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(71) Applicant(s)
Board Of Regents, the University of Texas System

(72) Inventor(s)
Cooper, Laurence J.N.;Korngold, Ana Beatriz;Rabinovich, Brian A.;Singh, Harjeet;Olivares, Simon

(74) Agent / Attorney
Pizzeys Patent and Trade Mark Attorneys Pty Ltd, GPO Box 1374, BRISBANE, QLD, 4001, AU

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(71) Applicant: **BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM** [US/US]; 201 West 7th St., Austin, TX 78701 (US).

(72) Inventors: **COOPER, Laurence, J.N.**; 311 West 8th St., Houston, TX 77007 (US). **KORNGOLD, Ana, Beatriz**; 402 Tuam St., Unit 9, Houston, TX 77006 (US). **RABINOVICH, Brian, A.**; 3815 Latma Dr., Houston, TX 77025 (US). **SINGH, Harjeet**; 9851 Meadowglen Lane, No.52, Houston, TX 77042 (US). **OLIVARES, Simon**; 2825 Bellefontaine St., Apt. 247A, Houston, TX 77025 (US).

(74) Agent: **FINDLAY, Geoffrey, S.**; Parker Highlander PLLC, 1120 S. Capital Of Texas Highway, Building One, Suite 200, Austin, TX 78746 (US).

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(54) **Title**: CHIMERIC ANTIGEN RECEPTORS AND METHODS OF MAKING

(57) **Abstract**: Provided are methods of generating chimeric antigen receptors (CAR). In some embodiments, library screening of CAR is performed by generating a vector encoding the CAR from random attachment of vectors from libraries of vectors encoding antigen-binding domains (*e.g.*, scFv regions), hinge regions, and endodomains. In some embodiments, the vectors contain a transposon.

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DESCRIPTION

CHIMERIC ANTIGEN RECEPTORS AND METHODS OF MAKING

BACKGROUND OF THE INVENTION

This application claims the benefit of United States Provisional Patent Application No. 61/940,339, filed February 14, 2014, the entirety of which is incorporated herein by reference.

Field of the Invention

[0001] The present invention relates generally to the field of molecular biology and medicine. More particularly, it concerns methods of generating chimeric antigen receptors (CAR).

Description of Related Art

[0002] Adoptive T cell transfer is a promising therapeutic approach that may be used for the treatment of cancer. Adoptive T cell transfer involves isolating and expanding antigen-specific T cells that can selectively kill tumor cells. Generally, T cells are removed from a subject and cultured *in vitro*. A Chimeric Antigen Receptor (CARs) may be introduced into a T cell *in vitro* to direct the T cell, once re-introduced into the subject, to selectively kill tumor cells based on expression of an antigen (*e.g.*, Wieczorek *et al.* 2013; Berry *et al.*, 2013).

[0003] One problem associated with adoptive T cell transfer is that significant variability exists between which CAR may work more effectively in certain populations of patients, *e.g.*, for treating a specific cancer. Due to the very large number of potential different CAR that could potentially be generated that might exhibit therapeutic activity against a cancer, it is presently very difficult for clinicians anticipate which CAR may display therapeutic activity against a given cancer or subtype of cancer. Due to the significant therapeutic potential of adoptive T cell transfer, there is a clear need for improved methods for identifying and generating new CARs.

SUMMARY OF THE INVENTION

[0005] The present invention provides, in some aspects, methods for the generation of CAR, and specific CAR are provided. In some aspects, methods are provided for the generation of large number of CAR that may be screened for activity against a particular cancer or sub-type of cancer; in this way, CAR may be generated and identified that can exhibit improved therapeutic potential against a particular cancer or sub-type of cancer. CAR provided herein may be therapeutically administered to a subject or human patient, *e.g.*, to treat a cancer.

[0006] Clinical data demonstrates that a particular chimeric antigen receptor (CAR) design targeting T cells to a given tumor-associated antigen (TAA) may have varying therapeutic potential in different patients. For example, second generation CD19-specific CARs activated via chimeric CD28/CD3zeta or CD137/CD3-zeta can exhibit superior clinical responses when autologous genetically modified T cells are administered to patients with acute, rather than chronic, B-lineage leukemia. To address this problem, provided herein are methods for generating CAR species that may exhibit an improved anti-tumor effect for a given tumor.

[0007] For example, methods are provided herein that may be used to generate and screen a large number of CAR for their ability to treat a cancer from a given patient; in this way, the methods may be used to personalize a therapy for a patient and select a particular CAR that displays an improved therapeutic potential for a particular patient or subset of patients with a particular cancer. A clinical approach to gene therapy may utilize the electro-transfer of DNA plasmids from the Sleeping Beauty (SB) transposon system, *e.g.*, to reduce the cost and complexity to manufacture individual CAR designs for small subsets of patients. These methods for personalizing CAR+ T cells may utilize the generation a large number of CAR molecules that can be screened and assessed for their ability to benefit a given patient.

[0008] In some aspects, provided are methods for the high throughput assembly of CAR molecules using a triple site-specific recombination system (also referred to as the "EZ-CAR" Platform). In some embodiments, these methods can allow for the rapid combination of 3 components of a prototypical CAR from (i) the single chain variable fragment (scFv) that defines specificity, (ii) the scaffold/hinge that appends the scFv from the cell surface, and (iii) one or more intracellular signaling domains. For example, as shown in the below examples, a CD19-specific CAR that is activated through chimeric CD28/CD3-zeta was generated using the EZ CAR platform in parallel with clinical-grade CD19RCD28mζ CAR+ T cells (CG CAR).

[0009] In some embodiments, a CAR provided herein or generated by methods according to the present invention may be co-expressed in a T cell with a membrane bound IL-15. In this way, the T cell may survive or exist in a quiescent state without significant proliferation *in vitro* or *in vivo*. In contrast, as described previously T-cells expressing CAR will typically die when cytokines are withdrawn *in vitro*, and this cell death may serve as a safety feature in certain instances when the T cells are administered clinically. T cell proliferation is typically measured using a autonomous cell assay. Thus, in contrast to certain previously identified CAR, where T cells cannot persist *in vitro* without antigenic stimulation, CAR are provided herein which may induce cytotoxicity without autonomous growth *in vitro*. Depending on the particular embodiment desired, a CAR produced by methods of the present invention or provided herein may be expressed in a T cell either with or without co-expression in the T cell of a membrane bound IL-15.

[0010] An aspect of the present invention relates to a composition comprising: (a) a plurality of first vectors encoding one or more distinct antigen binding domains; (b) a plurality of second vectors encoding one or more distinct hinge domains; and (c) a plurality of third vectors encoding one or more distinct endodomains; wherein at least two of the first, second and third vectors comprise a plurality of two or more vectors encoding distinct antigen binding domains, hinge domains and/or endodomains, respectively, and further wherein the vectors comprise sites for homologous recombination to permit the generation of a fourth vector encoding a chimeric antigen receptor (CAR).

[0011] In the present invention, as used in reference to protein domains and polypeptides such as antigen binding domains, hinge domains, transmembrane domains, and endodomains, the term "distinct" means domains having, comprising, or consisting of different polypeptide (amino acid) sequences. For example, two "distinct" antigen binding domains may bind the same antigen (indeed, even the same epitope on that antigen); however, the antigen binding domains are "distinct" if their sequential amino acid compositions differ from each other. Likewise, two "distinct" antigen binding domains, differing in sequential amino acid composition, may also specifically bind different antigens and epitopes. Conversely, as used herein, two molecules (polypeptides) of identical amino acid sequence are not "distinct" polypeptides.

[0012] In some embodiments, the plurality of first vectors encodes a plurality of distinct antigen binding domains, the plurality of second vectors encodes one hinge domain, and the plurality of third vectors encodes a plurality of distinct endodomains. In some embodiments, the plurality of first vectors encodes a plurality of distinct antigen binding domains, the plurality of second vectors encodes a plurality of distinct hinge domains, and the plurality of third vectors encodes a plurality of distinct endodomains. In some embodiments, the plurality of first vectors encodes a plurality of distinct antigen binding domains, the plurality of second vectors encodes a plurality of distinct hinge domains, and the plurality of third vectors encodes a one endodomain. In some embodiments, the plurality of first vectors encodes one antigen binding domain, the plurality of second vectors encodes a plurality of distinct hinge domains, and the plurality of third vectors encodes a plurality of distinct endodomains. In some embodiments, the antigen binding domains comprise or consist of scFv. The third vectors may encode a transmembrane domain. The second vectors may encode a transmembrane domain. In some embodiments, the composition further comprises a plurality of fifth vectors encoding one or more transmembrane domain; wherein the first vectors, the second vectors, the third vectors, and the fifth vectors comprise sites for homologous recombination to generate a fourth vector encoding a chimeric antigen receptor (CAR). The first vector may comprise a first sequence and a second site of homologous recombination. The second vector may comprise the second sequence of homologous recombination and a third sequence of homologous recombination. The third vector may comprise the third sequence of homologous recombination and a fourth sequence of homologous recombination. The third vector may comprise the third sequence of homologous recombination and a fourth sequence of homologous recombination. The fourth vector comprises the first sequence of homologous recombination and the fourth sequence of homologous recombination. The first vector, the second vector, and/or the third vector may encode a transposase. The transposase may be a salmonid-type Tc1-like transposase (SB). In some embodiments, 1, 2, 3, 4, or all of the first vector, the second vector, the third vector, the fourth vector, and/or the fifth vector is a Sleeping Beauty (SB) or *piggyBac* transposon vector. Alternately, in some embodiments, the first vector, the second vector, the third vector, the fourth vector, and/or the fifth vector is not a Sleeping Beauty (SB) or *piggyBac* transposon vector; for example, in some embodiments, a CAR may be generated without using a Sleeping Beauty (SB) or *piggyBac* vector, and then the CAR may subsequently be inserted in a vector suitable for transfecting T cells (*e.g.*, inserted into a Sleeping Beauty (SB) vector as described, *e.g.*, in Singh *et al.*, 2015). Nonetheless, in some embodiments, generating a CAR already present in a vector that is suitable for transfecting T cells may simply the process or reduce the number of steps required to both generate a CAR and transfect a T cell. The distinct antigen binding domains may selectively bind different antigens. In some embodiments, the distinct antigen binding domains selectively bind the same antigen. The antigen binding domain may selectively bind CD19, Universal Antigen (mouse), HER-3, GD2, Gp75, CS1 protein, mesothelin, phosphatidylserine, cMyc, CD22, CD4, CD44v6, CD45, CD28, CD3, CD3e, CD123, CD138, CD52, CD56, CD74, CD30, Gp75, CD38, CD33, CD20, Her1/HER3 fusion, GD2, a carbohydrate, *Aspergillus*, ROR1, c-MET, EGFR, Dectin, Ebola, a fungus, GP, HERV-K (HERVK), NY-ESO-1, VEGF-R2, TGF-b2R, IgG4, Biotin, or O-AcGD2. The distinct antigen binding domains may consist of or comprise scFv. The hinge region may consist of or comprise the 12 AA peptide (GAGAGCAAGTACGGCCCTCCCTGCCCCCCTTGCCCT; SEQ ID NO:1), t-20 AA peptide, IgG4 Fc Δ EQ, IgG4 Fc Δ Q, (t-12AA + t-20AA), mKate, phiLov, dsRed, Venus, eGFP, CH3 HA, (CD8 α + t-20AA), Double t-20 AA, (t-20AA + CD8α), (CD8α + Leucine Zipper Basep1), (CD8α + Leucine Zipper Acid1), 2D3, CD8 α, or IgG4 Fc. At least one of the endodomains may comprise CD3ζ. At least one of the endodomains may comprise one or more ITAM domains. In some embodiments, at least one of the endodomains comprise (CD28 +CD3ζ), (CD28 +CD27 + CD3ζ), (CD28 + OX40 + CD3ζ), (CD28 + 4-1BB + CD3ζ), (CD28 + CD27 + OX40 + CD3ζ), (CD28 + 4-1BB + CD27 + CD3ζ), (CD28 + 4-1BB + OX40 + CD3ζ), (4-1BB + CD3ζ), (4-1BB + OX40 + CD3ζ), (4-1BB + CD27 +CD3ζ), (CD27 + CD3ζ), (CD27 + OX 40 + CD3ζ), (CD28Δ +CD3ζ), (CD28Δ +CD27 + CD3ζ), (CD28Δ + OX40 + CD3ζ), (CD28Δ + 4-1BB + CD3ζ), (CD28Δ + 4-1BB + OX40 + CD3ζ), (CD28Δ + CD27 + OX40 + CD3ζ), (CD28Δ + 4-1BB + CD27 + CD3ζ), (4-1BB + ICOS + CD3ζ), (CD28 + ICOS + CD3ζ), (ICOS + CD3ζ), CD3ζ, or CD28 only. In some embodiments, the CARs may be tested for activity, *e.g.*, using the iQue™ Screener (IntelliCyt, Albuquerque, NM). In some embodiments CARs may evaluated for one or more characteristics (*e.g.*, viability, upregulation of activation signals, upregulation of CD25, cytokine release, and/or cell killing) when expressed in cells such as T cells using a technique such as, *e.g.*, flow cytometry.

[0013] Another aspect of the present invention relates to a composition comprising a collection of vectors encoding chimeric antigen receptors encoding a plurality of distinct antigen binding domains, hinge domains and endodomains, the vectors of said collection being randomized with respect to said domains.

[0014] Yet another aspect of the present invention relates to a method of producing a plurality of vectors each encoding a chimeric antigen receptor (CAR) comprising:(i) obtaining the composition comprising a plurality of vectors of the present invention (*e.g.*, as described above); and (ii) subjecting the composition to conditions sufficient to allow for the distinct antigen binding domains, hinge domains and/or endodomains comprised in or encoded by said vectors to recombine via homologous recombination to produce a plurality of fourth vectors, wherein each of said fourth vectors encodes a CAR. The method may further comprise expressing the CAR in a cell. The method may further comprise testing the CAR for activity. In some embodiments, one or more of the first vectors encodes a scFv region. In some embodiments, one or more of the third vectors encodes a transmembrane domain. In some embodiments, one or more of the second vectors encodes a transmembrane domain. The method may further comprise randomly incorporating by recombination a fifth vector encoding a transmembrane domain with said first vectors, second vectors, and third vectors to form said fourth vector. In some embodiments, said first vectors and said seconds vector are randomly attached from a plurality of vectors encoding a plurality of distinct scFv regions and a plurality of distinct hinge regions. In some embodiments, said first vectors and said third vectors are randomly attached from a plurality of vectors encoding a plurality of distinct scFv regions and a plurality of distinct endodomains. In some embodiments, said second vectors and said third vectors are randomly attached from a plurality of vectors encoding a plurality of distinct hinge regions and a plurality of distinct endodomains. In some embodiments, said first vectors, said second vectors, and said third vectors are randomly attached from a plurality of vectors encoding a plurality of distinct scFv regions, a plurality of distinct hinge regions, and a plurality of distinct endodomains. The method may further comprise generating said fourth vectors by random attachment of said first vectors from a first library of vectors encoding a plurality of scFv regions, random attachment of said second vectors from a second library of vectors encoding a plurality of scFv regions, and random attachment of said third vectors from a third library of vectors encoding a plurality of endodomains, to form said fourth vector encoding the CAR. The first vectors may comprise a first sequence and a second site of homologous recombination. The second vectors may comprise the second sequence of homologous recombination and a third sequence of homologous recombination. The third vectors may comprise the third sequence of homologous recombination and a fourth sequence of homologous recombination. The third vectors may comprise the third sequence of homologous recombination and a fourth sequence of homologous recombination. The fourth vectors may comprise the first sequence of homologous recombination and the fourth sequence of homologous recombination. The first vectors, the second vectors, and/or the third vectors may encode a transposase. In some embodiments, a sixth vector encodes a transposase, and wherein the method comprises introducing, electroporating, or transfecting one or more of said fourth vectors and said sixth vector into a cell. The transposase may be a salmonid-type Tc1-like transposase (SB). The method may further comprise culturing or providing cells transfected with the CAR in the presence of artificial antigen presenting cells (aAPCs) that can stimulate expansion of the CAR-expressing T-cells. In some embodiments, each of the scFv region, the hinge region, and the endodomain are each encoded in a Sleeping Beauty (SB) or *piggyBac* transposon vector. In some embodiments, each of the first vector, the second vector, and/or the third vector are randomly attached by said recombination from a plurality of vectors encoding multiple distinct scFv regions, the hinge regions, and endodomains. In some embodiments, said first vectors, the second vectors, and the third vectors each contain a transposon; and wherein said attaching via homologous recombination comprises site specific recombination. In some embodiments, the first vectors and the second vectors each have a first homologous recombination site; and wherein the second vectors and the third vectors each have a second homologous recombination site. In some embodiments, the first vectors have a third recombination site, and wherein the fourth vectors have a fourth recombination site, wherein the third recombination site and fourth recombination site can allow for homologous recombination into a cell. The cell may be a T cell such as, *e.g.*, an alpha beta T cell, a gamma delta T cell, or NK cell, or NKT cell. In some embodiments, the cell is a pluripotent cell such as, *e.g.*, a stem cell or an induced pluripotent stem cell. In some embodiments, the cell is derived from a stem cell, an induced pluripotent stem cell, or a stem cell. The cell may be a T cell or NK cell derived from an induced pluripotent stem cell. In some embodiments, said distinct antigen binding domains include at least 2, 3, 4, 5, 6, 7, 8, 9, or more scFv that selectively recognize different antigens. In some embodiments, said distinct antigen binding domains include at least 2, 3, 4, 5, 6, 7, 8, 9, or more scFv that selectively recognize (*i.e.*, specifically bind) the same antigen. In some embodiments, the antigen binding domains selectively (specifically) bind CD19, Universal Antigen (mouse), HER-3, GD2, Gp75, CS1 protein, mesothelin, phosphatidylserine, cMyc, CD22, CD4, CD44v6, CD45, CD28, CD3, CD3e, CD123, CD138, CD52, CD56, CD74, CD30, Gp75, CD38, CD33, CD20, Her1/HER3 fusion, GD2, a carbohydrate, *Aspergillus*, ROR1, c-MET, EGFR, Dectin, Ebola, a fungus, GP, HERV-K, NY-ESO-1, VEGF-R2, TGF-b2R, IgG4, Biotin, or O-AcGD2. In some embodiments, said antigen binding domains comprise or consist of scFv. The hinge region may encode the 12 AA peptide (GAGAGCAAGTACGGCCCTCCCTGCCCCCCTTGCCCT, SEQ ID NO:1), t-20 AA peptide, IgG4 Fc Δ EQ, IgG4 Fc Δ Q, (t-12AA + t-20AA), mKate, phiLov, dsRed, Venus, eGFP, CH3 HA, (CD8 α + t-20AA), Double t-20 AA, (t-20AA + CD8α), (CD8α + Leucine Zipper Basep1), (CD8α + Leucine Zipper Acid1), 2D3, CD8 α, or IgG4 Fc. The endodomain may encode CD3ζ. The endodomain may encode one or more ITAM domains. In some embodiments, the endodomain encodes (CD28 +CD3ζ), (CD28 +CD27 + CD3ζ), (CD28 + OX40 + CD3ζ), (CD28 + 4-1BB + CD3ζ), (CD28 + CD27 + OX40 + CD3ζ), (CD28 + 4-1BB + CD27 + CD3ζ), (CD28 + 4-1BB + OX40 + CD3ζ), (4-1BB + CD3ζ), (4-1BB + OX40 + CD3ζ), (4-1BB + CD27 +CD3ζ), (CD27 + CD3ζ), (CD27 + OX 40 + CD3ζ), (CD28Δ +CD3ζ), (CD28Δ +CD27 + CD3ζ), (CD28Δ + OX40 + CD3ζ), (CD28Δ + 4-1BB + CD3ζ), (CD28Δ + 4-1BB + OX40 + CD3ζ), (CD28Δ + CD27 + OX40 + CD3ζ), (CD28Δ + 4-1BB + CD27 + CD3ζ), (4-1BB + ICOS + CD3ζ), (CD28 + ICOS + CD3ζ), (ICOS + CD3ζ), CD3ζ, or CD28 only. In some embodiments, the CARs may be tested for activity, *e.g.*, using the iQue™ Screener (IntelliCyt, Albuquerque, NM). In some embodiments CARs may evaluated for one or more characteristics (*e.g.*, viability, upregulation of activation signals, upregulation of CD25, cytokine release, and/or cell killing) when expressed in cells such as T cells using a technique such as, *e.g.*, flow cytometry. In some embodiments, said activity comprises ability of the CAR to selectively bind a cancer cell, selectively bind a pathogen, selectively bind a cell involved in an autoimmune disease, or promote activation of a T-cell, destruction of a T cell, differentiation of a T cell, proliferation of a T cell, de-differentation of a T cell, movement of a T cell, cytokine production by a T cell, or killing by a T cell.

[0015] In some embodiments, the cancer cell is an ovarian cancer, a lymphoma, a renal cell carcinoma, a B-cell malignancy, CLL, B-ALL, ALL, a leukemia, a B-cell malignancy or lymphoma, mantle cell lymphoma, an indolent B-cell lymphoma, Hodgkin lymphoma, AML, cervical cancer, breast cancer, colorectal cancer, ovarian cancer, neuroblastoma, skin cancer, melanoma, a lung cancer, osteosarcoma, glioma, an epithelial derived tumor, prostate cancer, or a pediatric cancer. The pathogen may be a virus, a fungi, or a bacteria. In some embodiments, said testing comprises single cell imaging, single cell genetics, assessment of single T cells or populations of T cells; measuring specific killing or serial killing, gene expression, protein expression, movement towards or away from a target, proliferation, activation-induced cell death, secretion of cytokines, or secretion of chemokines. The method may further comprise selecting a single CAR from said plurality of vectors based on a property of the single CAR. The method may further comprise therapeutically administering the single CAR to a subject. The subject may be a mammal such as, *e.g.*, a human.

[0016] Another aspect of the present invention relates to a polypeptide comprising or consisting of CAR 217 (SEQ ID NO: 2), CAR 194 (SEQ ID NO: 3), CAR 212 (SEQ ID NO: 4), CAR 213 (SEQ ID NO: 5), CAR 265 (SEQ ID NO: 6), CAR 214 (SEQ ID NO:56), CAR 215(SEQ ID NO:57), CAR 216 (SEQ ID NO:58), CAR 218 (SEQ ID NO:59), CAR 193 (SEQ ID NO:55), or CAR 268 (SEQ ID NO: 7).

[0017] Yet another aspect of the present invention relates to a transformed T cell expressing the polypeptide comprising or consisting of CAR 217 (SEQ ID NO:2), CAR 194 (SEQ ID NO:3), CAR 212 (SEQ ID NO:4), CAR 213 (SEQ ID NO:5), CAR 265 (SEQ ID NO:6), CAR 214 (SEQ ID NO:56), CAR 215(SEQ ID NO:57), CAR 216 (SEQ ID NO:58), CAR 218 (SEQ ID NO:59), CAR 193 (SEQ ID NO:55), or CAR 268 (SEQ ID NO:7). The cell may be an immortalized cell. The T cell may be an alpha beta T cell, a gamma delta T cell, NK cell, NKT cell, stem cell, cells derived from stem cells, including cells of the immune system.

[0018] Another aspect of the present invention relates to a pharmaceutical preparation comprising the transformed T cell of the present invention.

[0019] Yet another aspect of the present invention relates to a nucleic acid encoding a chimeric antigen receptor comprising or consisting of CAR 217 (SEQ ID NO:2), CAR 194 (SEQ ID NO:3), CAR 212 (SEQ ID NO:4), CAR 213 (SEQ ID NO:5), CAR 265 (SEQ ID NO:6), CAR 214 (SEQ ID NO:56), CAR 215(SEQ ID NO:57), CAR 216 (SEQ ID NO:58), CAR 218 (SEQ ID NO:59), CAR 193 (SEQ ID NO:55), or CAR 268 (SEQ ID NO:7). The nucleic acid may be comprised in a T cell such as, *e.g.*, an alpha beta T cell, a gamma delta T cell, NK cell, NKT cell, stem cell, or a T cell derived from a pluripotent cell. The T cell may be comprised in a pharmaceutically acceptable carrier or excipient.

[0020] Another aspect of the present invention relates to a composition comprising a library of different CAR encoding vectors, the vectors of said library being randomized in terms of distinct antigen binding domains, hinge domains and/or endodomains. In some embodiments, he library randomized in terms of distinct antigen binding domains, hinge domains, and endodomains. In some embodiments, the library randomized in terms of distinct antigen binding domains and endodomains. In some embodiments, the library randomized in terms of distinct antigen binding domains and hinge domains. In some embodiments, the library randomized in terms of distinct antigen hinge domains and endodomains.

[0021] Examples of antigen binding domains, hinge regions, transmembrane domains, and endodomains that be used in methods of the present invention to generate a CAR are shown below in Table 1. The antigen binding domains, hinge regions, transmembrane domains, and endodomains are merely provided in Table 1 as non-limiting examples, and it is anticipated that one may select virtually any antigen binding domain (*e.g.*, targeting a cancerous cell, bacteria, fungi, virus, or virus-infected cell) as desired for the particular clinical application. In Table 1, the target of the antigen binding domain is provided (*e.g.*, "CD19" may refer to a scFv region that selectively binds CD19). In some embodiments, the antigen binding domain comprises or consists of a scFv that selectively binds the antigen. If desired, a portion of the scFv (*e.g.*, part of the variable region of the scFv) may be randomized if desired. In some embodiments, the antigen binding domain selectively binds a protein. Alternately, the antigen binding domain may selectively bind a carbohydrate expressed on a target such as, *e.g.*, a fungi, virus, bacteria, or cancerous cell. For example, in some embodiments, the antigen binding domain comprises or consists of Dectin-1, which can selectively bind β-glucans and carbohydrate found in fungal cell walls. In some embodiments, the CAR may selectively bind a virus, *e.g.*, the CAR may bind a viral protein such as a hepatitis envelope protein (*e.g.*, Krebs *et al.*, 2013). In some embodiments, the antigen binding domain is a cytokine. The antigen binding domain may selectively bind a protein, carbohydrate, or sugar. In some embodiments, a CAR is generated from a plurality of antigen binding domains that selectively bind a single target, antigen, or the antigen binding domains may have overlapping antigens. In some embodiments, a CAR is generated from a plurality of antigen binding domains that selectively bind different targets or antigens. The endodomain in a CAR may result in an inhibitory signal (*e.g.*, PD-1, CTLA-4, TIM-3, LAG-3, BTLA, ITIM, SHP-1, LAIR-1, TIGIT, Siglecs) or a stimulatory signal (*e.g.*,CD27,

CD28, ICOS, CD134, CD137, LCK, DAP10, ITAM, ZAP-70, LAT, SLP-76, cytokines as well as cytokine receptors; as well as combinations and mutations) in a cell expressing the CAR such as, *e.g.*, a T cell or a natural killer (NK) cell. When the antigen binding region selectively recognizes an antigen, the endodomain may cause or promote the cell (*e.g.*, T cell or NK cell) comprising the CAR to activate cell killing, migrate, differentiate, de-differentiate, or result in inducing an apoptotic signal in the cell. The apoptotic signal may comprise or consist of a CTLA4 apoptotic signal and/or a PD1 (protein death 1) apoptotic signal. In some embodiments, more than one distinct CAR may be expressed in a cell such as, *e.g.*, a T cell or a NK cell. For example, a first CAR and a second CAR may be expressed in a cell, wherein the first CAR selectively binds an antigen on a healthy cell and induces an inhibitory signal via a first endodomain (*e.g.*, reducing the probability that the T cell or NK cell will damage the healthy cell) and the second CAR selectively binds an antigen on a target cell (*e.g.*, cancerous cell, fungi, virus-infected cell, bacteria) and induces a stimulatory signal via a second endodomain (*e.g.*, promoting or causing cell killing of the target cell by the T cell or NK cell). A CAR generated via the methods of the present invention may be inserted in a target cell such as, *e.g.*, a T cell or a NK cell, as integrating DNA (*e.g.*, using electroporation and homologous recombination via a transposase/transposon vector or system) or as non-integrating DNA or RNA (*e.g.*, viral delivery of a mRNA using a viral vector such as, *e.g.*, a lentivirus or retrovirus). In some embodiments, the T cell encoding a CAR according to the present invention is an immortalized cell; such immortalized cells may function may be used to evaluate or measure the therapeutic potential or toxicity of the CAR. In this way, many CARs may be screened for a desired pharmacological profile, toxicity towards diseased cells or pathogens, lack of toxicity in healthy cells, and/or therapeutic efficacy.

Table 1. DNA molecules that can be combined as Antigen binding domain-hinge-signaling domains to generate CARs.

Antigen-binding Domain (*e.g.*, an ScFv that selectively bind a target listed below)
CD19 (mouse) (*e.g.*, SEQ ID NO:8)
CD19 (human) (*e.g.*, SEQ ID NO:9)
CD19 (humanized)
Universal Antigen (mouse) (Rushworth *et al.*, 2014)

CD22 (*e.g.*, scFv from Jabbour *et al.*, 2014 or Kong *et al.*, 2014)
CD4 (*e.g.*, scFv from Humblet-Baron *et al.*, 2015)
CD44v6 (*e.g.*, scFv from Leung 2010 or Verel 2002)
CD45 (*e.g.*, scFv from Shin *et al.*, 2011)
CD28 (*e.g.*, scFv from Czerwiński et al, 2015)
CD3 (*e.g.*, SEQ ID NO:10)
CD3e (*e.g.*, scFv from monoclonal antibody SPV-T3b, Life Technologies, Carlsbad, CA),
CD123 (*e.g.*, SEQ ID NO:11)
CD138 (*e.g.*, scFv from Sun *et al.*, 2007)
CD52 (*e.g.*, scFv from Wang *et al.*, 2015)
CD56 (*e.g.*, scFv from Kaufmann *et al.*, 1997)
CD74 (*e.g.*, scFv from Kaufman *et al.*, 2013)
CD30 (*e.g.*, SEQ ID NO:12)
Gp75 (*e.g.*, scFv from Patel *et al.*, 2008)
CD38 (*e.g.*, scFv from de Weers *et al.*, 2011)
CD33 (*e.g.*, scFv from Manero *et al.*, 2013)
CD20 (*e.g.*, scFv from Le Garff-Tavernier *et al.*, 2014 or Winiarska et al, 2014)
Her1/HER3 fusion (*e.g.*, scFv from Sarup *et al.*, 2008)
HER-3 (*e.g.*, SEQ ID NO:13)
GD2 (*e.g.*, SEQ ID NO:14)
Carbohydrates (such as an Aspergillus carbohydrate), *e.g.*, scfv from Stynen *et al.*, 1991)
ROR1 (*e.g.*, SEQ ID NO:15)
c-MET (*e.g.*, scFv from Zhuang *et al.*, 2014)
cMyc (*e.g.*, SEQ ID NO:16)
EGFR (*e.g.*, scFv from Funakoshi *et al.*, 2014)
Dectin (*e.g.*, Dectin 1 ectodomain, SEQ ID NO:17)
Dectin-1 binding site
Ebola virus (*e.g.*, scFv from Audet *et al.*, 2014 or Qiu *et al.*, 2012)
Fungal antigens (*e.g.*, scFv from Guimarães *et al.*, 2011)

GP (Qiu *et al.*, 2012)
Gp75 (*e.g.*, TA99, SEQ ID NO:18)
HERV-K (HERVK) (*e.g.*, SEQ ID NO:19)
NY-ESO-1 (*e.g.*, scFv from Schultz-Thater *et al.*, 2000)
VEGF-R2 (*e.g.*, scFv from Zhang *et al.*, 2002)
TGF-b2R (*e.g.*, scFv from Leung, 2011)
IgG4 (*e.g.*, scFv from Curtin *et al.*, 2015)
Biotin (*e.g.*, scFv from Vincent *et al.*, 1993)
O-AcGD2 (*e.g.*, scFv from Goldberg e*t al.*, 2014 or Ahmed *et al.*, 2014)
CS1 protein (*e.g.*, Elotuzumab or huLuc63, SEQ ID NO:20)
Mesothelin (*e.g.*, using the SS-1 scFv, SEQ ID NO:21)
Phosphatidylserine (*e.g.*, scFv from Gerber *et al.*, 2011)

Hinge/Scaffold
12 AA (peptide) (*e.g.*, SEQ ID NO:1)
t-20 AA (peptide) (*e.g.*, SEQ ID NO:22)
CD8 α (*e.g.*, SEQ ID NO:23)
IgG4 Fc (*e.g.*, SEQ ID NO:24)
2D3 (*e.g.*, SEQ ID NO:25)
IgG4 Fc Δ EQ (IgG4Fc N40Q) (*e.g.*, SEQ ID NO:26)
IgG4 Fc Δ Q (IgG4Fc L18E N40Q) (*e.g.* SEQ ID NO:27)
t-12AA + t-20AA
mKate (*e.g.*, SEQ ID NO:28)
phiLov (*e.g.*, SEQ ID NO:29)
dsRed (*e.g.*, SEQ ID NO:30)
Venus (*e.g.*, SEQ ID NO:31)
eGFP (*e.g.*, SEQ ID NO:32)
CH3 HA (*e.g.*, SEQ ID NO:33)
mTFP-1 (*e.g.*, SEQ ID NO:34)
CD8 α + t-20AA
Double t-20 AA

t-20AA + CD8α
CD8α + Leucine Zipper Basep1 (*e.g.*, SEQ ID NO:35)
CD8α + Leucine Zipper Acid1 (*e.g.*, SEQ ID NO:36)

Transmembrane domain
CD28 (*e.g.*, SEQ ID NO:37)
CD137 (4-1BB) (*e.g.*, SEQ ID NO:38)
CD8α (*e.g.*, SEQ ID NO:39)
CD3ζ (*e.g.*, SEQ ID NO:40)

Endo-domain (signaling domain)
CD28 +CD3ζ
CD28 +CD27 + CD3ζ
CD28 + OX40 + CD3ζ
CD28 + 4-1BB + CD3ζ
CD28 + CD27 + OX40 + CD3ζ
CD28 + 4-1BB + CD27 + CD3ζ
CD28 + 4-1BB + OX40 + CD3ζ
4-1BB + CD3ζ
4-1BB + OX40 + CD3ζ
4-1BB + CD27 +CD3ζ
CD27 + CD3ζ
CD27 + OX 40 + CD3ζ
CD28Δ +CD3ζ
CD28Δ +CD27 + CD3ζ
CD28Δ + OX40 + CD3ζ
CD28Δ + 4-1BB + CD3ζ
CD28Δ + 4-1BB + OX40 + CD3ζ
CD28Δ + CD27 + OX40 + CD3ζ
CD28Δ + 4-1BB + CD27 + CD3ζ
4-1BB + ICOS + CD3ζ
CD28 + ICOS + CD3ζ

ICOS + CD3ζ
CD3ζ
CD28 only

ζ - zeta; Δ- mutant; Note = 4-1BB is also referred to as CD137; "+" refers to the fusion of the different regions.

[0022] For example, in some embodiments, the following antigen-binding domains, hinge/scaffolds, transmembrane domains, and endodomains may be used, as shown in Table 2. Examples of sequences included in signaling domains, *e.g.*, in Table 1 or Table 2, include CD27 (SEQ ID NO:41), CD28 (SEQ ID NO:42), CD28Δ (SEQ ID NO:43), CD134 (OX40) (SEQ ID NO:44), CD137 (41BB) (SEQ ID NO:45), ICOS (SEQ ID NO:46)and CD3 zeta (SEQ ID NO:47). Examples of scFv Anti-EGFR domains as listed in Table 2 include <u>Nimotuximab</u> (SEQ ID NO:48) and Cetuximab (SEQ ID NO:49). An example of a scFv Anti-Phosphatidylserine as listed in Table 2 is Bavituximab (SEQ ID NO:50).

<u>Table 2: Example of libraries used to generate CAR</u>

ScFv
Anti –CS1 protein
Anti-mesothelin (SS-1)
Anti- CD123
Anti-CD19 human
Anti-CD19 mouse
Anti-CD3
Anti-CD30
Anti-Dectin
Anti-G2D
Anti-Gp75
Anti-HERVK
Anti-CD22
Anti-ROR-1
Anti-EGFR
Anti-HER-3
Anti-Phosphatidylserine

Hinge/Scaffold
t-12 AA (peptide)
t-20 AA (peptide)
CD8 α
IgG4 Fc
IgG4Fc Δ EQ
IgG4Fc Δ Q
t-12AA + t-20AA
mKate
phiLov
dsRed
Venus
eGFP
CH3 HA
CD8 α + t-20AA
Double t-20 AA
t-20AA + CD8α
CD8α + Leucine Zipper Basep1
CD8α + Leucine Zipper Acid1

Transmembrane domain
CD28
4-1BB
CD3ζ

Signaling Domain
CD28 +CD3ζ
CD28 +CD27 + CD3ζ
CD28 + OX40 + CD3ζ
CD28 + 4-1BB + CD3ζ
CD28 + CD27 + OX40 + CD3ζ
CD28 + 4-1BB + CD27 + CD3ζ
CD28 + 4-1BB + OX40 + CD3ζ
4-1BB + CD3ζ
4-1BB + OX40 + CD3ζ
4-1BB + CD27 +CD3ζ
CD28Δ +CD3ζ
CD28Δ +CD27 + CD3ζ
CD28Δ + OX40 + CD3ζ
CD28Δ + 4-1BB + CD3ζ
CD28Δ + 4-1BB + OX40 + CD3ζ
CD28Δ + CD27 + OX40 + CD3ζ
CD28Δ + 4-1BB + CD27 + CD3ζ
4-1BB + ICOS + CD3ζ
CD28 + ICOS + CD3ζ
ICOS + CD3 ζ
CD3 ζ
CD28 only

[0023] The term “chimeric antigen receptors (CARs)” or “CAR” as used herein, includes artificial T-cell receptors, chimeric T-cell receptors, or chimeric immunoreceptors. CARs are generally engineered receptors that may graft an artificial specificity onto a particular immune effector cell. CARs may be employed to impart the specificity of a monoclonal antibody onto a T cell, thereby allowing a large number of specific T cells to be generated, for example, for use in an adoptive cell therapy. In some embodiments, CARs direct specificity of the cell to a tumor associated antigen. In preferred embodiments, CARs comprise an endodomain (comprising an intracellular activation domain), a transmembrane domain, a hinge or scaffold region, and an extracellular domain comprising a targeting domain (*e.g.*, a scFv derived from a monoclonal antibody). In some embodiments, the extracellular targeting domain may be a ligand of a receptor (*e.g.*, a peptide that selectively binds a protein receptor). In some embodiments, one can target malignant cells by redirecting the specificity of T cells by using a CAR specific for the malignant cells (*e.g.*, by using an anti-CD19 scFv to target a cancerous B-lineage cell).

[0024] Examples of scFv regions, hinge / scaffold regions, transmembrane domains, and endodomains are shown in Table 1 and examples of related sequences are also provided herein. Note in Table 1 that the scFv regions may refer to a plurality of scFv regions for a particular target (*e.g.*, "CD19" in Table 1 may refer to a single monoclonal antibody sequence, or in some preferred embodiments, it may refer to a plurality of scFv regions derived from monoclonal antibodies that selectively target CD19). It is anticipated that methods of the present invention may be used to generate a CAR that comprises, *e.g.*, a fusion of any combination of a scFv region, hinge/scaffold, transmembrane domain, and endodomain of Table 1. For example, in some embodiments, the CAR may comprise a scFv region that selectively targets CD19 (*e.g.*, derived from a mouse, human, or humanized monoclonal antibody) fused to an IgG4 Fc hinge/scaffold region, a CD28 transmembrane domain, and an endodomain comprising CD28 and CD3ζ. In some embodiments, the CAR may comprise a scFv region that selectively targets ROR1 fused to IgG4 Fc hinge/scaffold region, a CD28 transmembrane domain, and an endodomain comprising CD28 and CD3ζ. In some embodiments, the CAR may comprise a scFv region that selectively targets ROR1 fused to IgG4 Fc hinge/scaffold region, a CD28 transmembrane domain, and an endodomain comprising 4-1BB and CD3ζ. In some embodiments, the CAR may comprise a scFv region that selectively targets CD19 (*e.g.*, derived from a mouse, human, or humanized monoclonal antibody) fused to IgG4 Fc hinge/scaffold region, a CD28 transmembrane domain, and an endodomain comprising CD28 and CD3ζ.

