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(71) Applicants: **CELLULAR BIOMEDICINE GROUP HK LIMITED** [CN/CN]; Room 417, 4th Floor, Lippo Centre, Tower Two, No.89 Queensway, Admiralty, Hong Kong (CN). **CELLULAR BIOMEDICINE GROUP INC.** [US/US]; 9605 Medical Center Drive, Suite 100, Rockville, MD 20850 (US).

(72) Inventors: **YAO, Yihong**; Room 417, 4th Floor, Lippo Centre, Tower Two, No.89 Queensway, Admiralty, Hong Kong (CN). **HUANG, Jiaqi**; Room 417, 4th Floor, Lippo Centre, Tower Two, No.89 Queensway, Admiralty, Hong Kong (CN). **YAO, Xin**; Room 417, 4th Floor, Lippo Centre, Tower Two, No.89 Queensway, Admiralty, Hong Kong (CN).

(74) Agent: **DAVITZ, Michael, A.** et al.; Leason Ellis LLP, One Barker Avenue, Fifth Floor, White Plains, NY 10601 (US).

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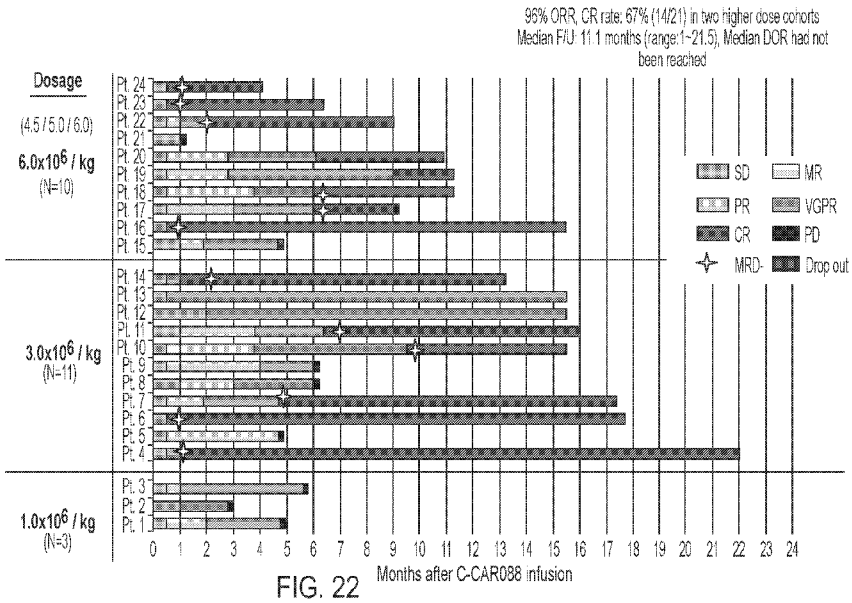

FIG. 22

(57) Abstract: The present disclosure provides BCMA-targeted chimeric antigen receptors (CARs) as well as preparation methods and applications thereof. The CARs of the present disclosure targets BCMA-positive cells, and can be used for treating BCMA-positive B-cell lymphoma, multiple myeloma and plasma cell leukemia.

WO 2022/119923 A1

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BCMA-TARGETED CHIMERIC ANTIGEN RECEPTORS

CROSS REFERENCE TO RELATED APPLICATIONS

The present application claims priority to U.S. Provisional Application Nos. 63/120,692 (filed on December 2, 2020), 63/153,666 (filed on February 25, 2021), and 63/212,289 (filed on June 18, 2021), and U.S. application No. 17/476,661 (filed on September 16, 2021), each of which is hereby incorporated by reference in its entirety.

SEQUENCE LISTING

This application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on December 1, 2021, is named 11299-008884-WO1_ST25.txt and is 41 KB in size.

TECHNICAL FIELD

The invention relates to the field of biomedicine, and more particularly to chimeric antigen receptors targeting BCMA, as well as preparation methods and applications thereof.

BACKGROUND

BCMA is a B cell maturation antigen, also known as CD269 or TNFRSF17, and is a member of the tumor necrosis factor receptor superfamily. Its ligands are B cell activating factor (BAFF) and a proliferation-induced ligand (APRIL).

Binding of BCMA to BAFF and APRIL activates NF-kB and induces up-regulation of anti-apoptotic Bcl-2 members such as Bcl-xL or Bcl-2 and Mcl-1. The interaction between BCMA and its ligands regulates humoral immunity as well as the growth and differentiation of B cells from different aspects to maintain a stable and balanced environment in the human body.

The expression of BCMA is restricted to B cell lines. It is expressed on plasma blasts, plasma cells and a portion of mature B cells, and increased at the differentiation of terminal B cells. While in most B cells, such as naive B cells, memory B cells and B cell germinal centers and other organs, BCMA is not expressed. It has been reported that the expression of BCMA is important for long-lived, fixed plasma cells in the bone marrow. Therefore, plasma cells in the bone marrow are reduced in BCMA-deficient mice, but plasma cell level in the spleen is not affected. Mature B

cells can normally differentiate into plasma cells in BCMA knockout mice. The BCMA knockout mice looked normal and seemed healthy, and the number of B cells was normal, but the plasma cells could not survive for a long time.

BCMA is also highly expressed in malignant plasma cells, such as multiple myeloma and plasma cell leukemia. BCMA is also detected in HRS cells of patients with Hodgkin's lymphoma. In America, malignant tumors of blood system account for about 10% of all malignant tumors, and myeloma accounts for 15% of all malignant hematological tumors. According to the literature, the expression of BCMA is associated with progression of multiple myeloma disease. The BCMA gene is highly expressed in myeloma samples, but is low expressed in chronic lymphocytic leukemia, acute lymphocytic leukemia, and acute T-cell lymphocytic leukemia. B cell lymphomas were significantly increased in a mouse model overexpressing BCMA ligands BAFF and APRIL. Ligands that bind to BCMA have been shown to regulate the growth and survival of multiple myeloma cells expressing BCMA. The combination of BCMA with BAFF and APRIL can make malignant plasma cells survive. Therefore, loss of tumor cells expressing BCMA and distribution of the interaction between BCMA ligand and receptor can improve outcome in the treatment of multiple myeloma or other BCMA positive B cell lines malignant lymphoma.

Multiple myeloma, also known as plasmacytoma or Keller's disease, is a malignant tumor of the refractory B cell line, characterized by abnormal proliferation of plasma cells. Plasma cells are a type of leukocyte that is responsible for production of antibodies. According to data released by the National Cancer Institute in 2017, myeloma accounts for 1.8% of all tumor cases, with a mortality rate of 2.1%. The statistical results of 2010-2014 show that the incidence rate is about 6.6 in 100,000 per year and the mortality rate is about 50%. Multiple myeloma is a middle-aged disease. The median age of onset in Europe and the United States is 68 years old. There are more males than females. The peak age of onset in China is 55-65 years old, and the ratio of male to female is 2.35:1. There is no confirmed epidemiological data on multiple myeloma in China. It is generally estimated that the incidence rate is similar to that in surrounding southeast Asia and Japan, about one in 100,000. Traditional treatments for multiple myeloma include chemotherapy and hematopoietic stem cell transplantation, but these methods have a high recurrence rate. Bortezomib (PS -341) is first proteasome inhibitor, which is approved by the FDA in 2003 for the treatment of relapsed refractory multiple myeloma, either alone or in combination with existing medications. The results were gratifying. The drug was also marketed in China in 2005 and has

become one of the options for the treatment of multiple myeloma with thalidomide and dexamethasone. The treatment of multiple myeloma is usually combined. However, if multiple drugs are used at the same time, there are also negative effects of costly and cumulative side effects. There is still a clinical need to develop new methods for the treatment of multiple myeloma.

Recently, immunotherapy, especially adoptive T-cell therapy, has shown strong efficacy and bright prospects in clinical trials for the treatment of malignant tumors of the blood system. T cells can be genetically modified to express a chimeric antigen receptor (CAR), which includes an antigen recognition portion and a T cell activation region. Using the antigen binding properties of monoclonal antibodies, CAR can redirect the specificity and reactivity of T cell and target in a non-MHC restricted manner. This non-MHC restricted antigen recognition allows CAR-expressing T cells to recognize antigen without antigen processing, thus avoiding a major mechanism of tumor escape. In addition, CAR does not produce dimers with alpha chain and beta chain of the endogenous TCR.

At present, two chimeric antigen receptor T cell therapy (CAR-T) products targeting CD19 have been approved for the treatment of acute lymphoblastic leukemia in children and young adult patients and adult second-line or multi-line system therapy of recurrent or refractory large B-cell lymphoma. However, CD19 is rarely expressed in malignant plasma cells of multiple myeloma. There is an urgent need to develop a CAR-T product that targets BCMA for the treatment of multiple myeloma.

SUMMARY

It is an object of the present disclosure to provide chimeric antigen receptors targeting BCMA as well as preparation methods and applications thereof.

The present disclosure provides for a chimeric antigen receptor (CAR). The CAR may comprise: an anti-BCMA antigen-binding region which comprises a light chain variable region (V_L) and a heavy chain variable region (V_H).

V_L may comprise three complementarity determining regions (CDRs), LCDR1, LCDR2 and LCDR3; V_H may comprise three CDRs, HCDR1, HCDR2 and HCDR3.

In certain embodiments, LCDR1, LCDR2 and LCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, respectively. HCDR1, HCDR2 and HCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, respectively.

In certain embodiments, LCDR1, LCDR2 and LCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, respectively. HCDR1, HCDR2 and HCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, respectively.

In certain embodiments, LCDR1, LCDR2 and LCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, respectively. HCDR1, HCDR2 and HCDR3 may have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, respectively.

V_L and V_H of the CAR may have amino acid sequences about 80% to about 100% identical to amino acid sequences set forth in (a) SEQ ID NO: 1 and SEQ ID NO: 2, respectively; (a) SEQ ID NO: 3 and SEQ ID NO: 4, respectively; or (a) SEQ ID NO: 5 and SEQ ID NO: 6, respectively.

In certain embodiments, V_L is located at the N-terminus of V_H.

The anti-BCMA antigen-binding region may be a single-chain variable fragment (scFv) that specifically binds BCMA.

The CAR may further comprise one or more of the following: (a) a signal peptide, (b) a hinge region, (c) a transmembrane domain, (d) a co-stimulatory region, and (e) a cytoplasmic signaling domain.

The co-stimulatory region may comprise a co-stimulatory region of (or may be derived from) 4-1BB (CD137), CD28, OX40, CD2, CD7, CD27, CD30, CD40, CD70, CD134, PD1, Dap10, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), NKG2D, GITR, TLR2, or combinations thereof.

The cytoplasmic signaling domain may comprise a cytoplasmic signaling domain of (or may be derived from) CD3ζ.

The hinge region may comprise a hinge region of (or may be derived from) CD8, CD28, CD137, Ig4, or combinations thereof.

The transmembrane domain may comprise a transmembrane domain of (or may be derived from) CD8, CD28, CD3ε, CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or combinations thereof.

The present disclosure provides for an immune cell expressing the present CAR. The immune cell may be a T cell or a natural killer (NK) cell. The immune cell may be allogeneic or autologous.

Also encompassed by the present disclosure is a nucleic acid encoding the present CAR.

The present disclosure further provides for a vector comprising the present nucleic acid.

The present disclosure provides for a method of treating cancer. The method may comprise administering the immune cell to a subject in need thereof.

The cancer may be a hematologic cancer. The cancer may be a plasma-cell malignancy. The cancer may be a BCMA-positive malignancy. The cancer may be multiple myeloma (MM), or plasma cell leukemia.

The immune cell may be administered by infusion, injection, transfusion, implantation, and/or transplantation.

The immune cell may be administered intravenously, subcutaneously, intradermally, intranodally, intratumorally, intramedullary, intramuscularly, or intraperitoneally.

The immune cell may be administered via intravenous infusion.

The subject may be a human.

The present disclosure provides for a method for treating cancer. The method may comprise administering the present immune cell to a subject in need of.

The chimeric antigen receptor (CAR) may generate an area under the curve (AUC) ranging from about 5.0e+05 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA, from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA, from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA, or from about 7.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA, in the blood of the subject in about 28 days after administration.

The chimeric antigen receptor (CAR) may generate a maximum plasma concentration (C_{max}) ranging from about $5x10^4$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA, from about $5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA, or from about $7.5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1x10^6$ copies/gDNA, in the blood of the subject.

The CAR may have a T_{max} ranging from about 12 days to about 25 days, from about 14 days to about 20 days, or from about 6 days to about 22 days.

In certain embodiments, the anti-BCMA antigen-binding region includes a light chain variable region (V_L) comprising an amino acid sequence at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5.

In certain embodiments, the anti-BCMA antigen-binding region includes a heavy chain variable region (V_H) comprising an amino acid sequence at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or

about 97%, at least or about 98%, at least or about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6.

A light chain variable region of the anti-BCMA antigen-binding region can comprise one, two, or three complementarity determining regions (CDRs) that are at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the CDRs of a light chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 1, respectively), or the CDRs of a light chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 3, respectively), or the CDRs of a light chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 5, respectively).

A heavy chain variable region of the anti-BCMA antigen-binding region can comprise one, two, or three complementarity determining regions (CDRs) that are at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the CDRs of a heavy chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 2, respectively), or the CDRs of a heavy chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 4, respectively), or the CDRs of a heavy chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 6, respectively).

A light chain variable region of the anti-BCMA antigen-binding region can comprise one,

two, or three complementarity determining regions (CDRs) that are at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the CDRs of a light chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, respectively), or the CDRs of a light chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, respectively), or the CDRs of a light chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, respectively).

A heavy chain variable region of the anti-BCMA antigen-binding region can comprise one, two, or three complementarity determining regions (CDRs) that are at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the CDRs of a heavy chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, respectively), or the CDRs of a heavy chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, respectively), or the CDRs of a heavy chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to CDRs of a heavy chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 1), and a heavy chain variable region of the

anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to CDRs of a heavy chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 2, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a light chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, respectively), and a heavy chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a heavy chain variable region of the BCMA-20 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to CDRs of a light chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 3, respectively), and a heavy chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to CDRs of a heavy chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 4, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a light chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, respectively), and a heavy chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a heavy chain variable region of the BCMA-CA8 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical to CDRs of a light chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in position 24-34, position 50-56, position 89-97 of SEQ ID NO: 5, respectively), and a heavy chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical to CDRs of a heavy chain

variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in position 31-35, position 50-66, position 99-110 of SEQ ID NO: 6, respectively).

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a light chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, respectively), and a heavy chain variable region of the anti-BCMA antigen-binding region includes three CDRs that are identical (e.g., 80% - 100% identical) to the CDRs of a heavy chain variable region of the BCMA-MO6 antibody (CDR1, CDR2 and CDR3 as set forth in SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, respectively).

In certain embodiments, the CAR may comprise an amino acid sequence about 80% to about 100%, about 85% to about 100%, about 90% to about 100%, about 95% to about 100%, at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the amino acid sequence set forth in SEQ ID NO: 59, SEQ ID NO: 61, or SEQ ID NO: 63.

In certain embodiments, the nucleic acid encoding the CAR may comprise a nucleic acid sequence about 80% to about 100%, about 85% to about 100%, about 90% to about 100%, about 95% to about 100%, at least or about 70%, at least or about 75%, at least or about 80%, at least or about 85%, at least or about 90%, at least or about 95%, at least or about 99%, at least or about 81%, at least or about 82%, at least or about 83%, at least or about 84%, at least or about 85%, at least or about 86%, at least or about 87%, at least or about 88%, at least or about 89%, at least or about 90%, at least or about 91%, at least or about 92%, at least or about 93%, at least or about 94%, at least or about 95%, at least or about 96%, at least or about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the amino acid sequence set forth in SEQ ID NO: 58, SEQ ID NO: 60, or SEQ ID NO: 62.

In certain embodiments, the CAR may generate an area under the curve (AUC) ranging from about 0.5e+06 copies/μg genomic DNA (copies/gDNA) to about 2e+07 copies/gDNA, from

about 5.0e+05 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA, from about 5.0e+05 copies/μg genomic DNA (copies/gDNA) to about 2e+07 copies/gDNA, from about 5.0e+05 copies/μg genomic DNA (copies/gDNA) to about 1.5e+07 copies/gDNA, from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA, from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA, from about 7.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA, from about 8.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA, from about 0.5e+06 copies/μg genomic DNA (copies/gDNA) to about 4e+06 copies/gDNA, from about 0.5e+06 copies/μg genomic DNA (copies/gDNA) to about 3.5e+06 copies/gDNA, from about 1e+06 copies/μg genomic DNA (copies/gDNA) to about 3.5e+06 copies/gDNA, from about 1.2e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, from about 0.8e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, from about 1.6e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, from about 1e+06 copies/μg genomic DNA (copies/gDNA) to about 2e+06 copies/gDNA, from about 0.6e+06 copies/μg genomic DNA (copies/gDNA) to about 1.8e+06 copies/gDNA, from about 3e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, from about 0.5e+06 copies/μg genomic DNA (copies/gDNA) to about 1.7e+06 copies/gDNA, from about 2e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, from about 1.5e+06 copies/μg genomic DNA (copies/gDNA) to about 2e+06 copies/gDNA, or from about 1e+06 copies/μg genomic DNA (copies/gDNA) to about 3.2e+06 copies/gDNA, in the blood of the subject in about 28 days after administration of the CAR to the subject. The AUC may be a median AUC.

In certain embodiments, the CAR generates a maximum plasma concentration (C_{max}) ranging from about $5x10^4$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA, from about $5x10^4$ copies/μg genomic DNA (copies/gDNA) to about $1.5x10^6$ copies/gDNA, from about $5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA, from about $7.5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1x10^6$ copies/gDNA, from about $7x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1x10^6$ copies/gDNA, from about $8x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1x10^6$

copies/gDNA, from about $7.5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.5x10^6$ copies/gDNA, from about $7x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.5x10^6$ copies/gDNA, from about $8x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.5x10^6$ copies/gDNA, from about 0.8e+05 copies/μg genomic DNA (copies/gDNA) to about 3.5e+05 copies/gDNA, from about 1e+05 copies/μg genomic DNA (copies/gDNA) to about 3.5e+05 copies/gDNA, from about 1e+05 copies/μg genomic DNA (copies/gDNA) to about 1.6e+05 copies/gDNA, from about 1e+05 copies/μg genomic DNA (copies/gDNA) to about 3.3e+05 copies/gDNA, from about 0.8e+05 copies/μg genomic DNA (copies/gDNA) to about 1.5e+05 copies/gDNA, from about 0.8e+05 copies/μg genomic DNA (copies/gDNA) to about 2e+05 copies/gDNA, from about 1e+05 copies/μg genomic DNA (copies/gDNA) to about 2e+05 copies/gDNA, from about 2e+05 copies/μg genomic DNA (copies/gDNA) to about 3e+05 copies/gDNA, from about 2e+05 copies/μg genomic DNA (copies/gDNA) to about 3.5e+05 copies/gDNA, from about 2e+05 copies/μg genomic DNA (copies/gDNA) to about 2.5e+05 copies/gDNA, or from about 1e+05 copies/μg genomic DNA (copies/gDNA) to about 3e+05 copies/gDNA, in the blood of the subject after administration of the CAR to the subject. The C_{max} may be a median C_{max}.

In certain embodiments, the CAR has a T_{max} (the time it takes the CAR to reach C_{max}) ranging from about 12 days to about 25 days, from about 14 days to about 20 days, from about 6 days to about 22 days, from about 3 days to about 20 days, from about 4 days to about 18 days, from about 5 days to about 17 days, from about 6 days to about 16 days, from about 7 days to about 15 days, from about 9 days to about 15 days, from about 10 days to about 15 days, from about 10 days to about 14 days, from about 8 days to about 12 days, from about 6 days to about 14 days, from about 12 days to about 14 days, from about 8 days to about 11 days, from about 8 days to about 15 days, or from about 10 days to about 14 days. The T_{max} may be a median T_{max}.

In certain embodiments, the CAR has a T_{last} (the time corresponding to the last quantifiable CAR level) ranging from about 30 days to about 200 days, from about 50 days to about 150 days, from about 50 days to about 100 days, from about 60 days to about 80 days, from about 60 days to about 150 days, from about 80 days to about 150 days, from about 50 days to about 200 days, from about 50 days to about 60 days, from about 50 days to about 80 days, from about 50 days to about 100 days, from about 60 days to about 100 days, from about 80 days to

about 100 days, from about 60 days to about 200 days, from about 80 days to about 200 days, from about 50 days to about 140 days, from about 60 days to about 140 days, or from about 80 days to about 140 days. The T_{last} may be a median T_{last}.

Specifically, it is an object of the present disclosure to provide a sequence of BCMA targeted chimeric antigen receptor as well as preparation method and activity identification of a modified T cell (CART-BCMA) thereof.

The present disclosure provides a chimeric antigen receptor structure for use in the treatment of BCMA positive B cell lymphoma.

In a first aspect, it provides a chimeric antigen receptor (CAR) (sequence), and its antigen binding domain is an antibody single chain variable region sequence that targets extracellular region of BCMA.

In another embodiment, the antigen binding domain is an antibody single chain variable region sequence that targets amino acid residues at positions 24 to 41 of the BCMA sequence.

In another embodiment, the NCBI accession number of the BCMA sequence is AY684975.1.

In another embodiment, the structure of the antigen binding domain is shown in formula I as below:

$$V_L\text{-}V_H \qquad (I)$$

wherein V_H is an antibody heavy chain variable region; V_L is an antibody light chain variable region; and "-" is a linker peptide or a peptide bond;

and, the amino acid sequence of V_L is as shown in SEQ ID NO: 1, and the amino acid sequence of V_H is as shown in SEQ ID NO: 2;

or, the amino acid sequence of V_L is as shown in SEQ ID NO: 3, and the amino acid sequence of V_H is as shown in SEQ ID NO: 4;

or, the amino acid sequence of V_L is as shown in SEQ ID NO: 5, and the amino acid sequence of V_H is as shown in SEQ ID NO: 6.

In another embodiment, the amino acid sequence of the linker peptide is as shown in SEQ ID NO: 10 or SEQ ID NO: 11.

In another embodiment, the antibody single chain variable region comprises a human, mouse, human-mouse chimeric antibody single chain variable region.

In another embodiment, the structure of the chimeric antigen receptor is shown in formula II as below:

$$S\text{-}V_L\text{-}V_H\text{-}H\text{-}TM\text{-}C\text{-}CD3\zeta \quad (II)$$

wherein,

S is an optional signal peptide;

H is a hinge region;

TM is a transmembrane domain;

C is a co-stimulatory signaling molecule;

CD3ζ is a cytoplasmic signaling sequence derived from CD3ζ;

V_H and V_L are as described above.

In another embodiment, the S is a signal peptide of a protein selected from the group consisting of CD8, CD28, GM-CSF, CD4, CD137, or a combination thereof.

In another embodiment, the S is a signal peptide derived from CD8.

In another embodiment, the amino acid sequence of S is as shown in SEQ ID NO: 9.

In another embodiment, the H is a hinge region of a protein selected from the group consisting of CD8, CD28, CD137, or a combination thereof.

In another embodiment, the H is a hinge region derived from CD8.

In another embodiment, the amino acid sequence of H is as shown in SEQ ID NO: 12.

In another embodiment, the TM is a transmembrane region of a protein selected from the group consisting of CD28, CD3ε, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or a combination thereof.

In another embodiment, the TM is a transmembrane region derived from CD8.

In another embodiment, the sequence of TM is as shown in SEQ ID NO: 13.

In another embodiment, the C is a co-stimulatory signaling molecule of a protein selected from the group consisting of OX40, CD2, CD7, CD27, CD28, CD30, CD40, CD70, CD134, 4-1BB (CD137), PD1, Dap10, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), NKG2D, GITR, TLR2, or a combination thereof.

In another embodiment, C is a co-stimulatory signaling molecule derived from 4-1BB.

In another embodiment, the amino acid sequence of C is as shown in SEQ ID NO: 14.

In another embodiment, the amino acid sequence of CD3ζ is as shown in SEQ ID NO: 15.

In a second aspect, it provides a nucleic acid molecule, encoding the chimeric antigen receptor (CAR) of the first aspect of.

In another embodiment, the nucleic acid molecule is isolated.

In a third aspect, it provides a vector, comprising the nucleic acid molecule of the second aspect.

In another embodiment, the vector is selected from the group consisting of DNA, RNA, plasmid, lentiviral vector, adenoviral vector, retroviral vector, transposon, or a combination thereof.

In another embodiment, the vector is a lentiviral vector.

In a fourth aspect, it provides a host cell, comprising the vector of the third aspect or having the exogenous nucleic acid molecule of the second aspect integrated into the chromosome or expressing the CAR of the first aspect.

In another embodiment, the cell is an isolated cell, and/or the cell is a genetically engineered cell.

In another embodiment, the cell is a mammalian cell.

In another embodiment, the cell is a T cell.

In a fifth aspect, it provides a method for preparing a CAR-T cell expressing the CAR of the first aspect, and the method comprises the steps of: transducing the nucleic acid molecule of the second aspect or the vector of the third aspect into a T cell, thereby obtaining the CAR-T cell.

In a sixth aspect, it provides a preparation, comprising the chimeric antigen receptor of the first aspect, the nucleic acid molecule of the second aspect, the vector of the third aspect, or the cell of the fourth aspect, and a pharmaceutically acceptable carrier, diluent or excipient.

In another embodiment, the preparation is a liquid preparation.

In another embodiment, the dosage form of the preparation is injection.

In another embodiment, the concentration of the CAR-T cells in the preparation is 1×10^{3}-1×10^{8} cells / ml, or 1×10^{4}-1×10^{7} cells / ml.

In a seventh aspect, it provides the use of the chimeric antigen receptor of the first aspect, the nucleic acid molecule of the second aspect, the vector of the third aspect, or the cell of the fourth aspect, for the preparation of a medicine or a preparation for preventing and/or treating tumor or cancer.

In another embodiment, the tumor is selected from the group consisting of a hematological tumor, a solid tumor, or a combination thereof.

In one embodiment, the cancer is B cell lymphoma.

In another embodiment, the blood tumor is selected from the group consisting of acute

myeloid leukemia (AML), multiple myeloma (MM), chronic lymphocytic leukemia (CLL), acute lymphoblastic leukemia (ALL), diffuse large B cell lymphoma (DLBCL), or a combination thereof.