[0025] As used herein, the term "antigen" is a molecule capable of being bound by an antibody or T-cell receptor. An antigen may generally be used to induce a humoral immune response and/or a cellular immune response leading to the production of B and/or T lymphocytes.

[0026] As used herein the specification, "a" or "an" may mean one or more. As used herein in the claim(s), when used in conjunction with the word "comprising", the words "a" or "an" may mean one or more than one.

[0027] The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or." As used herein "another" may mean at least a second or more.

[0028] Throughout this application, the term "about" is used to indicate that a value includes the inherent variation of error for the device, the method being employed to determine the value, or the variation that exists among the study subjects.

[0029] Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0030] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

[0031] FIG. 1. Cloning vectors used to re-assemble CARs using three donor plasmids expressing (i) specific scFv, (ii) extracellular hinge and (iii) endodomains. This approach will be adapted to generate panels of CARs that differ in hinge, transmembrane, and intracellular regions. Engineering CAR molecules from components scFv, IgG4 Fc (Long hinge); or CD8a (Medium hinge) or peptide only (Small hinge) and CD3ζ ιν combinations with different signaling domains using triple recombination site system. A library of scFv and distinct scaffolds and signaling domains encoded in three donor plasmids (entry clones), are recombined in to the expression DNA vector. This approach generated multiple CAR species in the format scFv-B-scaffold-C-signaling domain(s).

[0032] FIGS. 2A-B: (**FIG. 2A**) Expression of CAR (Fc) and $CD8^{+}$ in T cells after 66 days post electroporation by flow cytometry. The cells were expanded in aAPC loaded with CD19 antigen (clone 4) (**FIG. 2B**) Lysis of CD19+ EL-4 was compared to background lysis of $CD19^{neg}$ EL-4 using 4-h chromium release assay by CD19CAR+ T cells Clinical Grade (CG) CD19CAR+ T cells by triple recombination sites (EZ CAR) and CAR^{neg} T cells. The CAR^{neg} T were expanded in with irradiated and anti-CD3 (OKT3) loaded K562-derived aAPC clone #4.

[0033] FIG. 3: CAR Designs. CAR 212 = SEQ ID NO:4; CAR 213 = SEQ ID NO:5; CAR 214 = SEQ ID NO:56; CAR 215 = SEQ ID NO:57; CAR 216 = SEQ ID NO:58; CAR 217 = SEQ ID NO:2; CAR 218 = SEQ ID NO:59; CAR 193 = SEQ ID NO:55.

[0034] FIG. 4: Sleeping Beauty tracking plasmids

[0035] FIG. 5: CAR Expression.

[0036] FIG. 6: CAR Expression Kinetics

[0037] FIG. 7: Phenotype.

[0038] FIGS. 8A-B: Extended Phenotype is shown in FIG. 8A and FIG. 8B.

[0039] FIG. 9: Western Blot Analysis.

[0040] FIG. 10: Expansion Kinetics.

[0041] FIG. 11: Fold Expansion: Total Cells

[0042] FIG. 12: Fold Expansion: CAR+ T cells.

[0043] FIG. 13: Cytotoxicity.

[0044] FIG. 14: 4-1BB CARs: Cytotoxicity.

[0045] FIG. 15: TM domain: Cytotoxicity.

[0046] FIG. 16: Spacer (IgG4 vs CD8): Cytotoxicity

[0047] FIG. 17: IFN-γ production.

[0048] FIG. 18: 4-1BB CARs: IFN-γ production

[0049] FIG. 19: TM domain: IFN-γ production

[0050] FIG. 20: Spacer (IgG4 vs CD8): IFN-γ production.

[0051] FIG. 21: Safety: PCR for SB11 transposase.

[0052] FIG. 22: Safety: CAR copy number (qPCR).

[0053] FIG. 23: Safety: Autonomous Growth. As shown in the figure, a lack of autonomous growth was observed.

[0054] FIG. 24: CAR design. An example of a CAR is provided on the right-hand side of the figure.

[0055] FIG. 25: CD3-zeta. Query = SEQ ID NO:51; Subject – top = SEQ ID NO:52; Subject – middle = SEQ ID NO:53; Subject – bottom = SEQ ID NO:54.

[0056] FIG. 26: CAR designs.

[0057] FIG. 27: CARs.

[0058] FIG. 28: CAR Expression.

[0059] FIG. 29: Expansion Kinetics.

[0060] FIG. 30: Expansion Kinetics.

[0061] FIG. 31: Cytotoxicity.

[0062] FIG. 32: Cytotoxicity.

[0063] FIG. 33: Memory Markers. Percent expression of CD27, CD62L, CD28 and CCR7 on CAR^{+} T cells (expressing constructs shown in FIG. 26) are shown.

[0064] FIG. 34: IFN-γ production.

[0065] FIG. 35: IFN-γ production (PMA-Ion)

[0066] FIG. 36: Autonomous Growth.

[0067] FIG. 37: CAR Copy Number.

[0068] FIG. 38: CAR Copy Number.

[0069] FIG. 39: CAR Copy Number.

[0070] FIGS. 40A-E: Transfection of 293-HEK cells with plasmids carrying the CAR DNA (pSBSO EZ CAR) by lipofectamine was performed. The transfected cells were analyzed by flow cytometry after stained with anti-Fc or anti-idiotipic (antiCD19svFv) antibodies.

[0071] FIGS. 41A-B: **FIG. 41A**, Nalm-6; EL-4 CD19+ cells; patient tumor cells with MCL and CLL (targets) and were previously modified to express GFP. $5x10^{3}$ target cells were incubated with increasing concentration of CD19RIgG4CD28CAR T cells, CD19RCD8αCD28 CAR T cells and CAR^{neg} T cells (used as the control) for 4 hours. After 4 hours the cells were acquired by IntelliCyt's iQue and the data analyses were made in their proprietary software. **FIG. 42B**, The graphs are representing the killing percentage of CAR T cells against tumor cells. The ratio between effector and target cells ranged from 0 to 40 cells.

[0072] FIG. 42: 5x10^3 target cells (EL-4 CD19+ Granzyme B cells reporter) were incubated with increasing concentration of Clinical-grade CD19RIgG4CD28CAR T cells, EZ CD19RCD8αCD28 CAR T cells and CAR^{neg} T cells (used as the control) for 4 and 10 hours. After incubation time the cells were acquired by IntelliCyt's iQue and the data analyses were made in their proprietary software. The graphs are representing the killing percentage of CAR T cells against tumor cells. The ratio between effector and target cells ranged from 0 to 20 cells.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0073] Provided herein are methods for generating chimeric antigen receptors (CARs). The method utilizes a plurality of vectors each encoding an antigen binding domain (*e.g.*, a scFv region), a hinge region, a transmembrane region, and/or an endodomain. For example in some embodiments a first vector encodes the antigen binding domain, a second vector encodes the hinge region, and a third region encodes an endodomain. In some embodiments, the transmembrane region is encodes either in the second vector, in the third vector, or in a fourth vector. In some preferred embodiments, the vectors can homologously recombine to form a nucleic acid encoding a CAR comprising the antigen binding domain, the hinge region, the transmembrane region, and the endodomain. In this way, many CAR may be generated and screened for a desired activity such as, *e.g.*, selective recognition and killing of a cancerous cell expressing an antigen that is selectively bound by the CAR. The CAR may then be expressed in a cell such as a T cell or a natural killer (NK) cell as an integrating nucleic acid (*e.g.*, a DNA integrated into the host genome using a transposase/transposon) or as a non-integrating nucleic acid (*e.g.*, a mRNA delivered via a viral vector such as a lentivirus or retrovirus). The T cell or NK cell expressing the CAR may then be administered in a pharmaceutical preparation or excipient to a subject such as a human patient to treat or prevent a disease (*e.g.*, a cancer, a fungal infection, a bacterial infection, or a viral infection).

I. Library generation

[0074] Libraries encoding a plurality of scFv regions, hinge/scaffold regions, transmembrane domains, and endodomains (signaling domains) may be generated by methods known to one of skill in the art. In some embodiments, multiple possibilities are available for two or three of the scFv regions, hinge/scaffold regions, and endodomains (signaling domains). In some embodiments, multiple possibilities are available for two, three, or all of the scFv regions, hinge/scaffold regions, transmembrane domains, and endodomains (signaling domains). Examples of scFv regions, hinge/scaffold regions, transmembrane domains, and endodomains (signaling domains) are provided, *e.g.*, in Table 1. In some embodiments, the library may encode a plurality of scFv that target different antigens, such as such as multiple anti-cancer or tumor-targeting antigens; in other embodiments, the library may encode a plurality of different scFv that selectively bind a single target (*e.g.*, a single anticancer antigen such as CD19, *etc.*). In this way, the methods may be used to either identify which tumor-targeting construct may work more effectively for a given cell sample (*e.g.*, to be used in a personalized medicine) or the methods may be used to identify new CAR that function more effectively in targeting a given antigen. The scFv region generally comprises a variable light (VL) and a variable heavy (VH) chain derived from an antibody. In some embodiments, portions of the VL and VH regions may be randomized if desired. General methods for generating libraries include, *e.g.*, the generation of yeast libraries, bacterial, phage libraries, infiltrating B cells, hybridomas (including from human and rodents), or libraries from llamas, camels, equine libraries, and in silico methods (See, *e.g.*, Lennard, 2002).

[0075] In some embodiments, the different vectors encoding the scFv, hinge/scaffold region, transmembrane domain, and endodomain are fused to form a single vector encoding a CAR. The fusion may occur via transposon-mediated homologous recombination.

[0076] For example, in some embodiments, the vectors encoding the scFv, hinge/scaffold region, transmembrane domain, and/or endodomain may be *Sleeping Beauty* (SB) or *piggyBac* DNA plasmids. *Sleeping Beauty* (SB) and *piggyBac* DNA plasmids are described, *e.g.*, in Maiti *et al.* (2013), Singh *et al.* (2008), and Huls *et al.* (2013). In some embodiments, the transposon is mediated by a salmonid-type Tc1-like transposase (SB). In some preferred embodiments, the vector encoding the CAR is transfected or incorporated into T cells from a subject, such as a human patient with cancer, via the methods as described in Singh *et al.*, 2014 or Huls *et al.* For example, DNA vectors derived from the Sleeping Beauty (SB) system can be used to avoid expense and manufacturing difficulties associated with transducing T cells with recombinant viral vectors. After electroporation, the transposon/transposase can improve the efficiency of integration of plasmids used to express CAR and other transgenes in T cells. The SB system combined with artificial antigen-presenting cells (aAPC) can selectively propagate and produce CAR(+) T cells suitable for human application. In some embodiments, synchronous electro-transfer of two DNA plasmids, a SB transposon (encoding a CAR of interest) and a SB transposase (*e.g.*, SB11) may be followed by retrieval of stable integrants by the every-7-day additions (stimulation cycle) of γ-irradiated aAPC in the presence of soluble recombinant human IL-2 and IL-21. For example, 4 cycles (28 days of continuous culture) may be undertaken to generate clinically-appealing numbers of T cells that stably express a CAR of interest. Use of a transposon / transposase system may be utilized for delivery of T cells expressing a CAR as described, *e.g.*, in Hackett *et al.*

II. Chimeric Antigen Receptors

[0077] Embodiments of the present invention involve generation and identification of nucleic acids encoding an antigen-specific chimeric antigen receptor (CAR) polypeptide. In some embodiments, the CAR is humanized to reduce immunogenicity (hCAR).

[0078] In some embodiments, the CAR may recognize an epitope comprised of the shared space between one or more antigens. Pattern recognition receptors, such as Dectin-1, may be used to derive specificity to a carbohydrate antigen. In certain embodiments, the binding region may comprise complementary determining regions of a monoclonal antibody, variable regions of a monoclonal antibody, and/or antigen binding fragments thereof. In some embodiments the binding region is an scFv. In another embodiment, a peptide (*e.g.*, a cytokine) that binds to a receptor or cellular target may be included as a possibility or substituted for a scFv region in the binding region of a CAR. Thus, in some embodiments, a CAR may be generated from a plurality of vectors encoding multiple scFv regions and/or other targeting proteins. A complementarity determining region (CDR) is a short amino acid sequence found in the variable domains of antigen receptor (*e.g.*, immunoglobulin and T-cell receptor) proteins that complements an antigen and therefore provides the receptor with its specificity for that particular antigen. Each polypeptide chain of an antigen receptor contains three CDRs (CDR1, CDR2, and CDR3). Since the antigen receptors are typically composed of two polypeptide chains, there are six CDRs for each antigen receptor that can come into contact with the antigen -- each heavy and light chain contains three CDRs. Because most sequence variation associated with immunoglobulins and T-cell receptor selectivity are generally found in the CDRs, these regions are sometimes referred to as hypervariable domains. Among these, CDR3 shows the greatest variability as it is encoded by a recombination of the VJ (VDJ in the case of heavy chain and TCR αβ chain) regions.

[0079] A CAR-encoding nucleic acid generated via the present invention may comprise one or more human genes or gene fragments to enhance cellular immunotherapy for human patients. In some embodiments, a full length CAR cDNA or coding region may be generated via the methods described herein. The antigen binding regions or domain may comprise a fragment of the V_H and V_L chains of a single-chain variable fragment (scFv) derived from a particular human monoclonal antibody, such as those described in U.S. Patent 7,109,304, incorporated herein by reference. In some embodiments, the scFv comprises an antigen binding domains of a human antigen-specific antibody. In some embodiments, the scFv region is an antigen-specific scFv encoded by a sequence that is optimized for human codon usage for expression in human cells.

[0080] The arrangement of the antigen-binding domain of a CAR may be multimeric, such as a diabody or multimers. The multimers can be formed by cross pairing of the variable portions of the light and heavy chains into what may be referred to as a diabody. The hinge portion of the CAR may in some embodiments be shortened or excluded (*i.e.*, generating a CAR that only includes an antigen binding domain, a transmembrane region and an intracellular signaling domain). A multiplicity of hinges may be used with the present invention, *e.g.*, as shown in Table 1. In some embodiments, the hinge region may have the first cysteine maintained, or mutated by a proline or a serine substitution, or be truncated up to the first cysteine. The Fc portion may be deleted from scFv used to as an antigen-binding region to generate CARs according to the present invention. In some embodiments, an antigen-binding region may encode just one of the Fc domains, *e.g.*, either the CH2 or CH3 domain from human immunoglobulin. One may also include the hinge, CH2, and CH3 region of a human immunoglobulin that has been modified to improve dimerization and oligermerization. In some embodiments, the hinge portion of may comprise or consist of a 8-14 amino acid peptide (*e.g.*, a 12 AA peptide), a portion of CD8α, or the IgG4 Fc. In some embodiments, the antigen binding domain may be suspended from cell surface using a domain that promotes oligomerization, such as CD8 alpha. In some embodiments, the antigen binding domain may be suspended from cell surface using a domain that is recognized by monoclonal antibody (mAb) clone 2D3 (mAb clone 2D3 described, *e.g.*, in Singh *et al.*, 2008).

[0081] The endodomain or intracellular signaling domain of a CAR can generally cause or promote the activation of at least one of the normal effector functions of an immune cell comprising the CAR. For example, the endodomain may promote an effector function of a T cell such as, *e.g.*, cytolytic activity or helper activity including the secretion of cytokines. The effector function in a naive, memory, or memory-type T cell may include antigen-dependent proliferation. The terms “intracellular signaling domain” or “endodomain” refers to the portion of a CAR that can transduce the effector function signal and/or direct the cell to perform a specialized function. While usually the entire intracellular signaling domain may be included in a CAR, in some cases a truncated portion of an endodomain may be included.

Generally, endodomains include truncated endodomains, wherein the truncated endodomain retains the ability to transduce an effector function signal in a cell.

[0082] In some embodiments, an endodomain comprises the zeta chain of the T-cell receptor or any of its homologs (*e.g.*, eta, delta, gamma, or epsilon), MB1 chain, B29, Fc RIII, Fc RI, and combinations of signaling molecules, such as CD3ζ and CD28, CD27, 4-1BB, DAP-10, OX40, and combinations thereof, as well as other similar molecules and fragments. Intracellular signaling portions of other members of the families of activating proteins can be used, such as FcγRIII and FcεRI. Examples of these alternative transmembrane and intracellular domains can be found, *e.g.*, Gross *et al.* (1992), Stancovski *et al.* (1993), Moritz *et al.* (1994), Hwu *et al.* (1995), Weijtens *et al.* (1996), and Hekele *et al.* (1996), which are incorporated herein be reference in their entirety. In some embodiments, an endodomain may comprise the human CD3ζ intracellular domain.

[0083] The antigen-specific extracellular domain and the intracellular signaling-domain are preferably linked by a transmembrane domain. Transmembrane domains that may be included in a CAR include, *e.g.*, the human IgG4 Fc hinge and Fc regions, the human CD4 transmembrane domain, the human CD28 transmembrane domain, the transmembrane human CD3ζ domain, or a cysteine mutated human CD3ζ domain, or a transmembrane domains from a human transmembrane signaling protein such as, *e.g.*, the CD16 and CD8 and erythropoietin receptor. Examples of transmembrane domains are provided, *e.g.*, in Table 1.

[0084] In some embodiments, the endodomain comprises a sequence encoding a costimulatory receptors such as, *e.g.*, a modified CD28 intracellular signaling domain, or a CD28, CD27, OX-40 (CD134), DAP10, or 4-1BB (CD137) costimulatory receptor. In some embodiments, both a primary signal initiated by CD3 ζ, an additional signal provided by a human costimulatory receptor may be included in a CAR to more effectively activate a transformed T cells, which may help improve *in vivo* persistence and the therapeutic success of the adoptive immunotherapy. As noted in Table 1, the endodomain or intracellular receptor signaling domain may comprise the zeta chain of CD3 alone or in combination with an Fcγ RIII costimulatory signaling domains such as, *e.g.*, CD28, CD27, DAP10, CD137, OX40, CD2, 4-1BB. In some embodiments, the endodomain comprises part or all of one or more of TCR zeta chain, CD28, CD27, OX40/CD134, 4-1BB/CD137, FcεRIγ, ICOS/CD278, IL-2Rbeta/CD122, IL-2Ralpha/CD132, DAP10, DAP12, and CD40. In some embodiments, 1, 2, 3, 4 or more cytoplasmic domains may be included in an endodomain. For example, in some CARs it has been observed that at least two or three signaling domains fused together can result in an additive or synergistic effect.

[0085] In some aspects, an isolated nucleic acid segment and expression cassette including DNA sequences that encode a CAR may be generated. A variety of vectors may be used. In some preferred embodiments, the vector may allow for delivery of the DNA encoding a CAR to immune such as T cells. CAR expression may be under the control of regulated eukaryotic promoter such as, *e.g.*, the MNDU3 promoter, CMV promoter, EF1alpha promoter, or Ubiquitin promoter. Also, the vector may contain a selectable marker, if for no other reason, to facilitate their manipulation *in vitro*. In some embodiments, the CAR can be expressed from mRNA *in vitro* transcribed from a DNA template.

[0086] Chimeric antigen receptor molecules are recombinant and are distinguished by their ability to both bind antigen and transduce activation signals *via* immunoreceptor activation motifs (ITAM's) present in their cytoplasmic tails. Receptor constructs utilizing an antigen-binding moiety (for example, generated from single chain antibodies (scFv)) afford the additional advantage of being "universal" in that they can bind native antigen on the target cell surface in an HLA-independent fashion. For example, a scFv constructs may be fused to sequences coding for the intracellular portion of the CD3 complex's zeta chain (ζ), the Fc receptor gamma chain, and sky tyrosine kinase (Eshhar *et al.*, 1993; Fitzer-Attas *et al.*, 1998). Re-directed T cell effector mechanisms including tumor recognition and lysis by CTL have been documented in several murine and human antigen-scFv: ζ systems (Eshhar *et al.*, 1997; Altenschmidt *et al.*, 1997; Brocker *et al.*, 1998).

[0087] The antigen binding region may, *e.g.*, be from a human or non-human scFv. One possible problem with using non-human antigen binding regions, such as murine monoclonal antibodies, is reduced human effector functionality and a reduced ability to penetrate into tumor masses. Furthermore, non-human monoclonal antibodies can be recognized by the human host as a foreign protein, and therefore, repeated injections of such foreign antibodies might lead to the induction of immune responses leading to harmful hypersensitivity reactions. For murine-based monoclonal antibodies, this effect has been referred to as a Human Anti-Mouse Antibody (HAMA) response. In some embodiments, inclusion of human antibody or scFv sequences in a CAR may result in little or no HAMA response as compared to some murine antibodies. Similarly, the inclusion of human sequences in a CAR may be used to reduce or avoid the risk of immune-mediated recognition or elimination by endogenous T cells that reside in the recipient and might recognize processed antigen based on HLA.

[0088] In some embodiments, the CAR comprises: a) an intracellular signaling domain, b) a transmembrane domain, c) a hinge region, and d) an extracellular domain comprising an antigen binding region. In some embodiments, the intracellular signaling domain and the transmembrane domain are encoded with the endodomain by a single vector that can be fused (*e.g.*, via transposon-directed homologous recombination) with a vector encoding a hinge region and a vector encoding an antigen binding region. In other embodiments, the intracellular signaling region and the transmembrane region may be encoded by two separate vectors that are fused (*e.g.*, via transposon-directed homologous recombination).

[0089] In some embodiments, the antigen-specific portion of a CAR, also referred to as an extracellular domain comprising an antigen binding region, selectively targets a tumor associated antigen. A tumor associated antigen may be of any kind so long as it is expressed on the cell surface of tumor cells. Examples of tumor associated antigens that may be targeted with CARs generated via the present invention include, *e.g.*, CD19, CD20, carcinoembryonic antigen, alphafetoprotein, CA-125, MUC-1, CD56, EGFR, c-Met, AKT, Her2, Her3, epithelial tumor antigen, melanoma-associated antigen, mutated p53, mutated ras, Dectin-1, and so forth. In some embodiments that antigen specific portion of the CAR is a scFv. Examples of tumor-targeting scFv are provided in Table 1. In some embodiments, a CAR may be co-expressed with a membrane-bound cytokine, *e.g.*, to improve persistence when there is a low amount of tumor-associated antigen. For example, a CAR can be co-expressed with membrane-bound IL-15.

[0090] In some embodiments, an intracellular tumor associated antigen such as, *e.g.*, HA-1, survivin, WT1, and p53 may be targeted with a CAR. This may be achieved by a CAR expressed on a universal T cell that recognizes the processed peptide described from the intracellular tumor associated antigen in the context of HLA. In addition, the universal T cell may be genetically modified to express a T-cell receptor pairing that recognizes the intracellular processed tumor associated antigen in the context of HLA.

[0091] The pathogen recognized by a CAR may be essentially any kind of pathogen, but in some embodiments the pathogen is a fungus, bacteria, or virus. Exemplary viral pathogens include those of the families of Adenoviridae, Epstein–Barr virus (EBV), Cytomegalovirus (CMV), Respiratory Syncytial Virus (RSV), JC virus, BK virus, HSV, HHV family of viruses, Picornaviridae, Herpesviridae, Hepadnaviridae, Flaviviridae, Retroviridae, Orthomyxoviridae, Paramyxoviridae, Papovaviridae, Polyomavirus, Rhabdoviridae, and Togaviridae. Exemplary pathogenic viruses cause smallpox, influenza, mumps, measles, chickenpox, ebola, and rubella. Exemplary pathogenic fungi include *Candida*, *Aspergillus*, *Cryptococcus*, *Histoplasma*, *Pneumocystis*, and *Stachybotrys*. Exemplary pathogenic bacteria include *Streptococcus*, *Pseudomonas*, *Shigella*, *Campylobacter*, *Staphylococcus*, *Helicobacter*, *E. coli*, *Rickettsia*, *Bacillus*, *Bordetella*, *Chlamydia*, *Spirochetes*, and *Salmonella*. In some embodiments the pathogen receptor Dectin-1 may be used to generate a CAR that recognizes the carbohydrate structure on the cell wall of fungi such as *Aspergillus*. In another embodiment, CARs can be made based on an antibody recognizing viral determinants (*e.g.*, the glycoproteins from CMV and Ebola) to interrupt viral infections and pathology.

[0092] In some embodiments, naked DNA or a suitable vector encoding a CAR can be introduced into a subject's T cells (*e.g.*, T cells obtained from a human patient with cancer or other disease). Methods of stably transfecting T cells by electroporation using naked DNA are known in the art. See, *e.g.*, U.S. Pat. No. 6,410,319. Naked DNA generally refers to the DNA encoding a chimeric receptor of the present invention contained in a plasmid expression vector in proper orientation for expression. In some embodiments, the use of naked DNA may reduce the time required to produce T cells expressing a CAR generated via methods of the present invention.

[0093] Alternatively, a viral vector (*e.g.*, a retroviral vector, adenoviral vector, adeno-associated viral vector, or lentiviral vector) can be used to introduce the chimeric construct into T cells. Generally, a vector encoding a CAR that is used for transfecting a T cell from a subject should generally be non-replicating in the subject's T cells. A large number of vectors are known that are based on viruses, where the copy number of the virus maintained in the cell is low enough to maintain viability of the cell. Illustrative vectors include the pFB-neo vectors (STRATAGENE®) as well as vectors based on HIV, SV40, EBV, HSV, or BPV.

[0094] Once it is established that the transfected or transduced T cell is capable of expressing a CAR as a surface membrane protein with the desired regulation and at a desired level, it can be determined whether the chimeric receptor is functional in the host cell to provide for the desired signal induction. Subsequently, the transduced T cells may be reintroduced or administered to the subject to activate anti-tumor responses in the subject. To facilitate administration, the transduced T cells may be made into a pharmaceutical composition or made into an implant appropriate for administration *in vivo*, with appropriate carriers or diluents, which are preferably pharmaceutically acceptable. The means of making such a composition or an implant have been described in the art (see, for instance, Remington's Pharmaceutical Sciences, 16th Ed., Mack, ed. (1980)). Where appropriate, transduced T cells expressing a CAR can be formulated into a preparation in semisolid or liquid form, such as a capsule, solution, injection, inhalant, or aerosol, in the usual ways for their respective route of administration. Means known in the art can be utilized to prevent or minimize release and absorption of the composition until it reaches the target tissue or organ, or to ensure timed-release of the composition. Generally, a pharmaceutically acceptable form is preferably employed that does not ineffectuate the cells expressing the chimeric receptor. Thus, desirably the transduced T cells can be made into a pharmaceutical composition containing a balanced salt solution such as Hanks' balanced salt solution, or normal saline.

IV. Artificial Antigen Presenting Cells

[0095] In some cases, aAPCs are useful in preparing CAR-based therapeutic compositions and cell therapy products. For general guidance regarding the preparation and use of antigen-presenting systems, see, *e.g.*, U.S. Pat. Nos. 6,225,042, 6,355,479, 6,362,001 and 6,790,662; U.S. Patent Application Publication Nos. 2009/0017000 and 2009/0004142; and International Publication No. WO2007/103009).

[0096] aAPCs may be used to expand T Cells expressing a CAR. During encounter with tumor antigen, the signals delivered to T cells by antigen-presenting cells can affect T-cell programming and their subsequent therapeutic efficacy. This has stimulated efforts to develop artificial antigen-presenting cells that allow optimal control over the signals provided to T cells (Turtle *et al.*, 2010). In addition to antibody or antigen of interest, the aAPC systems may also comprise at least one exogenous assisting molecule. Any suitable number and combination of assisting molecules may be employed. The assisting molecule may be selected from assisting molecules such as co-stimulatory molecules and adhesion molecules.

Exemplary co-stimulatory molecules include CD70 and B7.1 (also called B7 or CD80), which can bind to CD28 and/or CTLA-4 molecules on the surface of T cells, thereby affecting, *e.g.*, T-cell expansion, Th1 differentiation, short-term T-cell survival, and cytokine secretion such as interleukin (IL)-2 (see Kim *et al.*, 2004). Adhesion molecules may include carbohydrate-binding glycoproteins such as selectins, transmembrane binding glycoproteins such as integrins, calcium-dependent proteins such as cadherins, and single-pass transmembrane immunoglobulin (Ig) superfamily proteins, such as intercellular adhesion molecules (ICAMs), that promote, for example, cell-to-cell or cell-to-matrix contact. Exemplary adhesion molecules include LFA-3 and ICAMs, such as ICAM-1. Techniques, methods, and reagents useful for selection, cloning, preparation, and expression of exemplary assisting molecules, including co-stimulatory molecules and adhesion molecules, are exemplified in, *e.g.*, U.S. Pat. Nos. 6,225,042, 6,355,479, and 6,362,001.

[0097] Cells selected to become aAPCs, preferably have deficiencies in intracellular antigen-processing, intracellular peptide trafficking, and/or intracellular MHC Class I or Class II molecule-peptide loading, or are poikilothermic (*i.e.*, less sensitive to temperature challenge than mammalian cell lines), or possess both deficiencies and poikilothermic properties. Preferably, cells selected to become aAPCs also lack the ability to express at least one endogenous counterpart (*e.g.*, endogenous MHC Class I or Class II molecule and/or endogenous assisting molecules as described above) to the exogenous MHC Class I or Class II molecule and assisting molecule components that are introduced into the cells. Furthermore, aAPCs preferably retain the deficiencies and poikilothermic properties that were possessed by the cells prior to their modification to generate the aAPCs. Exemplary aAPCs either constitute or are derived from a transporter associated with antigen processing (TAP)-deficient cell line, such as an insect cell line. An exemplary poikilothermic insect cells line is a Drosophila cell line, such as a Schneider 2 cell line (*e.g.,* Schneider, J.m 1972). Illustrative methods for the preparation, growth, and culture of Schneider 2 cells, are provided in U.S. Pat. Nos. 6,225,042, 6,355,479, and 6,362,001.

[0098] aAPCs may be subjected to a freeze-thaw cycle. For example, aAPCs may be frozen by contacting a suitable receptacle containing the aAPCs with an appropriate amount of liquid nitrogen, solid carbon dioxide (dry ice), or similar low-temperature material, such that freezing occurs rapidly. The frozen aAPCs are then thawed, either by removal of the aAPCs from the low-temperature material and exposure to ambient room temperature conditions, or by a facilitated thawing process in which a lukewarm water bath or warm hand is employed to facilitate a shorter thawing time. Additionally, aAPCs may be frozen and stored for an extended period of time prior to thawing. Frozen aAPCs may also be thawed and then lyophilized before further use. Preservatives that might detrimentally impact the freeze-thaw procedures, such as dimethyl sulfoxide (DMSO), polyethylene glycols (PEGs), and other preservatives, may be advantageously absent from media containing aAPCs that undergo the freeze-thaw cycle, or are essentially removed, such as by transfer of aAPCs to media that is essentially devoid of such preservatives.

[0099] In other preferred embodiments, xenogenic nucleic acid and nucleic acid endogenous to the aAPCs may be inactivated by crosslinking, so that essentially no cell growth, replication or expression of nucleic acid occurs after the inactivation. For example, aAPCs may be inactivated at a point subsequent to the expression of exogenous MHC and assisting molecules, presentation of such molecules on the surface of the aAPCs, and loading of presented MHC molecules with selected peptide or peptides. Accordingly, such inactivated and selected peptide loaded aAPCs, while rendered essentially incapable of proliferating or replicating, may retain selected peptide presentation function. The crosslinking can also result in aAPCS that are essentially free of contaminating microorganisms, such as bacteria and viruses, without substantially decreasing the antigen-presenting cell function of the aAPCs. Thus crosslinking can be used to maintain the important APC functions of aAPCs while helping to alleviate concerns about safety of a cell therapy product developed using the aAPCs. For methods related to crosslinking and aAPCs, see for example, U.S. Patent Application Publication No. 20090017000, which is incorporated herein by reference.

IV. Examples

[00100] The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

Materials and Methods

Generation of clinical-grade DNA plasmids

[00101] The SB transposon, CoOpCD19RCD28 ζ/pSBSO, expresses the human codon optimized (CoOp) 2nd generation CoOpCD19RCD28ζ CAR under EF-1/HTLV hybrid composite promoter (InvivoGen) comprised of Elongation Factor- 1a (EF-1a [Kim *et al.*, 1990] and 59 untranslated region of the Human T-Cell Leukemia Virus (HTLV) [Singh *et al.*, 2011; Davies *et al.*, 2010]. The derivation of this DNA plasmid is described in Figure S1. The SB transposase, SB11, under the cytomegalovirus (CMV) promoter is expressed in cis from the DNA plasmid pCMV-SB11 (Singh *et al.*, 2011; Singh *et al.*, 2008). Both plasmids were sequenced in their entirety and manufactured by Waisman Clinical Biomanufacturing Facility (Madison, WI) using kanamycin for selection of the bacterial strain E. Coli DH5a.

Generation of triple site-specific recombination DNA plasmids – EZ-Build-CARs

[00102] Using the DNA sequence from the CAR described above (CoOpCD19RCD28z/pSBSO), the parts CD19 ScFv, the hinge IgG4 Fc and the domain CD28 transmembrane and cytosolic portion conjugated with CD3ζ signaling domain were flanked by lambda recombination sites, synthetized by Geneart (Life Technologies) as PCR products. These three parts were individually inserted into pDonors221 plasmids (by the enzyme BP clonase (both from Invitrogen). The three plasmids were recombined with the triple site specific recombination Sleeping Beauty plasmid by the enzyme LR PLUS clonase (Invitrogen) generating the EZ-Build CD19CD28ζ CAR in the format scFv-**B**-scaffold-**C**-signaling domain(s) (**FIG. 1**).

Cell counting

[00103] Trypan-blue exclusion was used to distinguish live from dead cells and counted using Cellometer (Nexecelom Bioscience) (Singh *et al.*, 2011).

Isolation of PBMC

[00104] Leukapheresis products from two male volunteer healthy donors were purchased from Key Biologics LLC (Memphis, TN). The peripheral blood mononuclear cells (PBMC) were isolated by our adapting the Biosafe Sepax system (Eysins, Switzerland) for work in compliance with cGMP. Briefly, after closing all the clamps on the CS-900 kit, 100 mL Ficoll (GE Healthcare) was aseptically transferred via 60 mL syringes to a density gradient media bag (‘‘ficoll bag’’) via Luer-lock connector and the tubing was heat sealed using a hand held sealer (Sebra, Model# 2380). The kit was spike-connected to a 1,000 mL bag containing CliniMACS buffer (PBS/EDTA, Miltenyi, Cat#70026) with 20 mL 25% Human Serum Albumin (HSA) (Baxter) (2% v/v, wash buffer) for washes, a final product bag [300 mL Transfer Pack with Coupler (Baxter/ Fenwal 4R2014)] and a reagent/blood bag. Using the density gradient-based separation protocol (v126), the syringe piston was loaded into the centrifuge chamber and the cover of the Sepax aAPC (clone #4) to selectively propagate CAR+ T cells The c-irradiated aAPC were used to numerically expand the genetically modified T cells. Thawed aAPC from WCB were propagated in CM for up to 60 days in VueLife cell culture bags and harvested using Biosafe Sepax II harvest procedure. Briefly, CS-490.1 kit was connected to a 300 mL output bag (transfer pack) via Luer lock connection. The separation chamber was installed in the pit and the tubing was inserted into the optical sensor and stopcocks aligned in T-position. After connecting the pressure sensor line, the product bag and supernatant/plasma bags were hung on the holder. The modified protocol PBSCv302 was selected from the Sepax menu and the volume of input product to be processed (initial volume) was set to #840 mL. After validation and kit test, the procedure was started. Following completion, the bags were removed, clamps closed and the kit was removed. The cells from the final product bag were aseptically removed, washed twice with wash media (10% HSA in Plasmalyte) and counted. aAPC were irradiated (100 Gy) using a CIS BIO International radiator (IBL-437 C#09433) and cryopreserved for later use in cryopreservation media using controlled-rate freezer (Planer Kryo 750). The anti-CD3 (OKT3) loaded K562-derived aAPC clone #4 was used to propagate control (CARneg) autologous control T cells that had not undergone genetic modification. The aAPC, obtained from culture, were incubated overnight in serum-free X-Vivo 15 (cat # 04-744Q, Lonza) containing 0.2% acetyl cysteine (Acetadote, Cumberland Pharmaceuticals) termed Loading Medium (LM). The next day cells were washed, irradiated (100 Gy) using a Gamma Cell 1000 Elite Cs-137 radiator (MDS Nordion), resuspended in LM at a concentration of 106 cells/mL along with 1 mg/10^6 cells of functional grade purified anti-human CD3 (clone-OKT3, 16-0037-85, eBioscience) and incubated with gentle agitation on a 3-D rotator (Lab-Line) at 4^0C for 30 minutes. Following three washes with LM the cells were used in experiments or frozen in aliquots in liquid nitrogen in vapor layer for later use.

Manufacture of CAR+ T cells

[00105] Thawed PBMC were resuspended in (i) Human T-cell kit (cat# VPA-1002, Lonza; 100 μL for $2x10^7$ cells in one cuvette), with (ii) the DNA plasmid (CoOpCD19RCD28/pSBSO) coding for CD19RCD28 CAR transposon (15 μg supercoiled DNA per $2x10^7$ PBMC per cuvette), and (iii) the DNA plasmid (pCMVSB11) coding for SB11 transposase (5 μg supercoiled DNA per $2x10^7$ PBMC per cuvette). This mixture was immediately transferred to a cuvette (Lonza), electroporated (defining culture day 0) using Nucleofector II (Program U-14, Amaxa/Lonza), rested in 10% RPMI complete media for 2 to 3 hours, and after a half-media change, incubated overnight at 37°C, 5% CO_2. The following day, cells were harvested, counted, phenotyped by flow cytometry, and co-cultured with c-irradiated aAPC at a ratio of 1:2 (CAR + T cell:aAPC), which marked culture day 1 and the beginning of a 7-day stimulation cycle. IL-21 (cat # AF-200-21, PeproTech) and IL-2 (cat # NDC 65483-116-07, Novartis) were added on a Monday-Wednesday-Friday schedule onwards of day 1 and day 7 respectively. NK cells can prevent the numeric expansion of CAR + T cells, especially if their overgrowth occurs early in the tissue culturing process. Therefore, a CD56-depletion was performed if CD3negCD56 + cells $10% using CD56 beads (cat #70206, Miltenyi Biotech, 20 mL beads/107 cells) on LS columns (cat #130-042-401, Miltenyi Biotech) in CliniMACS buffer containing 25% HSA (80 mL/107 cells).

Generation of CAR^{neg} control T cells

[00106] As a control, $5x10^6$ mock transfected PBMC were co-cultured with irradiated and anti-CD3 (OKT3) loaded K562-derived aAPC clone #4 at a ratio of 1:1 in a 7-day stimulation cycle. All the cultures were supplemented with IL-21 (30 ng/mL) from culture day 1 onwards, and IL-2 (50 U/mL) starting 7 days after the start of the culture. All cytokines were subsequently added every other day

Immunophenotype of cells

[00107] Cells were stained using antibodies in 100 mL FACS Buffer (2% FBS, 0.1% Sodium Azide) for 30 minutes at 4°C. Acquisition was performed using FACSCalibur (BD Bioscience) and analyzed using FCS Express 3.00.0612

Chromium Release Assay

[00108] T cells were evaluated for their cytotoxicity in a standard 4-hour chromium release assay using ^{51}Cr-labeled target cells. T cells were plated in triplicate at 1x10^5, 0.5x10^5, 0.25x10^5, 0.125x10^5 bottom plate (Costar). After incubation, 50 μL of supernatant was harvested onto LumaPlate (Perkin Elmer), read in TopCount NXT (Perkin Elmer) and percent specific lysis was calculated per:

$$\frac{\text{Experimental } ^{51}\text{Cr released - Spontaneous } ^{51}\text{Cr released}}{\text{Maximum } ^{51}\text{Cr released - Spontaneous } ^{51}\text{Cr released}} \times 100$$

[00109] Spontaneous and maximum release was determined by measuring chromium in the conditioned supernatant from target cells incubated with CM or 0.1% Triton X-100 (Sigma), respectively and 0.0625x10^5 cells/well with 5x10^3 target cells in a 96-well V (Manufacturee Novo Software, Thornhill, Ontario, Canada).