In another embodiment, the solid tumor is selected from the group consisting of gastric cancer, peritoneal metastasis of gastric cancer, liver cancer, leukemia, renal cancer, lung cancer, small intestine cancer, bone cancer, prostate cancer, colorectal cancer, breast cancer, large intestine cancer, cervical cancer, ovarian cancer, lymphoma, nasopharyngeal carcinoma, adrenal tumor, bladder tumor, non-small cell lung cancer (NSCLC), glioma, endometrial cancer, or a combination thereof.

In another embodiment, the tumor is a BCMA positive tumor, such as a BCMA positive B cell lymphoma, multiple myeloma, or plasma cell leukemia.

In an eighth aspect, it provides a kit for the preparation of the cell of the fourth aspect, the kit comprises a container, and the nucleic acid molecule of the second aspect or the vector of the third aspect is located in the container.

In a ninth aspect, it provides a use of the cell of the fourth aspect, or the preparation of the sixth aspect for the prevention and/or treatment of cancer or tumor.

In a tenth aspect, it provides a method of treating a disease comprising administering an appropriate amount of the cell of the fourth aspect, or the preparation of the sixth aspect, to a subject in need of treatment.

In another embodiment, the disease is cancer or tumor.

It is to be understood that the various technical features of the present disclosure mentioned above and the various technical features specifically described hereinafter (as in the Examples) may be combined with each other within the scope of the present disclosure to constitute a new or preferred technical solution, which needs not be described one by one, due to space limitations.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A, 1B, and 1C show screening result of CART-BCMA comparative examples. FIG. 1A shows detection of transfection efficiency of engineered T cell with chimeric antigen receptors targeting BCMA. The expression level of the CAR gene-encoded protein on the surface of the T cell membrane in CAR-BCMA cells cultured on day 6 was identified by Fc fragment staining method of recombinant human BCMA protein. $1*10^5$ of CART-BCMA cells cultured on day 10 were cultured respectively with BCMA-positive K562-BCMA-B9 tumor cell line, MM.1S and RPMI8226 tumor cell lines naturally expressing BCMA, and BCMA-negative K562 tumor cell line, or without tumor cells, in 200 μl GT-551 medium for 18h at a ratio of 1:1. Then the expression level of CD137 on the surface of T cell membrane (FIG. 1B) and the secretion level of IFNγ in the culture supernatant was detected respectively (FIG. 1C).

Figure 2 shows structure of chimeric antigen receptor targeting BCMA. The structure of CAR includes a leader sequence, an antigen recognition sequence, a linker region, a transmembrane region, a co-stimulatory factor signal region, and a CD3ζ signaling region.

Figures 3A, 3B, and 3C show detection of transfection efficiency of engineered T cell with chimeric antigen receptors targeting BCMA. The expression levels of the CAR gene-encoded protein on the surface of the T cell membrane in CAR-BCMA cells cultured on day 7 (FIG. 3A) day 21 (FIG. 3B) and day 29 (FIG. 3C) were identified by Fc fragment staining method of recombinant human BCMA protein.

Figures 4A and 4B show the expression level of CD137 on the surface of T cell membrane (FIG. 4A) and the secretion level of IFNγ in the culture supernatant (FIG. 4B). Specifically, 1×10^5 of CART-BCMA cells cultured on day 7 were cultured respectively with BCMA-positive K562-BCMA-E7 tumor cell line and BCMA-negative K562 tumor cell line, or without tumor cells, in 200 μl GT-551 medium for 18h at a ratio of 1:1. Then the expression level of CD137 on the surface of T cell membrane and the secretion level of IFNγ in the culture supernatant was detected respectively.

Figure 5 shows detection of advanced apoptosis level of tumor cells induced by CART-BCMAs. Specifically, 1×10^4 CFSE-labeled BCMA-negative (NH929) or BCMA-positive (NH929-BCMA) tumor cell lines were co-cultured respectively with corresponding T cells in 100 μl of GT-551 medium for 4 h at a ratio as shown in the figure. The proportion of PI-positive cells

in CFSE-positive cells was analyzed by flow cytometry after staining with 100 μl of 25% PI dye for 15 min. The figure shows the statistical analysis of PI positive cells in the corresponding co-culture samples.

Figures 6A and 6B show detection of advanced apoptosis level of tumor cells induced by CART-BCMAs. FIG. 6A shows ratio of CART positive cells in the analyzed samples, wherein NT and BCMA-MO6 were calculated at 60%. 1 x 10^4 CFSE-labeled BCMA-negative (NH929) or BCMA-positive (NH929-BCMA, MM.1S) tumor cell lines were co-cultured respectively with corresponding T cells in 100 μl of GT-551 medium for 4 h at a ratio as shown in the figure. The proportion of PI-positive cells in CFSE-positive cells was analyzed by flow cytometry after staining with 100 μl of 25% PI dye for 15 min. FIG. 6B shows the statistical analysis of PI positive cells in the corresponding co-culture samples.

Figures 7A and 7B show the inhibitory effect of CART-BCMAs on the proliferation *in vivo* of myeloma cell line RPMI-8226 in B-NDG mice. RPMI-8226 cells in logarithmic growth phase were collected, and 4.0×10^6 tumor cells were inoculated subcutaneously in the right back of mice. When the tumor volume reached about 120 mm^3, the animals were randomly divided into 4 groups according to tumor volume. Then solvent control, 7.5×10^6 NT (T cells only) and 7.5×10^6 CART-BCMAs cells were injected through tail vein respectively. FIG. 7A shows that single injection of CART-BCMA-1 and CART-BCMA-20 through tail vein can effectively inhibit the growth of human myeloma RPMI-8226 cells. FIG. 7B shows that CART-BCMA-1 and CART-BCMA-20 can significantly prolong the survival of tumor-bearing mice with human myeloma RPMI-8226 cells.

Figure 8 shows results the expression of BCMA, CR2, CXADR, DDR2, and MAG in 293T cells after transfection of relevant plasmids by flow cytometry.

Figures 9A, 9B, and 9C show the cytokine detection results.

Figure 10 shows the killing ability of each cell to the target cell. Triangle: BCMA-20 (C-CAR088); square: positive control; circle: NT control (non-transfected (NT) T cells).

Figure 11 shows the effect of soluble BCMA on cell killing activity.

Figure 12 shows the survival rate of the mice in each group.

Figure 13 shows the experimental process of phase I clinical study.

Figure 14 shows the clinical response of phase I clinical study.

Figure 15 shows the treatment condition of the patient of ID Z0203-00801C008.

Figures 16A and 16B show the treatment condition of patient of ID Z0203-00701C001.

Figure 17 shows the expansion of C-CAR088 and the decrease of M-protein/sFLC levels in the blood.

Figures 18A-18C show the results of evaluating the binding specificity of the scFv of C-CAR088. Figure 18A shows the experimental scheme. Figure 18B shows the structure of the anti-BCMA CAR and scFv rabFc. Figure 18C shows the experimental results.

Figures 19A-19B show tissue cross reactivity IHC GLP study and validation. HAdCC, human primary adrenal cortical cells. HPTEC, human primary thyroid epithelial cells. A549 BCMA OE, a stable strain overexpressing BCMA.

Figures 20 shows an example of the CAR (C-CAR088) manufacture process. The process includes the usage of serum free media, a closed, modular integrated, semi-automated system, and digital monitoring. Stars indicate improved processes. Median vein to vein time is about 17 days (range: 13 to 83 days). Median manufacturing time is about 7 days (range: 5 to 10 days).

Figure 21 shows C-CAR088 phase I clinical study design (in treating relapsed or refractory multiple myeloma). Phase I, open-label, dose escalation and expansion studies were conducted at four medical centers. C-CAR088 is an embodiment of the present CAR which is based on the BCMA-20 antibody.

Figure 22 shows the C-CAR088 clinical response, including SD, MR, PR, CR, VGPR, MRD, and PD. SD: stable disease; PR: partial response; CR: complete response; PD: progressive disease; MR: minimal response; VGPR: very good partial response; MRD: minimal residual disease.

Figure 23 shows the C-CAR088 clinical response, including CR/sCR, VGPR and PR.

Figure 24 shows the Kaplan Meyer estimation of progression-free survival (PFS) for mid and high dose group.

Figure 25A shows the expansion of C-CAR088 in the blood of the patients after CAR administration. Figure 25B shows the expansion of C-CAR088 in the blood of the patients up to the most recent visit. Figure 25C shows C_{max} levels in the blood of the patients after CAR administration. Figure 25D shows AUC levels in the blood of the patients after CAR administration. Figure 25E shows T_{max} levels in the blood of the patients after CAR administration. Figure 25F shows T_{last} levels in the blood of the patients after CAR administration.

DETAILED DESCRIPTION

The present disclosure provides for chimeric antigen receptors (CARs) targeting BCMA. In certain embodiments, the CARs are based on four monoclonal antibodies: BCMA-1, BCMA-20, BCMA-CA8, and BCMA-MO6. The present disclosure also provides for the analysis and identification of the expression levels of the CARs in primary T cells, *in vitro* activation ability and tumor cell killing efficacy of these chimeric antigen receptors. Studies have shown that the chimeric antigen receptors of the present disclosure target BCMA positive cells and can be used to treat BCMA positive B cell lymphoma, multiple myeloma, plasma cell leukemia or other diseases.

Specifically, the present disclosure identifies the correlation between the expression time and the expression intensity of different CAR structures on the surface of the cell membrane after virus infection, and further identifies the difference in expression of different CAR structural proteins. This finding suggests that different CAR structures exist a difference in the expression level of CAR protein on the membrane surface and the persistence of CART in vivo activity under same infection condition. After extensive screening, the CAR structure of the present disclosure was obtained. The results show that the protein encoded by the CAR structure of the present disclosure can be fully expressed and membrane-localized.

In the present disclosure, the preparation process of CAR-modified T cell targeting BCMA antigen is improved. In one embodiement, GT-551 serum-free medium supplemented with 1% human albumin is used to culture lymphocytes in vitro.

Term

The term "about" may refer to a value or composition within an acceptable error range for a particular value or composition as determined by those skilled in the art, which will depend in part on how the value or composition is measured or determined. The term “about” in reference to a numeric value may refer to ±10% of the stated numeric value. In other words, the numeric value can be in a range of 90% of the stated value to 110% of the stated value.

The term "administering" refers to the physical introduction of a product of the disclosure into a subject using any one of various methods and delivery systems known to those skilled in the art, including, but not limited to, intravenous, intramuscular, subcutaneous, intraperitoneal, spinal

or other parenteral administration, such as by injection or infusion.

The term "antibody" (Ab) may include, but is not limited to, an immunoglobulin that specifically binds an antigen and contains at least two heavy (H) chains and two light (L) chains linked by disulfide bonds, or an antigen binding parts thereof. Each H chain contains a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region contains three constant domains, CH1, CH2, and CH3. Each light chain contains a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region contains a constant domain CL. The VH and VL regions can be further subdivided into hypervariable regions called complementarity determining regions (CDR), which are interspersed within more conservative regions called framework regions (FR). Each VH and VL contains three CDRs and four FRs, which are arranged from amino terminal to carboxy terminal in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen.

Chimeric antigen receptors (CARs)

The chimeric antigen receptors (CARs) of the present disclosure may comprise an extracellular domain, a transmembrane domain, and an intracellular domain. The extracellular domain comprises a target-specific binding element (also known as an antigen binding domain). The intracellular domain includes a co-stimulatory signaling region and a ζ chain. The co-stimulatory signaling region refers to a part of the intracellular domain that includes a co-stimulatory molecule. The co-stimulatory molecule is a cell surface molecule required for efficient response of lymphocytes to antigens, rather than an antigen receptor or its ligand.

A linker can be incorporated between the extracellular domain and the transmembrane domain of the CAR, or between the cytoplasmic domain and the transmembrane domain of the CAR. As used herein, the term "linker" generally refers to any oligopeptide or polypeptide that plays a role of linking the transmembrane domain to the extracellular domain or the cytoplasmic domain in a polypeptide chain. The linker may comprise 0-300 amino acids, 2-100 amino acids, or 3-50 amino acids.

In one embodiment, the extracellular domain of the CAR comprises an antigen binding domain targeting BCMA. When the CAR of the present disclosure is expressed in T cell, antigen recognition can be performed based on antigen binding specificity. When the CAR binds to its

associated antigen, it affects tumor cell, causing tumor cell to fail to grow, to death or to be affected otherwise, causing the patient's tumor burden to shrink or eliminate. The antigen binding domain may be fused to the intracellular domain from one or more of the co-stimulatory molecules and the ζ chain. The antigen binding domain may be fused with an intracellular domain of a combination of a 4-1BB signaling domain and a CD3ζ signaling domain.

As used herein, the "antigen binding domain" and "single-chain antibody fragment" may refer to a Fab fragment, a Fab' fragment, a F (ab') $_2$ fragment, or a single Fv fragment that has antigen-binding activity. The Fv antibody contains the heavy chain variable region and the light chain variable region of the antibody, but has no constant region. The Fv antibody has the smallest antibody fragment with all antigen-binding sites. Generally, Fv antibodies also include a polypeptide linker between the VH and VL domains, and can form the structure required for antigen binding. The antigen binding domain is usually a scFv (single-chain variable fragment). The size of scFv is typically 1/6 of a complete antibody. The single-chain antibody may be an amino acid chain sequence encoded by a nucleotide chain. In certain embodiments, the scFv may comprise an antibody which specifically recognizes the extracellular region of BCMA, such as amino acid residues at positions 24 to 41 of the BCMA sequence. The antibody may be a single chain antibody.