Example 2

Generation of CD19$^+$ CAR

[00110] A CD19+ CAR was generated using the methods described above in Example 1 (referred to as the "EZ" method). These CD19$^+$ CAR (CD19CAR) were compared to a clinical grade ("CG") CD19CAR generated via a previous method.

[00111] The data showed that the triple site-recombination system generated a CD19CAR (EZ) similar to the clinical grade CD19CAR (CG). The footprints left by recombination-sites in the plasmids did not interfere in the expression and function of the CAR (**FIGS. 2A-B**).

Example 3

Generation of CAR containing (CD8, CD28) Transmembrane Domains and (CD28, 4-1BB) Signaling Domains

[00112] Various CARs tested have shown similar expansion, cytotoxicity, and Th1 cytotoxicity. CD19-BB-z has shown lower production of Th2 cytokines; *in vivo*, it was efficient in controlling disease in mice (Molecular Therapy 17 (8): 1453–1464, 2009).

Nonetheless, a concern exists due to the fact that cells persisted *in vitro* without antigenic stimulation.

[00113] CARs in the clinic are shown below in Table 2. In some embodiments, a CAR of the present invention does not have the specific construct as shown in the below Table 2. Alternately, in some embodiments, methods of the present invention may be used to generate another variation of a CAR having the characteristics of the CAR mentioned below in Table 2 that is nonetheless distinct from the CAR currently being used in the clinic.

Table 2: CARs in the Clinic

Clinical Trial	UPenn	Cooper (MDACC)
Gene Transfer Method	Lentivirus	Electroporation/ Sleeping Beauty
scfv derived from	FMC63	FMC63
Scaffold	CD8alpha	IgG4
Space region	69 aa	230 aa
Transmembrane	CD8alpha	CD28
CAR signaling endomain(s)	CD137 and CD3-zeta	CD28 and CD3-zeta
Culture Method	CD3/CD28 beads	K562 aAPC
Cytokine	IL-2	IL-2 and IL-21
Culture Time	14 days	28 days
Transgene Expression in product infused	4-23%	>80%

[00114] Specific CAR construct designs are illustrated in FIG. 3. As shown in FIG. 3, a schematic of various CARs using a combination of CD19scfv, CD8a hinge or IgG4 Fc stalk, CD8 transmembrane (TM) or CD28 TM or CD137 TM and signaling through CD28 or CD137 endodomain along with CD3zeta endodomain were generated.

[00115] The CAR constructs shown in FIG. 3 were then cloned into Sleeping Beauty plasmids containing SIM and FRA tags to allow tracking in competitive repopulation studies, when amplified using a common CVseq7 primer. The Sleeping Beauty tracking plasmids are shown in FIG. 4.

[00116] The CAR constructs shown in FIG. 3 were electroporated into T cells using Amaxa Nucleofector II and co-cultured with aAPC for 28 days in the presence of cytokines (IL2, IL-21). CAR expression the day after electroporation (day 1) and after 28 days of co-culture with aAPC (day 28) is shown. Dot-plots for CD3 and CAR are shown, where CD3 and anti-CD19scfv specific Ab was used to distinguish T cells and CAR. CAR expression results are shown in FIG. 5.

[00117] The CAR constructs shown in FIG. 3 were evaluated for CAR expression over time for 28 days and is shown. After 21 days most of the cultures had >80% CAR expression. CAR expression kinetics are shown in FIG. 6.

[00118] Percent expression of CD4 and CD8 T cells in cultures nucleofected with CARs from Fig 3 is shown after 28 days of co-culture with aAPC. These phenotype results are shown in FIG. 7.

[00119] After 28 days of co-culture CAR^+ T cells (expressing the CAR described in FIG. 3) were evaluated for expression of markers pertaining to memory (CD45RA, CCR7, CD27), activation (CD69, HLA-DR), cytotoxic (Perforin, Granzyme B), exhaustion/senescence (CD57, KLRG1, PD1), and adhesion (CD39, CD150). Results for this extended phenotype are shoen in FIGS. 8A-B.

[00120] CAR^+ T cells (expressing the CAR described in FIG. 3) were evaluated for expression of CD3 ζ using western blot. Cell lysates were run under denaturing conditions, transferred and the expression of chimeric CD3 ζ was measured using a primary mouse anti-human CD3ζ mAb and HRP-conjugated goat anti-mouse IgG using SuperSignal West Femto Maximum Sensitivity substrate. Chimeric CD3ζ bands at 52, 71 and 78 kD are observed relative to size of CAR constructs. These western blot results are shown in FIG. 9.

[00121] T cells electroporated with the CAR constructs (described in FIG. 3) were stimulated with K562 aAPC at day 1 and every 7 days thereafter for 28 days. At the end of each stimulation cycle, cells were counted using trypan blue exclusion method and phenotyped for CD3 and CAR expression. The graphs shown in FIG. 10 depict inferred cell counts for total, CD3, and CAR^+ T cells over time.

[00122] Expansion of cells was measured. Fold expansion for Total Cells (FIG.11) and CAR^+ (FIG.12) T cells was calculated at day 14, 21 and 28 days of co-culture by comparing counts to day 1 (post electroporation). Results are shown in FIG. 11 and FIG. 12.

[00123] Cytotoxicity was measured for the CAR-expressing T Cells (CAR^+ T cells). CAR^+ T cells (expressing CAR described in FIG. 3) were evaluated for their cytotoxicity against $CD19^+$ tumor targets (Daudiβ_2m, NALM-6 and $CD19^+$ EL-4) as compared to $CD19^{neg}$ EL-4 in a standard 4-hr chromium release assay. Results are shown in FIG. 13, FIG. 14, FIG. 15, and FIG. 16.

[00124] Intracellular IFN-γ production. CAR^+ T cells (expressing the constructs described in FIG. 3) were incubated with ($CD19^+$ and $CD19^{neg}$) stimulator cells in the presence of protein transport inhibitor for 4-6 hr, fixed, permeabilized and stained with IFN-γ specific mAb. PMA-Ionomycin was used as a positive control. Results for intracellular IFN-γ production are shown in FIG. 17, FIG. 18, FIG. 19, and FIG. 20.

[00125] PCR for SB11 transposase. DNA isolated from CAR+ T cells (Fig 3) was amplified using SB11 specific primers in a thermal cycler. GAPDH was used as the housekeeping gene, and linearized pCMV-SB11 plasmid, genomic DNA from Jurkat cells expressing SB11 were used as positive controls. CAR^{neg} cells (No DNA) were used as negative controls. These PCR results are shown in FIG. 21.

[00126] CAR copy number was measured using quantitative PCR (qPCR). The integrated number of CAR transgene in cells (of the CAR constructs shown in FIG. 3) were evaluated by amplifying genomic DNA using primers and probes specific for the IgG4 Fc stalk and inverted/direct repeats (IR/DR). RNAse P gene was used as an internal control, and the Jurkat cell line expressing a single copy of CAR was used to generate a standard curve. Results are shown in FIG. 22.

[00127] Next, CAR+ T cells were measured for the presence or absence of autonomous growth. Aberrant growth of CAR+ T cells (expressing CAR constructs shown in FIG. 3) was monitored and measured by culturing T cells in the absence of cytokines and aAPC. Cells were counted every 7 days and the percents alive/dead cells (from day 1) were calculated and plotted. As shown in FIG. 23, more than 80% of T cells were observed to be dead by day 14 showing lack of autonomous growth.

[00128] Various CARs could be expressed (>80%), expanded (~1010) and were cytotoxic (~60%, Daudi) to similar extend. Scaffolding domains (IgG4 or CD8α) were used to build CAR and didn't effect expression or potency. Transmembrane domains (CD8, CD28) did not affect potency. 4-1BB transmembrane domain (216) affected expression (anti-scFv Ab), but not cytoxicity and cytokine production. Combination of signaling domains, CD28 and 4-1BB did not have an additive effect. CAR+ T cells exhibited memory/effector phenotype. CARs containing only 4-1BB domain (212, 214, 217) had higher CCR7 expression as compared to others. Cells expressed markers for memory (CD27hi, CD45RAhi, CCR7lo), activation (CD69med, HLA-DRhi), cytolysis (granzymehi, perforinlo), and adhesion (CD39hi, CD150lo), but negligible amounts of inhibitory markers (CD57, PD1, KLRG1) were observed. All the CARs including the ones containing 4-1BB domain lacked SB11 transposase and did not auto-proliferate.

Example 4

Generation of CAR containing CD3-zeta

[00129] CAR containing CD3ζ are provided in this example. A general diagram of CAR design is shown in FIG. 24. As shown in FIG. 24, a comparison of CAR design (FIG. 24, right) with an antibody molecule (FIG, 24, left) are shown.

[00130] CD3ζ sequences are shown in FIG. 25. The sequence of CD3zeta and its isoform are shown in FIG. 25. The CAR designs included CD3 zeta (isoform 1) which forms one of the endodomain signaling moieties and has three ITAMs.

[00131] Specific CAR constructs are shown in FIG. 26 and FIG. 27. FIG. 26 shows a schematic of CD19-specific CARs having long (IgG4), medium (CD8a hinge) and small (IgG 12 aa) stalks which signaling through CD28 or CD137 endodomains. Nomenclature of CAR molecules with different stalks and signaling are shown in FIG. 27.

[00132] CAR expression was measured. Expression of CAR (as described in FIG. 26) was measured the day after electroporation (day 1) and after 28 days of co-culture on aAPC (day 28). Dot plots of CD3 and CAR (as measured by CD19scfv-specific mAb) are shown in FIG. 28.

[00133] Expansion kinetics were measured for the CAR. T cells electroporated with CAR constructs (shown in FIG. 26) were co-cultured on aAPC in a 7-day stimulation cycle. Cells were counted and evaluated for expression of CD3 and CAR. Results are shown in FIG. 29 and FIG. 30.

[00134] Cytotoxicity of the CAR^+ T cells was measured. At the end of 28 days of co-culture CAR^+ T cells (expressing constructs shown in FIG. 26) were evaluated for cytotoxicity against tumor targets in a chromium release assay. As shown in FIG 31, percent cytotoxicity was measured at various effector-to-target ratio for CD19RCD28 (CAR 194) and CD19RCD137 (CAR 217) CARs against $CD19^+$ and $CD19^{neg}$ tumor targets. As shown in FIG 32, data were obtained for percent lysis of $CD19^+$ EL-4 by CAR^+ T cells (expressing CAR constructs shown in FIG. 26) at E:T ratio of 20:1. The percent expression of CD27, CD62L, CD28 and CCR7 on CAR^+ T cells (expressing constructs shown in FIG. 26) was measured, and results are shown in FIG. 33.

[00135] Intracellular cytokine production was measured for the CAR^+ T cells. Stimulator cells ($CD19^+$ and $CD19^{neg}$) were incubated with CAR^+ T cells (expressing CAR shown in FIG. 26) for 4 hr in the presence of protein transport inhibitor and stained with IFN-γ and IL-2 mAb. PMA-Ionomycin served as a positive control and T cells alone served as negative control. FIG 34 shows percentage of IFN- γ producing cells after stimulation. FIG 35 shows breakdown of IFN- γ and or, IL-2 producing cells after incubation with cell stimulation cocktail (PMA-Ionomycin).

[00136] The CAR^+ T cells were measured for the presence of absence of autonomous growth. CAR^+ T cells (expressing CAR described in FIG. 26) were evaluated for their lack of aberrant growth in the absence of external stimulation (cytokines and aAPC) for 18 days. At the end of 18 days, more than 80% of the cells were dead showing lack of unwanted growth. As shown in FIG. 36, a lack of autonomous growth was observed.

[00137] CAR copy number was measured in the CAR^+ T cells. The number of copies of integrated CAR molecule was evaluated using primers/probes specific for IgG4-Fc and IR/DR regions by qPCR. As shown in FIG 37, CAR copy number integrated (of CAR shown in FIG. 26) was observed using the IR/DR probe. As shown in FIG 38 and FIG. 39, a compilation of CAR copy number data are provided in a table and graphical form for CAR constructs (for both CAR constructs shown in FIG. 3 and CAR constructs shown in FIG. 26) as tested in two separate experiments (P491;C714 and GCR357861).

[00138] These data show that CARs with various spacers can be expressed and grown *in vitro* in the culture system as described herein. All CARs were observed to have similar CAR expression. The maximum cytotoxicity of CD19+ EL-4s was observed in CARs with a CD8 hinge region. Similar expression of CD62L and CD28 was observed on all CARs tested. High integration frequency as measured by CAR copy number was observed in all CAR, except for CAR containing IgG4-Fc stalk. A lack of autonomous growth and SB11 was observed by PCR. Contrary to previous reports, inclusion of a 12aa spacer in the CAR did not confer improved functionality in these studies.

Example 5

Rapid Assembly of CARs from Principal Components

[00139] The inventors generated a CD19-specific CAR that is activated through chimeric CD28/CD3-zeta using the EZ CAR platform in parallel with clinical-grade CD19RCD28mζ CAR+ T cells (CG CAR). Both, Clinical Grade CD28/CD3-ζ and EZ CAR CD19RCD28mζ CARs sequences were inserted into Sleeping Beauty transposon vectors and electroporated into T cells. After electroporation the T cells were cultivated in presence of CD19+ artificial Antigen Presenting Cells (also called Activating and Propagating Cells, or AaPCs) for antigen specific expansion of the T cells. The expression of the CARs in the T cell's surface was measured every week by flow cytometry (Fc+ expression), showing similar CAR expression in Clinical Grade CD19 CAR T cells and EZ CD19 CAR T cells. A Chromium Release Assay (CRA) was also performed to evaluate the killing function of T cells CD19 CAR+ generated by EZ CAR platform against tumor cells. After 4 hours of incubation the percentage of specific cell lysis was observed to be 52% by the EZ CAR T cells and 49% by the CG CAR T cells.

[00140] These results demonstrate that functional CAR^+ T cells were generated using these methods. The inventors then performed a rapid production of CARs using methods as described above in combination with a library of plasmids containing the following three components of a CAR molecule: (i) anti-CD19 scFv (ii) 5 hinges with different sizes (long - IgG4a and IgG4ΔEQ, medium - CD8α, short – t-20AA and t-12AA) and (iii) different combinations of 7 signaling domains (CD27, CD28, $CD28\Delta Y^{173} \rightarrow F^{173}$, CD134, CD137, CD278) with the CD3ζ domain. Transfection of HEK 293 cells with plasmid containing the CAR transgene were used to screen 27 different CARs constructs to ensure the expression of the CAR protein in the cell surface. The high throughput testing of individual CAR molecules was undertaken using the iQue™ Screener (Intellicyt, Albuquerque, NM), a high throughput flow cytometer, where cytotoxic assays are performed using engineered target cells expressing a fluorescent granzyme B reporter or GFP. Results are shown in FIGS. 40A-E.

[00141] Additional experiments were performed to screen the CAR molecules using IntelliCyt's iQue™. iQue™ uses high throughput flow cytometry, a complementary technology that generates information by studying large populations using multiplexing capabilities and cell-by-cell analysis. The inventors adapted this technology to inform on the therapeutic potential of T cells modified with panels of CARs. T cells from the wells can be stained for viability, as well as activation signals (*e.g.*, upregulation of CD25), cytokine release, and killing. Thus the inventors adapted the iQue Screener and harnessed its ability to perform multiplexed bead-based cytokine detection and cell-based assays. The results obtained indicate that this technology may be used to test a large number of different CAR T cells generated by the EZ CAR platform. Data was generated using IntelliCyt's iQue™, where 2 populations of CAR T cells were evaluated on their abilities to kill target cells. Results are shown in FIGS. 41A-B and FIG. 42. These results demonstrate that the CAR molecules were active and the iQue™ method may be effectively used to evaluate CAR activity.

* * *

[00142] All of the methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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WHAT IS CLAIMED IS:

1. A polypeptide comprising a chimeric antigen receptor encoded by a DNA sequence according to SEQ ID NO:5.

2. A transformed T cell expressing the polypeptide of claim 1.

3. The transformed T cell of claim 2, wherein the cell is an immortalized cell.

4. The transformed T cell of claim 2, wherein the T cell is an alpha beta T cell, a gamma delta T cell, or a NKT cell.

5. A pharmaceutical preparation comprising the transformed T cell of any one of claims 2-4.

6. A nucleic acid encoding a chimeric antigen receptor comprising a sequence according to SEQ ID NO:5.

7. The nucleic acid of claim 6, wherein the nucleic acid is comprised in a T cell.

8. The nucleic acid of claim 7, wherein the T cell is an alpha beta T cell, a gamma delta T cell, a NKT cell, or a T cell derived from a pluripotent cell.

9. A Sleeping Beauty transposon comprising a nucleic acid encoding a chimeric antigen receptor comprising a sequence according to SEQ ID NO: 5.

10. A T cell comprising a nucleic acid encoding a chimeric antigen receptor encoded by a sequence according to SEQ ID NO. 5.

11. A T cell comprising a Sleeping Beauty transposon vector comprising a nucleic acid of claim 6.

12. The T cell of claim 10 further comprising a membrane-bound cytokine.

13. The T cell of claim 12, wherein the membrane-bound cytokine is membrane-bound IL-15.

14. The T cell according to claims 10-13 when used in treating cancer.

15. The T cell according to claim 14, wherein the cancer is a B-cell malignancy or lymphoma.

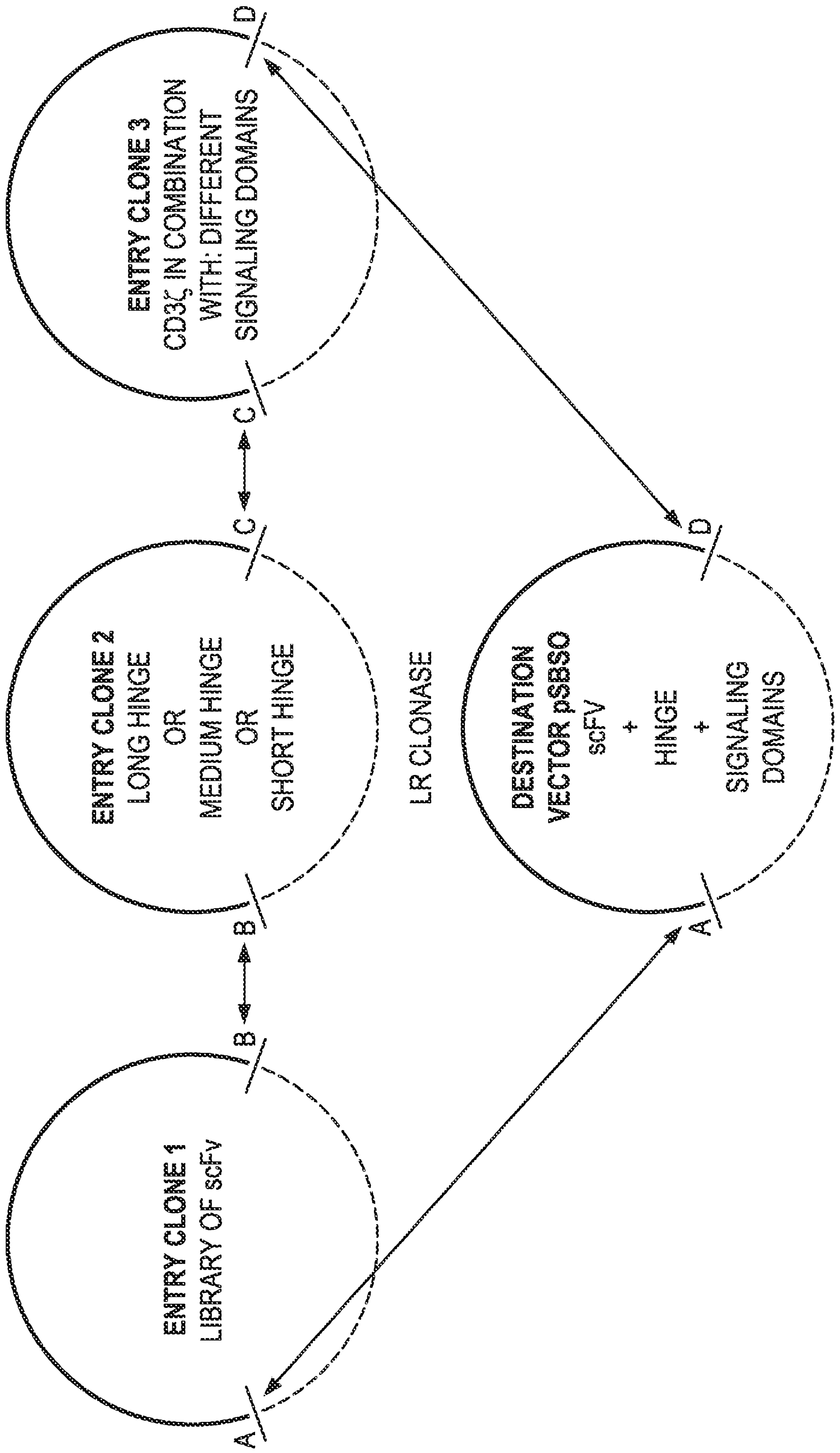

ENTRY CLONE 1
LIBRARY OF scFv
ENTRY CLONE 2
LONG HINGE
OR
MEDIUM HINGE
OR
SHORT HINGE
ENTRY CLONE 3
CD3ζ IN COMBINATION
WITH: DIFFERENT
SIGNALING DOMAINS
LR CLONASE
DESTINATION
VECTOR pSBSO
scFV
+
HINGE
+
SIGNALING
DOMAINS
A
B
B
C
C
D
D
A

FIG. 1

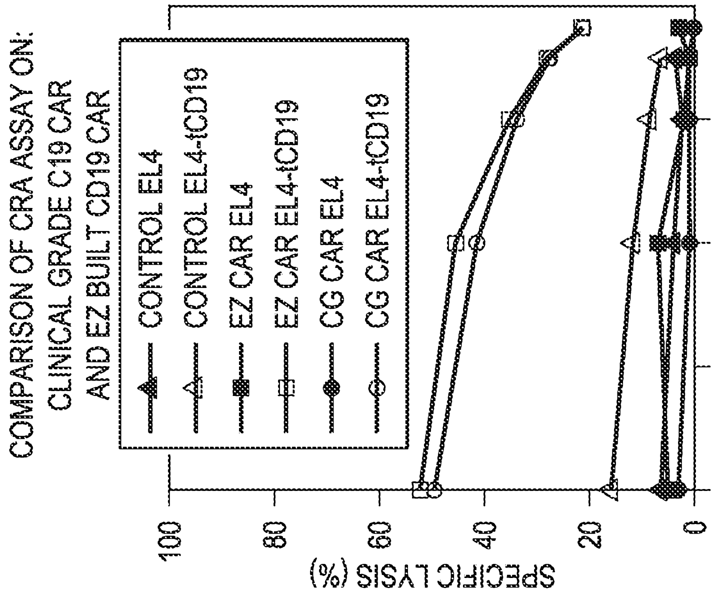

COMPARISON OF CRA ASSAY ON:
CLINICAL GRADE C19 CAR
AND EZ BUILT CD19 CAR
CONTROL EL4
CONTROL EL4-tCD19
EZ CAR EL4
EZ CAR EL4-tCD19
CG CAR EL4
CG CAR EL4-tCD19
SPECIFIC LYSIS (%)
100
80
60
40
20
0
20
15
10
5
E:T (X:1)

FIG. 2B

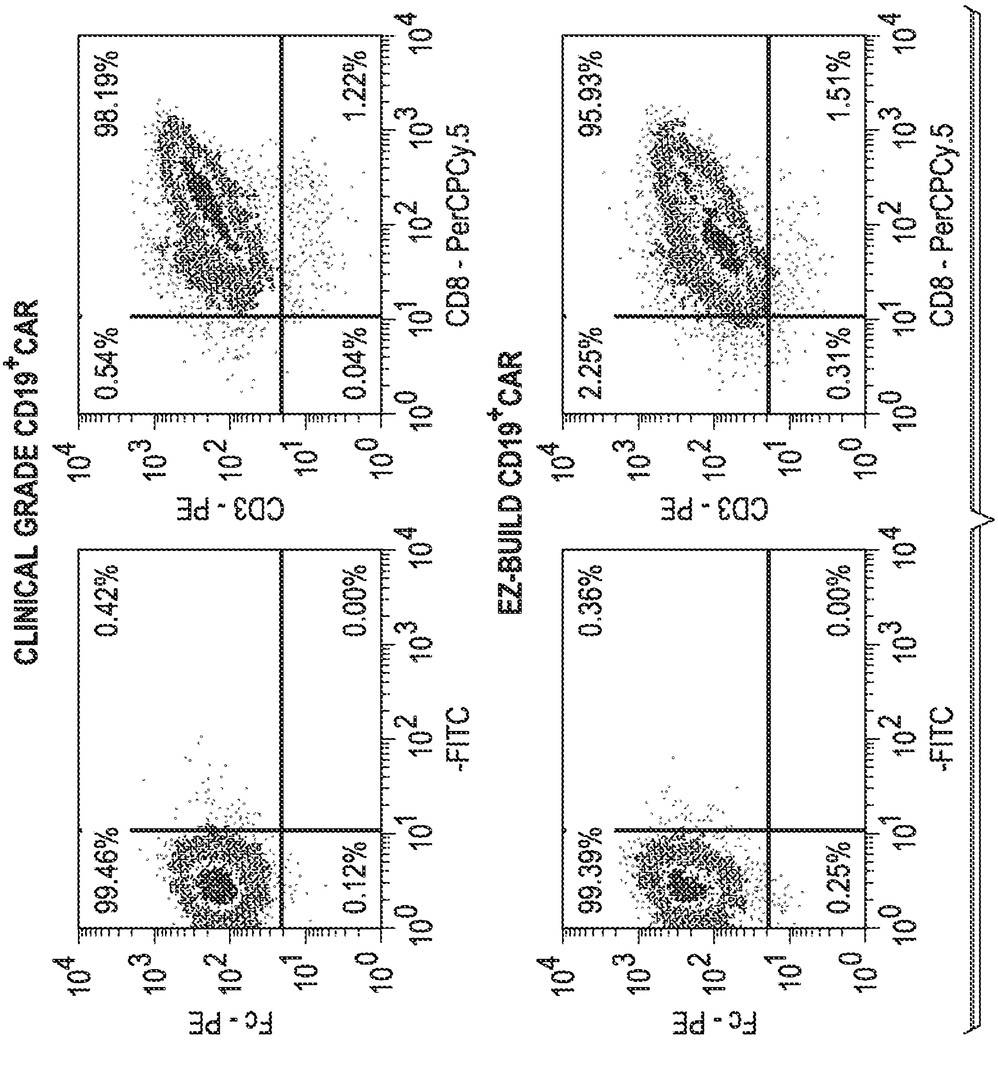
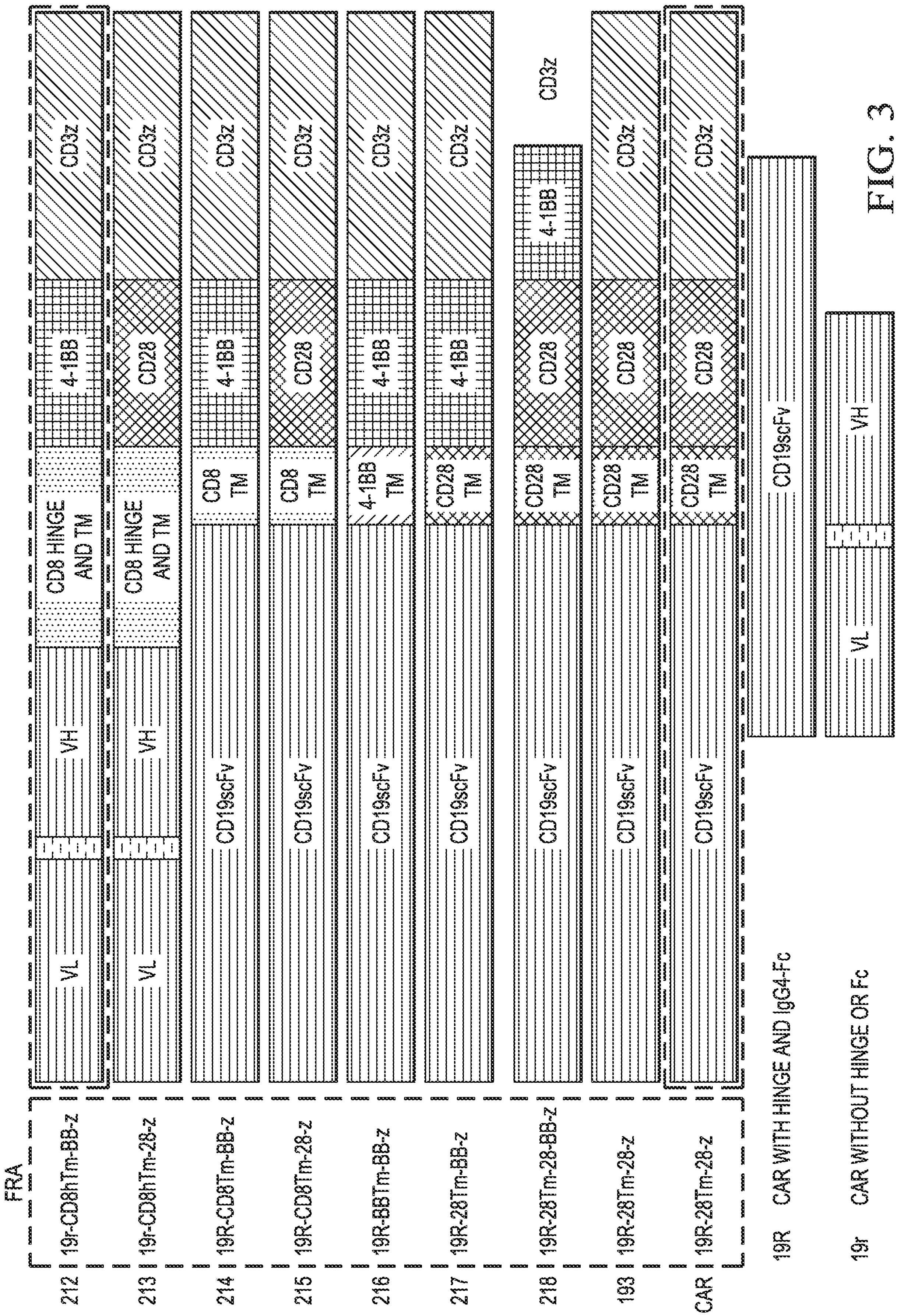

CLINICAL GRADE CD19+CAR
Fc - PE
-FITC
99.46%
0.42%
0.12%
0.00%
CD3 - PE
CD8 - PerCPCy.5
0.54%
98.19%
0.04%
1.22%
EZ-BUILD CD19+CAR
99.39%
0.36%
0.25%
0.00%
2.25%
95.93%
0.31%
1.51%

FIG. 2A


FRA
212 19r-CD8hTm-BB-z
VL
VH
CD8 HINGE AND TM
4-1BB
CD3z
213 19r-CD8hTm-28-z
VL
VH
CD8 HINGE AND TM
CD28
CD3z
214 19R-CD8Tm-BB-z
CD19scFv
CD8 TM
4-1BB
CD3z
215 19R-CD8Tm-28-z
CD19scFv
CD8 TM
CD28
CD3z
216 19R-BBTm-BB-z
CD19scFv
4-1BB TM
4-1BB
CD3z
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CD28 TM
4-1BB
CD3z
218 19R-28Tm-28-BB-z
CD19scFv
CD28 TM
CD28
4-1BB
CD3z
193 19R-28Tm-28-z
CD19scFv
CD28 TM
CD28
CD3z
CAR 19R-28Tm-28-z
CD19scFv
CD28 TM
CD28
CD3z
19R CAR WITH HINGE AND IgG4-Fc
CD19scFv
19r CAR WITHOUT HINGE OR Fc
VL
VH

FIG. 3

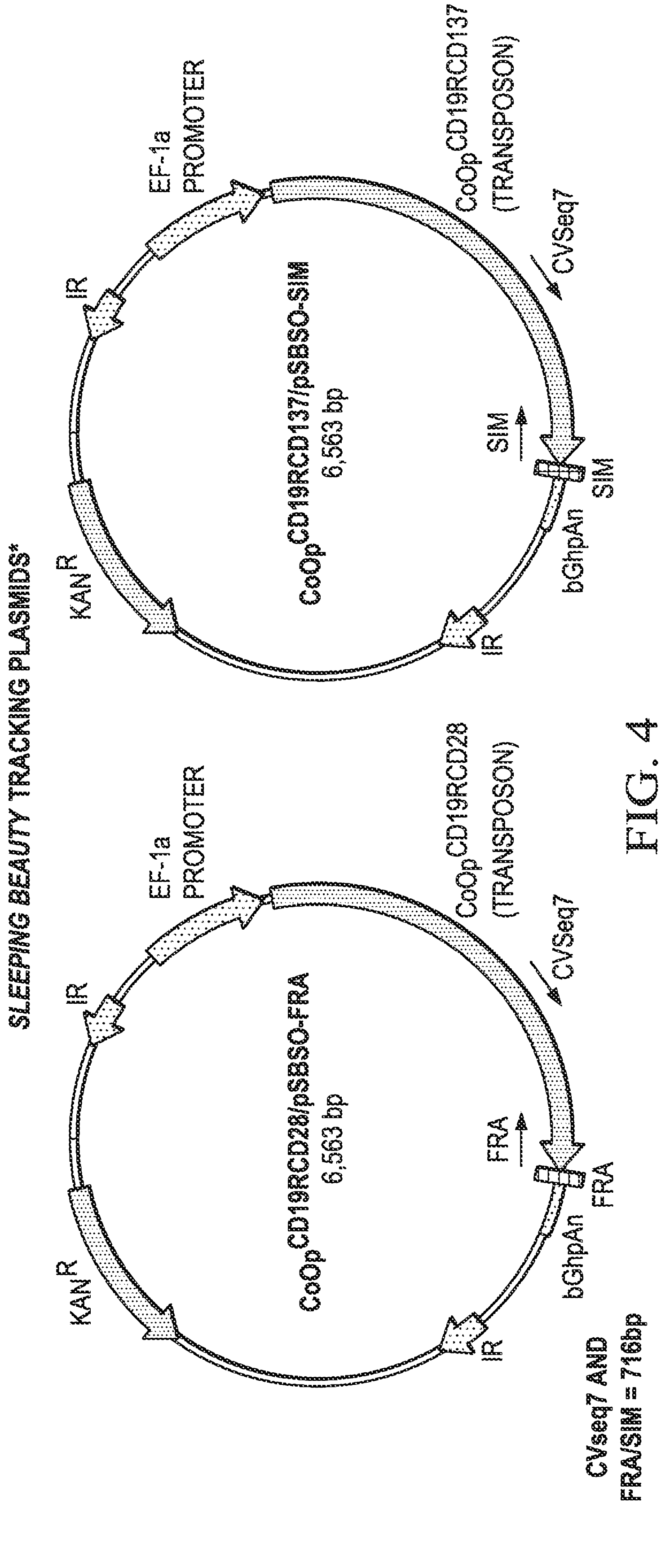

SLEEPING BEAUTY TRACKING PLASMIDS*
CoOpCD19RCD28/pSBSO-FRA
6,563 bp
IR
EF-1a
PROMOTER
CoOpCD19RCD28
(TRANSPOSON)
CVSeq7
FRA
FRA
bGhpAn
IR
KANR
CVseq7 AND
FRA/SIM = 716bp
CoOpCD19RCD137/pSBSO-SIM
6,563 bp
IR
EF-1a
PROMOTER
CoOpCD19RCD137
(TRANSPOSON)
CVSeq7
SIM
SIM
bGhpAn
IR
KANR

FIG. 4

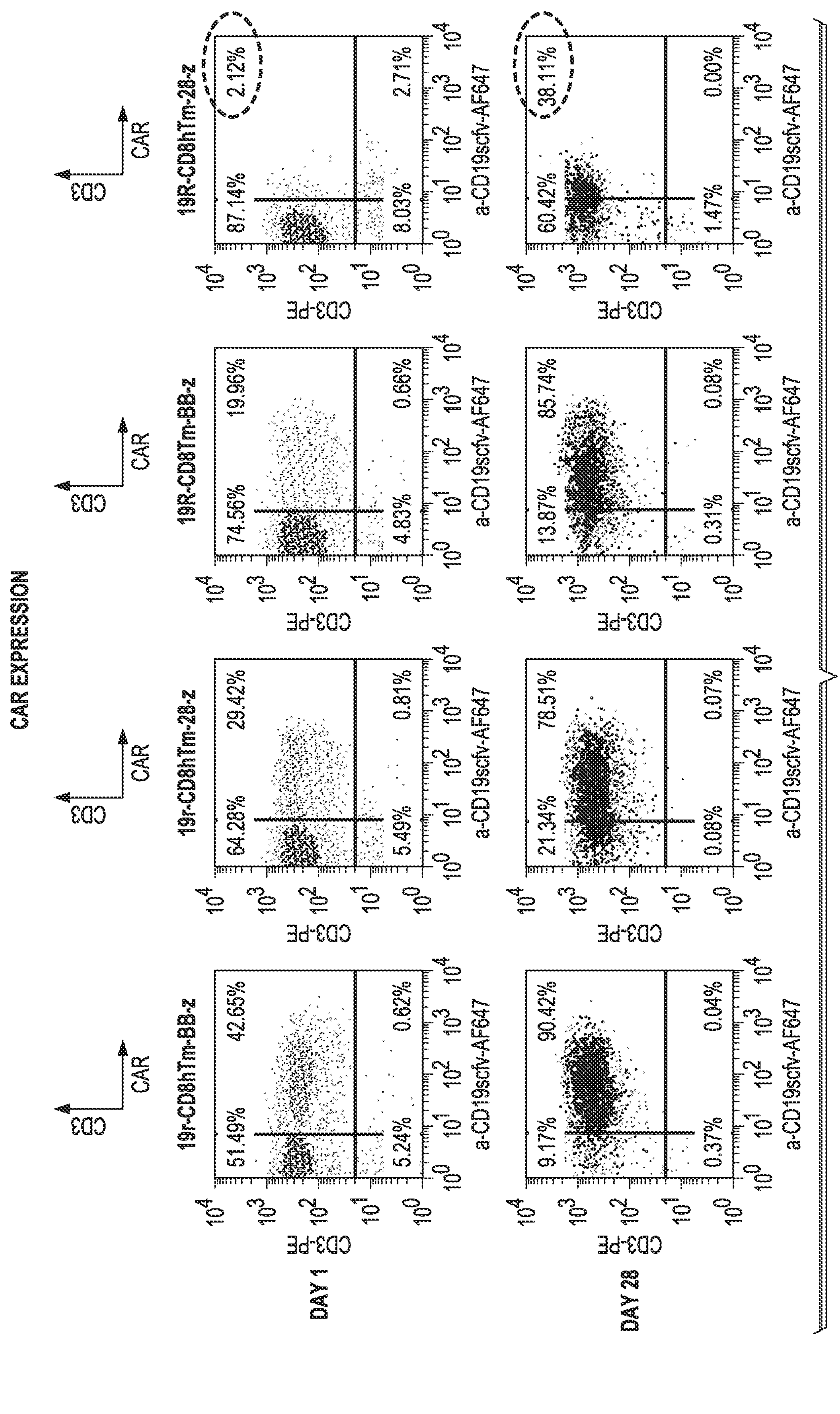

CAR EXPRESSION
CD3
CAR
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8hTm-28-z
DAY 1
DAY 28
CD3-PE
a-CD19scfv-AF647
51.49%
42.65%
5.24%
0.62%
64.28%
29.42%
5.49%
0.81%
74.56%
19.96%
4.83%
0.66%
87.14%
2.12%
8.03%
2.71%
9.17%
90.42%
0.37%
0.04%
21.34%
78.51%
0.08%
0.07%
13.87%
85.74%
0.31%
0.08%
60.42%
38.11%
1.47%
0.00%

FIG. 5-1

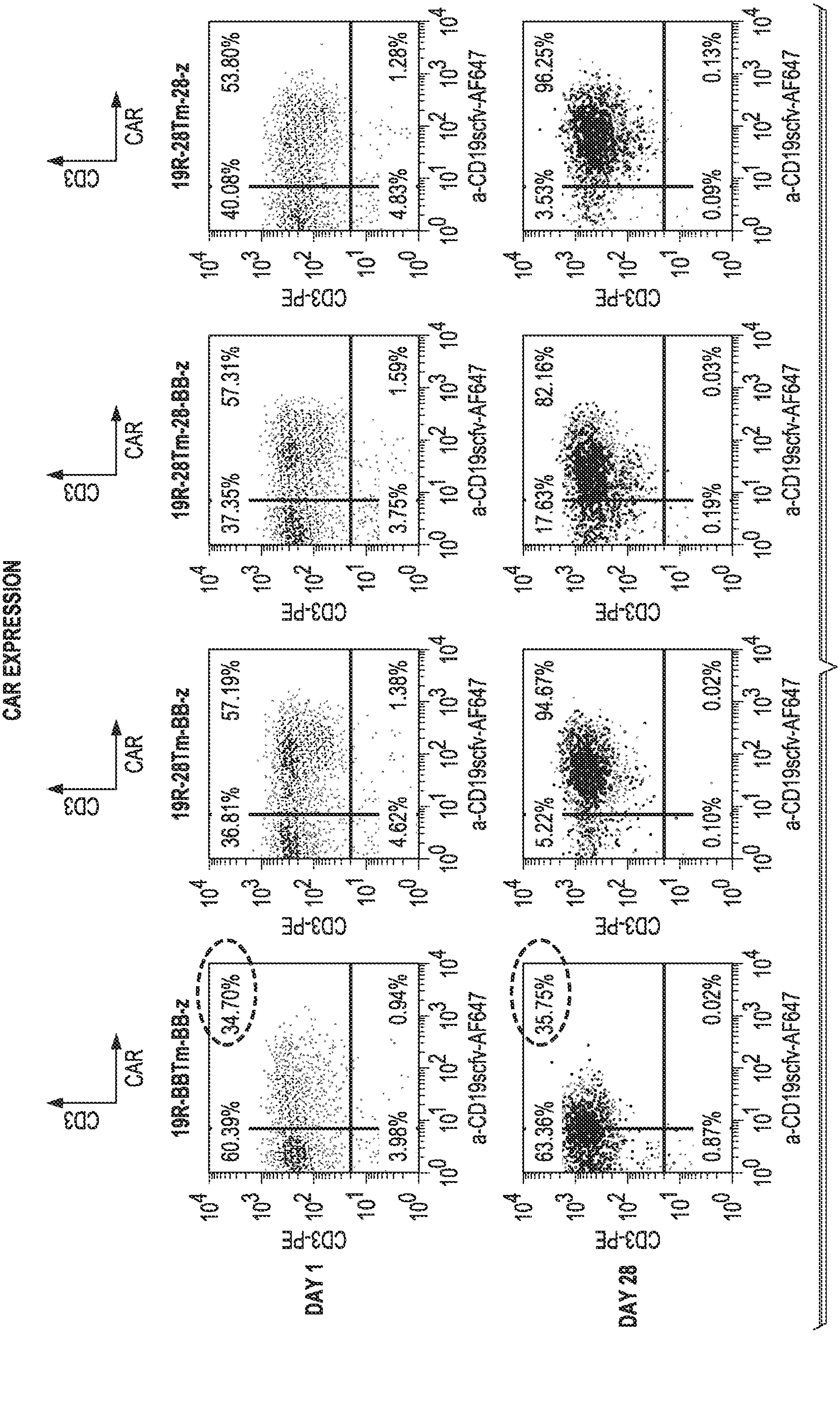

CAR EXPRESSION
DAY 1
DAY 28
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
CD3
CAR
CD3-PE
a-CD19scfv-AF647
60.39%
34.70%
3.98%
0.94%
63.36%
35.75%
0.87%
0.02%
36.81%
57.19%
4.62%
1.38%
5.22%
94.67%
0.10%
0.02%
37.35%
57.31%
3.75%
1.59%
17.63%
82.16%
0.19%
0.03%
40.08%
53.80%
4.83%
1.28%
3.53%
96.25%
0.09%
0.13%

FIG. 5-2

FIG. 6

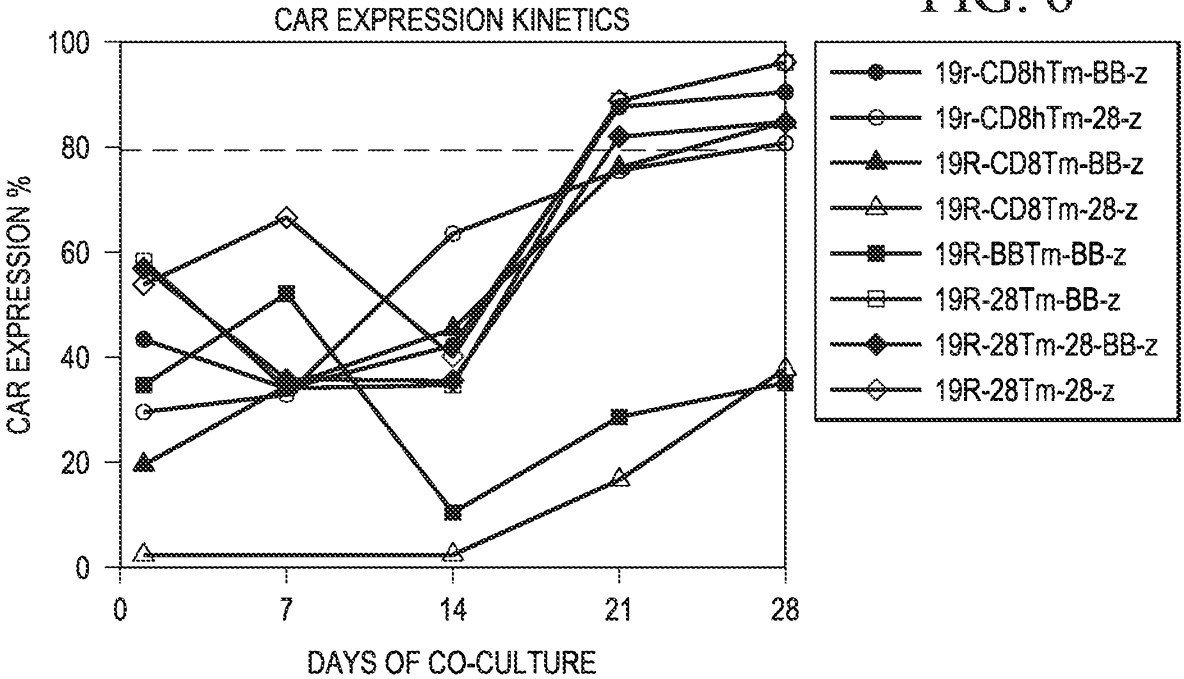
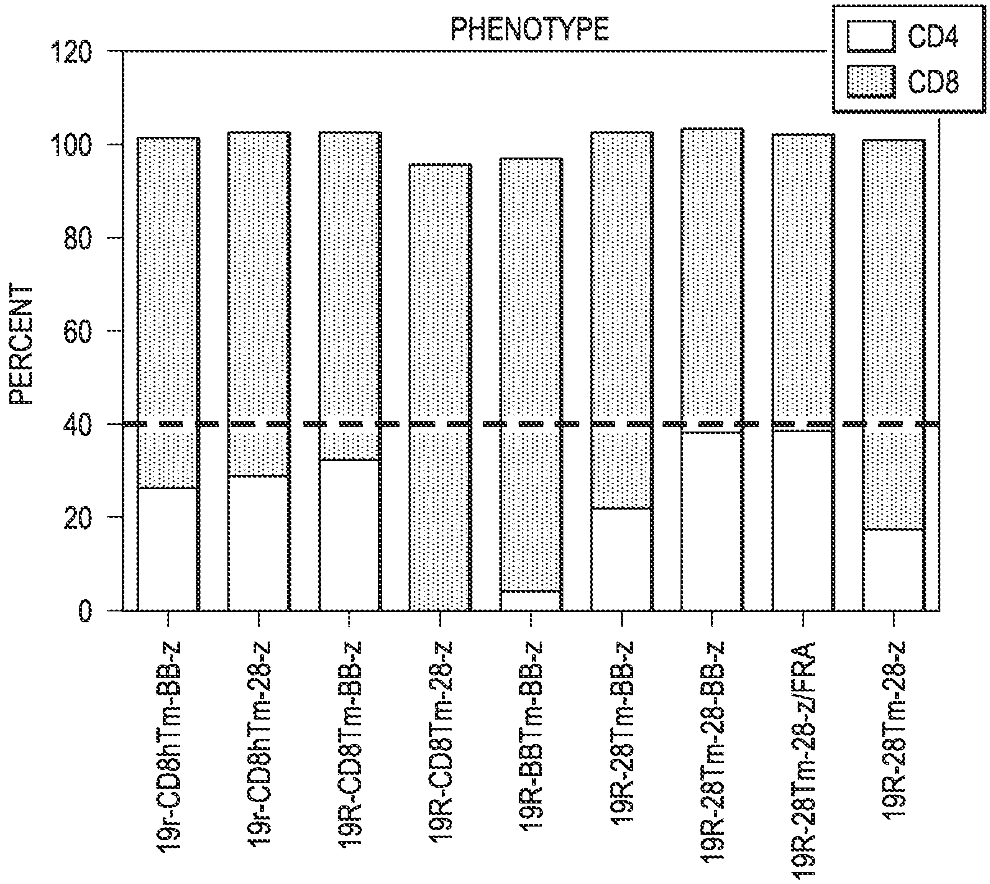

CAR EXPRESSION KINETICS
CAR EXPRESSION %
100
80
60
40
20
0
0
7
14
21
28
DAYS OF CO-CULTURE
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z

FIG. 7


PHENOTYPE
CD4
CD8
PERCENT
120
100
80
60
40
20
0
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z/FRA
19R-28Tm-28-z

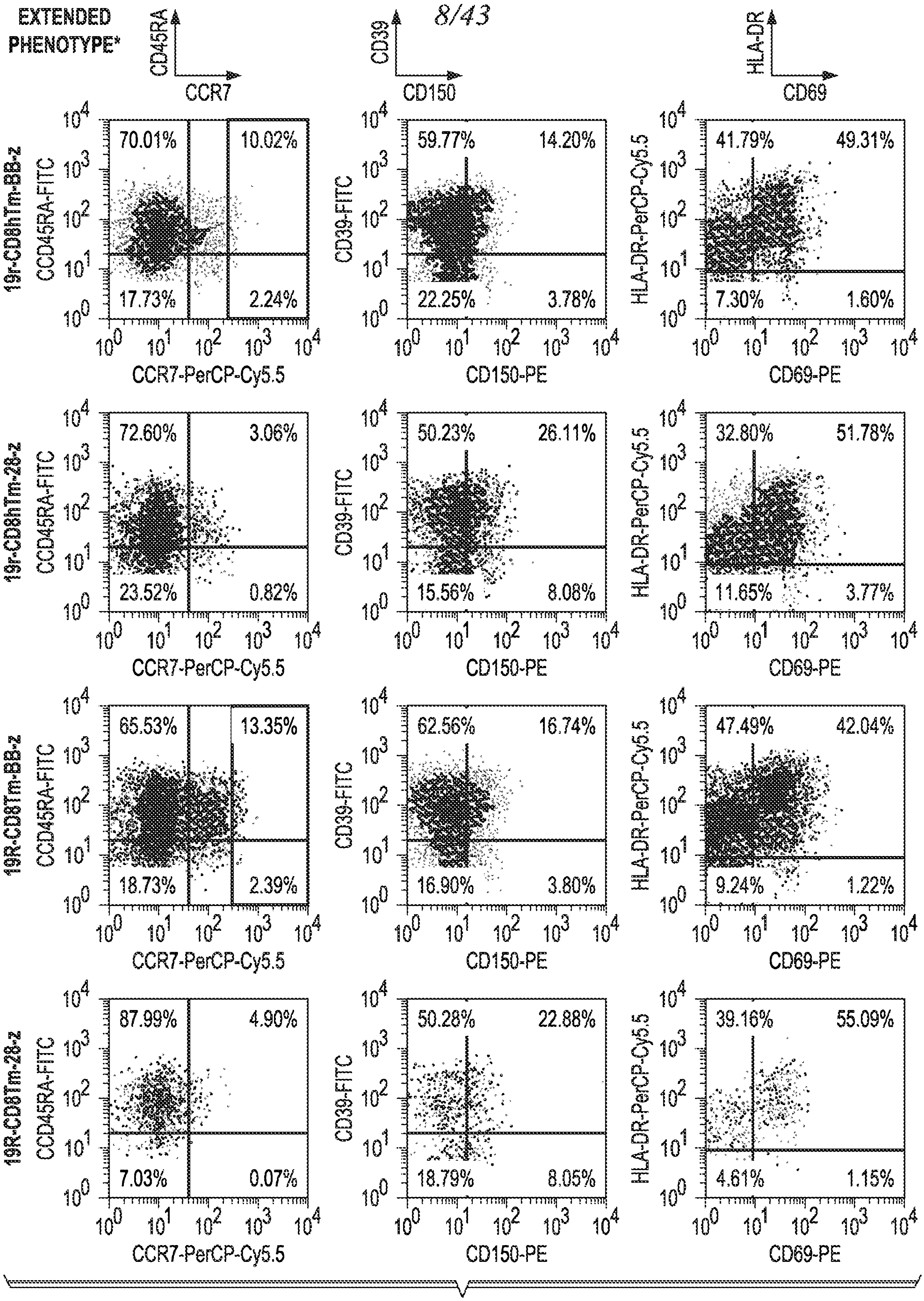

EXTENDED PHENOTYPE*
CD45RA
CCR7
CD39
CD150
HLA-DR
CD69
19r-CD8hTm-BB-z
CCD45RA-FITC
70.01%
10.02%
17.73%
2.24%
CCR7-PerCP-Cy5.5
CD39-FITC
59.77%
14.20%
22.25%
3.78%
CD150-PE
HLA-DR-PerCP-Cy5.5
41.79%
49.31%
7.30%
1.60%
CD69-PE
19r-CD8hTm-28-z
72.60%
3.06%
23.52%
0.82%
50.23%
26.11%
15.56%
8.08%
32.80%
51.78%
11.65%
3.77%
19R-CD8Tm-BB-z
65.53%
13.35%
18.73%
2.39%
62.56%
16.74%
16.90%
3.80%
47.49%
42.04%
9.24%
1.22%
19R-CD8Tm-28-z
87.99%
4.90%
7.03%
0.07%
50.28%
22.88%
18.79%
8.05%
39.16%
55.09%
4.61%
1.15%

FIG. 8A-1

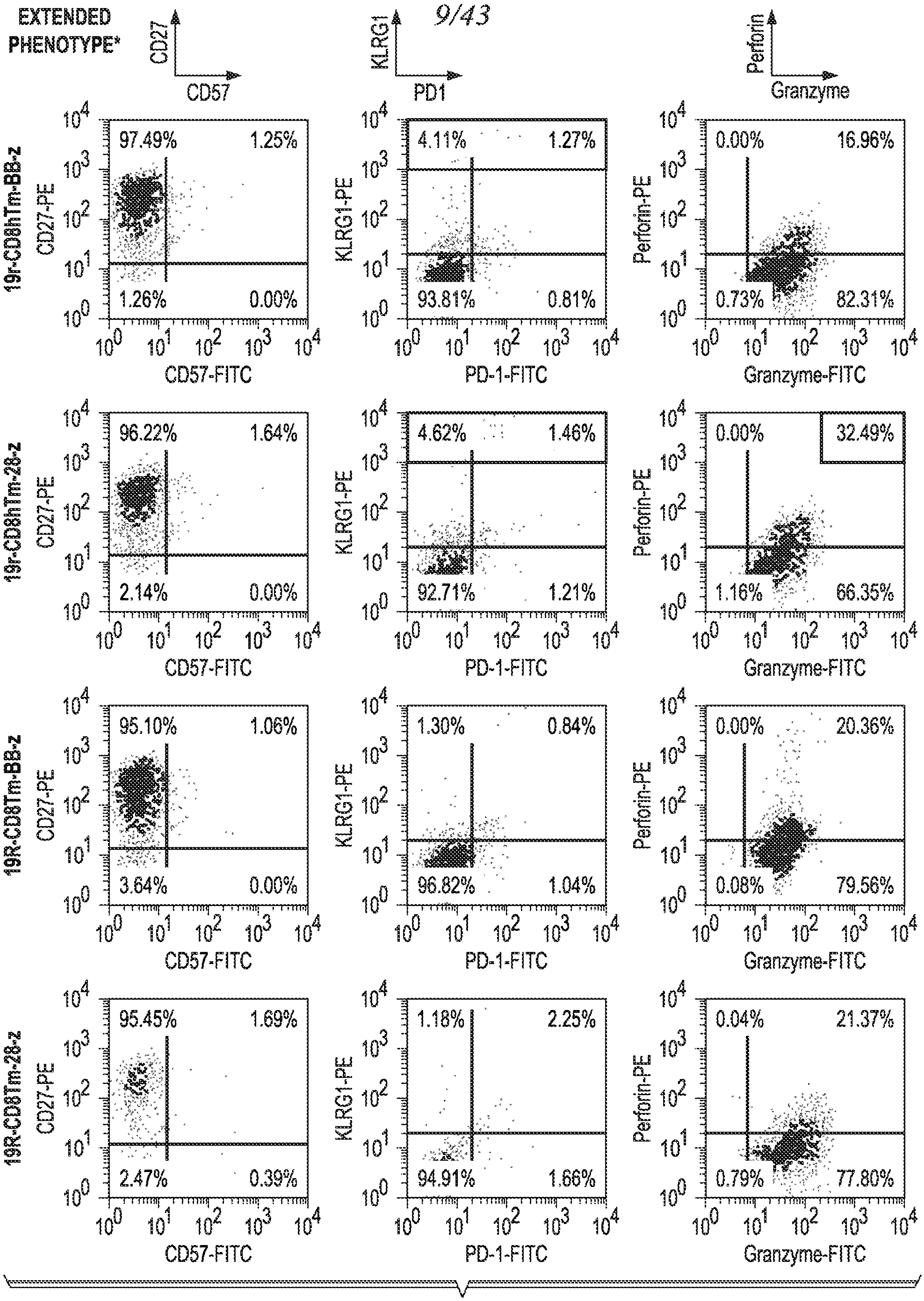

EXTENDED PHENOTYPE*
CD27
CD57
KLRG1
PD1
Perforin
Granzyme
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
CD27-PE
CD57-FITC
KLRG1-PE
PD-1-FITC
Perforin-PE
Granzyme-FITC
97.49%
1.25%
1.26%
0.00%
4.11%
1.27%
93.81%
0.81%
0.00%
16.96%
0.73%
82.31%
96.22%
1.64%
2.14%
0.00%
4.62%
1.46%
92.71%
1.21%
0.00%
32.49%
1.16%
66.35%
95.10%
1.06%
3.64%
0.00%
1.30%
0.84%
96.82%
1.04%
0.00%
20.36%
0.08%
79.56%
95.45%
1.69%
2.47%
0.39%
1.18%
2.25%
94.91%
1.66%
0.04%
21.37%
0.79%
77.80%

FIG. 8A-2

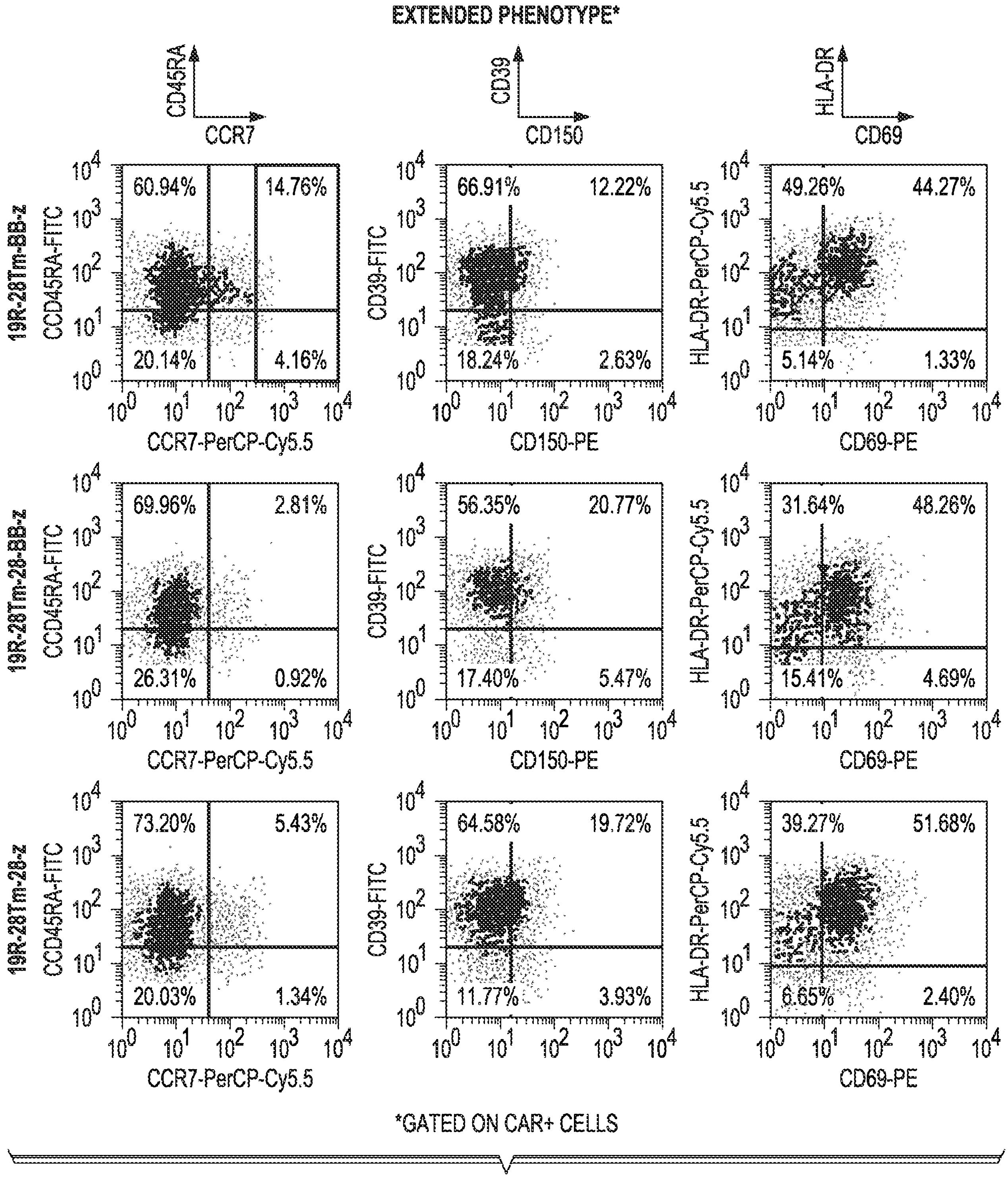

EXTENDED PHENOTYPE*
CD45RA
CCR7
CD39
CD150
HLA-DR
CD69
19R-28Tm-BB-z
CCD45RA-FITC
60.94%
14.76%
20.14%
4.16%
CCR7-PerCP-Cy5.5
CD39-FITC
66.91%
12.22%
18.24%
2.63%
CD150-PE
HLA-DR-PerCP-Cy5.5
49.26%
44.27%
5.14%
1.33%
CD69-PE
19R-28Tm-28-BB-z
CCD45RA-FITC
69.96%
2.81%
26.31%
0.92%
CCR7-PerCP-Cy5.5
CD39-FITC
56.35%
20.77%
17.40%
5.47%
CD150-PE
HLA-DR-PerCP-Cy5.5
31.64%
48.26%
15.41%
4.69%
CD69-PE
19R-28Tm-28-z
CCD45RA-FITC
73.20%
5.43%
20.03%
1.34%
CCR7-PerCP-Cy5.5
CD39-FITC
64.58%
19.72%
11.77%
3.93%
CD150-PE
HLA-DR-PerCP-Cy5.5
39.27%
51.68%
6.65%
2.40%
CD69-PE
*GATED ON CAR+ CELLS

FIG. 8B-1

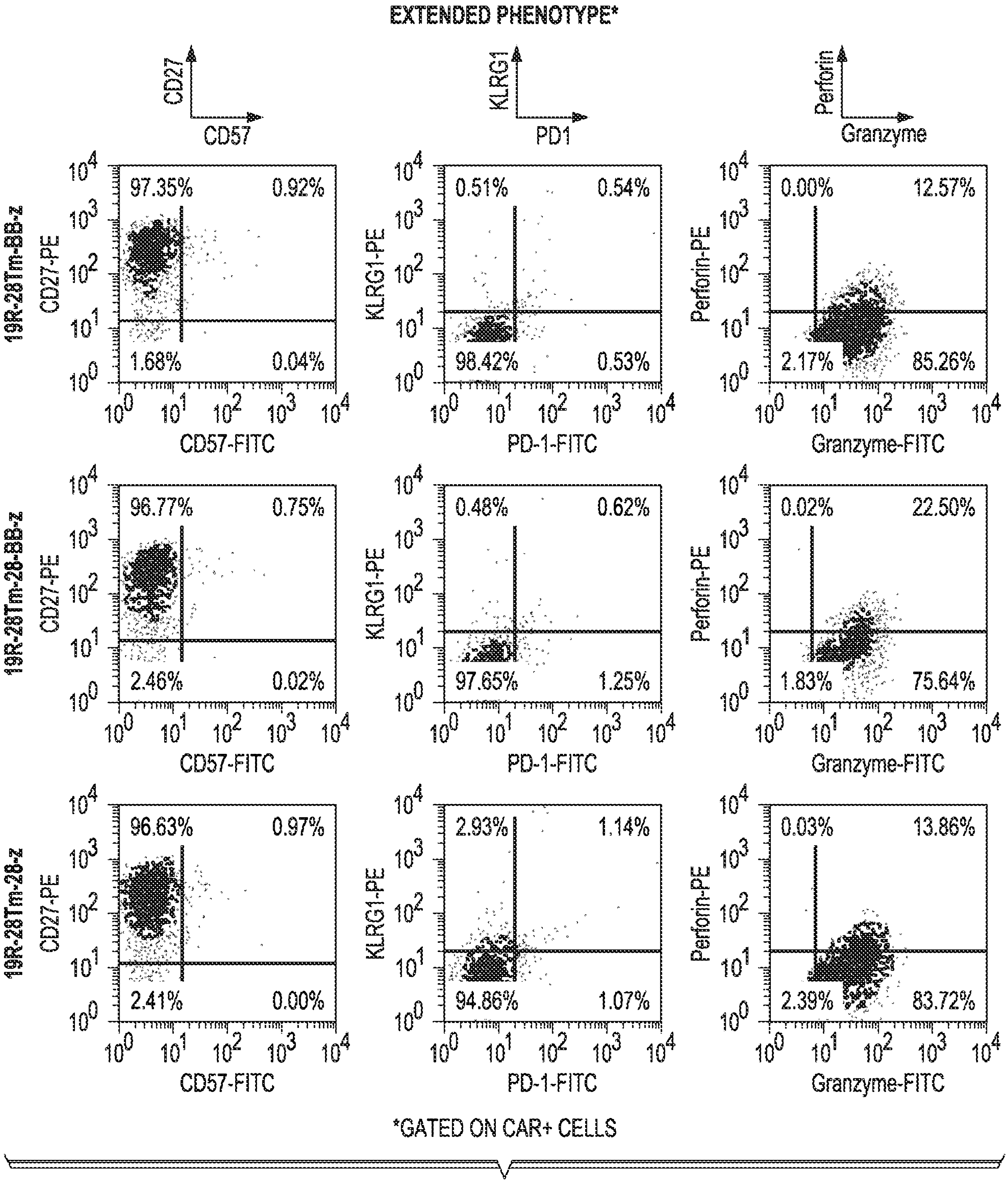

EXTENDED PHENOTYPE*
CD27
CD57
KLRG1
PD1
Perforin
Granzyme
19R-28Tm-BB-z
CD27-PE
97.35%
0.92%
1.68%
0.04%
CD57-FITC
KLRG1-PE
0.51%
0.54%
98.42%
0.53%
PD-1-FITC
Perforin-PE
0.00%
12.57%
2.17%
85.26%
Granzyme-FITC
19R-28Tm-28-BB-z
96.77%
0.75%
2.46%
0.02%
0.48%
0.62%
97.65%
1.25%
0.02%
22.50%
1.83%
75.64%
19R-28Tm-28-z
96.63%
0.97%
2.41%
0.00%
2.93%
1.14%
94.86%
1.07%
0.03%
13.86%
2.39%
83.72%
*GATED ON CAR+ CELLS

FIG. 8B-2

CONSTRUCT	MOLECULAR WT (kDS)	
	EXPTD	OBSD
19R-28Tm-28-z		71.4
19R-28Tm-28-z/FRA	73.1	70.1
19r-CD8hTm-BB-z	52.2	51.4
19r-CD8hTm-28-z	52.1	51.9
19R-CD8Tm-BB-z	73.3	73.5
19R-CD8Tm-28-z	73.2	70.7
19R-BBTm-BB-z	73.3	72.8
19R-28Tm-BB-z	73.2	72.8
19R-28Tm-28-BB-z	78.0	77.9

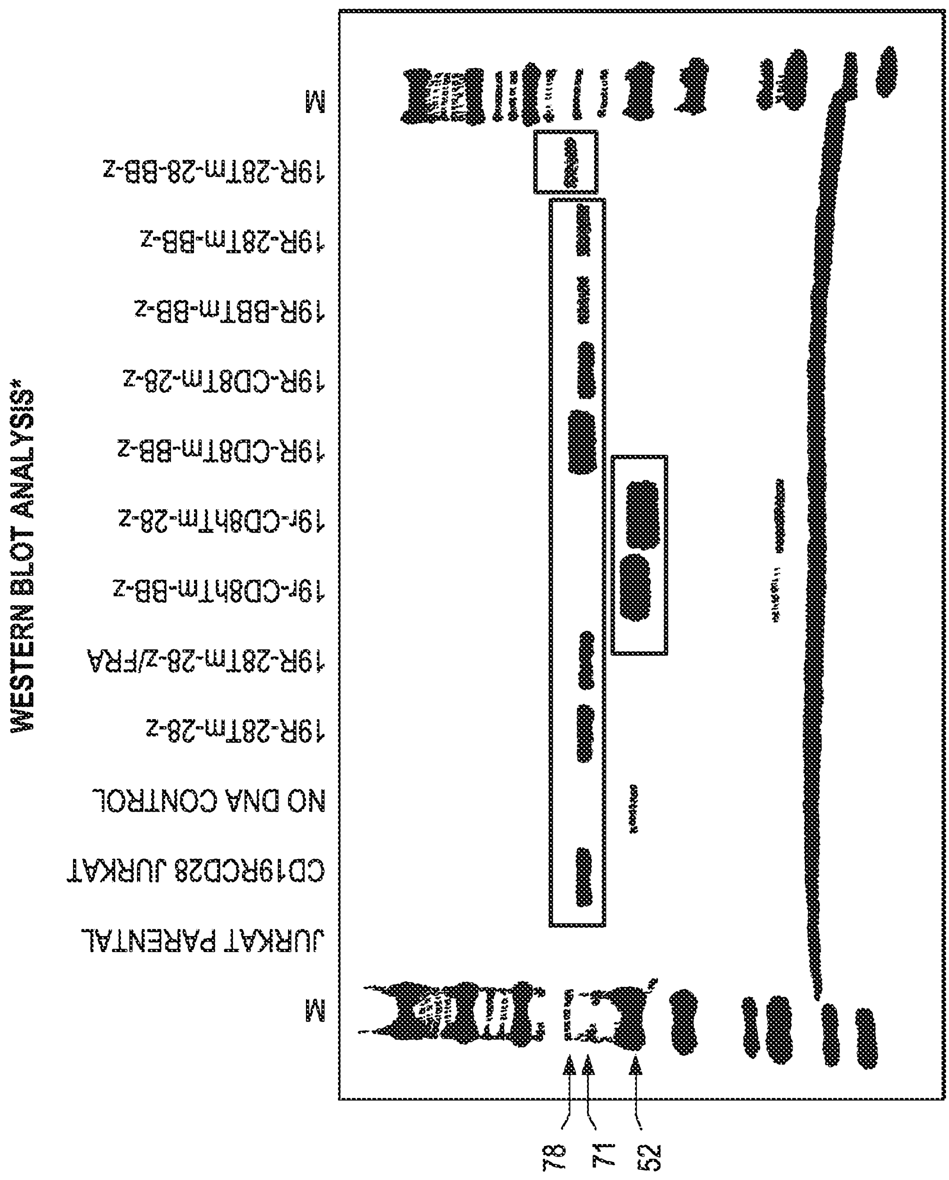
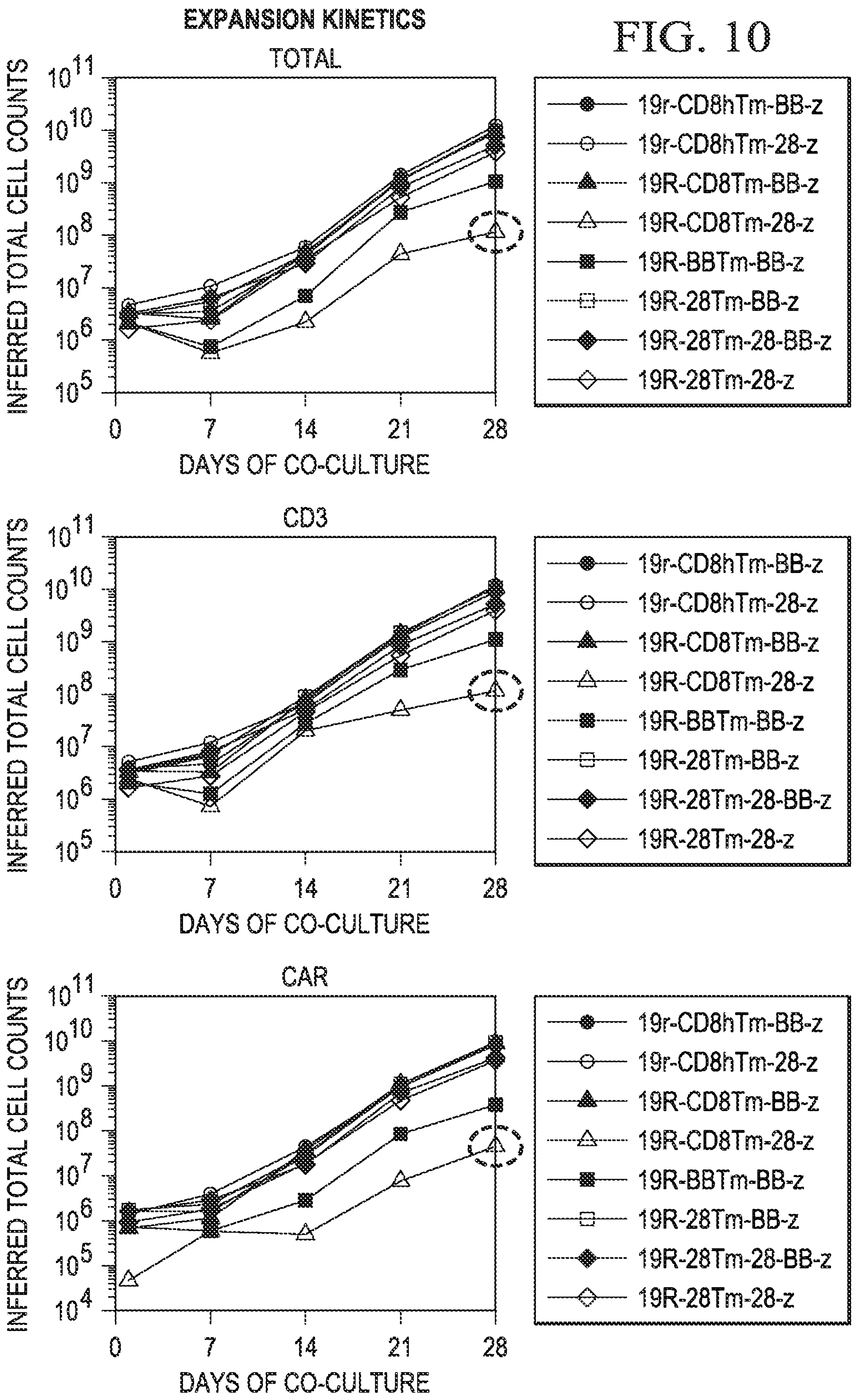


FIG. 9

FIG. 10


EXPANSION KINETICS
TOTAL
CD3
CAR
INFERRED TOTAL CELL COUNTS
DAYS OF CO-CULTURE
0
7
14
21
28
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z

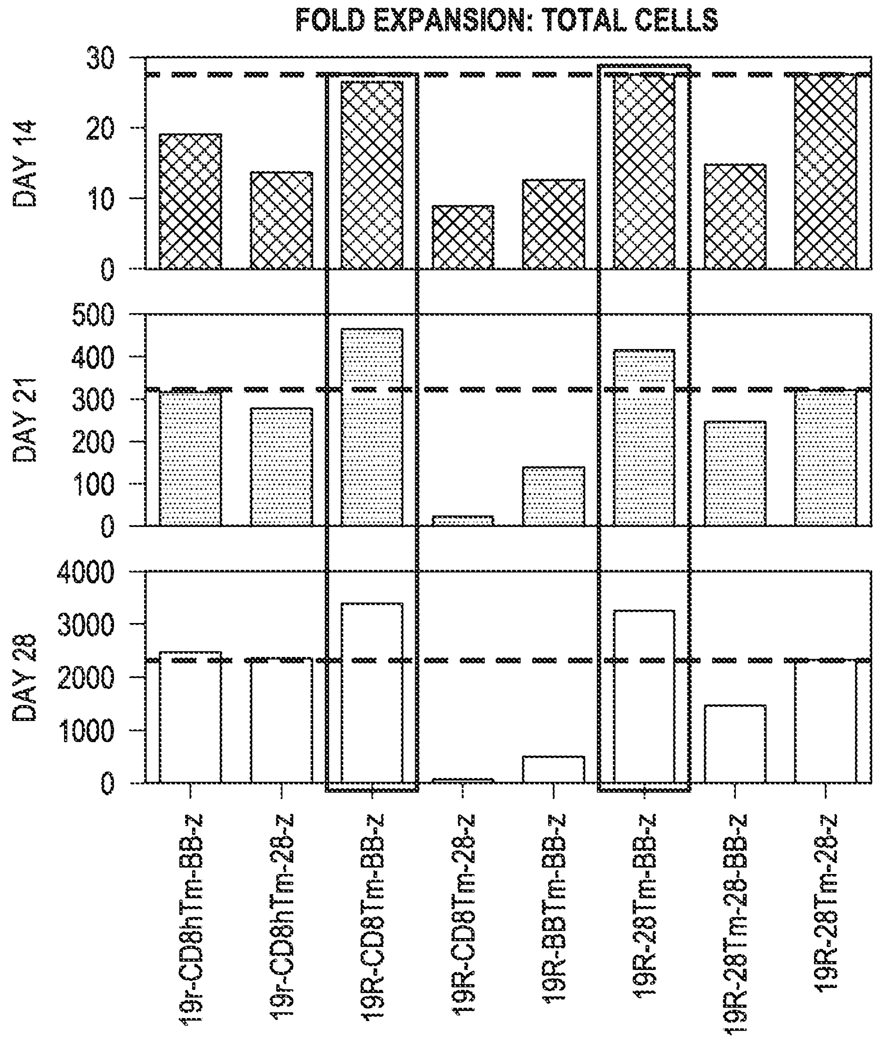

FOLD EXPANSION: TOTAL CELLS
DAY 14
DAY 21
DAY 28
30
20
10
0
500
400
300
200
100
0
4000
3000
2000
1000
0
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z