As for the hinge region and the transmembrane region (transmembrane domain), the CAR can be designed to comprise a transmembrane domain fused to the extracellular domain of the CAR. In one embodiment, a transmembrane domain that is naturally associated with one of the domains in the CAR is used. In some embodiments, transmembrane domains may be selected or modified by amino acid substitutions to avoid binding such domains to the transmembrane domain of the same or different surface membrane proteins, thereby minimizing the interaction with other members of the receptor complexes.

The intracellular domain in the CAR comprises the signaling domain of 4-1BB and the signaling domain of CD3ζ.

In certain embodiments, the CAR structure of the present disclosure comprises a signal peptide, an antigen recognition sequence (antigen-binding domain), a linker region, a transmembrane region, a co-stimulatory factor signal region, and a CD3zeta signaling region (ζ chain portion). The order of connection is as follows:

[CD8 S]-[VL-Linker-VH]-[hinge-CD8TM]-[4-1BB]-[CD3zeta]

In certain embodiments, the sequence selected in the present disclosure is as follows:

(1) The signal peptide is a signal peptide sequence derived from CD8:

MALPVTALLLPLALLLHAARP (SEQ ID NO: 9)

(2) light chain (VL) sequence of single-chain variable region derived from BCMA-1 antibody:

DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIHWYQQKPGQPPTLLIQLASNV QTGVPARFSGS GSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK (SEQ ID NO: 7)

(3) heavy chain (VH) sequence of single-chain variable region derived from BCMA-1 antibody:

QIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTETREPA YAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTVSS (SEQ ID NO: 8)

Among them, BCMA-1 is an antibody sequence contained in a published Car-T sequence, and is used as a control in the present application.

(4) light chain (V_L) sequence of single-chain variable region derived from BCMA-20 antibody:

DIQMTQSPSSLSASVGDRVTITC**RASQGISNYLN**WYQQKPGKAPKPLIY**YTSNLQS** GVPSRFSGSGSGT DYTLTISSLQPEDFATYYC**MGQTISSYT**FGQGTKLEI (SEQ ID NO: 1)

V_L Region	**Sequence**	**Residues of SEQ ID NO: 1**	**Length** (number of amino acid residues)
LFR1	DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO: 16)	1 - 23	23
CDR-L1	RASQGISNYLN (SEQ ID NO: 17)	24 - 34	11
LFR2	WYQQKPGKAPKPLIY (SEQ ID NO: 18)	35 - 49	15
CDR-L2	YTSNLQS (SEQ ID NO: 19)	50 - 56	7
LFR3	GVPSRFSGSGSGTDYTLTISSLQPEDFATY YC (SEQ ID NO: 20)	57 - 88	32

CDR-L3	MGQTISSYT (SEQ ID NO: 21)	89 - 97	9
LFR4	FGQGTKLEI (SEQ ID NO: 22)	98 - 106	9

(5) heavy chain (VH) sequence of single-chain variable region derived from BCMA-20 antibody:

EVQLVESGGGLVQPGGSLRLSCAASGFTFS**NFDMA**WVRQAPGKGLVWVS**SITTG ADHAIYADSVKG**RFTISRDNAKNTLYLQMNSLRAEDTAVYYCVR**HGYYDGYHLFDY** WGQGTLVTVSS (SEQ ID NO: 2)

V_H Region	**Sequence**	**Residues of SEQ ID NO: 2**	**Length** (number of amino acid residues)
HFR1	EVQLVESGGGLVQPGGSLRLSCAASGF TFS (SEQ ID NO: 23)	1 - 30	30
CDR-H1	NFDMA (SEQ ID NO: 24)	31 - 35	5
HFR2	WVRQAPGKGLVWVS (SEQ ID NO: 25)	36 - 49	14
CDR-H2	SITTGADHAIYADSVKG (SEQ ID NO: 26)	50 - 66	17
HFR3	RFTISRDNAKNTLYLQMNSLRAEDTAV YYCVR (SEQ ID NO: 27)	67 - 98	32
CDR-H3	HGYYDGYHLFDY (SEQ ID NO: 28)	99 - 110	12
HFR4	WGQGTLVTVSS (SEQ ID NO: 29)	111 - 121	11

(6) light chain (VL) sequence of single-chain variable region derived from BCMA-CA8 antibody:

DIQLTQTTSSLSASLGDRVTISC**SASTTTSNYLN**WYQQKPDGTVELVIY**YTSNLHG** GGPSRFSGSGSGTDYSLTIGYLEPEDVATYYC**QQYRKLPWT**FGGGSKLEIKR (SEQ ID NO: 3)

V_L Region	**Sequence**	**Residues of SEQ ID NO: 3**	**Length** (number of amino acid residues)
LFR1	DIQLTQTTSSLSASLGDRVTISC (SEQ ID NO: 30)	1 - 23	23
CDR-L1	SASTTTSNYLN (SEQ ID NO: 31)	24 - 34	11
LFR2	WYQQKPDGTVELVIY (SEQ ID NO: 32)	35 - 49	15
CDR-L2	YTSNLHG (SEQ ID NO: 33)	50 - 56	7
LFR3	GGPSRFSGSGSGTDYSLTIGYLEPEDV ATYYC (SEQ ID NO: 34)	57 - 88	32
CDR-L3	QQYRKLPWT (SEQ ID NO: 35)	89 - 97	9
LFR4	FGGGSKLEIKR (SEQ ID NO: 36)	98 - 108	11

(7) heavy chain (VH) sequence of single-chain variable region derived from BCMA-CA8 antibody:

EVQLQQSGAVLARPGASVKMSCKGSGYTFT**NYWMH**WVKQRPGQGLEWIG**ATY RGHSDTYYNQKFKG**KAKLTAVTSTSTAYMELSSLTNEDSAVYYCTR**GAIYNGYDVLD N**WGQGTLVTVSS (SEQ ID NO: 4)

V_H Region	**Sequence**	**Residues of SEQ ID NO: 4**	**Length** (number of amino acid residues)
HFR1	EVQLQQSGAVLARPGASVKMSCKGSG YTFT (SEQ ID NO: 37)	1 - 30	30
CDR-H1	NYWMH (SEQ ID NO: 38)	31 - 35	5
HFR2	WVKQRPGQGLEWIG (SEQ ID NO: 39)	36 - 49	14
CDR-H2	ATYRGHSDTYYNQKFKG (SEQ ID NO:	50 - 66	17

	40)		
HFR3	KAKLTAVTSTSTAYMELSSLTNEDSAV YYCTR (SEQ ID NO: 41)	67 - 98	32
CDR-H3	GAIYNGYDVLDN (SEQ ID NO: 42)	99 - 110	12
HFR4	WGQGTLVTVSS (SEQ ID NO: 43)	111 - 121	11

(8) light chain (VL) sequence of single-chain variable region derived from BCMA-MO6 antibody:

DIQMTQSPSSLSASVGDRVTITC**SASQDISNYLN**WYQQKPGKAPKLLIY**YTSNLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQYRKLPWT**FGQGTKLEIKR (SEQ ID NO: 5)

V_L Region	**Sequence**	**Residues of SEQ ID NO: 5**	**Length** (number of amino acid residues)
LFR1	DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO: 44)	1 - 23	23
CDR-L1	SASQDISNYLN (SEQ ID NO: 45)	24 - 34	11
LFR2	WYQQKPGKAPKLLIY (SEQ ID NO: 46)	35 - 49	15
CDR-L2	YTSNLHS (SEQ ID NO: 47)	50 - 56	7
LFR3	GVPSRFSGSGSGTDFTLTISSLQPEDF ATYYC (SEQ ID NO: 48)	57 - 88	32
CDR-L3	QQYRKLPWT (SEQ ID NO: 49)	89 - 97	9
LFR4	FGQGTKLEIKR (SEQ ID NO: 50)	98 - 108	11

(9) heavy chain (VH) sequence of single-chain variable region derived from BCMA-MO6 antibody:

QVQLVQSGAEVKKPGSSVKVSCKASGGTFS**NYWMH**WVRQAPGQGLEWMG**ATY RGHSDTYYNQKFKG**RVTITADKSTSTAYMELSSLRSEDTAVYYCAR**GAIYDGYDVLD**

NWGQGTLVTVSS (SEQ ID NO: 6)

V_H Region	**Sequence**	**Residues of SEQ ID NO: 6**	**Length** (number of amino acid residues)
HFR1	QVQLVQSGAEVKKPGSSVKVSCKASG GTFS (SEQ ID NO: 51)	1 - 30	30
CDR-H1	NYWMH (SEQ ID NO: 52)	31 - 35	5
HFR2	WVRQAPGQGLEWMG (SEQ ID NO: 53)	36 - 49	14
CDR-H2	ATYRGHSDTYYNQKFKG (SEQ ID NO: 54)	50 - 66	17
HFR3	RVTITADKSTSTAYMELSSLRSEDTAV YYCAR (SEQ ID NO: 55)	67 - 98	32
CDR-H3	GAIYDGYDVLDN (SEQ ID NO: 56)	99 - 110	12
HFR4	WGQGTLVTVSS (SEQ ID NO: 57)	111 - 121	11

(10) The linker sequence between heavy chain and light chain of BCMA-1 single-chain variable region is:

GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10)

(11) The linker sequence between heavy chain and light chain of BCMA-20, BCMA-CA8, and BCMA-MO6 single-chain variable region is:

GGGGSGGGGSGGGGS (SEQ ID NO: 11)

(12) Sequence of hinge region and linker region:

FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 12)

(13) The transmembrane region is a transmembrane region sequence of CD8 (CD8TM) antigen:

IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 13)

(14) The co-stimulatory factor signal region is derived from the sequence of 4-1BB

cytoplasmic signaling motif:

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 14)

(15) The signaling region of CD3 zeta is derived from the sequence of immunorecceptor tyrosine-based activation motif (ITAM) of CD3zeta in the TCR complex:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPQRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR (SEQ ID NO: 15)

In certain embodiments, the nucleic acid encoding the CAR (derived from the BCMA-20 antibody) may have the following sequence (SEQ ID NO: 58):

atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggacatccagatgacccagtcccc
ctcctccctgtccgcctccgtgggcgaccgggtgaccatcacctgccgggcctcccagggcatctccaactacctgaactggtacc
agcagaagcccggcaaggcccccaagcccctgatctactacacctccaacctgcagtccggcgtgccctcccggttctccggctc
cggctccggcaccgactacaccctgaccatctcctccctgcagcccgaggacttcgccacctactactgcatgggccagaccatct
cctcctacaccttcggccagggcaccaagctggagatcaagggtggcggtggctcgggcggtggtgggtcgggtggcggcgga
tctgaggtgcagctggtggagtccggcggcggcctggtgcagcccggcggctccctgcggctgtcctgcgccgcctccggcttc
accttctccaacttcgacatggcctgggtgcggcaggcccccggcaagggcctggtgtgggtgtcctccatcaccaccggcgccg
accacgccatctacgccgactccgtgaagggccggttcaccatctcccgggacaacgccaagaacaccctgtacctgcagatgaa
ctccctgcgggccgaggacaccgccgtgtactactgcgtgcggcacggctactacgacggctaccacctgttcgactactggggc
cagggcaccctggtgaccgtgtcctccttcgtgccggtcttcctgccagcgaagcccaccacgacgccagcgccgcgaccacca
acaccggcgcccaccatcgcgtcgcagcccctgtccctgcgcccagaggcgtgccggccagcggcgggggggcgcagtgcaca
cgagggggctggacttcgcctgtgatatctacatctgggcgcccttggccgggacttgtggggtccttctcctgtcactggttatcac
cctttactgcaaacggggcagaaagaaactcctgtatatattcaaacaaccatttatgagaccagtacaaactactcaagaggaagat
ggctgtagctgccgatttccagaagaagaagaaggaggatgtgaactgagagtgaagttcagcaggagcgcagacgcccccgc
gtaccagcagggccagaaccagctctataacgagctcaatctaggacgaagagaggagtacgatgttttggacaagagacgtggc
cgggaccctgagatgggggaaagccgagaaggaagaaccctcaggaaggcctgtacaatgaactgcagaaagataagatgg
cggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaaggggcacgatggcctttaccagggtctcagtaca
gccaccaaggacacctacgacgcccttcacatgcaggccctgcccccctcgctaa

In certain embodiments, the CAR (derived from the BCMA-20 antibody) may have

the following amino acid sequence (SEQ ID NO: 59):

MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNYLNWY
QQKPGKAPKPLIYYTSNLQSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCMGQTISS
YTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFS
NFDMAWVRQAPGKGLVWVSSITTGADHAIYADSVKGRFTISRDNAKNTLYLQMNS
LRAEDTAVYYCVRHGYYDGYHLFDYWGQGTLVTVSSFVPVFLPAKPTTTPAPRPPT
PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLY
CKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ
QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA
EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In certain embodiments, the nucleic acid encoding the CAR (derived from the BCMA-CA8 antibody) may have the following sequence (SEQ ID NO: 60):

atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggatatccagctgacccagaccac
aagcagcctgagcgcctccctgggcgacagggtgaccattagctgcagcgccagccaggacatcagcaactacctgaactggta
ccagcagaagcccgacggcaccgtggagctcgtgatctactacacctccaacctgcacagcggcgtgcccagcaggttctctggc
agcggcagcggcaccgactacagcctgaccatcggctatctggagcccgaggacgtcgccacctactactgccagcagtacagg
aagctgccctggaccttcggcggaggctctaagctggagattaagcgtggtggcggtggctcgggcggtggtgggtcgggtggc
ggcggatctgaggtgcagctgcagcagagcggcgccgtgctggccaggcccggagctagcgtgaagatgagctgcaagggca
gcggctacaccttcaccaactactggatgcactgggtgaaacagaggcccggccagggactggagtggatcggcgccacctaca
ggggccacagcgacacctactacaaccagaagttcaagggcaaggccaagctgaccgccgtgacctcaaccagcaccgcctac
atggaactgagcagcctgaccaacgaggacagcgccgtctattactgcaccaggggcgccatctacaacggctacgacgtgctg
gacaattggggccagggaacactagtgaccgtgtccagcttcgtgccggtcttcctgccagcgaagcccaccacgacgccagcg
ccgcgaccaccaacaccggcgcccaccatcgcgtcgcagcccctgtccctgcgcccagaggcgtgccggccagcggcgggggg
gcgcagtgcacacgaggggggctggacttcgcctgtgatatctacatctgggcgcccttggccgggacttgtggggtccttctcctgt
cactggttatcacccttactgcaaacggggcagaaagaaactcctgtatatattcaaacaaccatttatgagaccagtacaaactact
caagaggaagatggctgtagctgccgatttccagaagaagaagaaggaggatgtgaactgagagtgaagttcagcaggagcgca
gacgcccccgcgtaccagcagggccagaaccagctctataacgagctcaatctaggacgaagagaggagtacgatgttttggac
aagagacgtggccgggaccctgagatgggggggaaagccgagaaggaagaaccctcaggaaggcctgtacaatgaactgcaga

aagataagatggcggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaaggggcacgatggcctttaccag
ggtctcagtacagccaccaaggacacctacgacgcccttcacatgcaggccctgcccccctcgctaa

In certain embodiments, the CAR (derived from the BCMA-CA8 antibody) may have the following amino acid sequence (SEQ ID NO: 61):

MALPVTALLLPLALLLHAARPDIQLTQTTSSLSASLGDRVTISCSASQDISNYLNWYQ
QKPDGTVELVIYYTSNLHSGVPSRFSGSGSGTDYSLTIGYLEPEDVATYYCQQYRKLP
WTFGGGSKLEIKRGGGGSGGGGSGGGGSEVQLQQSGAVLARPGASVKMSCKGSGY
TFTNYWMHWVKQRPGQGLEWIGATYRGHSDTYYNQKFKGKAKLTAVTSTSTAYM
ELSSLTNEDSAVYYCTRGAIYNGYDVLDNWGQGTLVTVSSFVPVFLPAKPTTTPAPR
PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVIT
LYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPA
YQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK
MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In certain embodiments, the nucleic acid encoding the CAR (derived from the BCMA-MO6 antibody) may have the following sequence (SEQ ID NO: 62):

atggccttaccagtgaccgccttgctcctgccgctggccttgctgctccacgccgccaggccggacatccagatgacccagagccctagct
cactgagcgccagcgtgggcgacagggtgaccattacctgctccgccagccaggacatcagcaactacctgaactggtaccagcagaag
cccggcaaggcccccaagctgctgatctactacacctccaacctgcactccggcgtgcccagcaggttcagcggaagcggcagcggca
ccgatttcaccctgaccatctccagcctgcagcccgaggacttcgccacctactactgccagcagtacaggaagctcccctggactttcggc
cagggcaccaaactggagatcaagcgtggtggcggtggctcgggcggtggtgggtcgggtggcggcggatctcaggtgcagctggtcc
agagcggcgccgaagtgaagaagcccggcagctccgtgaaagtgagctgcaaggccagcggcggcaccttcagcaactactggatgc
actgggtgaggcaggcccccggacagggcctggagtggatgggcgccacctacaggggccacagcgacacctactacaaccagaagt
tcaagggccgggtgaccatcaccgccgacaagagcaccagcaccgcctacatggaactgagcagcctcaggagcgaggacaccgctg
tgtattactgcgccaggggcgccatctacgacggctacgacgtgctggacaactggggccagggcacactagtgaccgtgtccagcttcg
tgccggtcttcctgccagcgaagcccaccacgacgccagcgccgcgaccaccaacaccggcgcccaccatcgcgtcgcagcccctgtc
cctgcgcccagaggcgtgccggccagcggcgggggggcgcagtgcacacgaggggctggacttcgcctgtgatatctacatctgggcg
cccttggccgggacttgtggggtccttctcctgtcactggttatcacccttactgcaaacggggcagaaagaaactcctgtatatattcaaac

aaccatttatgagaccagtacaaactactcaagaggaagatggctgtagctgccgatttccagaagaagaagaaggaggatgtgaactgag
agtgaagttcagcaggagcgcagacgcccccgcgtaccagcagggccagaaccagctctataacgagctcaatctaggacgaagagag
gagtacgatgttttggacaagagacgtggccgggaccctgagatgggggggaaagccgagaaggaagaaccctcaggaaggcctgtaca
atgaactgcagaaagataagatggcggaggcctacagtgagattgggatgaaaggcgagcgccggaggggcaaggggcacgatggcc
tttaccagggtctcagtacagccaccaaggacacctacgacgcccttcacatgcaggccctgcccccctcgctaa

In certain embodiments, the CAR (derived from the BCMA-BCMA-MO6 antibody) may have the following amino acid sequence (SEQ ID NO: 63):

MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
KPGKAPKLLIYYTSNLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYRKLPWTF
GQGTKLEIKRGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKASGGTFSNY
WMHWVRQAPGQGLEWMGATYRGHSDTYYNQKFKGRVTITADKSTSTAYMELSSLRS
EDTAVYYCARGAIYDGYDVLDNWGQGTLVTVSSFVPVFLPAKPTTTPAPRPPTPAPTIAS
QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL
LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL
NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR
RGKGHDGLYQGLSTATKDTYDALHMQALPPR

Chimeric antigen receptor T cells (CAR-T cells)

As used herein, the terms "CAR-T cell", "CAR-T", and "CART", may be used interchangeably.

The present disclosure relates to the construction of a chimeric antigen receptor structure targeting BCMA, a preparation method of a chimeric antigen receptor engineered T cell targeting BCMA, and activity identification thereof.

Vector

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

gene of interest can be produced synthetically.

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

In brief summary, the expression cassette or nucleic acid sequence is typically and operably linked to a promoter, and incorporated into an expression vector. The vectors can be suitable for replication and integration in eukaryotes. Typical cloning vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the desired nucleic acid sequence.

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

The nucleic acid can be cloned into a number of types of vectors. For example, the nucleic acid can be cloned into a vector including, but not limited to a plasmid, a phagemid, a phage derivative, an animal virus, and a cosmid. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors, and sequencing vectors.

Further, the expression vector may be provided to a cell in the form of a viral vector. Viral vector technology is well known in the art and is described, for example, in Sambrook et al, (2001 , Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York), and in other virology and molecular biology manuals. Viruses, which are useful as vectors include, but are not limited to, retroviruses, adenoviruses, adeno-associated viruses, herpes viruses, and lentiviruses. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers, (e.g., WO 01/96584; WO 01/29058; and U.S, Pat. No. 6,326, 193).

A number of viral based systems have been developed for gene transfer into mammalian cells. For example, retroviruses provide a convenient platform for gene delivery systems. A selected gene can be inserted into a vector and packaged in retroviral particles using techniques

known in the art. The recombinant virus can then be isolated and delivered to cells of the subject either *in vivo* or *ex vivo*. A number of retroviral systems are known in the art. In some embodiments, adenovirus vectors are used. A number of adenovirus vectors are known in the art. In one embodiment, lentivirus vectors are used.

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

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

In order to assess the expression of a CAR polypeptide or portions thereof, the expression vector to be introduced into a ceil can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the population of cells sought to be transfected or infected through viral vectors. In other aspects, the selectable

marker may be carried on a separate piece of DNA and used in a co- transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as neo and the like.

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

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

Physical methods for introducing a polynucleotide into a host cell include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and the like. Methods for producing cells comprising vectors and/or exogenous nucleic acids are well-known in the art. See, for example, Sambrook et al. (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York). A method for the introduction of a polynucleotide into a host cell is calcium phosphate transfection.

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

Chemical means for introducing a polynucleotide into a host cell include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. An exemplary colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (e.g., an artificial membrane vesicle).

In the case where a non-viral delivery system is utilized, an exemplary delivery vehicle is a liposome. The use of lipid formulations is contemplated for the introduction of the nucleic acids into a host cell (*in vitro*, *ex vivo* or *in vivo*). In another aspect, the nucleic acid may be associated with a lipid. The nucleic acid associated with a lipid may be encapsulated in the aqueous interior of a liposome, interspersed within the lipid bilayer of a liposome, attached to a liposome via a linking molecule that is associated with both the liposome and the oligonucleotide, entrapped in a liposome, complexed with a liposome, dispersed in a solution containing a lipid, mixed with a lipid, combined with a lipid, contained as a suspension in a lipid, contained or complexed with a micelle, or otherwise associated with a lipid. Lipid, lipid/DNA or lipid/expression vector associated compositions are not limited to any particular structure in solution. For example, they may be present in a bilayer structure, as micelles, or with a "collapsed" structure. They may also simply be interspersed in a solution, possibly forming aggregates that are not uniform in size or shape. Lipids are fatty substances which may be naturally occurring or synthetic lipids. For example, lipids include the fatty droplets that naturally occur in the cytoplasm as well as the class of compounds which contain long-chain aliphatic hydrocarbons and their derivatives, such as fatty acids, alcohols, amines, amino alcohols, and aldehydes.

In one embodiment, the vector is a lentiviral vector.

Compositions

The disclosure provides a composition comprising the immune cell (e.g., CAR-T cell), and a pharmaceutically acceptable carrier, diluent and/or excipient. In one embodiment, the composition is a liquid composition. For example, the composition is an injectable composition. In certain embodiments, the concentration of the CAR-T cells in the composition is 1×10^3-1×10^8 cells/ml, or 1×10^4-1×10^7 cells/ml.

In one embodiment, the composition may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or

dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. The composition may be formulated for intravenous administration.

Therapeutic application

The disclosure comprises therapeutic applications using cells (e.g., T cells) transduced with a lentiviral vector (LV) encoding the expression cassette of the disclosure. The transduced T cells can target the tumor cell marker BCMA, synergistically activate T cells, and cause T cell immune responses, thereby significantly increasing the killing efficiency against tumor cells.

Thus, the present disclosure also provides a method for stimulating a T cell-mediated immune response to a target cell population or tissue in a mammal comprising the step of administering to the mammal a CAR-T cell of the disclosure.

In one embodiment, the present disclosure comprises a class of cell therapies, wherein T cells from autologous patient (or heterologous donor) are isolated, activated and genetically modified to generate CAR-T cells, and then injected into the same patient. The probability of graft versus host disease in the way is extremely low, and antigens are recognized by T cells in a non-MHC-restricted manner. In addition, one CAR-T can treat all cancers that express the antigen. Unlike antibody therapies, CAR-T cells are able to replicate *in vivo* resulting in long-term persistence that can lead to sustained tumor control

In one embodiment, the CAR-T cells of the disclosure can undergo robust in vivo T cell expansion and can persist for an extended amount of time. In addition, the CAR mediated immune response may be part of an adoptive immunotherapy approach in which CAR-modified T cells induce an immune response specific to the antigen binding moiety in the CAR. For example, an anti-BCMA CAR-T cell elicits an immune response specific against cells expressing BCMA.

Although the data disclosed herein specifically disclose lentiviral vector comprising BCMA scFv, hinge and transmembrane domain, and 4-1BB and CD3ζ signaling domains, the disclosure should be construed to include any number of variations for each of the components of the construct as described elsewhere herein.

Cancers that may be treated include tumors that are unvascularized or largely unvascularized, and tumors that are vascularized. Cancers may include non-solid tumors (such as hematological tumors, for example, leukemias and lymphomas) or solid tumors. Types of cancers

to be treated with the CARs include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies e.g., sarcomas, carcinomas, and melanomas. Adult tumors/cancers and pediatric tumors/cancers are also included.

Hematologic cancers are cancers of the blood or bone marrow. Examples of hematological (or hematogenous) cancers include leukemias, including acute leukemias (such as acute lymphocytic leukemia, acute myelocytic leukemia, acute myelogenous leukemia and myeloblasts, promyeiocytic, myelomonocytic, monocytic and erythroleukemia), chronic leukemias (such as chronic myelocytic (granulocytic) leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia), polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma (indolent and high grade forms), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia and myelodysplasia.

Solid tumors are abnormal masses of tissue that usually do not contain cysts or liquid areas. Solid tumors can be benign or malignant. Different types of solid tumors are named for the type of cells that form them (such as sarcomas, carcinomas, and lymphomas). Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, mesothelioma, malignant lymphoma, pancreatic cancer and ovarian cancer.

The CAR-modified T cells may also serve as a type of vaccine for *ex vivo* immunization and/or *in vivo* therapy in a mammal. Preferably, the mammal is a human.

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

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

In addition to using a cell-based vaccine in terms of *ex vivo* immunization, the present

disclosure also provides compositions and methods for *in vivo* immunization to elicit an immune response directed against an antigen in a patient.

The present disclosure provides methods for treating tumors comprising administering to a subject in need thereof, a therapeutically effective amount of the CAR-modified T cells.

The CAR-modified T cells of the present disclosure may be administered either alone, or as a pharmaceutical composition in combination with diluents and/or with other components such as IL-2, IL-17 or other cytokines or cell populations. Briefly, pharmaceutical compositions of the present disclosure may comprise a target cell population as described herein, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present disclosure may be formulated for intravenous administration.

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

When "an immunologically effective amount", "an anti-tumor effective amount", "an tumor-inhibiting effective amount", or "therapeutic amount" is indicated, the precise amount of the compositions of the present disclosure to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical composition comprising the T cells described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, or 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. T cell compositions may also be administered multiple times at these dosages. The cells can be administered by using infusion techniques that are commonly known in immunotherapy (see, e.g., Rosenberg et al,, New Eng. J. of Med. 319: 1676, 1988). The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly.

The administration of the subject compositions may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient subcutaneously, intradermaliy, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous injection, or intraperitoneally. In one embodiment, the T cell compositions of the present disclosure are administered to a patient by intradermal or subcutaneous injection. In another embodiment, the T cell compositions of the present disclosure may be administered by intravenous injection. The compositions of T cells may be injected directly into a tumor, lymph node, or site of infection.

In certain embodiments of the present disclosure, cells activated and expanded using the methods described herein, or other methods known in the art where T cells are expanded to therapeutic levels, are administered to a patient in conjunction with (e.g., before, simultaneously or following) any number of relevant treatment modalities, including but not limited to treatment with agents such as antiviral therapy, cidofovir and interleukin-2, Cytarabine (also known as ARA-C) or natalizumab treatment for MS patients or efalizumab treatment for psoriasis patients or other treatments for PML patients. In further embodiments, the T cells of the disclosure may be used in combination with chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunotherapeutic agents. In a further embodiment, the cell compositions of the present disclosure are administered to a patient in conjunction with (e.g., before, simultaneously or following) bone marrow transplantation, or the use of chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide. For example, in one embodiment, subjects may undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain embodiments, following the transplant, subjects receive an infusion of the expanded immune cells of the present disclosure. In an additional embodiment, expanded cells are administered before or following surgery.

The dosage of the above treatments to be administered to a patient will vary with the precise nature of the condition being treated and the recipient of the treatment. The scaling of dosages for patient administration can be performed according to art-accepted practices. In general, 1×10^6 to 1×10^{10} of the modified T cells of the disclosure (e.g., CAR-T-BCMA cells) can be applied to patients by means of, for example, intravenous infusion each treatment or each course of treatment.

The main advantages of the present disclosure include:

(a) As for the chimeric antigen receptor of the present disclosure, the extracellular antigen binding domain is a specific anti-BCMA scFv; the CARs have shown a great ability of killing tumor cells with low cytotoxicity and low side effects.

(b) The chimeric antigen receptor provided by the disclosure can achieve stable expression and membrane localization of CAR protein after T cells are infected by viral vectors (e.g., lentiviruses) carrying the CAR gene.

(c) The CAR-modified T cells of the present disclosure have a longer survival time *in vivo* and strong anti-tumor effect. The scFv used in the present disclosure may be a humanized or human-derived antibody, and is less likely to produce specific immunological rejection.

The present disclosure will be further illustrated below with reference to the specific examples. It is to be understood that these examples are for illustrative purposes only and are not intended to limit the scope of the invention. For the experimental methods in the following examples the specific conditions of which are not specifically indicated, they are performed under routine conditions, e.g., those described by Sambrook. et al., in Molecule Clone: A Laboratory Manual, New York: Cold Spring Harbor Laboratory Press, 1989, or as instructed by the manufacturers, unless otherwise specified. Percentages and parts are by weight unless otherwise stated.

Example 1 Construction of lentiviral expression vector

The full-length DNA synthesis and cloning were commissioned by Shanghai Boyi Biotechnology Co., Ltd to achieve the construction of coding plasmids. The pWPT lentiviral vector was selected as a cloning vector, and the cloning sites were BamH I and Sal I sites. The specific sequence is as described above.

Example 2 Preparation of CAR-T cell

(1) Mononuclear cells (PBMCs) were isolated from venous blood of healthy people by density gradient centrifugation.

(2) On day 0, PBMCs were seeded in a cell culture flask previously coated with CD3 monoclonal antibody (OKT3) at a final concentration of 5 μg/mL and Retronectin (purchased from

TAKARA) at a final concentration of 10 μg/mL. The medium was GT-551 cell culture medium containing 1% human albumin. Recombinant human interleukin 2 (IL-2) was added to the medium at a final concentration of 1000 U/mL. The cells were cultured in an CO_2 incubator with a saturated humidity of 5% at 37 ℃.

(3) On day 1, the supernatant of the cultured PBMCs was slowly aspirated and discarded. New GT-551 cell culture medium containing 1% human albumin was added, and recombinant human interleukin 2 (IL-2) was added to the medium at a final concentration of 1000 U/mL. The cells were continuously cultured in an CO_2 incubator with a saturated humidity of 5% at 37 ℃.

(4) On day 3, fresh medium, concentrated and purified CAR-BCMAs lentivirus solution, protamine sulfate (12 ug/ml), and IL-2 (at a final concentration of 1000 U/mL) were added. After 12 hours of infection in a 5% CO_2 incubator at 37 °C, the culture medium was discarded, fresh medium was added, and cultivation was continued in a 5% CO_2 incubator at 37 °C.

(5) Starting from day 6, CAR-BCMAs cells can be taken for the corresponding activity assay.

Example 3 Detection of the integration rate of the CAR gene in the T cell genome and the expression level of the encoded protein thereof on the membrane surface

0.5×10^6 of CART-BCMAs cell samples cultured on day 7 (Fig. 3A), day 21 (Fig. 3B) and day 29 (Fig. 3C) in Example 2 were taken, respectively. The expression level of CAR-BCMA protein on the surface of T cell membrane was analyzed by flow cytometry after Fc fragment staining of recombinant human BCMA protein.

The result is shown in Figures 3A, 3B and 3C, and four CAR structures designed in the present disclosure can be expressed in their corresponding modified T cells and complete the cell membrane surface localization.

Example 4 Detection of the in vitro activation ability of CAR-BCMAs

Cell activation level indicator proteins CD137 and IFNγ was detected using CART-BCMAs cells cultured on day 7 in Example 2. 1×10^5 of CART-BCMA cells cultured on day 7 were cultured respectively with BCMA-positive K562-BCMA+E7 tumor cell line and BCMA-negative K562 tumor cell line, or without tumor cells, in 200 μl GT-551 medium for 18h at a ratio of 1:1. Then the expression level of CD137 on the surface of T cell membrane was detected by flow cytometry

and the secretion level of IFNγ in the culture supernatant was detected by ELISA.

The results are shown in Fig. 4A and Fig. 4B, the expression of CD137 was detected on the surface of four CART cells, and the expression of IFNγ was detected in the culture supernatant. Among them, CAR-BCMA-20 shows best CD137 activation level and IFNγ release level. CART-BCMA-MO6 which is constructed based on humanized MO6 antibody sequence shows a weaker level of CD137 activation but a higher level of IFNγ release than CART-BCMA-CA8 which is constructed based on mouse antibody sequence.

Additionally, C-CAR088 induced higher levels of IFN-γ release (Figure 4B) and CD137 expression (Figure 4A) in BCMA-positive tumor cells, compared to CARs based on BCMA-1, BCMA-CA8 and BCMA-MO6.

CART-BCMA-20 induced greater apoptosis of BCMA-positive tumor cells than CART-BCMA-1 (positive control), CART-BCMA-MO6 and CART-BCMA-CA8 (Figure 5).

Example 5 Detection of advanced apoptosis activity of tumor cells induced by CART-BCMAs cells

(1) The CART-BCMAs cells cultured on day 17 in Example 2 were mixed respectively with 1×10^4CFSE-labeled BCMA-negative cells (NH929) or BCMA-positive self-constructed cells (NH929-BCMA overexpressing tumor cell line) at a ratio of 1:1, 2.5:1, 5:1, 10:1, 20:1 (as shown in Fig. 5). The mixed cells were co-cultured in 100 μl GT-551 medium for 4 h, and then stained with 100 μl 25% PI dye for 15 min. The proportion of PI positive cells in CFSE positive cells was analyzed by flow cytometry.

(2) The CART-BCMAs cells cultured on day 22 in Example 2 were mixed respectively with 1×10^4 CFSE-labeled BCMA-negative cells (NH929), BCMA-positive self-constructed cells (NH929-BCMA overexpressing tumor cell line) or MM.1S cell line naturally expressed BCMA at a ratio of 1:1, 5:1, 10:1, 10:1, 40:1 (as shown in Fig. 6B). The mixed cells were co-cultured in 100 μl GT-551 medium for 4 h, and then stained with 100 μl 25% PI dye for 15 min. The proportion of PI positive cells in CFSE positive cells was analyzed by flow cytometry.

The results are shown in Fig. 5 and Figures 6A and 6B, all four CART cells can induce apoptosis of BCMA-positive tumor cells. Among them, CART-BCMA-20 can induce advanced apoptosis of BCMA-positive tumor cells better than CART-BCMA-1. The ability of CART-BCMA-MO6 and CART-BCMA-CA8 to induce advanced apoptosis of BCMA-positive tumor

cells is similar.

Example 6 Inhibition of CART-BCMAs on RPMI-8226 myeloma xenograft model

RPMI-8226 cells in logarithmic growth phase were collected, and 4.0×10^6 tumor cells were inoculated subcutaneously in the right back of 6-8 week old B-NDG mice. When the tumor volume reached about 120 mm^3, the animals were randomly divided into 4 groups according to tumor volume, so that the tumor volume difference of each group was less than 10% of the mean value. Then the solvent control, 7.5×10^6 NT and 7.5×10^6 CART-BCMAs cells were injected through tail vein respectively.

The results are shown in Figures 7A and 7B, compared with the control group, single injection of CART-BCMA-1 and CART-BCMA-20 through tail vein can effectively inhibit the growth of human myeloma RPMI-8226 cells (relative tumor proliferation rate %T/CRTV≤40%, P<0.05), and can significantly prolong the survival time of human myeloma-bearing mice (median survival of the control group is 23 days, median survival of the CART-BCMAs treatment group > 33 days). There was no significant difference in tumor proliferation rate and median survival between the mice treated with CART-BCMA-1 and CART-BCMA-20.

For *in vivo* studies, B-NDG mice were xenografted with human myeloma RPMI-8226 cells. When the tumor volume reached about 120 mm^3, the solvent control, non-transfected (NT) T cells (a negative control) or CART-BCMAs cells were injected through the tail vein of the mice.

Compared with the control group, a single injection of CART-BCMA-1 and CART-BCMA-20 effectively inhibited the growth of the myeloma cells, and significantly prolonged the survival time of human myeloma-bearing mice: median survival of the CART-BCMA-treated groups was >33 days, while median survival of the control group was 23 days. There was no significant difference in the tumor proliferation rate and median survival between the mice treated with CART-BCMA-1 and the mice treated with CART-BCMA-20 (Figures 7A and 7B).

The results suggest that BCMA-20 (C-CAR088) had high *in vivo* anti-tumor efficacy.

Comparative example

In the screening process of the chimeric antigen receptor of the present application, the

inventors tested a large number of candidate sequences, which are illustrated below with examples.

The antibodies to be screened include: BCMA-1, BCMA-2, BCMA-69, BCMA-72, BCMA-2A1, BCMA-1E1, BCMA-J22.9, BCMA-20, BCMA-CA8, and BCMA-MO6. Structures of chimeric antigen receptor targeting BCMA were constructed on the basis of the above antibodies. Among them, BCMA-1 and BCMA-2 are published Car-T sequences and used as a positive control for screening. CAR-T cells were prepared in the same way as in Example 2, and detected in the same way as in Examples 3 and 4.

The results are shown in Figures 1A, 1B and 1C, which are the experimental results of two batches of CAR-T cells. The expression of Car-T was detected with BCMA-Fc fusion protein. It can be seen that there is a high expression in primary T cells, as seen in Fig. 1A. In Fig. IB, it can be seen that BCMA-1, BCMA-20, BCMA-1E1, BCMA-CA8, BCMA-MO6, and BCMA-J22.9 can be activated by the BCMA antigen. Fig. 1C shows that the activated BCMA-1, BCMA-20, BCMA-1E1, BCMA-CA8, BCMA-MO6, and BCMA-J22.9 CAR-Ts can produce higher levels of IFN-γ. The results show that the CAR-T functions obtained by BCMA-1, BCMA-20, CA8 and MO6 are similar, so BCMA-20, CA8 and MO6CAR-T were further analyzed and studied.

Example 7 Membrane protein array experiment

The light chain variable region of SEQ ID NO: 1 and the heavy chain variable region of SEQ ID NO: 2 were used to prepare a single chain antibody B20-scFv-rabFc, and membrane protein array experiment was performed.