FIG. 11

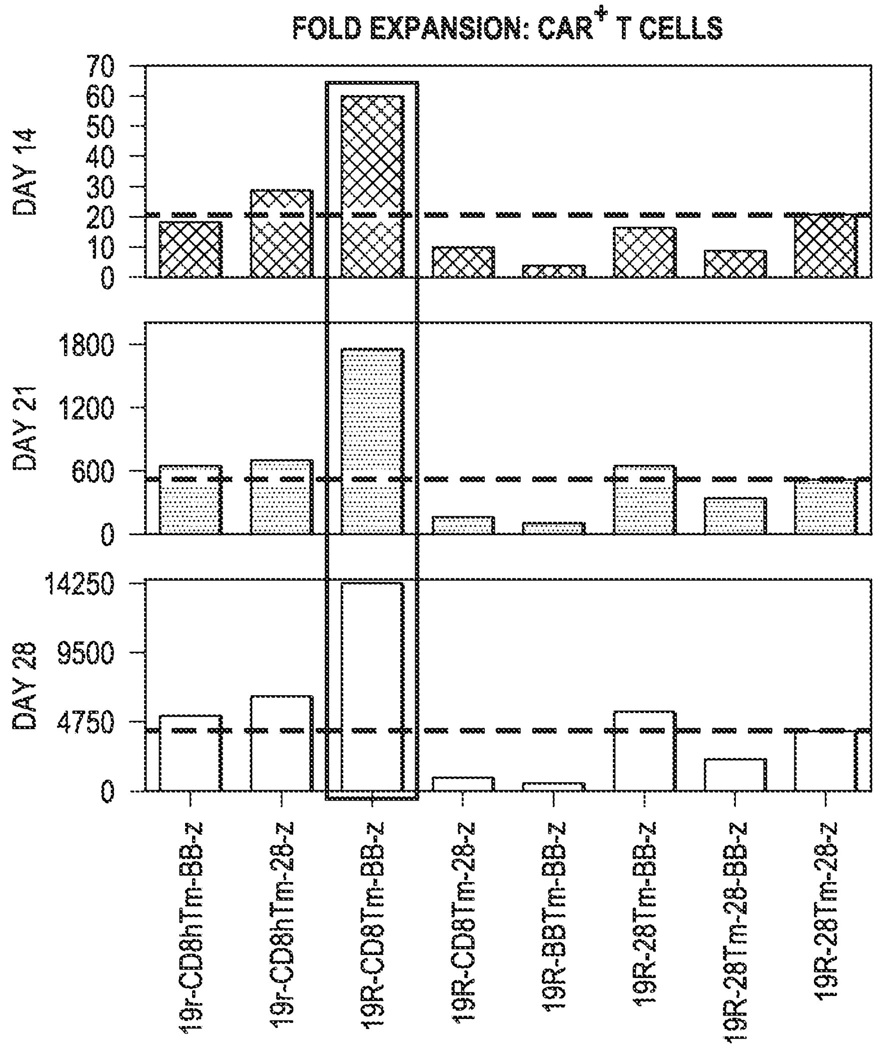
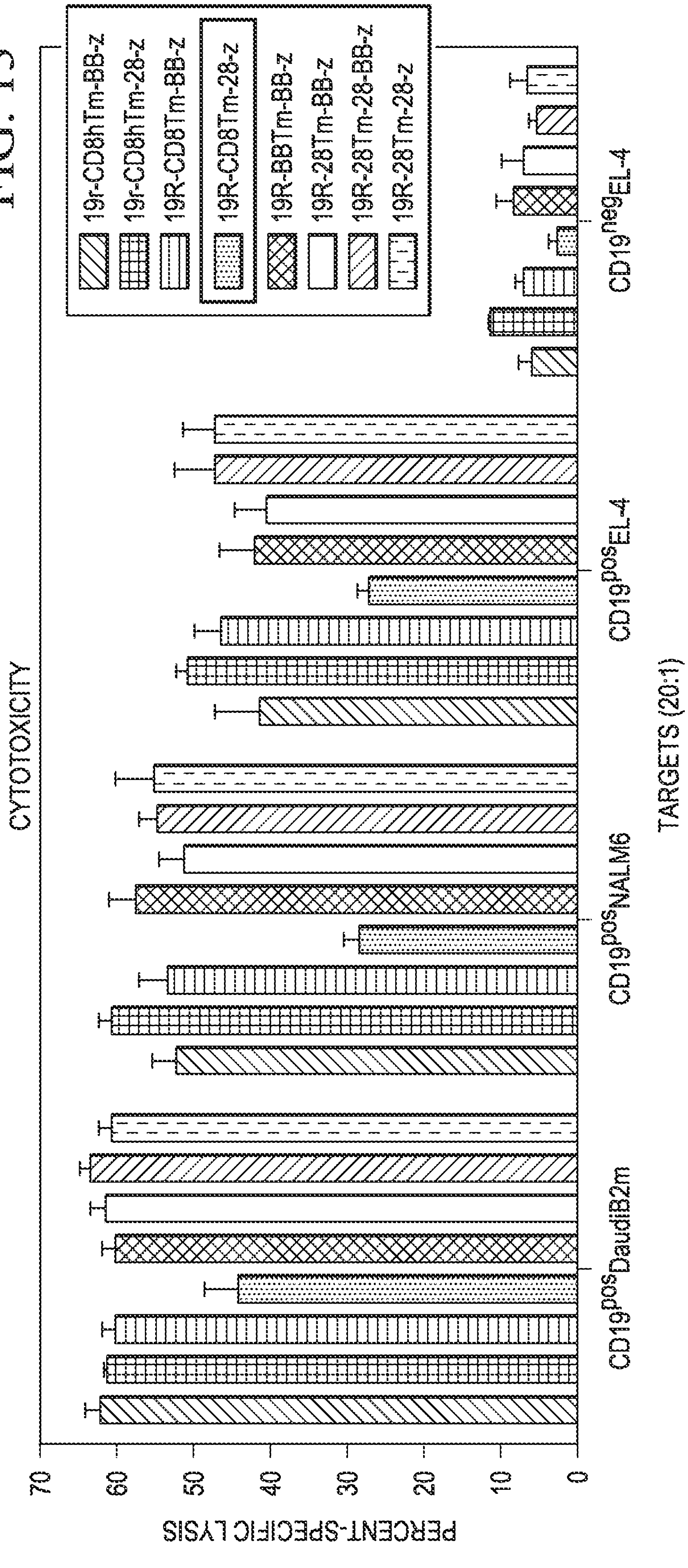

FOLD EXPANSION: CAR+ T CELLS
DAY 14
70
60
50
40
30
20
10
0
DAY 21
1800
1200
600
0
DAY 28
14250
9500
4750
0
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z

FIG. 12

FIG. 13


CYTOTOXICITY
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
PERCENT-SPECIFIC LYSIS
0
10
20
30
40
50
60
70
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)

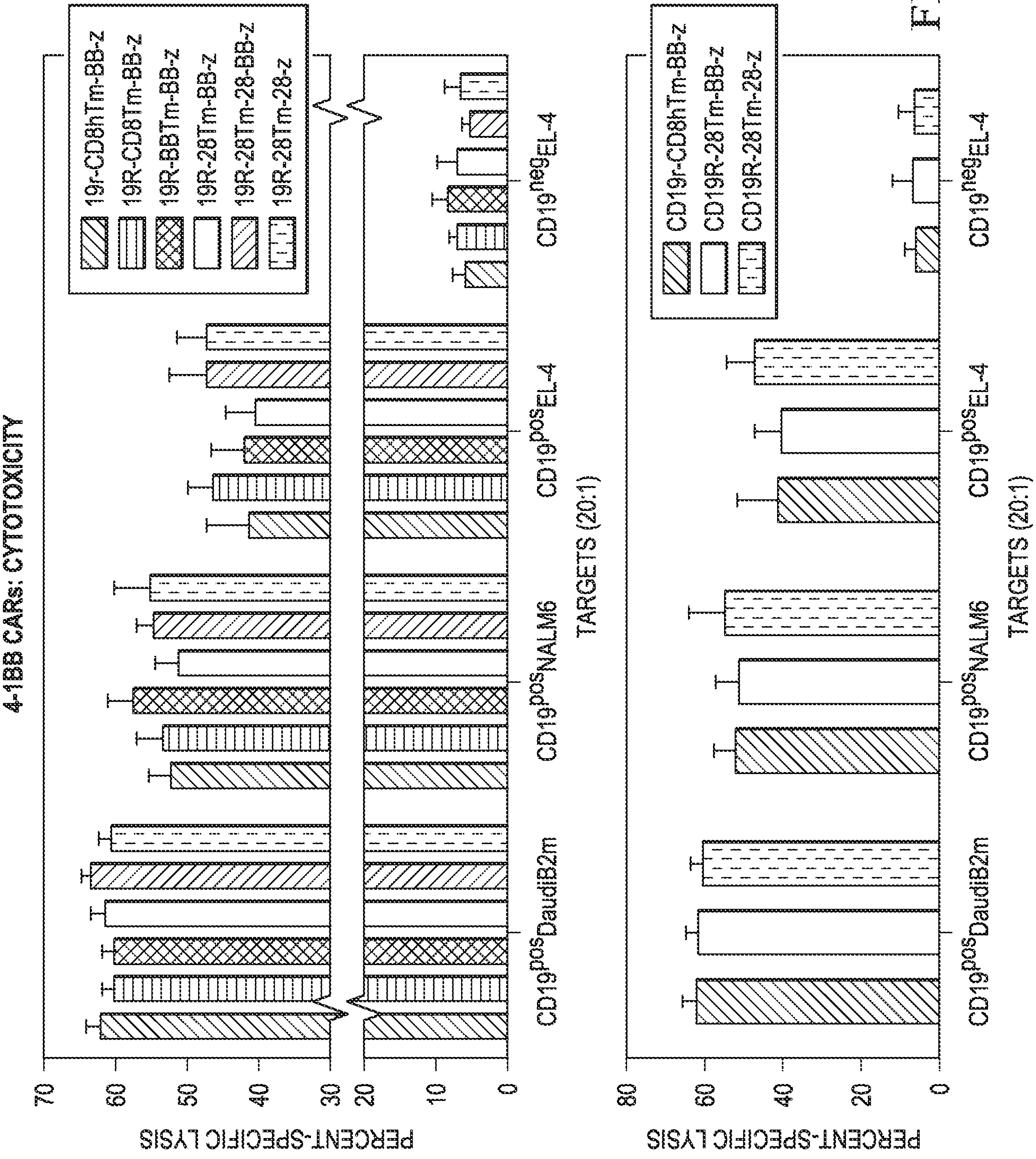

4-1BB CARs; CYTOTOXICITY
PERCENT-SPECIFIC LYSIS
70
60
50
40
30
20
10
0
19r-CD8hTm-BB-z
19R-CD8Tm-BB-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)
PERCENT-SPECIFIC LYSIS
80
60
40
20
0
CD19r-CD8hTm-BB-z
CD19R-28Tm-BB-z
CD19R-28Tm-28-z
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)

FIG. 14

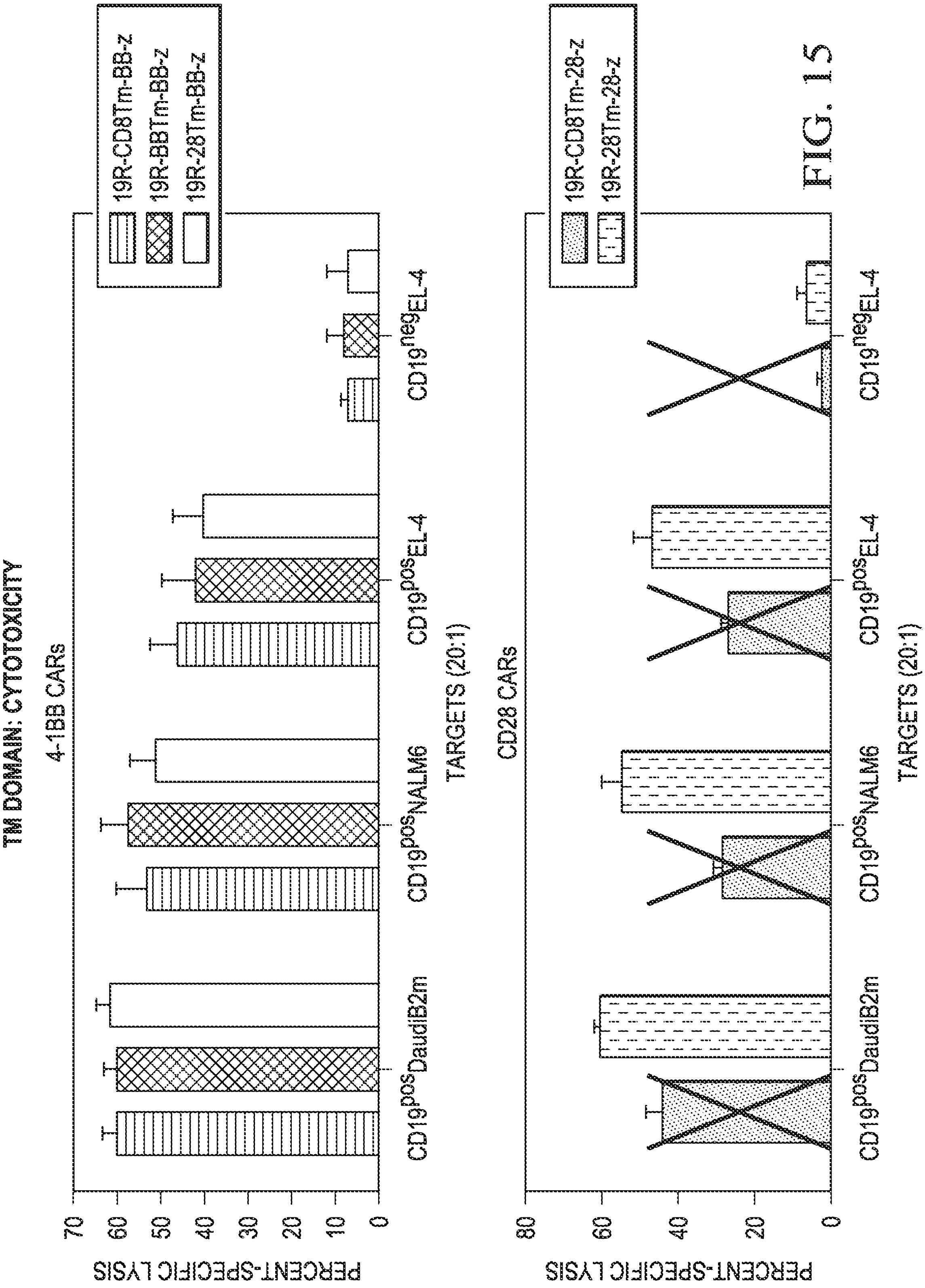

TM DOMAIN: CYTOTOXICITY
4-1BB CARs
19R-CD8Tm-BB-z
19R-BBTm-BB-z
19R-28Tm-BB-z
PERCENT-SPECIFIC LYSIS
70
60
50
40
30
20
10
0
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)
CD28 CARs
19R-CD8Tm-28-z
19R-28Tm-28-z
PERCENT-SPECIFIC LYSIS
80
60
40
20
0
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)

FIG. 15

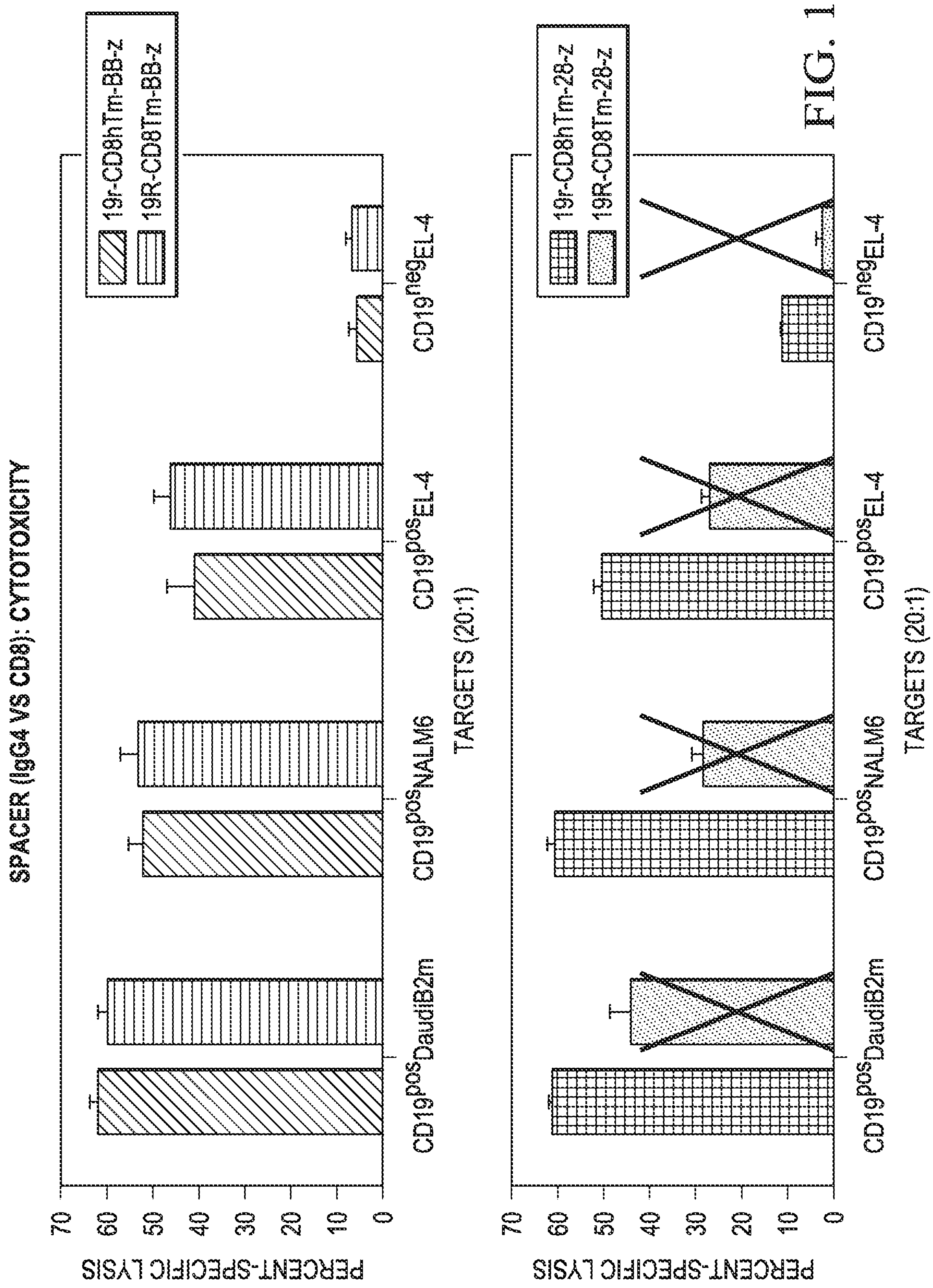

SPACER (IgG4 VS CD8): CYTOTOXICITY
19r-CD8hTm-BB-z
19R-CD8Tm-BB-z
PERCENT-SPECIFIC LYSIS
70
60
50
40
30
20
10
0
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)
19r-CD8hTm-28-z
19R-CD8Tm-28-z
PERCENT-SPECIFIC LYSIS
70
60
50
40
30
20
10
0
CD19posDaudiB2m
CD19posNALM6
CD19posEL-4
CD19negEL-4
TARGETS (20:1)

FIG. 16

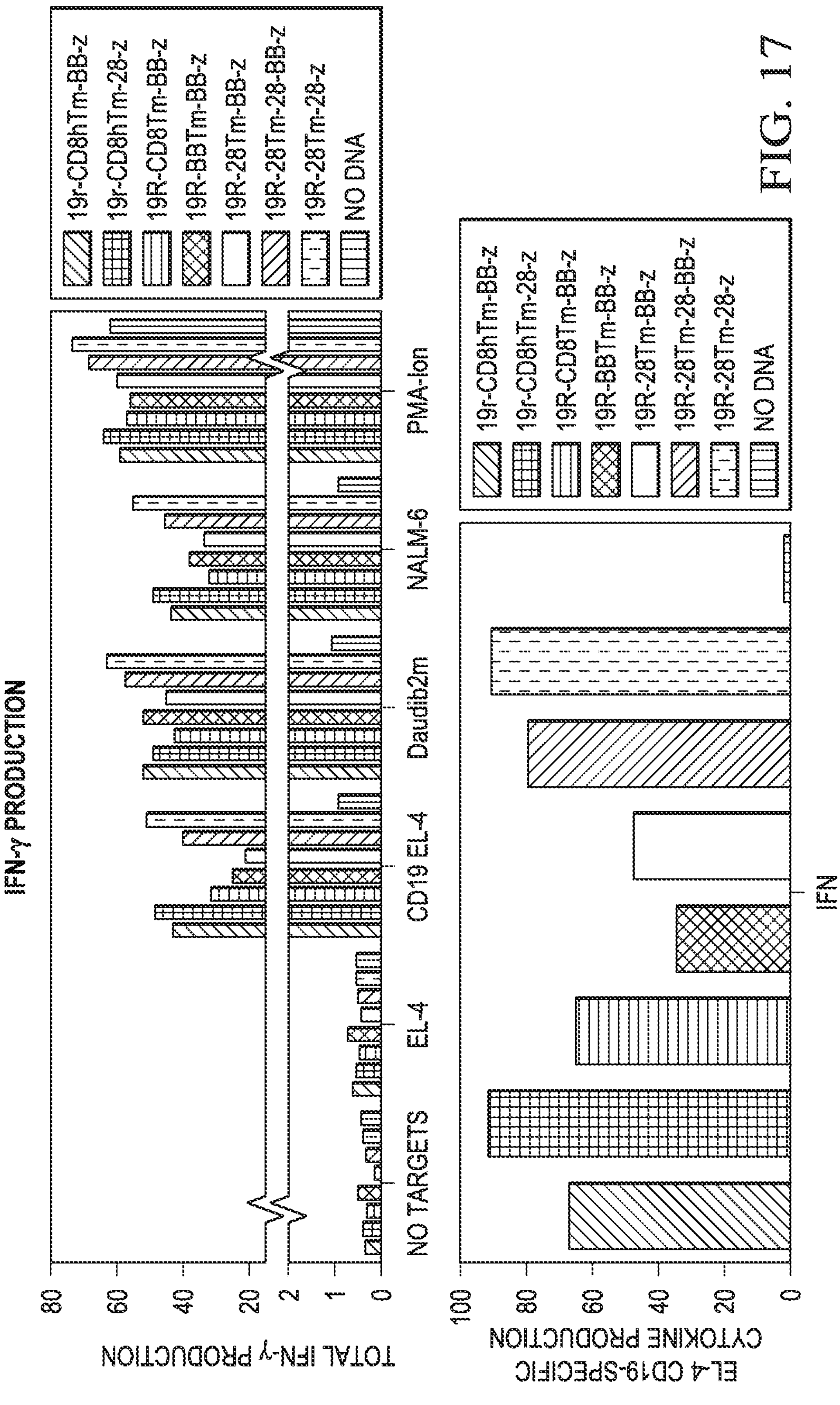

IFN-γ PRODUCTION
TOTAL IFN-γ PRODUCTION
80
60
40
20
2
1
0
NO TARGETS
EL-4
CD19 EL-4
Daudib2m
NALM-6
PMA-Ion
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
NO DNA
EL-4 CD19-SPECIFIC CYTOKINE PRODUCTION
100
80
60
40
20
0
IFN

FIG. 17

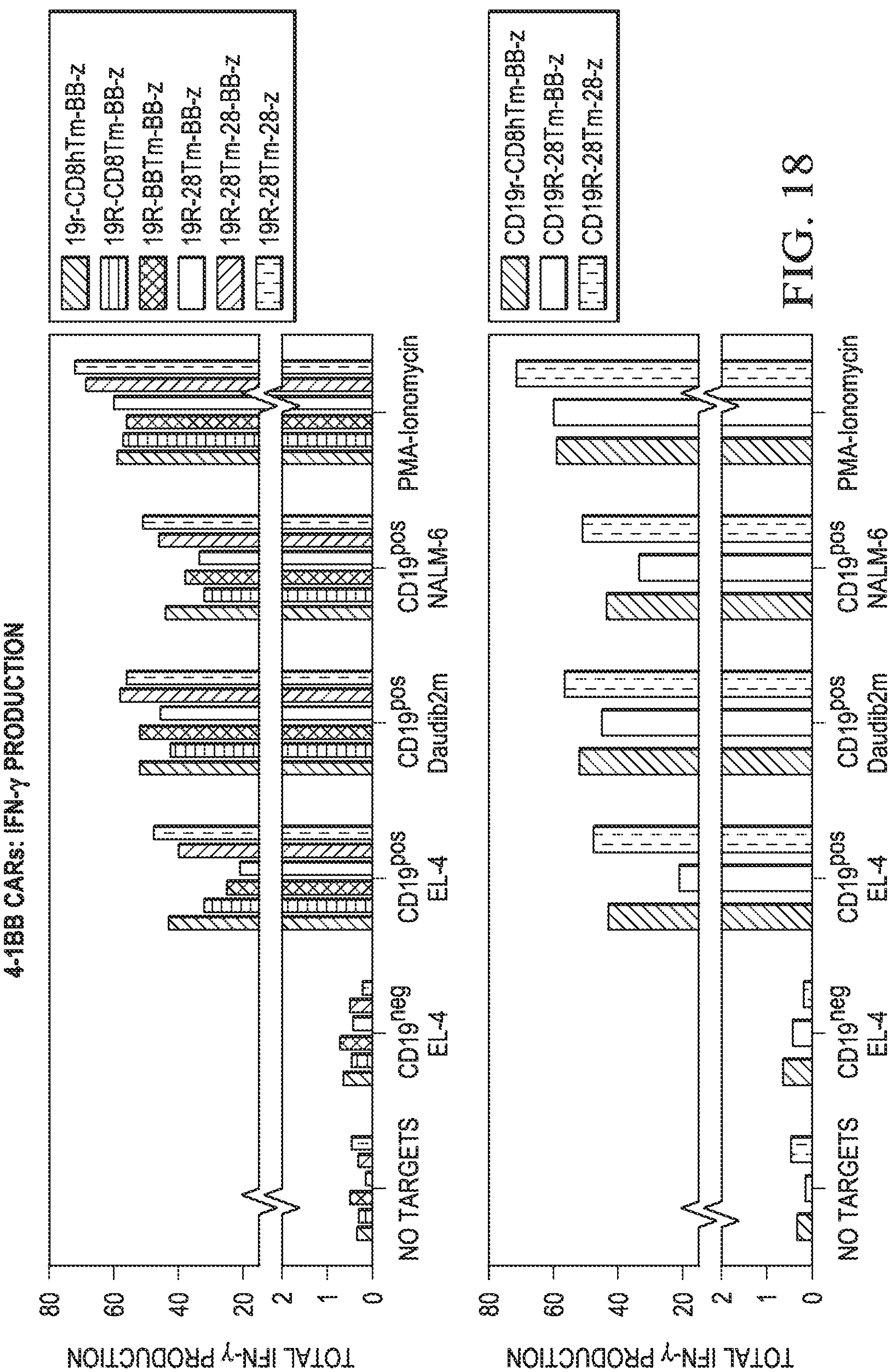

4-1BB CARs: IFN-γ PRODUCTION
TOTAL IFN-γ PRODUCTION
80
60
40
20
2
1
0
NO TARGETS
CD19neg EL-4
CD19pos EL-4
CD19pos Daudib2m
CD19pos NALM-6
PMA-Ionomycin
19r-CD8hTm-BB-z
19R-CD8Tm-BB-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
CD19r-CD8hTm-BB-z
CD19R-28Tm-BB-z
CD19R-28Tm-28-z

FIG. 18

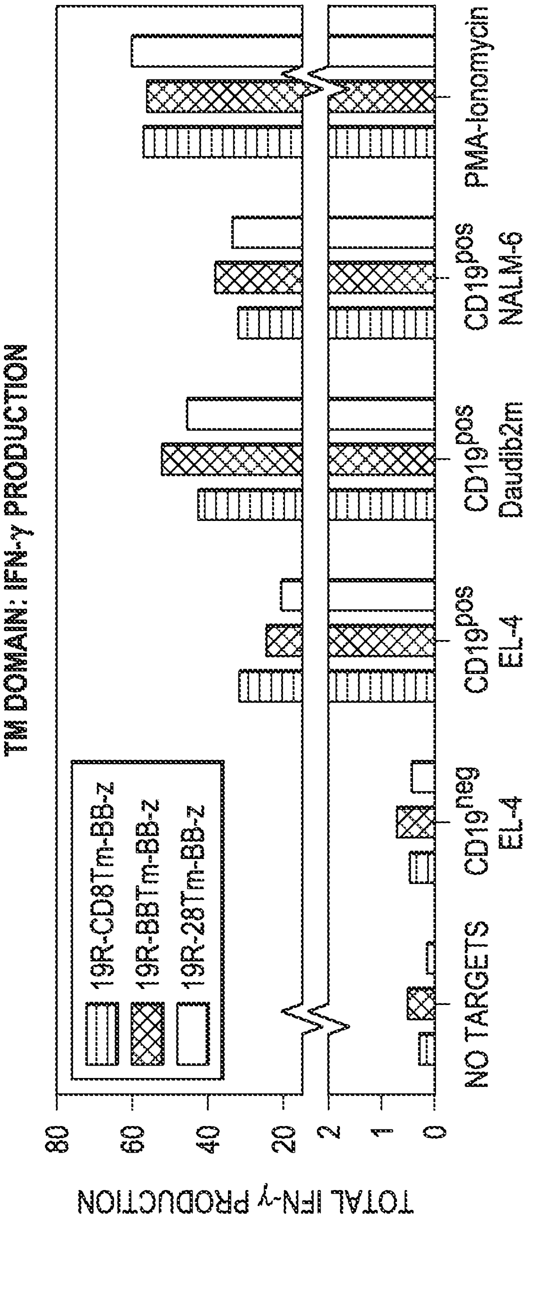

TM DOMAIN: IFN-γ PRODUCTION
TOTAL IFN-γ PRODUCTION
80
60
40
20
2
1
0
19R-CD8Tm-BB-z
19R-BBTm-BB-z
19R-28Tm-BB-z
NO TARGETS
CD19neg EL-4
CD19pos EL-4
CD19pos Daudib2m
CD19pos NALM-6
PMA-Ionomycin

FIG. 19

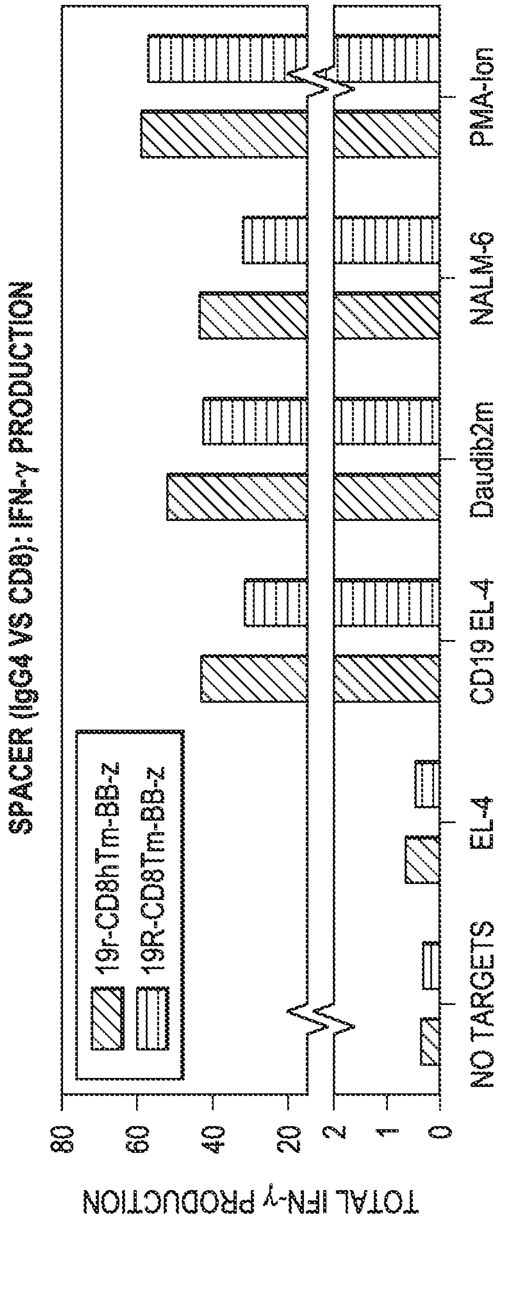
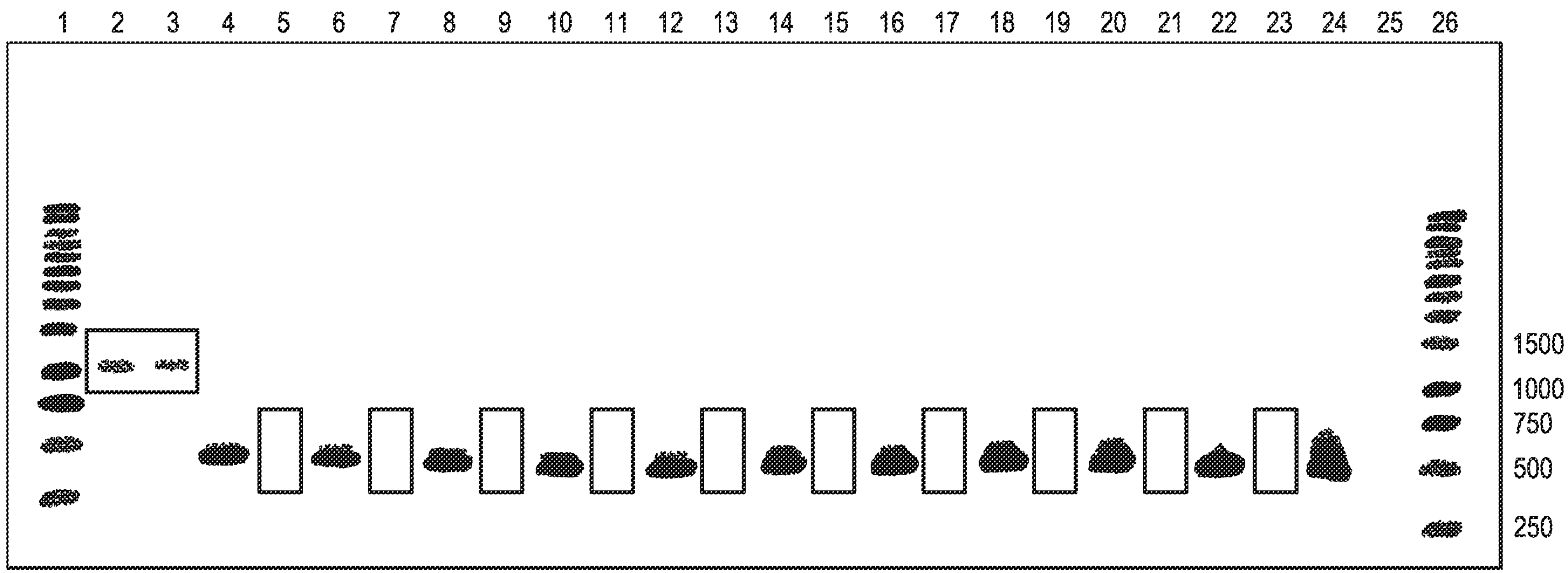

SPACER (IgG4 VS CD8): IFN-γ PRODUCTION
TOTAL IFN-γ PRODUCTION
80
60
40
20
2
1
0
19r-CD8hTm-BB-z
19R-CD8Tm-BB-z
NO TARGETS
EL-4
CD19 EL-4
Daudib2m
NALM-6
PMA-Ion

FIG. 20

FIG. 21

SAFETY: SB11 PCR*



1,26 = 1kb LADDER
25 = BLANK

SB11 PRIMERS

2 = SB11-IRES2-EGFP PLASMID
3 = JURKAT/SB11-IRES2-EGFP
5 = NO DNA
7 = 217
9 = 215
11 = 213
13 = 218
15 = 214
17 = CAR
19 = 193
21 = 216
23 = 212

GAPDH PRIMERS

4 = JURKAT/SB11-IRES2-EGFP
6 = NO DNA
8 = 217
10 = 215
12 = 213
14 = 218
16 = 214
18 = CAR
20 = 193
22 = 216
24 = 212

FIG. 22

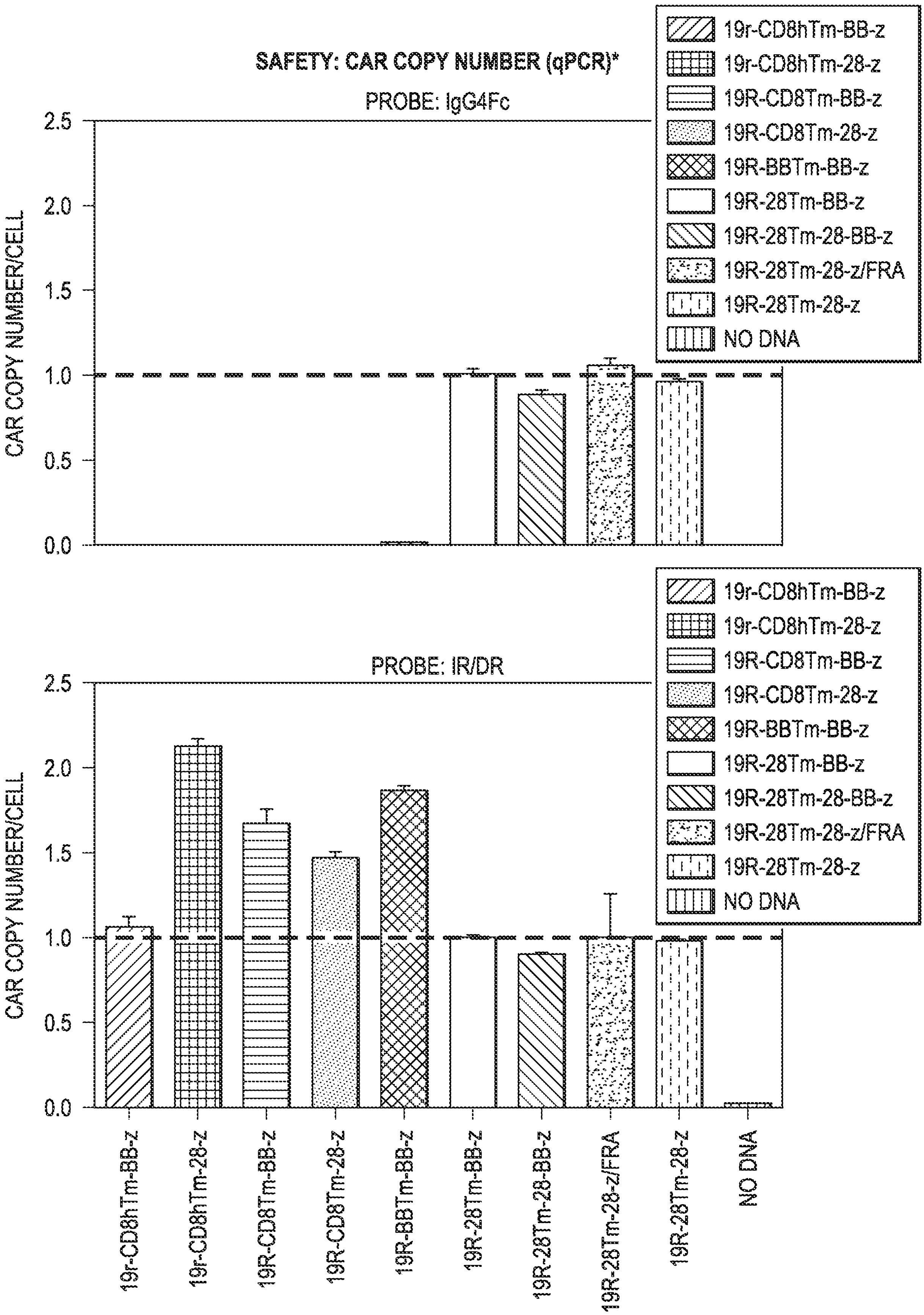
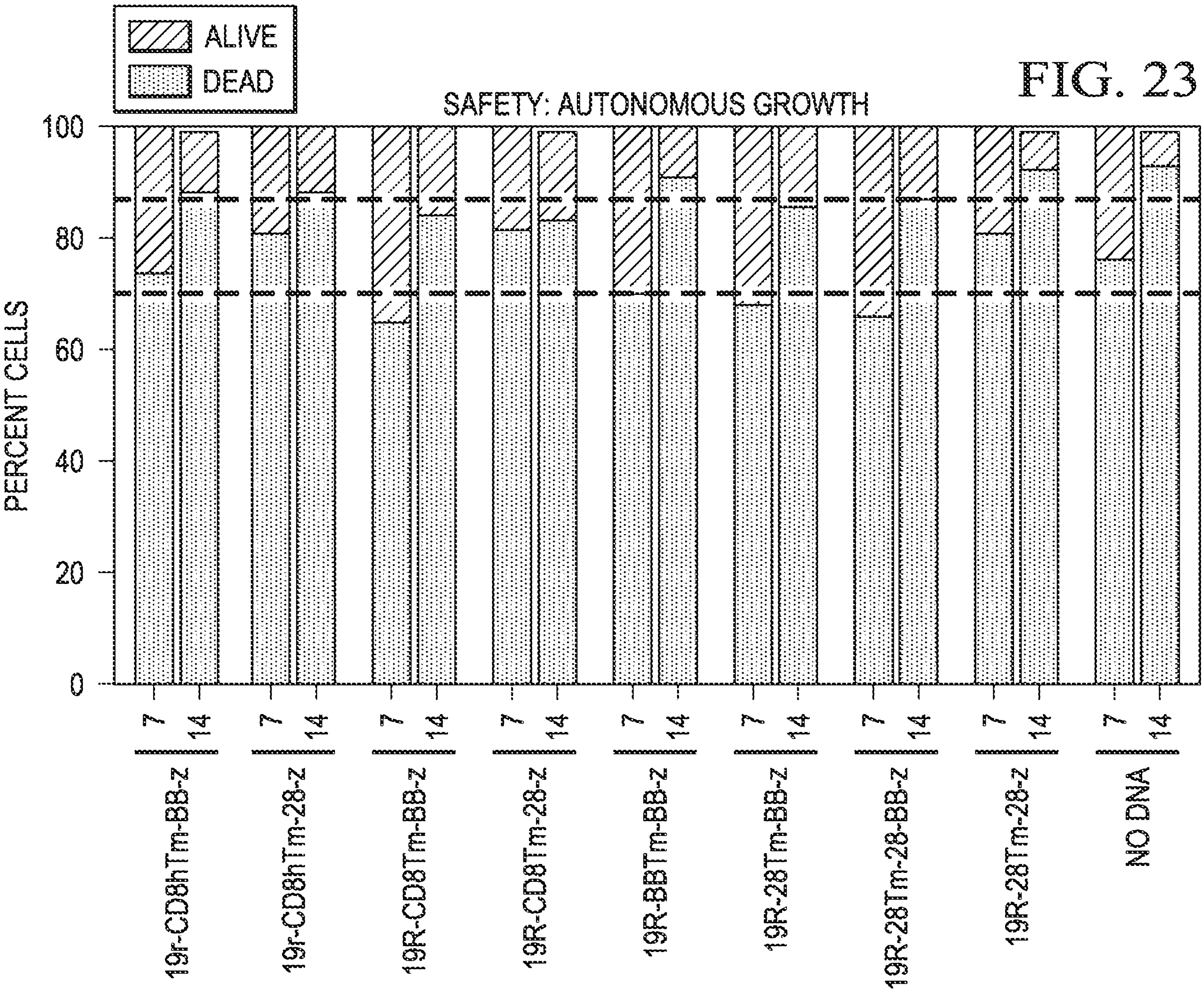

SAFETY: CAR COPY NUMBER (qPCR)*
PROBE: IgG4Fc
CAR COPY NUMBER/CELL
2.5
2.0
1.5
1.0
0.5
0.0
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z/FRA
19R-28Tm-28-z
NO DNA
PROBE: IR/DR
CAR COPY NUMBER/CELL
2.5
2.0
1.5
1.0
0.5
0.0
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z/FRA
19R-28Tm-28-z
NO DNA

FIG. 23


ALIVE
DEAD
SAFETY: AUTONOMOUS GROWTH
PERCENT CELLS
100
80
60
40
20
0
7
14
19r-CD8hTm-BB-z
19r-CD8hTm-28-z
19R-CD8Tm-BB-z
19R-CD8Tm-28-z
19R-BBTm-BB-z
19R-28Tm-BB-z
19R-28Tm-28-BB-z
19R-28Tm-28-z
NO DNA

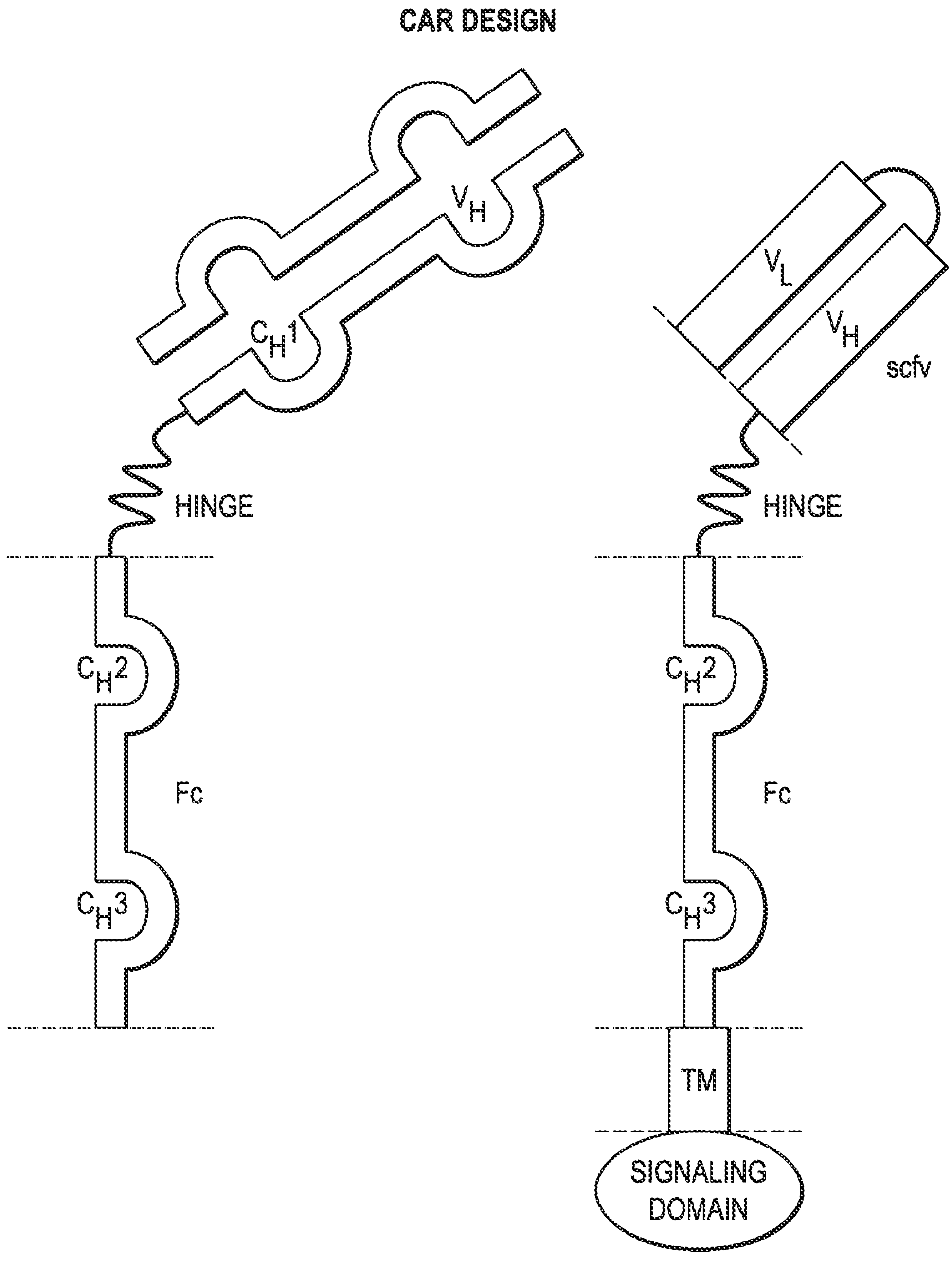

CAR DESIGN
VH
CH1
HINGE
CH2
Fc
CH3
VL
VH
scfv
HINGE
CH2
Fc
CH3
TM
SIGNALING DOMAIN

FIG. 24

CD3ζ

HOMO SAPIENS CD247 MOLECULE (CD247), TRANSCRIPT VARIANT 1, mRNA
NCBI REFERENCE SEQUENCE: NM_198053.2

```
Query   1  RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP-RRKNPQEGLY  59
Sbjct      RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPQRRKNPQEGLY

Query  60  NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR  112
Sbjct      NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA
```

T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN ISOFORM 1 PRECURSOR [HOMO SAPIENS]
NCBI REFERENCE SEQUENCE: NP_932170.1

```
Query   1  RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP-RRKNPQEGLY  59
Sbjct  52  RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPQRRKNPQEGLY  111

Query  60  NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR  112
Sbjct 112  NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR  164
```

T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN ISOFORM 2 PRECURSOR [HOMO SAPIENS]
NCBI REFERENCE SEQUENCE: NP_000725.1

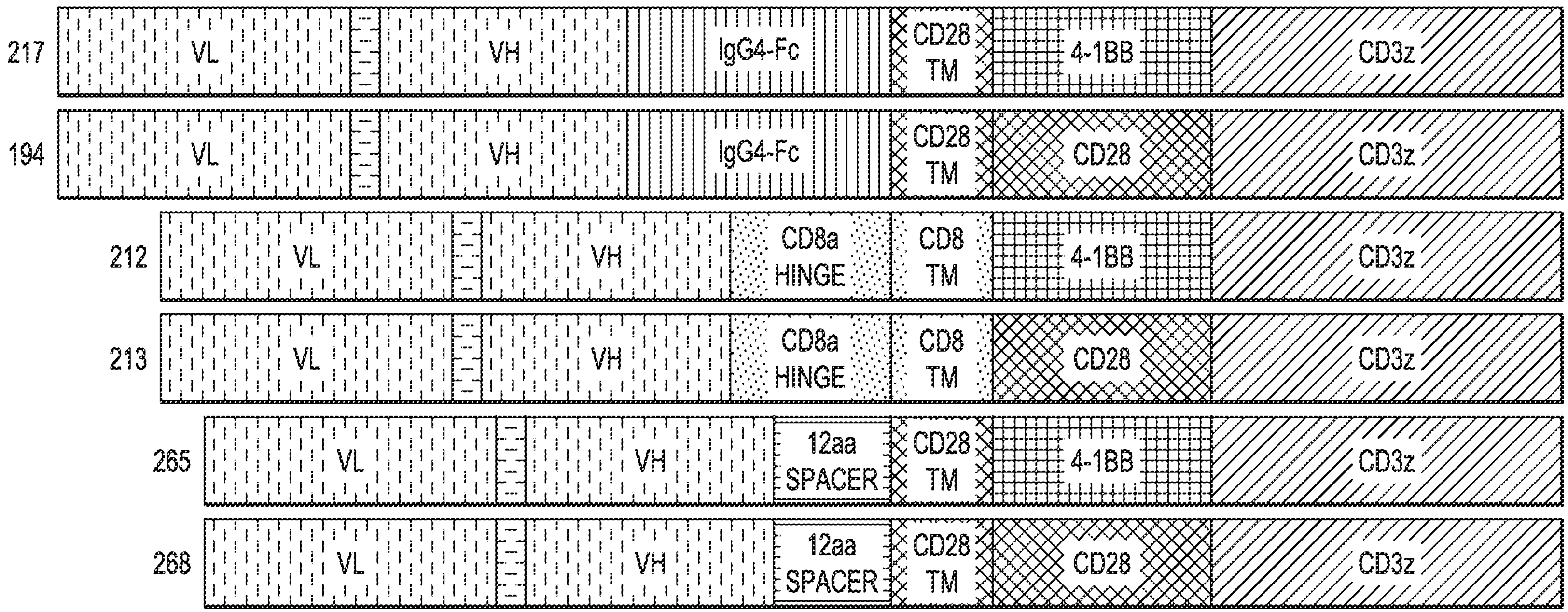
```
                     ITAM1                                ITAM2
Query   1  RVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGK PRRKNPQEGLYN  60
Sbjct  52  RVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGK PRRKNPQEGLYN  111

                                      ITAM3
Query  61  ELQKDKMAEAYSEIGM KG ERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR  112
Sbjct 112  ELQKDKMAEAYSEIGM KG ERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR  163
```

FIG. 25

FIG. 26

CARs*



ESKYGPPCPPCP = IgG4 Fc HINGE = 12aa SPACER

FIG. 27

CARs

CAR →	COOPER	
SPACER	CD28	CD137
Fc (230aa)	194	217
CD8 (47aa)	213	212
SHORT (12aa)	265	268
CD3ζ	WT	WT

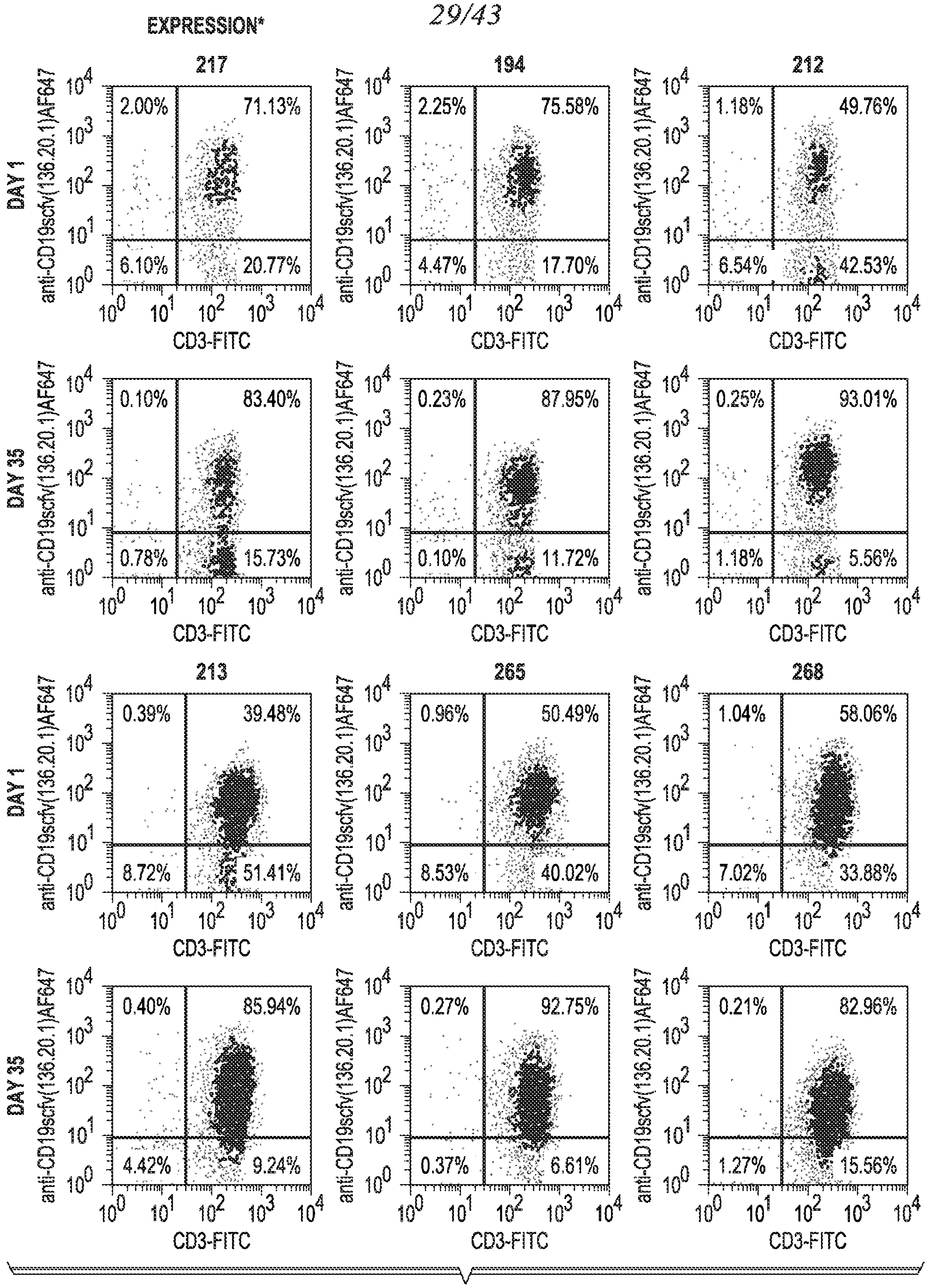

EXPRESSION*
217
194
212
DAY 1
DAY 35
213
265
268
DAY 1
DAY 35
anti-CD19scfv(136.20.1)AF647
CD3-FITC
2.00% 71.13% 6.10% 20.77%
2.25% 75.58% 4.47% 17.70%
1.18% 49.76% 6.54% 42.53%
0.10% 83.40% 0.78% 15.73%
0.23% 87.95% 0.10% 11.72%
0.25% 93.01% 1.18% 5.56%
0.39% 39.48% 8.72% 51.41%
0.96% 50.49% 8.53% 40.02%
1.04% 58.06% 7.02% 33.88%
0.40% 85.94% 4.42% 9.24%
0.27% 92.75% 0.37% 6.61%
0.21% 82.96% 1.27% 15.56%

FIG. 28

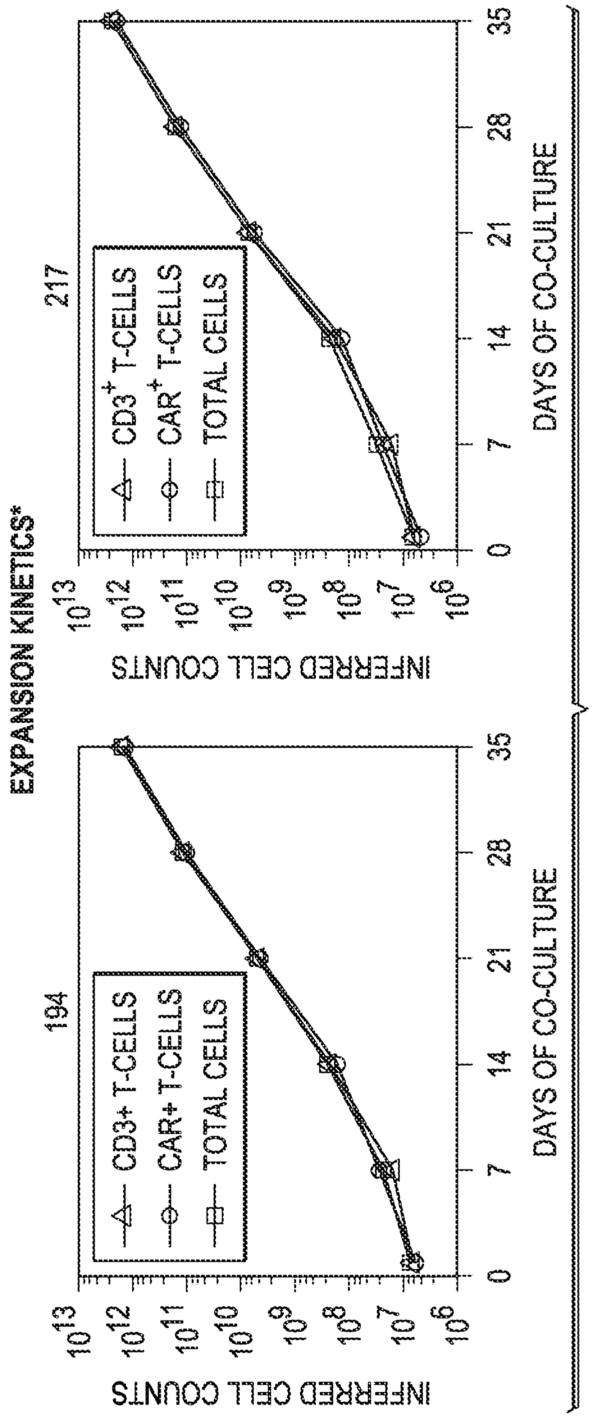

EXPANSION KINETICS*
194
217
INFERRED CELL COUNTS
CD3+ T-CELLS
CAR+ T-CELLS
TOTAL CELLS
DAYS OF CO-CULTURE

FIG. 29

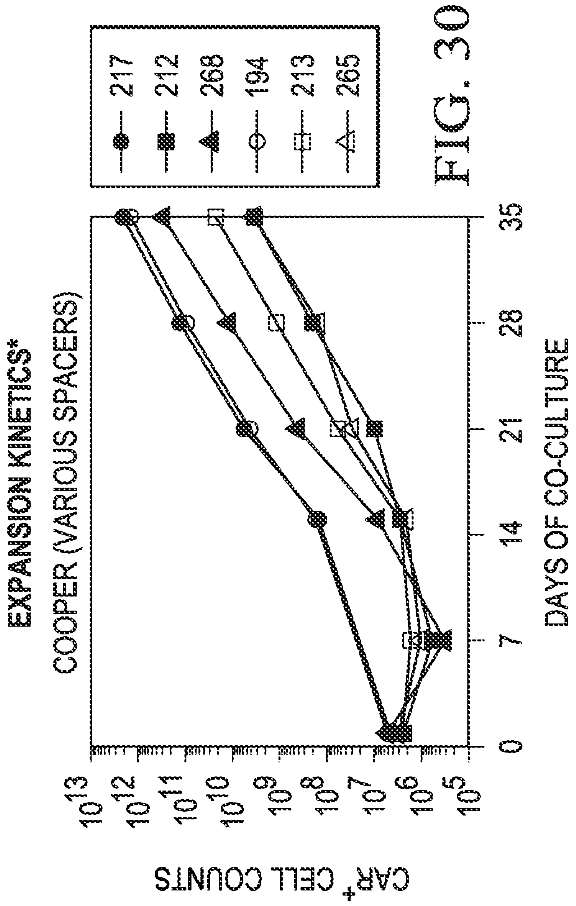

EXPANSION KINETICS*
COOPER (VARIOUS SPACERS)
CAR+ CELL COUNTS
217
212
268
194
213
265
DAYS OF CO-CULTURE

FIG. 30

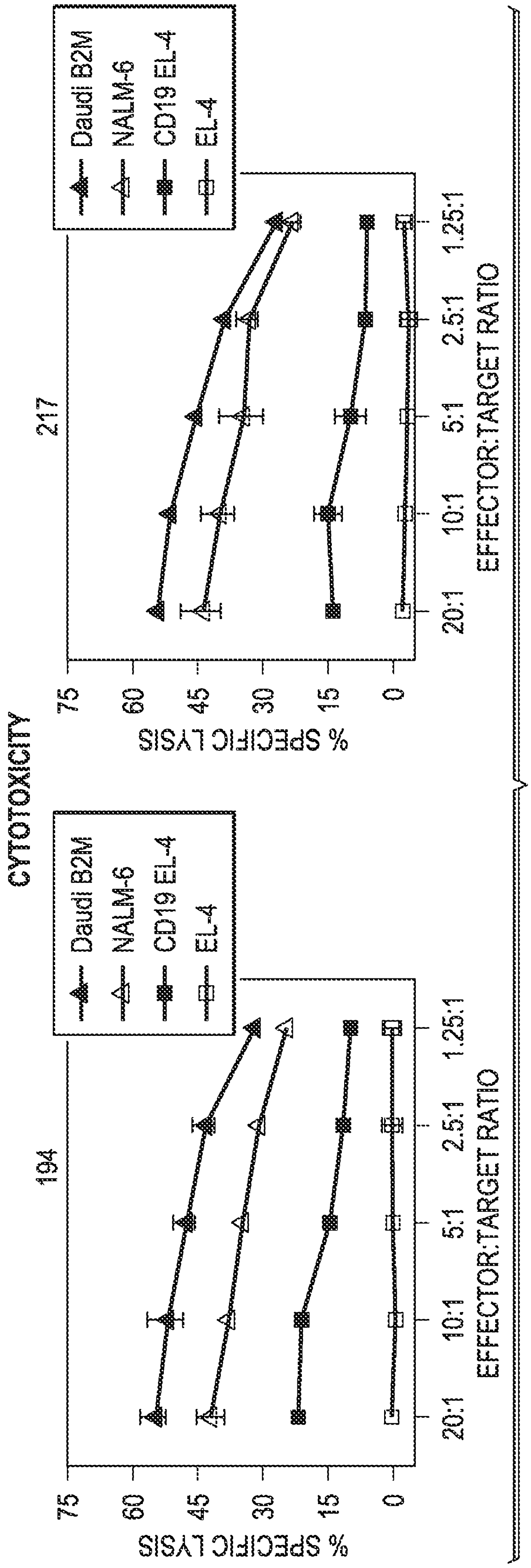


FIG. 31

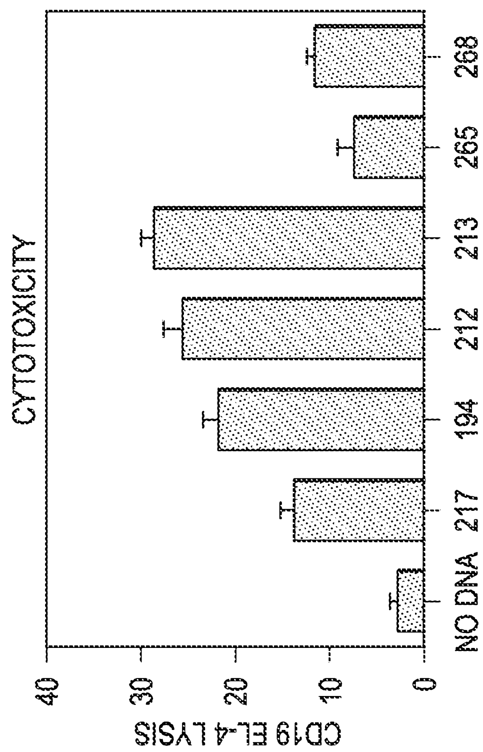


FIG. 32

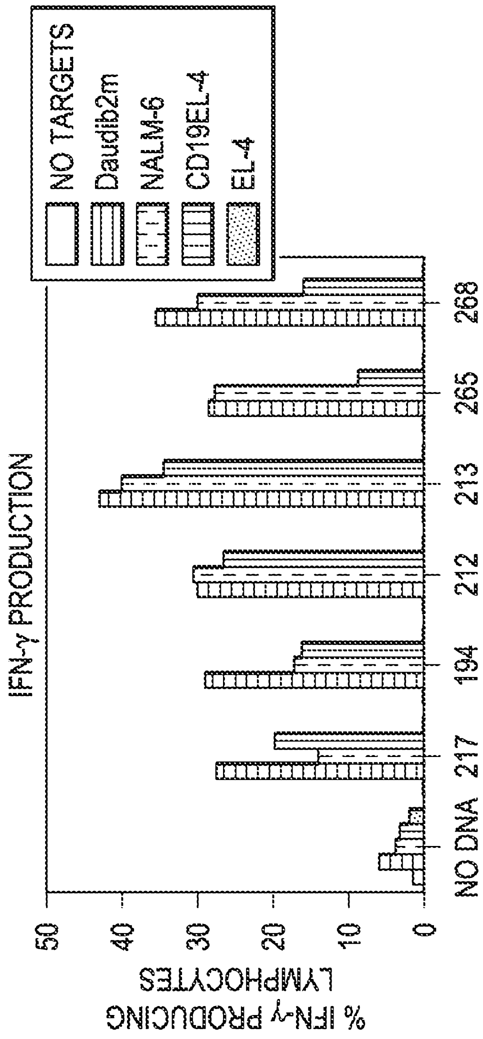


FIG. 34

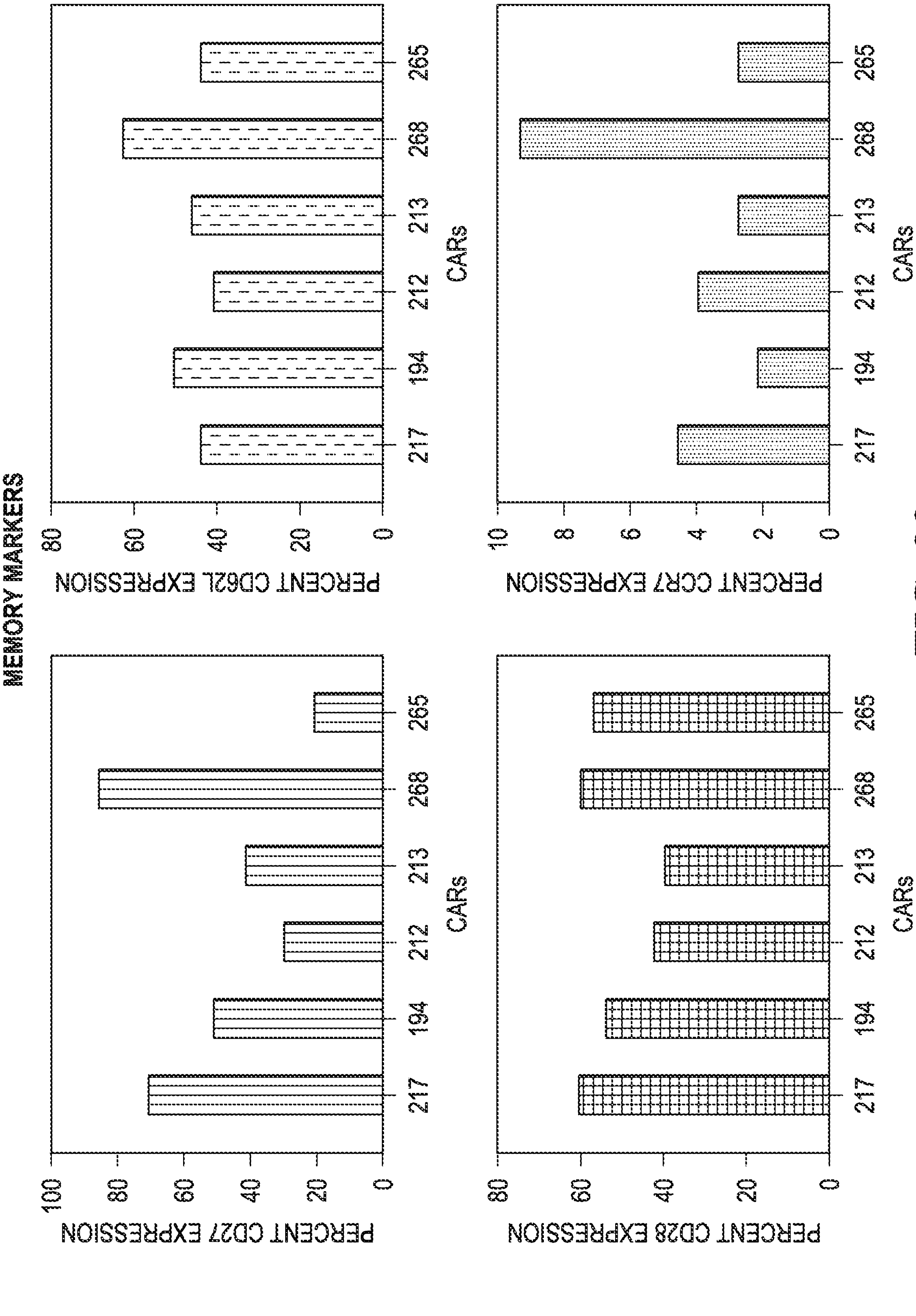

MEMORY MARKERS
PERCENT CD27 EXPRESSION
100
80
60
40
20
0
217
194
212
213
268
265
CARs
PERCENT CD62L EXPRESSION
80
60
40
20
0
217
194
212
213
268
265
CARs
PERCENT CD28 EXPRESSION
80
60
40
20
0
217
194
212
213
268
265
CARs
PERCENT CCR7 EXPRESSION
10
8
6
4
2
0
217
194
212
213
268
265
CARs

FIG. 33

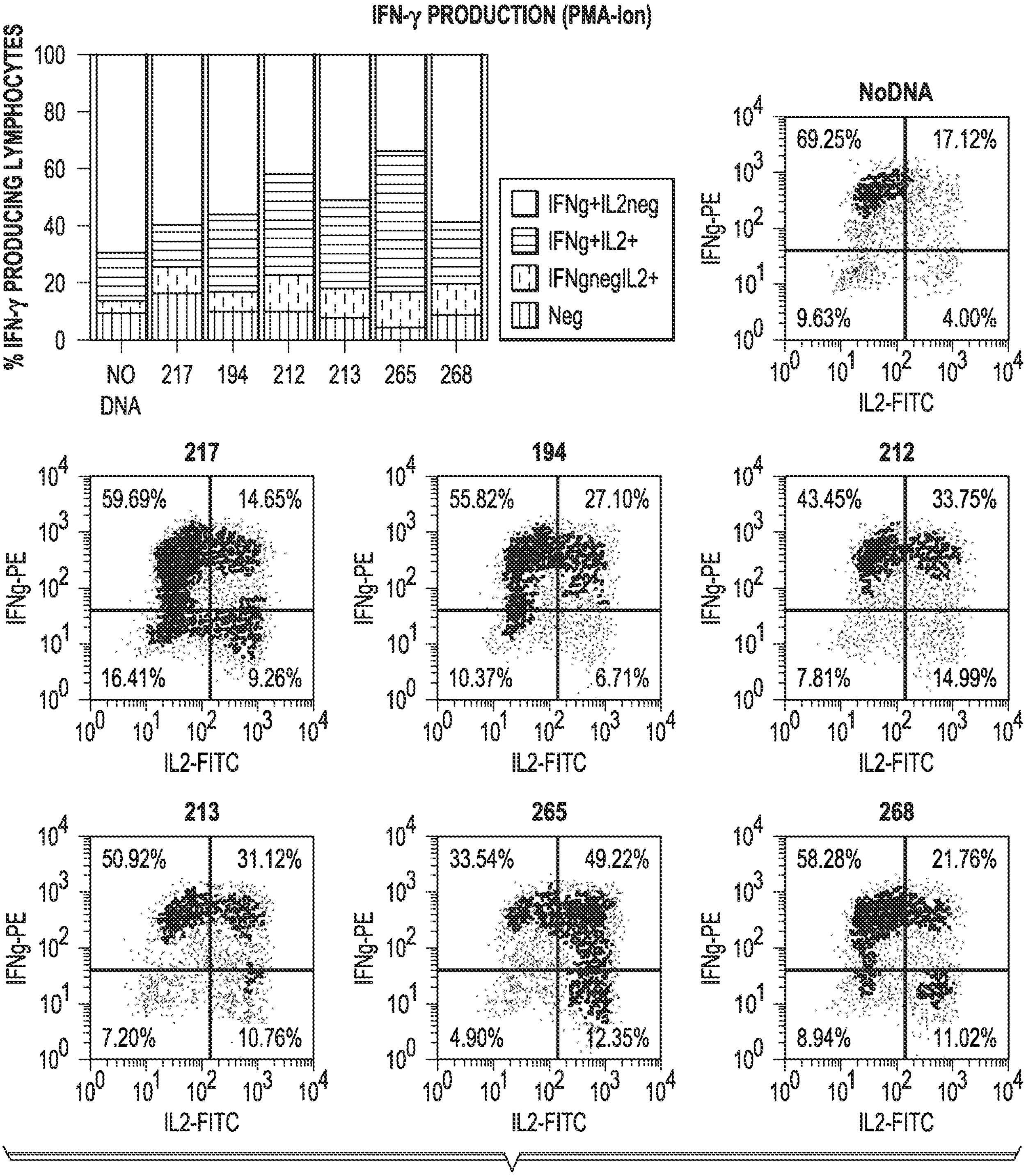

IFN-γ PRODUCTION (PMA-Ion)
% IFN-γ PRODUCING LYMPHOCYTES
NO DNA
217
194
212
213
265
268
IFNg+IL2neg
IFNg+IL2+
IFNgnegIL2+
Neg
NoDNA
69.25%
17.12%
9.63%
4.00%
217
59.69%
14.65%
16.41%
9.26%
194
55.82%
27.10%
10.37%
6.71%
212
43.45%
33.75%
7.81%
14.99%
213
50.92%
31.12%
7.20%
10.76%
265
33.54%
49.22%
4.90%
12.35%
268
58.28%
21.76%
8.94%
11.02%
IFNg-PE
IL2-FITC