20 ug/mL of B20-scFv-rabFc was added to HEK293T cell array transiently transfected with 5344 membrane proteins, respectively. Flow cytometry found that, under this test condition, B20-scFv-rabFc may cross-recognize with TNFRSF17 (Q02223), MAG (P20916), CR2 (P20023), CXADR (P78310) and DDR2 (Q16832), wherein TNFRSF17, i.e., BCMA is the specific target of B20-scFv, and MAG, CR2, CXADR and DDR2 are suspected non-specific targets.

To further confirm whether the suspected target can cause the activation of CAR-T, CBM.BCMA CAR-T was co-cultured with 293T cells transfected with BCMA, CR2, CXADR, DDR2, and MAG, respectively. The IFNγ, TNF, IL-2 and other cytokines in co-culture supernatant were detected. 293T cells transfected with empty vector were used as a negative control, and 293T cells transfected with BCMA were used as a positive control.

Figure 8 shows results the expression of BCMA, CR2, CXADR, DDR2, and MAG in 293T

cells after transfection of relevant plasmids by flow cytometry.

The cytokine detection results are shown in Figures 9A, 9B and 9C. Only the BCMA expressed on 293T cells can induce CBM. BCMA CAR-T cells to produce large amounts of IFNγ/TNF/IL-2, while the other four non-specific surface markers cannot activate CBM. BCMA CAR-T cells.

Figure 8 and Figures 9A-9C show whole genome membrane proteome array and validation. TNFRSF17, MAG, CR2, CXADR and DDR2 were identified with moderate binding with B-20 scFv rabFc at the concentrations of 20.0 μg/mL. Only cells expressing TNFRSF17(BCMA) can induce BCMA-CAR-T cells producing a large number of cytokines (IFNγ/TNF/IL-2).

Specific membrane staining was observed on human lymphocytes in thymus, spleen, lymph nodes, bone marrow and scattered lymphocytes in thyroid gland, adrenal gland at the concentrations of 20.0 μg/mL (Table 1 and Figures 19A-19B).

Table 1

Staining site	**Tissue**	**5.0 μg/mL**	**20.0 μg/mL**
Nucleus	Esophagus, mucosal layer	1/3[a], +[b]	1/3, +
Cytoplasm	Stomach, mucosal layer	1/3, +	2/3, +
	Kidney, cortex	1/3, +	2/3, +
	Bladder, mucosal layer	-	1/3, +
Membrane	Thyroid	-	3/3, +
	Thymus, cortex, medulla	3/3, +	3/3, +
	Spleen, splenic cord	2/3, +	3/3, +~++
	Lymph node, medulla	3/3, +	3/3, +
	Adrenal gland, cortex	-	3/3, +
	Bone marrow	-	3/3, +

a) number of positive staining in 3 donors.

b) staining intensity of positive cells and percentage of positive cells in the cells of the same type.

"-" No stained cells,

"+" weakly positive staining, < 10% cells are stained,

"++" moderately positive staining, 11%-50% cells are stained.

Example 8 *In vitro* anti-tumor activity of C-CAR088 cells

The chimeric antigen receptor BCMA-20 (hereafter named C-CAR088) was selected for subsequent experiments. C-CAR088 cells, NT cells (non-transfected T cells, used as negative control) and positive control cells (Bluebird bb2121) were co-cultured with BCMA negative cells (NH929) or BCMA positive cells (NH929-BCMA) at different effect target ratios, The killing ability of each cell to the target cell was analyzed.

The results are shown in Figure 10. C-CAR088 cells and positive control cells only have a strong killing effect on NH929-BCMA cells, but no significant killing effect on negative target cells NH929. The non-transfected group (NT) also have no significant killing effect on the target cells.

T cells with C-CAR088, non-transfected (NT) T cells (a negative control) and positive control cells (Bluebird bb2121) were co-cultured with BCMA negative cells (NH929) or BCMA positive cells (NH929-BCMA) at different effect/target ratios. Then the cytotoxicity was assayed.

Figure 10 shows that C-CAR088 T cells and the positive control demonstrated strong cytotoxicity on NH929-BCMA cells, but not NH929 cells.

Example 9 Effect of soluble BCMA on cell killing activity

In the co-cultivation system of C-CAR088 cells with BCMA negative target cells A549 and BCMA positive target cells A549-BCMA-2E9, 100 ng/ml and 500 ng/ml soluble BCMA protein was added respectively to detect its effect on CD137 expression.

The results are shown in Figure 11. Soluble BCMA protein have no effect on the upregulation of CD137 expression, indicating that soluble BCMA does not block the specific recognition of CAR and target antigen. In the test of *in vitro* cell killing ability and ELISA of IFN-γ release, the killing effect of C-CAR088 cells on target cells and the release of IFN-γ were reduced by 500ng/ml soluble BCMA protein, but there was no significant difference. The above results indicate that the cell killing activity of C-CAR088 cells is basically unaffected by soluble BCMA

Example 10 Dose dependent effect of C-CAR088 cells

6 week old B-NDG mice (half male and half female) were selected and intraperitoneally injected with 2.5×10^6 human multiple myeloma cells RPMI-8226. Mice with similar tumor burden were selected and divided into 5 groups, and were injected with 2.5×10^6 C-CAR088 cells (low-dose group), 5×10^6 C-CAR088 cells (medium-dose group), 1×10^7 C-CAR088 cells (high-dose group), T cells and vehicle (with cryoprotectant (CBMG C-CFMC) as vehicle), respectively. The experiment lasted 54 days. During the experiment, the tumor burden of the mice was evaluated every 5 days. At the end of the experiment, the survival rate of the mice was calculated.

The results are shown in Figure 12. Single administration of doses of 5×10^6 cells /mouse and 1×10^7 cells /mouse C-CAR088 cells can effectively inhibit the growth of B-NDG mouse xenograft tumor of human myeloma RPMI-8226 cell. The relative tumor proliferation rates were 6.12% and 0.75%, respectively ($p < 0.05$). At the end of the experiment, the survival rate of tumor-bearing mice in the middle-dose group was 91.7% (11/12). No death occurred in the tumor-bearing mice in the high-dose group, and the survival rate was 100.0% (12/12), having a significant difference ($p < 0.05$) compared with the vehicle group (survival rate 58.3%). The above results indicate that C-CAR088 exhibits dose dependent *in vivo* anti-tumor activity.

Example 11 Phase I clinical study of C-CAR088

With the approval of the Ethics Committee, a total of 15 volunteers conducted phase I clinical trials. The key eligibility criteria for volunteer are as follows: patients with multiple myeloma aged 18-75 years old, MM cells express BCMA, have measurable MM, and have received 2 prior lines of therapy for MM and have received treatment with PI and IMiD, have adequate hepatic, renal, cardiac and hematopoietic function.

The experimental process is shown in Figure 13.

The treatment results are shown in Figure 14 and Table 2. Two patients were evaluated at week 2, one SD and one CR. The remaining 13 patients were evaluated at week 4 and the objective response rate ORR reached 100%. In all patients, there were 3 CR, 5 VGPR (including 1 Daratumumab-resistant patient), and 6 PR.

Table 2 Clinical response

Research center	Patient ID	Follow up length	Serum M protien /sFLC type	Clinical response								Best ORR
				Baseline	2w	4w	8w	12w	16w	20w	6 m	
Jiangsu Provincial People's Hospital	Z0203-00801C001	6m	IgG	71.0g/L	42.0g/L	26.3g/L	1.8g/L UIF(-)	6.2g/L UIF(-)	7.0g/L UIF(-)	16.4g/L	45g/L	VGPR
	Z0203-00801C003	12w	k	3250mg/L	3050mg/L	75 mg/L SIF(-) UIF(+) UPEP(-)	170mg/L	960mg/L	PD			VGPR
	Z0203-00801C004	6m	IgG	46.5g/L	7.9g/L	9.0g/L	SPEP(-) UIF(-) SIF(+)	SPEP(-) UIF(-) SIF(+)	SPEP(-) UIF(-) SIF(+)	SPEP(-) UIF(-) SIF(+)	21.6g/L	VGPR
	Z0203-00801C008	20w	IgG	26.1g/L	9.1g/L	4.8g/L	4.6g/L	9g/L*	10g/L*	17g/L *	PD	PR
	Z0203-00801C010	4e	IgG	55.7g/L	45.4g/L	23.3g/L						PR
	Z0203-00801C011	3w	IgG	22.5g/L	18.8g/L							SD
Tianjin Hematology Hospital	Z0203-01301C001	8w	IgA	16.7g/L	7.4g/L	3.6g/L	SPEP(-) UIF(-) SIF(+)					VGPR
	Z0203-01301C003	4w	IgG	50.2g/L	27.1g/L	15.0g/L						PR
	Z0203-01301C006	4w	λ	760mg/L	SPEP(-) UIF(-) SIF(+)	SPEP(-) UIF(-) SIF(+)						VGPR
Peking Union	Z0203-00701C001	4w	IgG	17.4g/L	10.8g/L	5.3g/L						PR
	Z0203-00701C002	4w	IgG	21.7g/L	15.8g/L	7.9g/L						PR

Medical College Hospital													
	Z0203-00601C002	12w	λ	187mg/L	3.28mg/L	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-	sCR
Daupei Hospital	Z0203-00601C004	4w	κ	209mg/L	SIF-UIF-MRD-	SIF-UIF-MRD-	SIF-UIF-MRD-						sCR
	Z0203-00601C005	4w	IgG	28.27g/L	24.3g/L	8.6g/L							PR
	Z0203-00601C006	2W	κ	121mg/L	SIF-UIF-MRD-								sCR

The treatment-emerging adverse events are shown in Table 3. Only one patient occurred grade 3 cytokine release syndrome in 15 patients. No neurotoxicity events and no dose-limiting toxicity (DLTs) were observed in the dose escalation. The cytopenias is mostly related to Cy/Flu lymphodepletion. It should be noted that the occurrence of a certain degree of cytokine release syndrome after treatment also illustrates the effectiveness of CART treatment from the side. None of the 15 patients had particularly serious cytokines, and C-CAR088 has better safety.

Table 3 Treatment-Emerging Adverse Events

Treatment-Emerging Adverse Events	**n (%) Overall**	**n (%) Grade 3/4**
Cytokine release syndrome	14 (93)	1(7)
Neutropenia	15 (100)	15 (100)
Thrombocytopenia	13 (87)	11(73)
Anemia	12 (80)	6(40)
Increased AST	5(33)	3(20)
Infection	3(20)	3(20)

Figure 15 shows the treatment condition of the patient of ID Z0203-00801C008. Figure 16 shows the treatment condition of patient of ID Z0203-00701C001. The PET-CT images of the cancer lesions for one patient show that abnormal plasma cells in the bone marrow were significantly decreased after the C-CAR088 treatment (Figure 15). Figures 16A and 16B show that majority of the PCs were abnormal (>90% were CD45lo/-), were BCMA+ and clonal for Kappa light chain at the beginning of the experiment (Baseline). Figure 16B shows that after 14 or 28 days of BCMA CAR-T treatment, abnormal PC in BM were significantly decreased, especially Kappa + PC, which decreased from the baseline level of 85.2% to 0%.

Figure 17 shows the expansion of C-CAR088 and the decrease of M-protein/sFLC levels in the blood. The results showed that C-CAR088 cells expanded effectively after injection, and the level of M-protein/sFLC markers continued to decrease. The M-marker level of one patient was

dropped to 0 on day 14.

Summary of observations for C-CAR088 was as follow.

- In preclinical studies, C-CAR088 showed antitumor activity both *in vitro* and *in vivo.*
- Early C-CAR088 trial results in patients with r/r MM support preclinical findings, showed promising efficacy and manageable safety profile.
- The early clinical efficacy signal at low, suboptimal dose was encouraging.
- Compared to KarMMa data, our current dose level from infused patients was well below the optimal dose of bb2121. 53% (8/15) were recently dosed (at ~4 weeks).
- Dose dependence was observed based on PK profile. C-CAR088 was well tolerated in patients.

Example 12 An Anti-BCMA CAR T-Cell Therapy (C-CAR088) Showed Promising Safety and Efficacy Profile in Treating Relapsed or Refractory Multiple Myeloma (r/r MM)

Our studies demonstrated that C-CAR088 was considerably more cytotoxic towards tumor cells both *in vitro* and *in vivo*, compared to other anti-BCMA CARs.

We conducted a clinical trial of an anti-BCMA CAR (BCMA-20, also termed "C-CAR088") in treating relapsed/refractory multiple myeloma (R/R MM) in patients.

Clinical trials are evaluated along a number of different criteria. Two key measures are overall response rate (ORR) and complete response rate (CR). When compared with other anti-BCMA CARs, the CARs of the claimed method offer better therapeutic efficacy in a clinical trial, as reflected by high response rates (95% overall response rate or ORR, and 67% complete response rate or CR) in treating relapsed/refractory multiple myeloma (R/R MM). Even when compared with JNJ-4528 (CARTITUDE-1), the percentage of adverse events, such as neurotoxicity, in the C-CAR088 was significantly lower. Specifically, for C-CAR088, only 4% patients experienced grade 1 neurotoxicity which resolved spontaneously. Thus, the CAR-T cells of the claimed method offered a favorable safety profile.