FIG. 35

FIG. 36

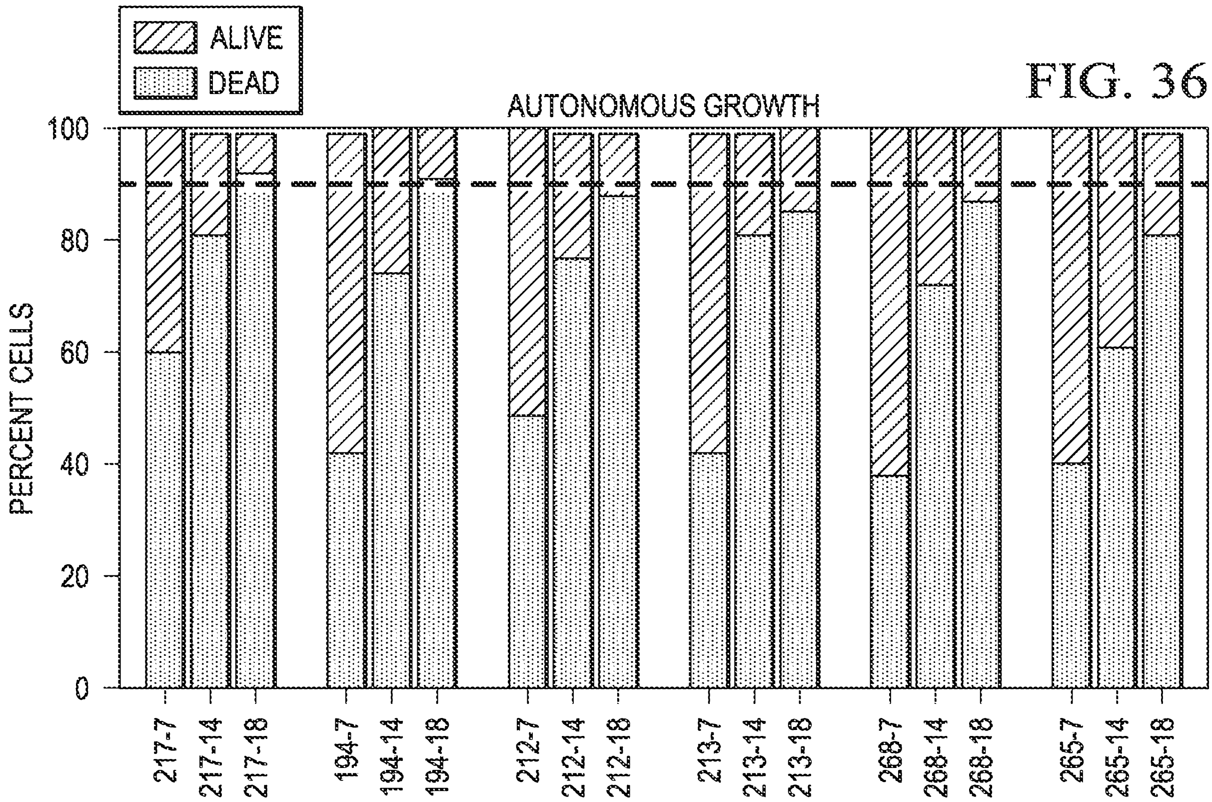
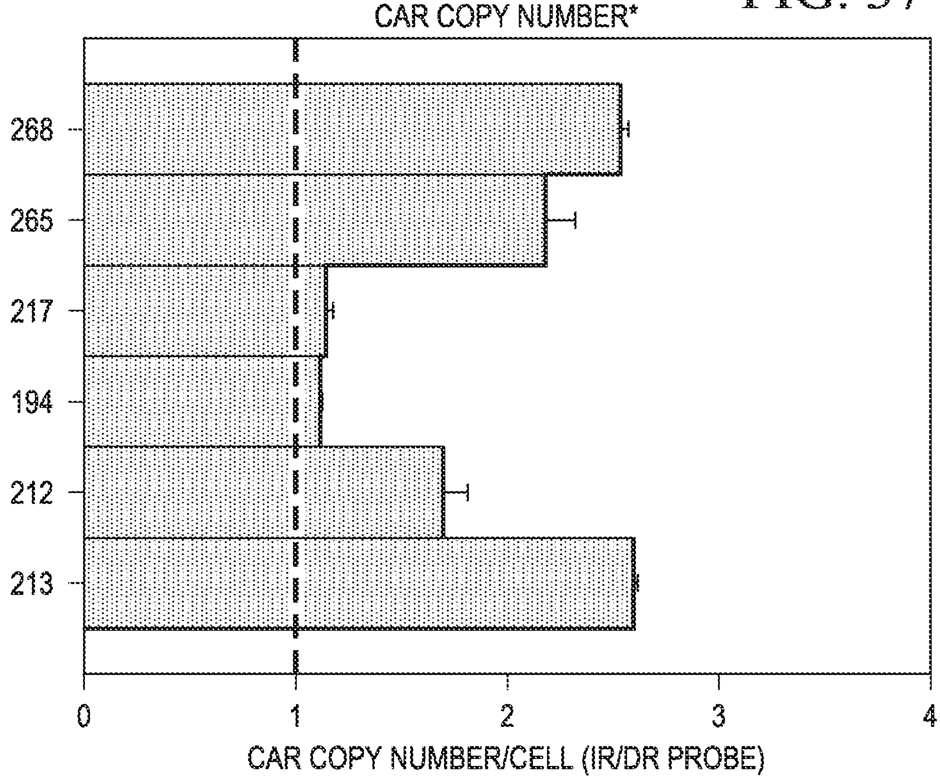

ALIVE
DEAD
AUTONOMOUS GROWTH
PERCENT CELLS
100
80
60
40
20
0
217-7
217-14
217-18
194-7
194-14
194-18
212-7
212-14
212-18
213-7
213-14
213-18
268-7
268-14
268-18
265-7
265-14
265-18

FIG. 37


CAR COPY NUMBER*
268
265
217
194
212
213
0
1
2
3
4
CAR COPY NUMBER/CELL (IR/DR PROBE)

DONOR P491C714
DONOR GCR357861

FIG. 38

CAR COPY NUMBER

DOMAINS	COOPER						
INTRACELLULAR SIGNALING	CD28			CD137			CD28+ CD137
TM/SPACER	CD8	CD28	CD137	CD8	CD28	CD137	CD28
Fc (230aa)	215 (1.48)	194 (1.12) 193 (1.01) 118 (0.98)		214 (1.67)	217 (1.01, 1.14)	216 (1.87)	218 (0.90)
CD8 (47aa)	213 (2.13, 2.6)			212 (1.06, 1.7)			
SHORT (12aa)		265 (2.18)			268 (2.53)		
CD3ζ	WT	WT	WT	WT	WT	WT	WT

FIG. 39

CAR COPY NUMBER

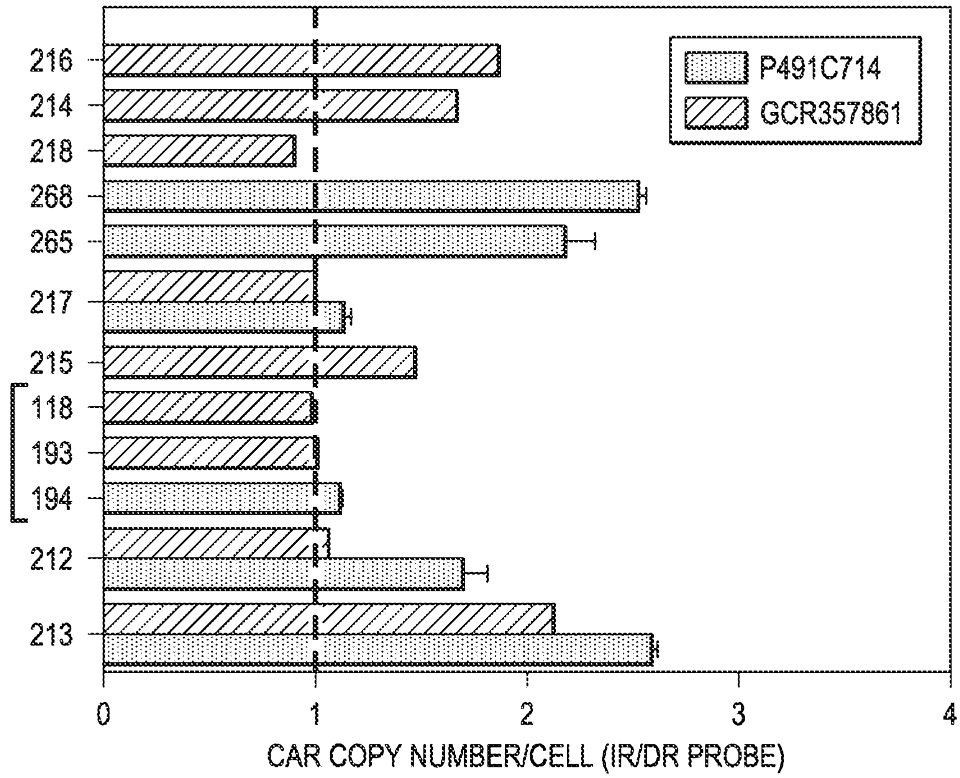
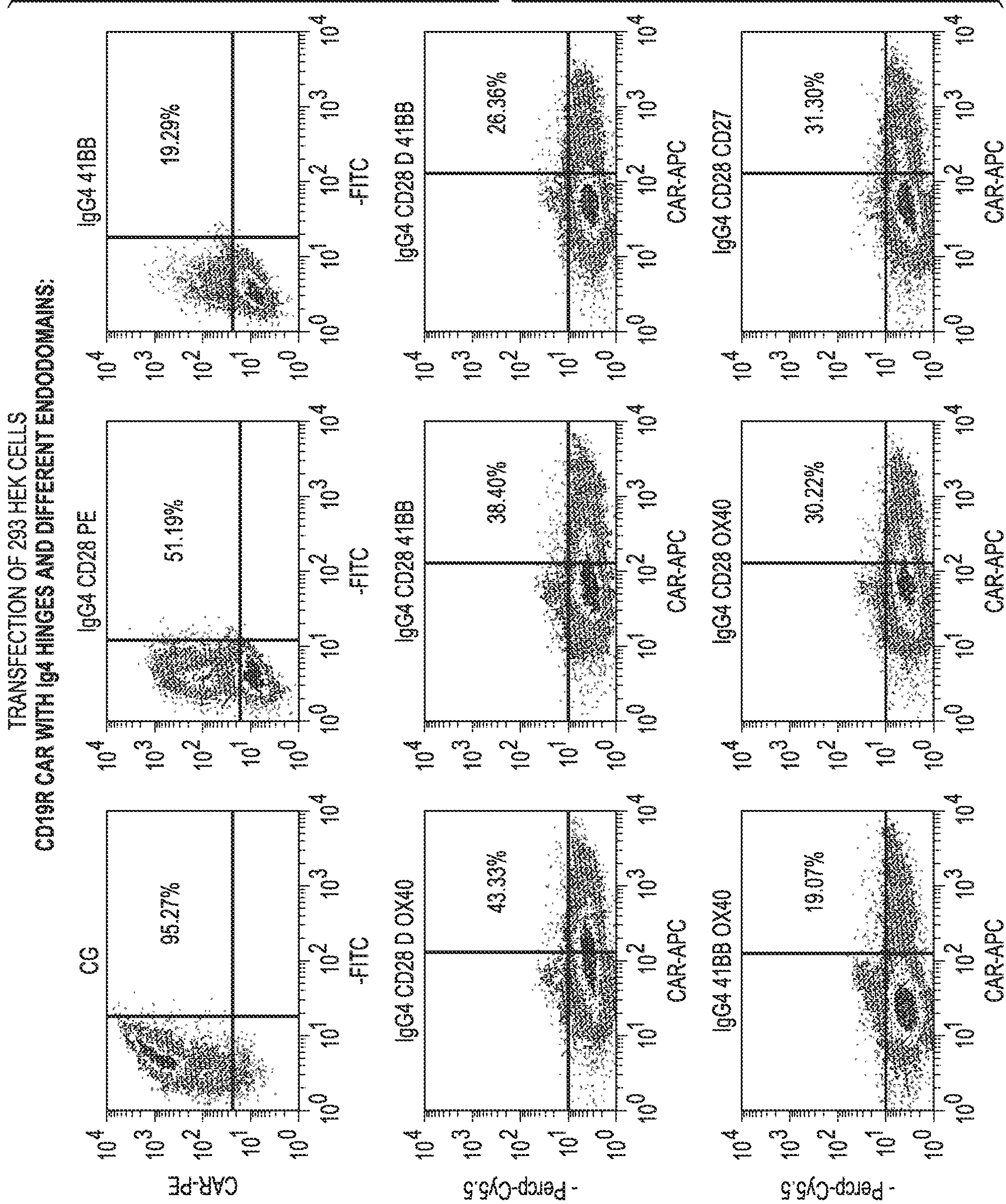


FIG. 40A


TRANSFECTION OF 293 HEK CELLS
CD19R CAR WITH Ig4 HINGES AND DIFFERENT ENDODOMAINS:
CG
95.27%
IgG4 CD28 PE
51.19%
IgG4 41BB
19.29%
IgG4 CD28 D OX40
43.33%
IgG4 CD28 41BB
38.40%
IgG4 CD28 D 41BB
26.36%
IgG4 41BB OX40
19.07%
IgG4 CD28 OX40
30.22%
IgG4 CD28 CD27
31.30%
CAR-PE
-FITC
- Percp-Cy5.5
CAR-APC

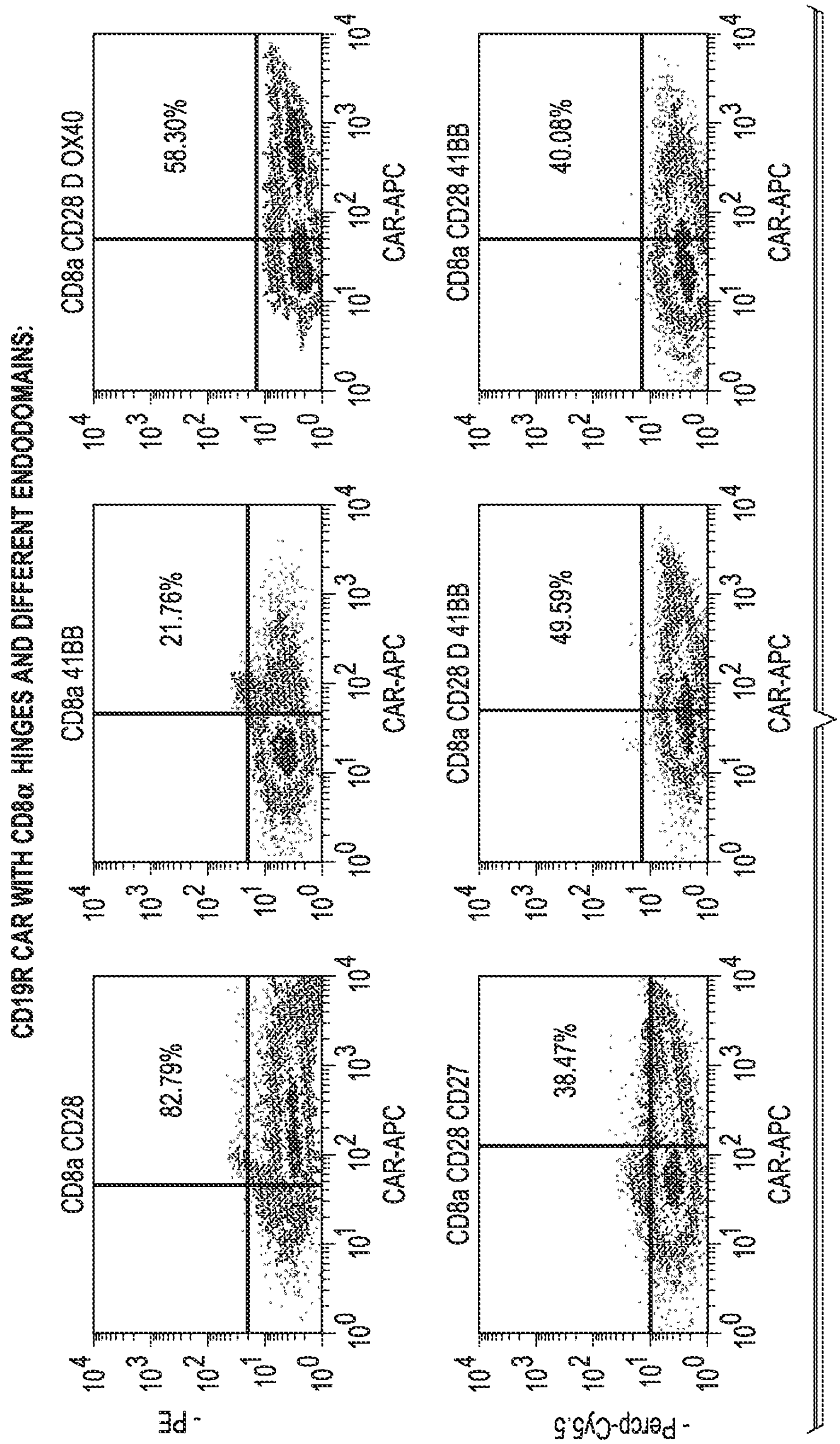

CD19R CAR WITH CD8α HINGES AND DIFFERENT ENDODOMAINS:
CD8a CD28
82.79%
CD8a 41BB
21.76%
CD8a CD28 D OX40
58.30%
CD8a CD28 CD27
38.47%
CD8a CD28 D 41BB
49.59%
CD8a CD28 41BB
40.08%
CAR-APC
- PE
- Percp-Cy5.5

FIG. 40B

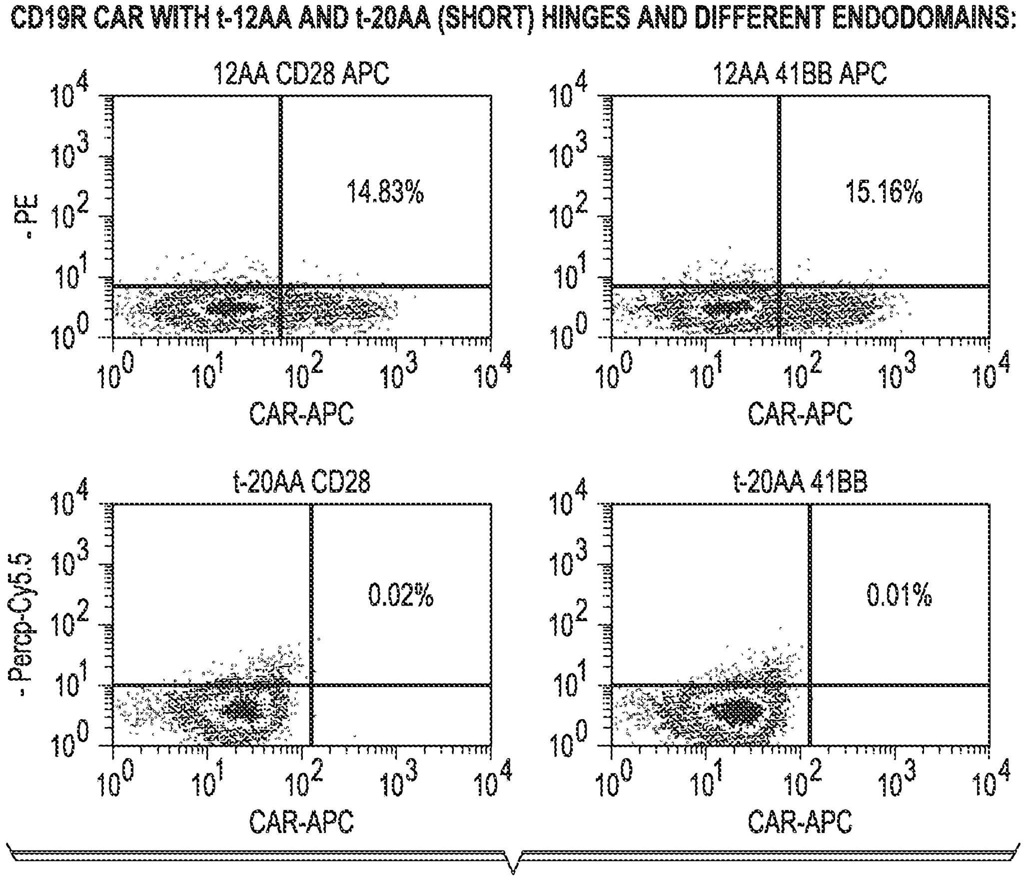

CD19R CAR WITH t-12AA AND t-20AA (SHORT) HINGES AND DIFFERENT ENDODOMAINS:
12AA CD28 APC
14.83%
-PE
CAR-APC
12AA 41BB APC
15.16%
CAR-APC
t-20AA CD28
0.02%
- Percp-Cy5.5
CAR-APC
t-20AA 41BB
0.01%
CAR-APC

FIG. 40C

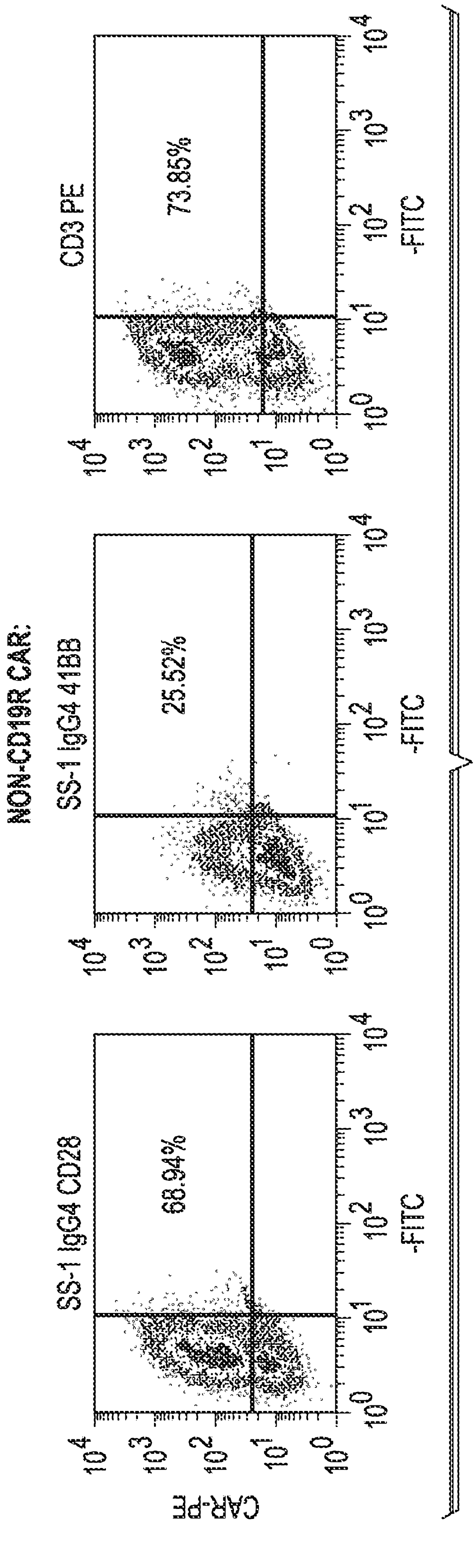


FIG. 40D

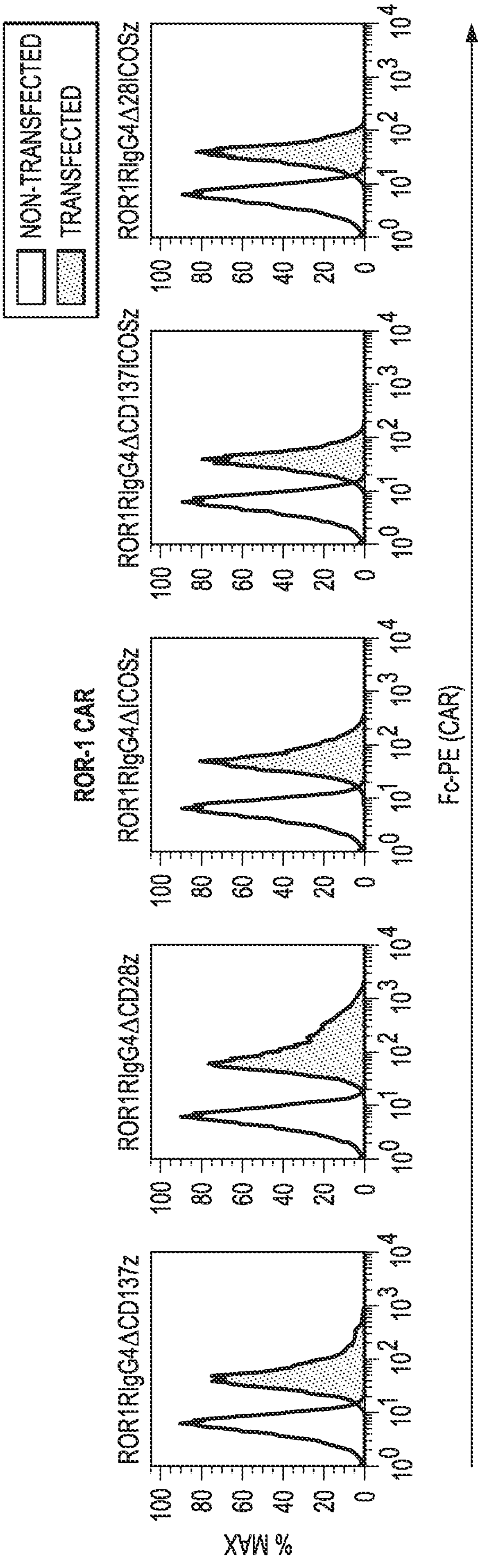


FIG. 40E

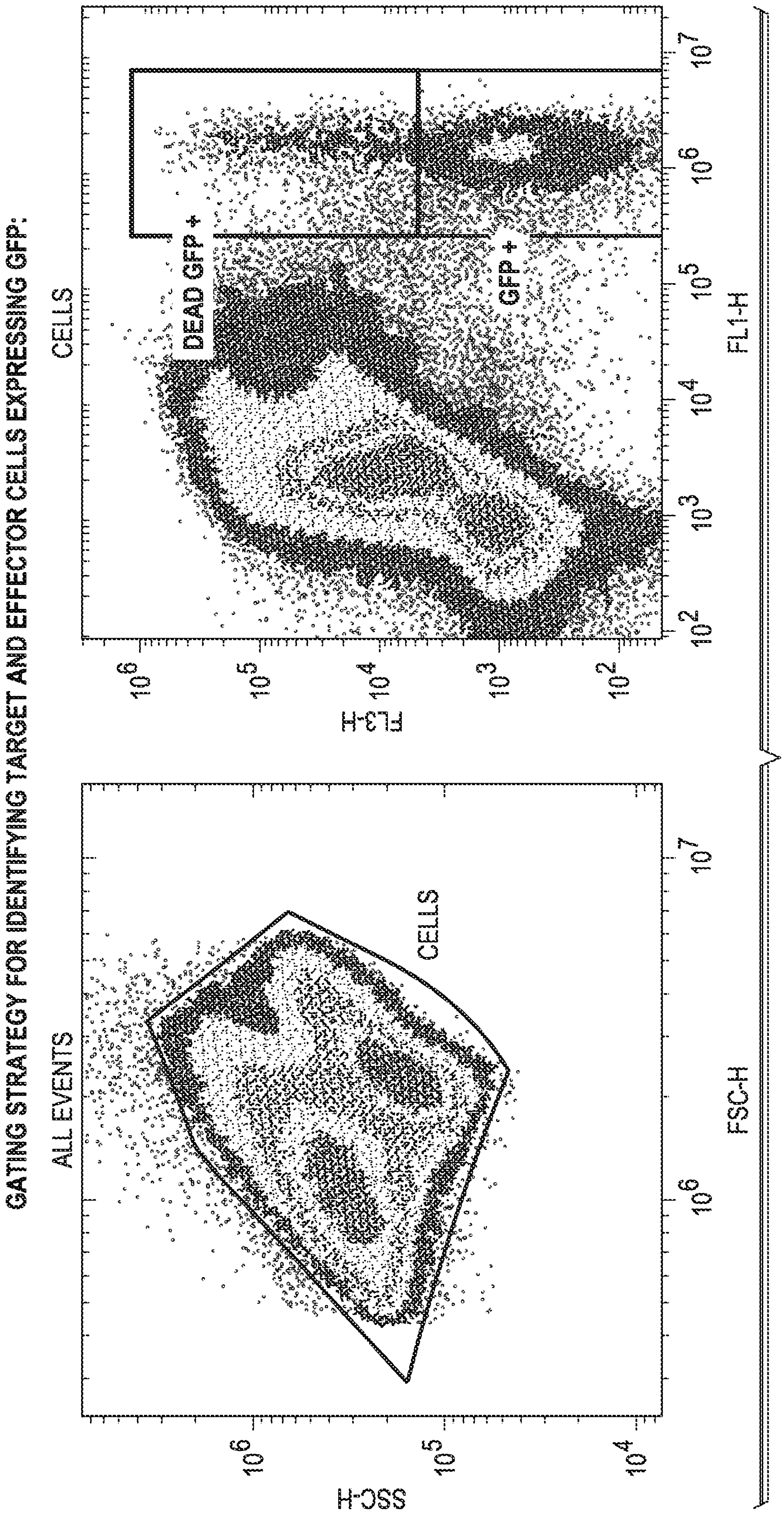

GATING STRATEGY FOR IDENTIFYING TARGET AND EFFECTOR CELLS EXPRESSING GFP:
ALL EVENTS
CELLS
SSC-H
FSC-H
CELLS
DEAD GFP +
GFP +
FL3-H
FL1-H

FIG. 41A-1

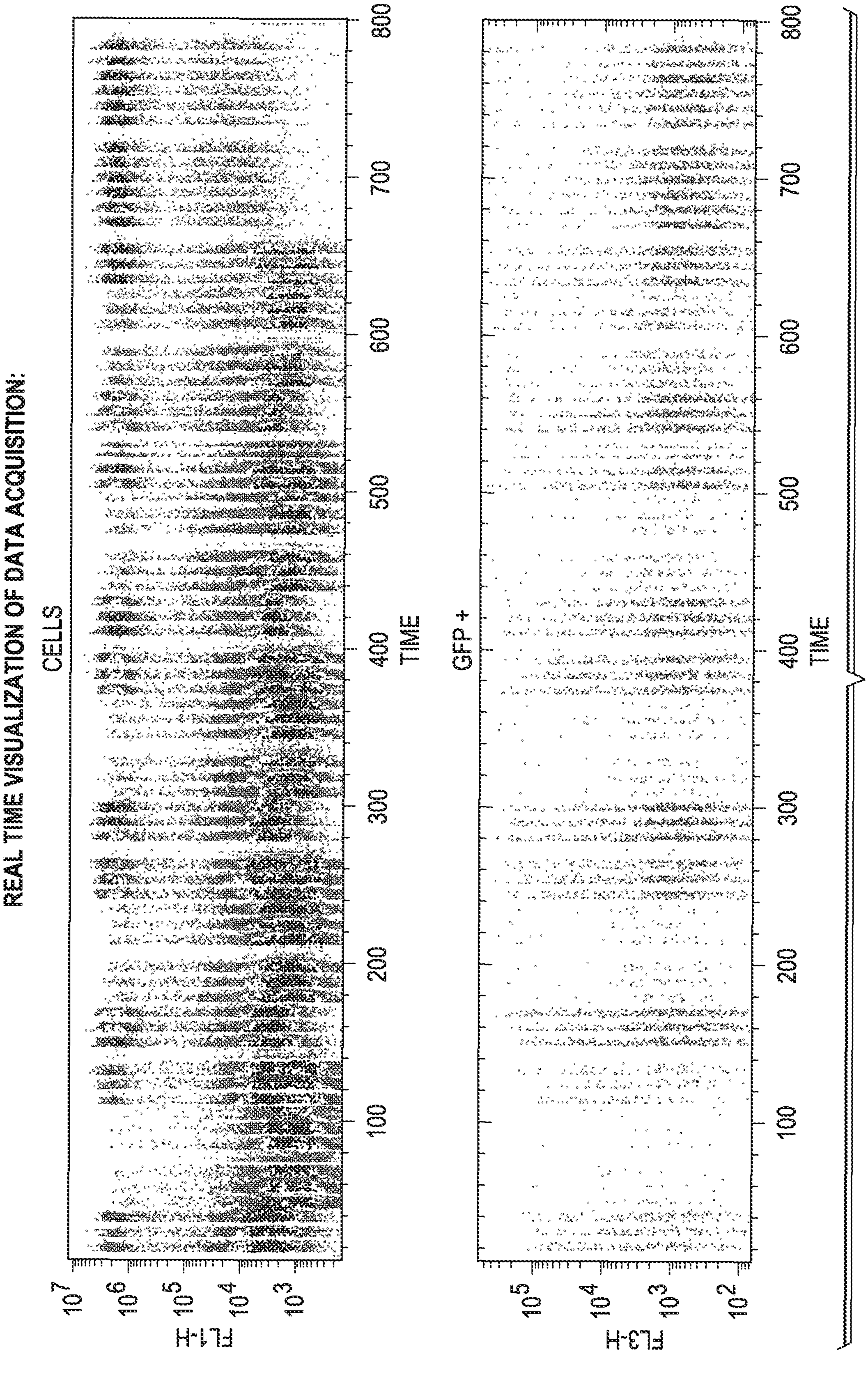

REAL TIME VISUALIZATION OF DATA ACQUISITION:
CELLS
GFP +
TIME
TIME
FL1-H
FL3-H
10^7 10^6 10^5 10^4 10^3
10^5 10^4 10^3 10^2
100 200 300 400 500 600 700 800
100 200 300 400 500 600 700 800

FIG. 41A-2

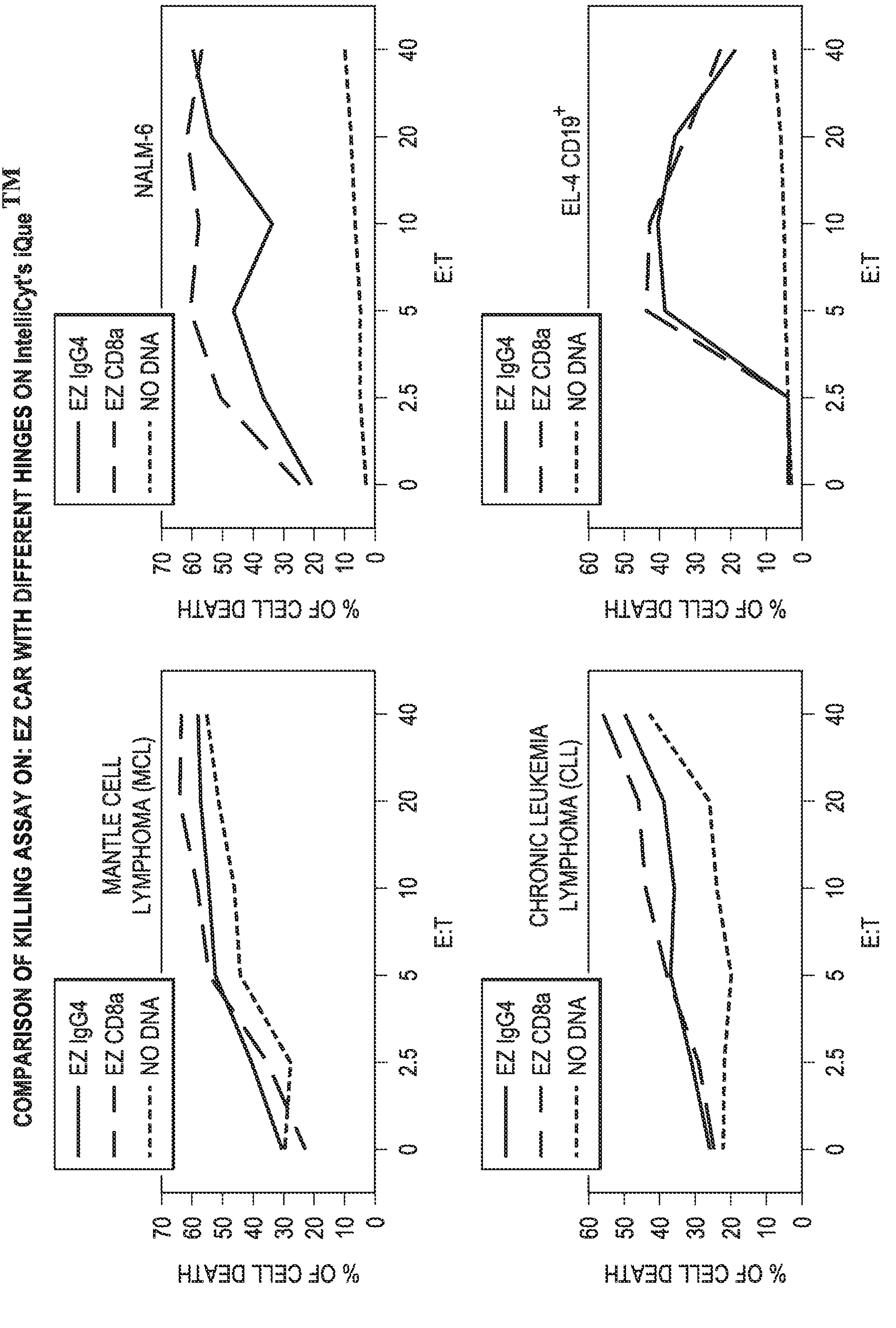
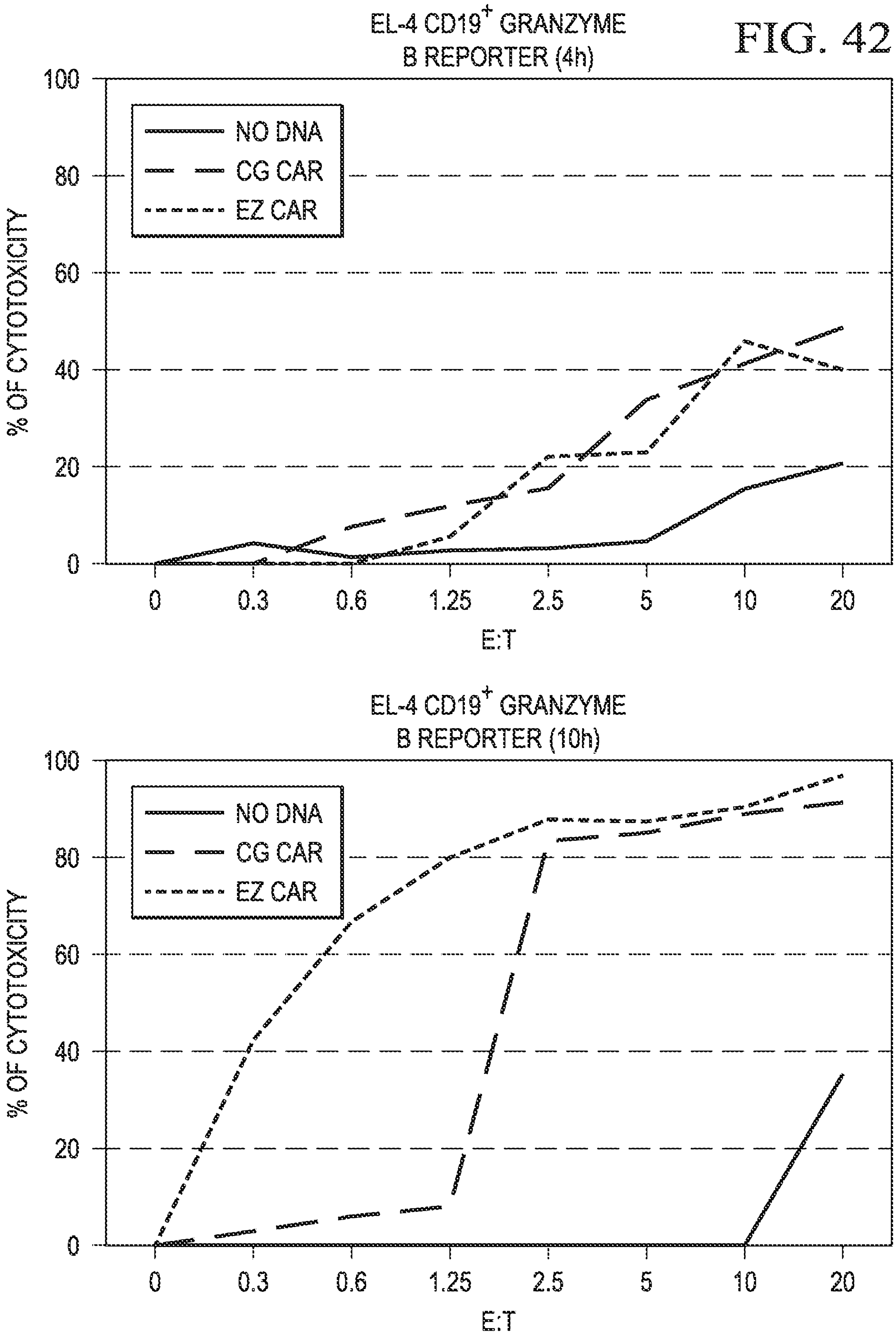

COMPARISON OF KILLING ASSAY ON: EZ CAR WITH DIFFERENT HINGES ON IntelliCyt's iQue™
EZ IgG4
EZ CD8a
NO DNA
MANTLE CELL LYMPHOMA (MCL)
% OF CELL DEATH
E:T
NALM-6
CHRONIC LEUKEMIA LYMPHOMA (CLL)
EL-4 CD19+
0
2.5
5
10
20
40
10
20
30
40
50
60
70

FIG. 41B

FIG. 42


EL-4 CD19+ GRANZYME B REPORTER (4h)
% OF CYTOTOXICITY
100
80
60
40
20
0
NO DNA
CG CAR
EZ CAR
0
0.3
0.6
1.25
2.5
5
10
20
E:T
EL-4 CD19+ GRANZYME B REPORTER (10h)
% OF CYTOTOXICITY
100
80
60
40
20
0
NO DNA
CG CAR
EZ CAR
0
0.3
0.6
1.25
2.5
5
10
20
E:T

SEQUENCE LISTING

<110> BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM

<120> CHIMERIC ANTIGEN RECEPTORS AND METHODS OF MAKING

<130> UTFC.P1231WO

<140> UNKNOWN
<141> 2015-02-16

<150> 61/940,339
<151> 2014-02-14

<160> 59

<170> PatentIn version 3.5

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<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 1
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<210> 2
<211> 2037
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

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atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120

gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300

gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

ggcggcggaa caaagctgga gatcaccggc agcacctccg gcagcggcaa gcctggcagc 420

ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaga gcggccctgg cctggtggcc 480

cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc 540

gtgtcctgga tccggcagcc ccctaggaag ggcctggagt ggctgggcgt gatctggggc 600

agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac 660

agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720

tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780

accagcgtga ccgtgtccag cgagagcaag tacggccctc cctgcccccc ttgccctgcc 840

cccgagttcc tgggcggacc cagcgtgttc ctgttccccc ccaagcccaa ggacaccctg 900 atgatcagcc ggacccccga ggtgacctgt gtggtggtgg acgtgtccca ggaggacccc 960

gaggtccagt tcaactggta cgtggacggc gtggaggtgc acaacgccaa gaccaagccc 1020

cgggaggagc agttcaatag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 1080

gactggctga acggcaagga atacaagtgt aaggtgtcca acaagggcct gcccagcagc 1140

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ccccctagcc aagaggagat gaccaagaat caggtgtccc tgacctgcct ggtgaagggc 1260

ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1320

aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc 1380

gtggacaaga gccggtggca ggagggcaac gtctttagct gctccgtgat gcacgaggcc 1440

ctgcacaacc actacaccca gaagagcctg tccctgagcc tgggcaagat gttctgggtg 1500

ctggtcgtgg tgggtggcgt gctggcctgc tacagcctgc tggtgacagt ggccttcatc 1560

atcttttggg tgaagagagg ccggaagaaa ctgctgtaca tcttcaagca gcccttcatg 1620

cggcccgtgc agaccaccca ggaagaggac ggctgcagct gccggttccc cgaggaagag 1680

gaaggcggct gcgaactgcg ggtgaagttc agccggagcg ccgacgcccc tgcctaccag 1740

cagggccaga accagctgta caacgagctg aacctgggcc ggagggagga gtacgacgtg 1800

ctggacaagc ggagaggccg ggaccctgag atgggcggca agccccggag aaagaaccct 1860

caggagggcc tgtataacga actgcagaaa gacaagatgg ccgaggccta cagcgagatc 1920

ggcatgaagg gcgagcggcg gaggggcaag ggccacgacg gcctgtacca gggcctgagc 1980

accgccacca aggataccta cgacgccctg cacatgcagg ccctgccccc cagatga 2037

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<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

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atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120

gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300

gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

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ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaga gcggccctgg cctggtggcc 480

cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc 540

gtgtcctgga tccggcagcc ccctaggaag ggcctggagt ggctgggcgt gatctggggc 600 agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac 660

agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720

tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780

accagcgtga ccgtgtccag cgagagcaag tacggccctc cctgcccccc ttgccctgcc 840

cccgagttcc tgggcggacc cagcgtgttc ctgttccccc ccaagcccaa ggacaccctg 900

atgatcagcc ggacccccga ggtgacctgt gtggtggtgg acgtgtccca ggaggacccc 960

gaggtccagt tcaactggta cgtggacggc gtggaggtgc acaacgccaa gaccaagccc 1020

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gactggctga acggcaagga atacaagtgt aaggtgtcca acaagggcct gcccagcagc 1140

atcgagaaaa ccatcagcaa ggccaagggc cagcctcggg agccccaggt gtacaccctg 1200

ccccctagcc aagaggagat gaccaagaat caggtgtccc tgacctgcct ggtgaagggc 1260

ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1320

aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc 1380

gtggacaaga gccggtggca ggagggcaac gtctttagct gctccgtgat gcacgaggcc 1440

ctgcacaacc actacaccca gaagagcctg tccctgagcc tgggcaagat gttctgggtg 1500

ctggtcgtgg tgggtggcgt gctggcctgc tacagcctgc tggtgacagt ggccttcatc 1560

atcttttggg tgaggagcaa gcggagcaga ggcggccaca gcgactacat gaacatgacc 1620

ccccggaggc ctggccccac ccggaagcac taccagccct acgcccctcc cagggacttc 1680

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ggccagaacc agctgtacaa cgagctgaac ctgggccgga gggaggagta cgacgtgctg 1800

gacaagcgga gaggccggga ccctgagatg ggcggcaagc cccggagaaa gaaccctcag 1860

gagggcctgt ataacgaact gcagaaagac aagatggccg aggcctacag cgagatcggc 1920

atgaagggcg agcggcggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1980

gccaccaagg atacctacga cgccctgcac atgcaggccc tgccccccag atga 2034

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gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

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<210> 5
<211> 1488
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 5
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gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300

gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

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ggcgagcggc ggaggggcaa gggccacgac ggcctgtacc agggcctgag caccgccacc 1440
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<210> 6
<211> 1380
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 6
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gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180
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accagcgtga ccgtgtccag cgagagcaag tacggccctc cctgcccccc ttgccctttc 840

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ttcatcatct tttgggtgag gagcaagcgg agcagaggcg gccacagcga ctacatgaac 960

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gacttcgccg cctaccggag ccgggtgaag ttcagccgga gcgccgacgc ccctgcctac 1080

cagcagggcc agaaccagct gtacaacgag ctgaacctgg gccggaggga ggagtacgac 1140

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cctcaggagg gcctgtataa cgaactgcag aaagacaaga tggccgaggc ctacagcgag 1260

atcggcatga agggcgagcg gcggaggggc aagggccacg acggcctgta ccagggcctg 1320

agcaccgcca ccaaggatac ctacgacgcc ctgcacatgc aggccctgcc ccccagatga 1380

<210> 7
<211> 1383
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 7
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atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120

gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300

gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

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ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaga gcggccctgg cctggtggcc 480

cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc 540

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agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720

tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780

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aaccctcagg agggcctgta taacgaactg cagaaagaca agatggccga ggcctacagc 1260

gagatcggca tgaagggcga gcggcggagg ggcaagggcc acgacggcct gtaccagggc 1320

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tga 1383

<210> 8
<211> 720
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 8
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gtgaccatcc agtgtcaggc cagcgaggac atctactctg gcctggcttg gtatcagcag 120

aagcccggca agagccctca gctgctgatc tacggcgcca gcgacctgca ggacggcgtg 180

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ggaggaggca ccaagctgga actgaagggc ggaggcggaa gtggaggcgg aggatctggc 360

ggcggaggct ctgaagtgca gctgcagcag tctggcgctg aactggtccg gcctggcact 420

agcgtgaagc tgtcctgcaa ggtgtccggc gacaccatca ccttctacta catgcacttc 480

gtgaagcaga ggccaggaca gggcctggaa tggatcggca gaatcgaccc tgaggacgag 540

agcaccaagt acagcgagaa gttcaagaac aaggccaccc tgaccgccga caccagcagc 600

aacaccgcct acctgaagct gtctagcctg acctccgagg acaccgccac ctacttttgc 660

atctacggcg gctactactt cgactactgg ggccagggcg tgatggtcac cgtgtccagc 720

<210> 9
<211> 741
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 9
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cgggtgacca tcagctgccg ggccagccag gacatcagca agtacctgaa ctggtatcag 120

cagaagcccg acggcaccgt caagctgctg atctaccaca ccagccggct gcacagcggc 180

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tttggcggcg gaacaaagct ggagatcacc ggcagcacct ccggcagcgg caagcctggc 360

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ggcgtgtcct ggatccggca gccccctagg aagggcctgg agtggctggg cgtgatctgg 540

ggcagcgaga ccacctacta caacagcgcc ctgaagagcc ggctgaccat catcaaggac 600

aacagcaaga gccaggtgtt cctgaagatg aacagcctgc agaccgacga caccgccatc 660

tactactgtg ccaagcacta ctactacggc ggcagctacg ccatggacta ctggggccag 720

ggcaccagcg tgaccgtgtc c 741

<210> 10
<211> 723
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 10
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atgacctgca gcgccagcag cagcgtgagc tacatgaact ggtatcagca gaagagcggc 120

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cagagacccg gccagggcct ggaatggatc ggctacatca accccagccg gggctacacc 540

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gcctacatgc agctgtccag cctgacctcc gaggacagcg ccgtgtacta ctgcgcccgg 660

tactacgacg accactactg cctggactac tggggccagg gcaccacact gaccgtgagc 720

agc 723

<210> 11
<211> 735
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 11
ctgatccccg acgtgcagat cacccagagc cccagctacc tggccgccag ccctggcgag 60

acaatcacca tcaactgccg ggccagcaag agcatcagca aggacctggc ctggtatcag 120

gaaaagcccg gcaagaccaa caagctgctg atctacagcg gcagcaccct gcagagcggc 180

atccccagca gattcagcgg cagcggctcc ggaaccgact tcaccctgac catcagcagc 240

ctggaacccg aggacttcgc catgtactac tgccagcagc acaacaagta cccctacacc 300 ttcggcggag gcaccaagct ggaaatcaag ggcagcacct ccggcagcgg caagcctggc 360

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aaacctggcg cccctgtgaa gctgagctgc aaggccagcg gctacacctt caccaactac 480

tggatgaact ggatcaagca gaggcccggc agaggcctgg aatggatcgg cagaatcgac 540

cccagcgaca gcgagagcca ctacaaccag aagttcaagg acaaggccac actgaccgtg 600

gacaagagca gcaacaccgc ctacatccag ctgtcttctc tgaccagcga ggacagcgcc 660

gtgtactatt gcgccagata cgactacgac gacaccatgg actactgggg ccagggcacc 720

agcgtgaccg tgtct 735

<210> 12
<211> 810
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 12
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agaatggccc aggtgcaact gcagcagtca ggggctgagc tggctagacc tggggcttca 120

gtgaagatgt cctgcaaggc ttctggctac acctttacta cctacacaat acactgggta 180

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tctgaagact tggcagagta tttctgtcag caatatcaca cctatcctct cacgttcgga 780

gggggcacca agctggaaat caaacggtcg 810

<210> 13
<211> 735
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 13
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agctgcgcgg cgagcggctt tacctttagc agctatgaaa tgaactgggt gcgccaggcg 120 ccgggcaaag gcctggaatg ggtgagcggc attagcggca gcggcggcag cacctattat 180

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tatctgcaga tgaaccgcct gcgcgcggaa gataccgcgg tgtattattg cgcgcgcgat 300

aacggctggg aactgaccga ttggtatttt gatctgtggg gccgcggcac catggtgacc 360

gtgagcagcg gcggcggcgg cagcggcggc ggcggcagcg gcggcggcgg cagcgatatt 420

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gcgccgaaac tgctgattta taaagcgagc agcctggcga gcggcgcgcc gagccgcttt 600

agcggcagcg gcagcggcac cgattttacc ctgaccatta gcagcctgca gccggatgat 660

tttgcgacct attattgcca gcagtatagc aactatccgc tgacctttgg cggcggcacc 720

aaactggaaa ttaaa 735

<210> 14
<211> 747
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 14
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atcagctgca gaagcagcca gagcctgctg aagaacaacg gcaacacctt cctgcactgg 120

tatctgcaga agtccggcca gtcccccaag ctgctgatct acaaggtgtc caaccggctg 180

agcggcgtgc ccgatagatt ttctggctct ggcagcggca cctacttcac cctgaagatc 240

agccgggtgg aagccgagga cctgggcgtg tacttctgta gccagagcac ccacatccct 300

tacaccttcg gcggaggcac caagctggaa ctgaagcggg gcagcacctc cggcagcggc 360

aagcctggca gcggcgaggg cagcaccaag ggcgaagtga agctggtgga aagcggcgga 420

ggcctggtgc tgcctggcga ttctctgaga ctgagctgcg ccaccagcga gttcaccttc 480

accgactact acatgacctg ggtgcgccag ccccccagaa aggctctgga atggctgggc 540

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ttcaccatca gccgggacaa cagccagagc atcctgtacc tgcagatgaa caccctgcgg 660

accgaggaca gcgccaccta ctactgtgct cgggtgtcca actgggcctt cgactattgg 720

ggccagggca ccaccctgac cgtgtct 747

<210> 15
<211> 759
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 15
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atcacctgta aagccagccc cgacatcaac agctacctga gctggttcca gcagaagccc   120

ggcaagagcc ccaagaccct gatctaccgg gccaacagac tggtggatgg cgtgcccagc   180

agattcagcg gcggaggctc tggccaggac tacagcctga ccatcaactc cctggaatac   240

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aacatcctgt acctgcagat gagcagcctg cggagcgagg acaccgccat gtactactgt   660

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accgtgtcta gccagggaac ctccgtgaca gtgtccagc   759

<210> 16
<211> 759
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 16
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tcctgtgcag cctctggatt cactttcagt cactatggca tgtcttgggt tcgccagact   120

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ccagacagtg tgaagggacg attcaccatc tccagagaca atgacaagaa cgccctgtac   240

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gaattttatt actacggtaa tacctactat tactctgcta tggactactg gggccaaggc   360

accacggtca ccgtctcctc aggtggcggt ggcagcggcg gtggtgggtc cggtggcggc   420

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ccgtggacgt tcggagctgg caccaagctc gagatcaaa   759

<210> 17
<211> 543
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 17
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cggaacaaag agaaccacag ccagcccacc cagagcagcc tggaagatag cgtgaccccc   120

accaaggccg tgaaaaccac cggcgtgctg tccagcccct gccctcccaa ctggatcatc   180

tacgagaaga gctgctacct gttcagcatg agcctgaaca gctgggacgg cagcaagcgg   240

cagtgctggc agctgggcag caacctgctg aagatcgaca gcagcaacga gctgggcttc   300

atcgtgaagc aggtgtccag ccagcccgac aactccttct ggatcggcct gagcaggccc   360

cagaccgagg tgccctggct gtgggaggac ggctccacct tcagctccaa cctgttccag   420

atccggacca ccgccacaca ggaaaacccc agccccaact gcgtgtggat ccacgtgagc   480

gtgatctacg accagctgtg cagcgtgccc agctacagca tctgcgagaa gaaattcagc   540

atg   543

<210> 18
<211> 987
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 18
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatgtct   60

agacaattcc aagtgaagct ggaggagtct ggggctgagc ttgtgaggcc aggggccttg   120

gtcaagttgt cctgcaaaac ttctggcttc aacattaaag actacttttt acactgggtg   180

agacagaggc ctgaccaggg cctggagtgg attggatgga ttaatcctga taatggtaat   240

actgtttatg acccgaagct tcagggcacg gccagtttaa cagcagacac atcctccaac   300

acagtctact tgcagctcag cggcctgaca tctgaggaca ctgccgtcta tttctgtact   360

cggagggact atacttatga aaaggctgct ctggactact ggggtcaggg agcctcagtc   420

atcgtctcct cagccaaaac aacagcccca tcggtctatc cactggcccc tgtgtgtgga   480

gatacaactg gctcctcggt gactctagga tgcctggtca agagatctgg cggtggcggt   540

tctggtggcg gtggctccgg cggtggcggt tctggagctc gacattgtgc tcacacagac   600

tccaaatcca tgtccatgtc agtaggagag agggtcacct tgacctgcaa ggccagtgag   660

aatgtggtta cttatgtttc ctggtatcaa cagaaaccag agcagtctcc taaactgctg   720

atatacgggg catccaaccg gtacactggg gtccccgatc gcttcacagg cagtggatct   780

gcaacagatt tcactctgac catcagcagt gtgcaggctg aagaccttgc agattatcac   840

tgtggacagg gttacagcta tccgtacacg ttcggagggg ggaccaagct ggaaataaaa   900

cgggctgatg ctgcaccaac ttatccgcat caccatcatc atcatcatct gcagatatcc   960

agcacagtgg cggccgctcg agtctag   987

<210> 19
<211> 753
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 19
ctgatcccca tggcccaggt gaagctgcag cagagcggcc ctgatctggt gaagcctggc   60

gccagcgtga agatcagctg caaggccagc ggctacagct tcaccggcta ctacatgcac   120

tgggtgaaac agagccacgg caagagcctg gaatggatcg gcagagtgaa ccccaatagc   180

ggcggcacca gctacaacca gaagttcaag gacaaggcca tcctgaccgt ggacaagagc   240

agcagcaccg cctacatgga actgcggagc ctgaccagcg aggacagcgc cgtgtactac   300

tgcgcccggt ccaagggcaa ctacttctac gccatggact actggggcca gggcaccacc   360

gtgaccgtgt ctagcagcgg cggaggaagc ggaggggag gatctggcgg aggcggcagc   420

gatatcgagc tgacccagag ccctagcagc ctggccgtgt cactgggcca gagagccacc   480

atcagctgca gagcctccga gagcgtggat agccacggca ccagcctgat gcactggtat   540

cagcagaagc ccggccagcc ccccaagttc ctgatctacc gggccagcaa cctggaaagc   600

ggcatccccg ccagattttc cggcagcggc agcagaaccg acttcaccct gaccatcaac   660

cccgtggaga cagacgacgt ggccatctac tactgccagc agagcaacga ggaccctccc   720

acctttggcg gaggcaccaa gctggaactg aag   753

<210> 20
<211> 732
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 20
gaagtgcagc tggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg   60

agctgtgccg ccagcggctt cgacttcagc cggtactgga tgagctgggt gcgccaggcc   120

cctggcaaag gcctggaatg gatcggcgag atcaaccccg acagcagcac catcaactac   180

gcccccagcc tgaaggacaa gttcatcatc agccgggaca acgccaagaa cagcctgtac   240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actattgcgc cagacccgac   300

ggcaactact ggtacttcga cgtgtggggc cagggcaccc tcgtgacagt gtctggcagc   360

acaagcggct ctggcaagcc tggatctggc gagggctcta ccaagggcga catccagatg   420

acccagagcc ccagcagcct gtctgccagc gtgggcgaca gagtgaccat cacatgcaag   480

gccagccagg acgtgggaat cgccgtggcc tggtatcagc agaaacccgg caaggtgccc   540

aagctgctga tctactgggc cagcaccaga cacaccggcg tgcccgatag attttccggc   600

agcggctccg gcaccgactt caccctgaca atcagctccc tgcagcctga ggacgtggcc   660 acctactact gccagcagta cagcagctac ccctacacct tcggacaggg caccaaggtg 720

gaaatcaagc gg 732

<210> 21
<211> 720
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 21
caggtgcagc tgcagcagtc tggccccgag ctggaaaaac ctggcgcctc cgtgaagatc 60

agctgcaagg ccagcggcta cagcttcacc ggctacacca tgaactgggt caagcagagc 120

cacggcaaga gcctggaatg gatcggcctg atcacccccct acaacggcgc cagcagctac 180

aaccagaagt tccggggcaa ggccaccctg accgtggaca agtctagcag caccgcctac 240

atggacctgc tgagcctgac cagcgaggac agcgccgtgt acttctgtgc cagaggcggc 300

tacgacggca gaggcttcga ttattggggc cagggcacca ccgtgacagt gtctagcgga 360

gtgggaggat ctggcggagg cggaagtggc ggaggggggat ctgatatcga gctgacccag 420

agccccgcca tcatgtctgc tagccctggc gagaaagtga ccatgacctg cagcgccagc 480

tccagcgtgt cctacatgca ctggtatcag cagaagtccg gcaccagccc caagcggtgg 540

atctacgaca caagcaagct ggcctctggc gtgcccggca gattttctgg cagcggctcc 600

ggcaacagct actccctgac aatcagcagc gtggaagccg aggacgacgc cacctactac 660

tgccagcagt ggagcggcta ccccctgact tttggagccg gcaccaagct ggaaatcaag 720

<210> 22
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 22
agccaggaag agatgaccaa gaaccaggtg tccctgacct gcctcgtgaa gggcttctac 60

<210> 23
<211> 141
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 23
aagcctacca caacccctgc ccccagacct cctacacccg cccctacaat tgccagccag 60

cctctgtctc tgaggcccga ggcttgtaga cctgctgctg gcggagccgt gcacaccaga 120

ggactggatt tcgcctgcga c 141

<210> 24
<211> 696
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 24
agcgagagca agtacggccc tccctgcccc ccttgccctg cccccgagtt cctgggcgga 60

cccagcgtgt tcctgttccc ccccaagccc aaggacaccc tgatgatcag ccggaccccc 120

gaggtgacct gtgtggtggt ggacgtgtcc caggaggacc ccgaggtcca gttcaactgg 180

tacgtggacg gcgtggaggt gcacaacgcc aagaccaagc cccgggagga gcagttcaat 240

agcacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaag 300

gaatacaagt gtaaggtgtc caacaagggc ctgcccagca gcatcgagaa aaccatcagc 360

aaggccaagg gccagcctcg ggagccccag gtgtacaccc tgccccctag ccaagaggag 420

atgaccaaga atcaggtgtc cctgacctgc ctggtgaagg gcttctaccc cagcgacatc 480

gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac cccccctgtg 540

ctggacagcg acggcagctt cttcctgtac agcaggctga ccgtggacaa gagccggtgg 600

caggagggca acgtctttag ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 660

cagaagagcc tgtccctgag cctgggcaag atgttc 696

<210> 25
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 25
agccaggaag agatgaccaa gaaccaggtg tccctgacct gcctcgtgaa gggcttctac 60

<210> 26
<211> 696
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 26
agcgagagca agtacggccc tccctgcccc ccttgccctg cccccgagtt cctgggcgga 60

cccagcgtgt tcctgttccc ccccaagccc aaggacaccc tgatgatcag ccggaccccc 120

gaggtgacct gtgtggtggt ggacgtgtcc caggaggacc ccgaggtcca gttcaactgg 180

tacgtggacg gcgtggaggt gcacaacgcc aagaccaagc cccgggagga gcagttccag 240

agcacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaag 300

gaatacaagt gtaaggtgtc caacaagggc ctgcccagca gcatcgagaa aaccatcagc 360

aaggccaagg gccagcctcg ggagccccag gtgtacaccc tgccccctag ccaagaggag 420 atgaccaaga atcaggtgtc cctgacctgc ctggtgaagg gcttctaccc cagcgacatc 480

gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac ccccccctgtg 540

ctggacagcg acggcagctt cttcctgtac agcaggctga ccgtggacaa gagccggtgg 600

caggagggca acgtctttag ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 660

cagaagagcc tgtccctgag cctgggcaag atgttc 696

<210> 27
<211> 696
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 27
agcgagagca agtacggccc tccctgcccc ccttgccctg cccccgagtt cgaaggcgga 60

cccagcgtgt tcctgttccc ccccaagccc aaggacaccc tgatgatcag ccggaccccc 120

gaggtgacct gtgtggtggt ggacgtgtcc caggaggacc ccgaggtcca gttcaactgg 180

tacgtggacg gcgtggaggt gcacaacgcc aagaccaagc cccgggagga gcagttccag 240

agcacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaag 300

gaatacaagt gtaaggtgtc caacaagggc ctgcccagca gcatcgagaa aaccatcagc 360

aaggccaagg gccagcctcg ggagccccag gtgtacaccc tgcccccctag ccaagaggag 420

atgaccaaga atcaggtgtc cctgacctgc ctggtgaagg gcttctaccc cagcgacatc 480

gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac ccccccctgtg 540

ctggacagcg acggcagctt cttcctgtac agcaggctga ccgtggacaa gagccggtgg 600

caggagggca acgtctttag ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 660

cagaagagcc tgtccctgag cctgggcaag atgttc 696

<210> 28
<211> 711
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 28
atggtgtcca agggcgagga actgatcaaa gaaaacatgc acatgaagct gtacatggaa 60

ggcaccgtga acaaccacca cttcaagtgc accagcgagg gagagggcaa gccctacgag 120

ggcacccaga ccatgcggat caaggtggtc gagggcggac ctctgccctt cgccttcgac 180

atcctggcca caagcttcat gtacggcagc aagaccttca tcaaccacac ccagggcatc 240

cccgatttct tcaagcagag cttccccgag ggcttcacct gggagagagt gaccacctac 300

gaggacggcg gcgtgctgac cgccacccag gacaccagcc tgcaggacgg ctgcctgatc 360

tacaacgtga agatccgggg cgtgaacttc cccagcaacg gccccgtgat gcagaagaaa 420 accctgggct gggaggccag caccgagatg ctgtaccctg ccgatggcgg cctggaaggc 480

agagccgaca tggccctgaa actggtcggc ggagggcacc tgatctgcaa cctgaaaacc 540

acctacagaa gcaagaagcc cgccaagaac ctgaagatgc ccggcgtgta ctacgtggac 600

cggcggctgg aaaggatcaa agaggccgac aaagaaacct acgtggagca gcacgaggtg 660

gccgtggccc ggtactgcga cctgccctcc aagctgggcc acaaactgaa c 711

<210> 29
<211> 333
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 29
atgatcgaga agtccttcgt gatcaccgac ccccggctgc ccgactaccc tatcatcttt 60

gccagcgacg gcttcctgga actgaccgag tacagccggg aagagatcat gggccggaac 120

gccagattcc tgcagggccc cgaaaccgat caggccaccg tgcagaagat ccgggacgcc 180

atcagggacc agcgggaaac cacagtgcag ctgatcaact acaccaagag cggcaagaag 240

ttctggaacc tgctgcatct gcagcccgtg cgggatagaa agggcggcct gcagtacttc 300

atcggcgtgc agctcgtggg cagcgaccac gtg 333

<210> 30
<211> 675
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 30
atggccagca gcgaggacgt gatcaaagaa ttcatgcggt tcaaagtgcg gatggaaggc 60

agcgtgaacg gccacgagtt cgagattgag ggcgagggcg aaggcagacc ctacgaggga 120

acacagaccg ccaagctgaa agtgaccaag ggcggacccc tgcccttcgc ctgggatatc 180

ctgagccccc agttccagta cggcagcaag gtgtacgtga agcaccccgc cgacatcccc 240

gactacaaga agctgagctt ccccgagggc ttcaagtggg agagagtgat gaacttcgag 300

gacggcggcg tcgtgaccgt gacccaggat agctctctgc aggacggcag cttcatctac 360

aaagtgaagt ttatcggcgt gaacttcccc agcgacggcc ccgtgatgca gaaaaagacc 420

atgggctggg aggccagcac cgagagactg taccctagag atggcgtgct gaagggcgag 480

atccacaagg ccctgaagct gaaggatggc ggccactacc tggtggaatt caagagcatc 540

tacatggcca agaaacccgt gcagctgccc ggctactact acgtggacag caagctggac 600

atcaccagcc acaacgagga ctacaccatc gtggaacagt acgagcgggc cgagggccgg 660

caccatctgt ttctg 675

<210> 31
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 31
atggtgtcca agggcgagga actgttcacc ggcgtggtgc ccatcctggt ggaactggat   60

ggcgacgtga acggccacaa gttcagcgtg tccggcgagg gcgaaggcga cgccacatat   120

ggcaagctga ccctgaagct gatctgcacc accggcaagc tgcccgtgcc ttggcctacc   180

ctcgtgacca cactgggcta cggcctgcag tgcttcgcca gataccccga ccatatgaag   240

cagcacgact tcttcaagag cgccatgccc gagggctacg tgcaggaacg gaccatcttc   300

tttaaggacg acggcaacta caagaccagg gccgaagtga agttcgaggg cgacaccctc   360

gtgaaccgga tcgagctgaa gggcatcgac ttcaaagagg acggcaacat cctgggccac   420

aagctggagt acaactacaa cagccacaac gtgtacatca ccgccgacaa gcagaagaac   480

ggcatcaagg ccaacttcaa gatccggcac aacatcgagg acggcggcgt gcagctggcc   540

gatcactacc agcagaacac ccctatcggc gacggccctg tgctgctgcc cgacaatcac   600

tacctgagct accagagcgc cctgagcaag gaccccaacg agaagcggga ccacatggtg   660

ctgctggaat tcgtgaccgc cgctggcatc accctgggca tggacgagct gtacaag   717

<210> 32
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 32
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac   60

ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac   120

ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc   180

ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag   240

cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc   300

ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg   360

gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac   420

aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac   480

ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc   540

gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac   600

tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc   660

ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaag   717

<210> 33
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 33
gccaagggcc agcctcggga gccccaggtg tacaccctgc cccctagcca agaggagatg   60

accaagaatc aggtgtccct gacctgcctg gtgaagggct tctaccccag cgacatcgcc   120

gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg   180

gacagcgacg gcagcttctt cctgtacagc aggctgaccg tggacaagag ccggtggcag   240

gagggcaacg tctttagctg ctccgtgatg cacgaggccc tgcacaacca ctacacccag   300

aagagcctgt ccctgagcct gggcaagatg ttctacccat acgatgttcc agattacgct   360

tac   363

<210> 34
<211> 708
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 34
atggtgagca agggcgagga gaccacaatg ggcgtaatca agcccgacat gaagatcaag   60

ctgaagatgg agggcaacgt gaatggccac gccttcgtga tcgagggcga gggcgagggc   120

aagccctacg acggcaccaa caccatcaac ctggaggtga aggagggagc ccccctgccc   180

ttctcctacg acattctgac caccgcgttc gcctacggca acagggcctt caccaagtac   240

cccgacgaca tccccaacta cttcaagcag tccttccccg agggctactc ttgggagcgc   300

accatgacct tcgaggacaa gggcatcgtg aaggtgaagt ccgacatctc catggaggag   360

gactccttca tctacgagat acacctcaag ggcgagaact tcccccccaa cggccccgtg   420

atgcagaaga agaccaccgg ctgggacgcc tccaccgaga ggatgtacgt gcgcgacggc   480

gtgctgaagg gcgacgtcaa gcacaagctg ctgctggagg gcggcggcca ccaccgcgtt   540

gacttcaaga ccatctacag ggccaagaag gcggtgaagc tgcccgacta tcactttgtg   600

gaccaccgca tcgagatcct gaaccacgac aaggactaca acaaggtgac cgtttacgag   660

agcgccgtgg cccgcaactc caccgacggc atggacgagc tgtacaag   708

<210> 35
<211> 423
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 35
aagcctacca caacccctgc ccccagacct cctacacccg cccctacaat tgccagccag   60

cctctgtctc tgaggcccga ggcttgtaga cctgctgctg gcggagccgt gcacaccaga 120

ggactggatt tcgcctgcga caagcctacc acaacccctg cccccagacc tcctacaccc 180

gcccctacaa ttgccagcca gcctctgtct ctgaggcccg aggcttgtag acctgctgct 240

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acagcagcgg cggcggcggc 300

agcggcggcg gcggcagcgg cggcggcggc agcgcgcagc tgaaaaaaaa actgcaggcg 360

ctgaaaaaaa aaaacgcgca gctgaaatgg aaactgcagg cgctgaaaaa aaaactggcg 420

cag 423

<210> 36
<211> 423
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 36
aagcctacca caacccctgc ccccagacct cctacacccg cccctacaat tgccagccag 60

cctctgtctc tgaggcccga ggcttgtaga cctgctgctg gcggagccgt gcacaccaga 120

ggactggatt tcgcctgcga caagcctacc acaacccctg cccccagacc tcctacaccc 180

gcccctacaa ttgccagcca gcctctgtct ctgaggcccg aggcttgtag acctgctgct 240

ggcggagccg tgcacaccag aggactggat ttcgcctgcg acagcagcgg cggcggcggc 300

agcggcggcg gcggcagcgg cggcggcggc agcgcccagc tggaaaaaga gctgcaggcc 360

ctggaaaaag aaaacgctca gctggaatgg gaactgcagg ctctggaaaa agagctggcc 420

cag 423

<210> 37
<211> 69
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 37
tgggtgctgg tcgtggtggg tggcgtgctg gcctgctaca gcctgctggt gacagtggcc 60

ttcatcatc 69

<210> 38
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 38
attatctcat tcttcctggc cctgacctct accgccctgc tgtttctgct gttctttctg 60

accctgcggt tcagcgtggt g 81

<210> 39
<211> 84
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 39
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc   60

accctttact gcaaccacag gaac   84

<210> 40
<211> 63
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 40
ctctgctacc tgctggatgg aatcctcttc atctatggtg tcattctcac tgccttgttc   60

ctg   63

<210> 41
<211> 144
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
cagcggcgga agtacagaag caacaagggc gagagccccg tggaacctgc cgagccttgc   60

agatacagct gccccagaga ggaagagggc agcaccatcc caatccagga agattaccgg   120

aagcccgagc ccgcctgtag ccct   144

<210> 42
<211> 132
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
ttttgggtga ggagcaagcg gagcagaggc ggccacagcg actacatgaa catgaccccc   60

cggaggcctg gccccacccg gaagcactac cagccctacg cccctcccag ggacttcgcc   120

gcctaccgga gc   132

<210> 43
<211> 132
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 43
ttttgggtga ggagcaagcg gagcagaggc ggccacagcg acttcatgaa catgaccccc   60

cggaggcctg gccccacccg gaagcactac cagccctacg cccctcccag ggacttcgcc   120

gcctaccgga gc   132

<210> 44
<211> 108
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
agggaccaga gactgcctcc cgatgcccac aaacctccag gcggcggaag cttcagaacc   60

cccatccagg aagaacaggc cgacgcccac agcaccctgg ccaagatt   108

<210> 45
<211> 126
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 45
aagcggggca gaaagaagct gctgtacatc ttcaagcagc ccttcatgcg gcccgtgcag   60

accacccagg aagaggacgg ctgctcctgc agattccccg aggaagaaga aggcggctgc   120

gagctg   126

<210> 46
<211> 102
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 46
aagaaaaagt acagcagcag cgtgcacgac cccaacggcg agtacatgtt catgcgggcc   60

gtgaacaccg ccaagaagtc cagactgacc gacgtgaccc tg   102

<210> 47
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 47
cgggtgaagt tcagccggag cgccgacgcc cctgcctacc agcagggcca gaaccagctg   60

tacaacgagc tgaacctggg ccggagggag gagtacgacg tgctggacaa gcggagaggc   120

cgggaccctg agatgggcgg caagccccgg agaaagaacc ctcaggaggg cctgtataac   180 gaactgcaga aagacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagcgg 240

cggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggatacc 300

tacgacgccc tgcacatgca ggccctgccc cccaga 336

<210> 48
<211> 759
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 48
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60

attacctgcc gcagcagcca gaacattgtg catagcaacg gcaacaccta tctggattgg 120

tatcagcaga ccccgggcaa agcgccgaaa ctgctgattt ataaagtgag caaccgcttt 180

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cctggcagcg gcgagggcag caccaagggc agccaggtgc agctgcagca gagcggcgcg 420

gaagtgaaaa aaccgggcag cagcgtgaaa gtgagctgca aagcgagcgg ctataccttt 480

accaactatt atatttattg ggtgcgccag gcgccgggcc agggcctgga atggattggc 540

ggcattaacc cgaccagcgg cggcagcaac tttaacgaaa aatttaaaac ccgcgtgacc 600

attaccgcgg atgaaagcag caccaccgcg tatatggaac tgagcagcct gcgcagcgaa 660

gataccgcgt tttatttttg cacccgccag ggcctgtggt ttgatagcga tggccgcggc 720

tttgattttt ggggccaggg caccaccgtg accgtgagc 759

<210> 49
<211> 732
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 49
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aacggcagcc cgcgcctgct gattaaatat gcgagcgaaa gcattagcgg cattccgagc 180

cgctttagcg gcagcggcag cggcaccgat tttaccctga gcattaacag cgtggaaagc 240

gaagatattg cggattatta ttgccagcag aacaacaact ggccgaccac ctttggcgcg 300

ggcaccaaac tggaactgaa aggcagcacc tccggcagcg gcaagcctgg cagcggcgag 360

ggcagcacca agggcagcca ggtgcagctg aaacagagcg gcccgggcct ggtgcagccg 420

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ggcaacaccg attataacac cccgtttacc agccgcctga gcattaacaa agataacagc 600

aaaagccagg tgtttttaa aatgaacagc ctgcagagca acgataccgc gatttattat 660

tgcgcgcgcg cgctgaccta ttatgattat gaatttgcgt attggggcca gggcaccctg 720

gtgaccgtga gc 732

<210> 50
<211> 726
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
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agctgcaaag cgagcggcta tagctttacc ggctataaca tgaactgggt gaaacagagc 120

catggcaaaa gcctggaatg gattggccat attgatccgt attatggcga taccagctat 180

aaccagaaat ttcgcggcaa agcgaccctg accgtggata aaagcagcag caccgcgtat 240

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tattatggcc attggtattt tgatgtgtgg ggcgcgggca ccaccgtgac cgtgagcagc 360

ggcggaggcg gctctggcgg cggaggatca ggtggcggag gatccgatat tcagatgacc 420

cagagcccga gcagcctgag cgcgagcctg ggcgaacgcg tgagcctgac ctgccgcgcg 480

agccaggata ttggcagcag cctgaactgg ctgcagcagg gcccggatgg caccattaaa 540

cgcctgattt atgcgaccag cagcctggat agcggcgtgc cgaaacgctt tagcggcagc 600

cgcagcggca gcgattatag cctgaccatt agcagcctgg aaagcgaaga ttttgtggat 660

tattattgcc tgcagtatgt gagcagcccg ccgacctttg gcgcgggcac caaactggaa 720

ctgaaa 726

<210> 51
<211> 111
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic polypeptide

<400> 51

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50   55   60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                85   90   95

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100   105   110

<210> 52
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic polypeptide

<400> 52

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    50   55   60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65   70   75   80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
            100   105

<210> 53
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic polypeptide

<400> 53

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    50   55   60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65   70   75   80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100   105   110

<210> 54
<211> 111
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic polypeptide

<400> 54

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        35   40   45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    50   55   60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                85   90   95

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100   105   110

<210> 55
<211> 2034
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
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atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg   120

gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag   180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg   240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg   300

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cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc   540

gtgtcctgga tccggcagcc ccctaggaag ggcctggagt ggctgggcgt gatctggggc   600

agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac   660

agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac   720

tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc   780

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gaggtccagt tcaactggta cgtggacggc gtggaggtgc acaacgccaa gaccaagccc   1020

cgggaggagc agttcaatag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag   1080

gactggctga acggcaagga atacaagtgt aaggtgtcca acaagggcct gcccagcagc   1140

atcgagaaaa ccatcagcaa ggccaagggc cagcctcggg agccccaggt gtacaccctg   1200

ccccctagcc aagaggagat gaccaagaat caggtgtccc tgacctgcct ggtgaagggc   1260

ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac   1320

aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc   1380

gtggacaaga gccggtggca ggagggcaac gtctttagct gctccgtgat gcacgaggcc   1440

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gacaagcgga gaggccggga ccctgagatg ggcggcaagc cccggagaaa gaaccctcag   1860

gagggcctgt ataacgaact gcagaaagac aagatggccg aggcctacag cgagatcggc   1920 atgaagggcg agcggcggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1980

gccaccaagg atacctacga cgccctgcac atgcaggccc tgccccccag atga 2034

<210> 56
<211> 2040
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
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gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

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gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

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cctcaggagg gcctgtataa cgaactgcag aaagacaaga tggccgaggc ctacagcgag 1920

atcggcatga agggcgagcg gcggaggggc aagggccacg acggcctgta ccagggcctg 1980

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<210> 57
<211> 2037
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
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<210> 58
<211> 2037
<212> DNA
<213> Artificial sequence

<220>
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gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

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tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780

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ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1320

aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc 1380

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gaaggcggct gcgaactgcg ggtgaagttc agccggagcg ccgacgcccc tgcctaccag 1740

cagggccaga accagctgta caacgagctg aacctgggcc ggagggagga gtacgacgtg 1800

ctggacaagc ggagaggccg ggaccctgag atgggcggca agccccggag aaagaaccct 1860

caggagggcc tgtataacga actgcagaaa gacaagatgg ccgaggccta cagcgagatc 1920

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<210> 59
<211> 2160
<212> DNA
<213> Artificial sequence

<220>
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