C-CAR088 demonstrated a manageable safety profile.

- Most cases of CRS were grade 1/2 with median time to onset of 6 days.
- Neurotoxicity (ICANS) was infrequent and generally low-grade with 1 grade 1 event.

Dose dependent responses occurred early and deepened.

- ORR: 95.7%, with 43.5% CR rate at median time to CR: 1.6 months (range: 0.5-9.5). Median time to response: 0.5 month.
- At median 6.2 months follow up, 65.1% patients were progression-free at 6 months

In preclinical studies, C-CAR088 showed very good in vitro and in vivo anti-tumor activity and target specificity. Clinical trial results in 24 patients with r/r MM showed strong therapeutic index with promising efficacy and manageable safety profile.

We conducted a clinical trial of an anti-BCMA CAR (BCMA-20, also termed "C-CAR088") in treating relapsed/refractory multiple myeloma (R/R MM) in patients. The patients' baseline demographics and clinical characteristics prior to the start of our anti-BCMA CAR treatment are shown in Table 4.

The median age of the patients dosed was 60 years (range: 45–74 years). The median number of prior lines of therapy was 4 (ranging from 2-12 prior therapies). All patients had received prior treatment with IMiDs (immunomodulatory drug) and proteasome inhibitors. 25% patents were previously treated with anti-CD38 monoclonal antibody, while 25% patents had received autologous hematopoietic stem cell transplant.

Table 4 Summary of baseline clinical characteristics of the patients

Characteristic	**N=24**
Median age, yrs (range)	60 (45-74)
• Age ≥ 65, n (%)	9 (37.5)
Male/Female, n	14/10
MM subtype, n (%)	
• IgG	14 (58.3)
• IgA	3 (12.5)
• IgD	1 (4.2)
• Light Chain	6 (25)

Characteristic	**N=24**
High Risk Cytogenetics*, n (%)	
•0	3 (12.5)
•1	5 (20.8)
•2	11 (45.8)
•3	2 (8.3)
•Unknown	3 (12.5)
Median number of prior lines of therapy, n (range)	4 (2-12)
Prior regimens, n (%)	
• Prior PIs and IMiDs	24 (100)

ECOG PS, n (%)	
• 0	15 (62.5)
• 1	9 (37.5)
ISS stage, n (%)	
• I	7 (29.2)
• II	11 (45.8)
• III	6 (25)
• Prior ASCT	6 (25.0)
• Prior CD38 mAb	6 (25.0)
Received bridging therapy, n (%)	4 (16.7)

* Including 1q21 gain, del (17p), t (4;14) and t (14;16).

The clinical protocol, as well as the key inclusion criteria, is shown in Figure 21. Specifically, qualified subjects were enrolled, and the collected peripheral blood leukocytes were used to produce the CAR-T cells (C-CAR088). The CAR-T cells were then frozen and stored below -135°C until use. For CAR-T treatment, the CAR-T cells were thawed, and administration completed within 30-45 minutes.

At -5 and -3 days before the CAR-T infusion, the patients received lymphodepletion pretreatment, including fludarabine (30 mg/m^2/d, intravenous, once per day for three days), and cyclophosphamide (300 mg/m^2/d, intravenous, once per day for three days).

Approximately 72 hours after lymphodepletion, the patients were administered 1.0-6.0 x 10^6 CAR-T cells/kg on day 0 as 3 + 3 dose escalation. Follow-ups with the patients were carried out after the infusion starting on day 1 through month 24.

The primary objectives included safety: rated of dose limiting toxicities; incidence and severity of treatment-emergent adverse events (CTCAEV5.0). Secondary objectives included efficacy: IMWG 2016 ORR; DOR; PFS; OS. Exploratory objectives included CAR-T expansion and persistence.

As shown in Figure 22, an overall response rate (ORR, including CR and PR) of our anti-BCMA CAR-T trial is 96%. The best overall response (BOR) included 12 stringent complete responses (sCRs), 2 complete responses (CR), 8 very good partial responses (VGPRs) and 1 partial response (PR). The complete response (CR) is 67%. (SD: stable disease; PR: partial response; CR:

complete response; PD: progressive disease; MR: minimal response; VGPR: very good partial response; MRD: minimal residual disease.)

The CR/sCR, VGPR and PR for overall and each dose group are shown in Table 5 and Figure 23. In the 3.0-6.0 x10^6 CAR-T cells/kg dose groups, 14/21 (66.7%) patients achieved a CR/sCR and all (14/14) patients achieved MRD negative by flow cytometry at 10^{-4} -10^{-6}.

Table 5

Response	**Overall** (n=24)	**1.0 x 10^6 /kg** (n=3) (low dose)	**3.0 x 10^6 /kg** (n=11) (mid dose)	**4.5-6.0 x 10^6 /kg** (n=10)* (high dose)
ORR, n (%)	23 (95.8%)	3 (100%)	11 (100%)	9 (90.0%)
CRR, n (%)	13 (54.2%)	0	6 (54.5%)	7 (70.0%)

*1 patient received 4.5 x 10^6 /kg and 1 received 5.0 x 10^6 /kg.

Table 6 below compares the C-CAR088 trial with those of Munshi et al. (KarMMa: Idecabtagene Vicleucel), Mailankody et al. (EVOLVE: Orvacabtagene Autoleucel) and Madduri et al. (CARTITUDE-1: JNJ-4528).

Table 6 Comparison of C-CAR088 clinical trial with other BCMA-specific CARs

	KarMMa: Idecabtagene Vicleucel (n=128)	EVOLVE: Orvacabtagene Autoleucel (n=62)	CARTITUDE-1: JNJ-4528 (n=97)	**C-CAR088** (n=24)
Median age, yrs (range)	61 (33-78)	61 (33-77)	61 (43-78)	60 (45-74)
High risk cytogenetics	35%	41%*	24%	75%*
Tumor burden in BM, %	>50% PC: 51	-	>60% PC: 22	>50% PC: 17
Extramedullary PCs	39%	23%	13%	8%
Median prior lines of therapies, No. (range)	6 (3-16)	6 (3-18)	6 (3-18)	4 (2-12)

Triple refractory, %	84%	94%	88%	25%
Bridging therapy	88%	63%	-	17%
CRS: all / grade ≥ 3	84%/6%	89%/3%	95%/5%	92%/4%
ICANS: all / grade ≥ 3	17%/3%	13%/3%	21%/10% (Neurotoxicity)	**4%/0**
ORR	73%	92%	97%	**95%**
sCR/CR	33%	36%	67%	**67%**
Evaluable patients with MRD neg ≥ 10^5	94%	84%	55%	83%
PFS, mos	8.8	9.3$^+$	12-mo PFS: 76.6%	6-mo PFS: 78.7%$^\#$

* Includes +1q21. $^+$ PFS in lowest dose cohort (300 x 10^6 cells). $^\#$ Results in 3-6 x 10^6 CAR-T cell/ kg dose cohort.

ICANS: immune effector cell-associated neurotoxicity syndrome.

See, Munshi et al., Idecabtagene vicleucel (ide-cel; bb2121), a BCMA-targeted CAR T-cell therapy, in patients with relapsed and refractory multiple myeloma (RRMM): Initial KarMMa results, Journal of Clinical Oncology, 2020, 38(15) suppl., Abstract 8503; Mailankody et al., Orvacabtagene autoleucel (orva-cel), a B-cell maturation antigen (BCMA)-directed CAR T cell therapy for patients (pts) with relapsed/refractory multiple myeloma (RRMM): update of the phase 1/2 EVOLVE study (NCT03430011), Journal of Clinical Oncology, 2020, 38(15) suppl., Abstract 8504; Madduri et al., CARTITUDE-1: Phase 1b/2 Study of Ciltacabtagene Autoleucel, a B-Cell Maturation Antigen–Directed Chimeric Antigen Receptor T Cell Therapy, in Relapsed/Refractory Multiple Myeloma, 62nd ASH Annual Meeting and Exposition, December 5-8, 2020, Abstract 177.

For our clinical trial of C-CAR088, the Kaplan Meier progression-free survival (PFS) estimates include a 6-month PFS of 78.7% for the mid- and high-dose group, with 95% confidence intervals (CIs) of 62.1% - 99.7%. Median duration of response (DOR) was not reached. See Table 7 and Figure 24.

Table 7

Time (month)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
n.risk	21	19	19	18	16	16	13	13	10	9	8	8	5	3	2	1	1	1	1
n.event	1	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0

The time course of the CAR copies in the blood of the patients is shown in Figures 25A and 25B. Thus, the CAR levels were maintained in the blood after administration.

C-CAR088 treatment was well tolerated. The patients' adverse reactions (adverse events, AEs) were recorded (Tables 8 and 9). There was only 1 (4.2%) grade ≥3 cytokine release syndrome (CRS). Neurotoxicity was observed only in one patient (4.2%) which resolved spontaneously, with no grade ≥3 neurotoxicity. Cytopenia, such as neutropenia and thrombocytopenia, was mostly related to the fludarabine/cyclophosphamide (Cy/Flu) lymphodepletion. No dose-limiting toxicities were observed, and all adverse events were reversible. These demonstrated that our anti-BCMA CAR had an excellent safety profile.

Table 8

AEs (≥25%), n (%)	**Any Grade (n=24)**	**Grade ≥3 (n=24)**
Neutropenia	24 (100%)	22 (91.7%)
Lymphopenia	22 (91.7%)	20 (83.3%)
Thrombocytopenia	22 (91.7%)	9 (37.5%)
Anemia	20 (83.3%)	12 (50.0%)
Elevated AST/ALT	13 (54.2%) / 8 (33.3%)	4 (16.7%) / 0 (0)
Infection	12 (50.0%)	6 (25.0%)

Table 9

CRS & Neurotoxicity *	**Any Grade (n=24)**	**Grade ≥3 (n=24)**
CRS, n (%)	22 (91.7%)	1 (4.2%)
• Median days to onset, d (range)	6 (1-11)	

• Median days to resolution, d (range)	5 (2-9)	
• Treated with Tocilizumab, n (%)	6 (26.1)	
• Treated with Steroids, n (%)	2 (8.7)	
Neurotoxicity, n (%)	1 (4.2%)	0 (0)
• Days to onset, d	8	
• Days to resolution, d	1	

*ASTCT Consensus Grading for Cytokine Release Syndrome and Neurologic Toxicity Associated with Immune Effector Cells 2019.

CRS: Cytokine release syndrome

The scope of the present invention is not limited by what has been specifically shown and described hereinabove. Those skilled in the art will recognize that there are suitable alternatives to the depicted examples of materials, configurations, constructions and dimensions. Numerous references, including patents and various publications, are cited and discussed in the description of this invention. The citation and discussion of such references is provided merely to clarify the description of the present invention and is not an admission that any reference is prior art to the invention described herein. All references cited and discussed in this specification are incorporated herein by reference in their entirety. Variations, modifications and other implementations of what is described herein will occur to those of ordinary skill in the art without departing from the spirit and scope of the invention. While certain embodiments of the present invention have been shown and described, it will be obvious to those skilled in the art that changes and modifications may be made without departing from the spirit and scope of the invention. The matter set forth in the foregoing description and accompanying drawings is offered by way of illustration only and not as a limitation.

Claims

1. A chimeric antigen receptor (CAR), comprising: an anti-BCMA antigen-binding region which comprises a light chain variable region (V_L) and a heavy chain variable region (V_H), V_L comprising three complementarity determining regions (CDRs), LCDR1, LCDR2 and LCDR3, V_H comprising three CDRs, HCDR1, HCDR2 and HCDR3,

(a) wherein LCDR1, LCDR2 and LCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, respectively, wherein HCDR1, HCDR2 and HCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, respectively;

(b) wherein LCDR1, LCDR2 and LCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, respectively, wherein HCDR1, HCDR2 and HCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, respectively; or

(c) wherein LCDR1, LCDR2 and LCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, respectively, wherein HCDR1, HCDR2 and HCDR3 have amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, respectively.

2. The CAR of claim 1, wherein V_L is located at the N-terminus of V_H.

3. The CAR of claim 1, wherein V_L and V_H have amino acid sequences about 80% to about 100% identical to amino acid sequences set forth in (a) SEQ ID NO: 1 and SEQ ID NO: 2, respectively; (a) SEQ ID NO: 3 and SEQ ID NO: 4, respectively; or (a) SEQ ID NO: 5 and SEQ ID NO: 6, respectively.

4. The CAR of claim 1, wherein the anti-BCMA antigen-binding region is a single-chain variable fragment (scFv) that specifically binds BCMA.

5. The CAR of claim 1, wherein the CAR further comprises one or more of the following:

(a) a signal peptide,

(b) a hinge region,

(c) a transmembrane domain,

(d) a co-stimulatory region, and

(e) a cytoplasmic signaling domain.

6. The CAR of claim 5, wherein the co-stimulatory region comprises a co-stimulatory region of 4-1BB (CD137), CD28, OX40, CD2, CD7, CD27, CD30, CD40, CD70, CD134, PD1, Dap10, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), NKG2D, GITR, TLR2, or combinations thereof.

7. The CAR of claim 5, wherein the cytoplasmic signaling domain comprises a cytoplasmic signaling domain of CD3ζ.

8. The CAR of claim 5, wherein the hinge region comprises a hinge region of CD8, CD28, CD137, Ig4, or combinations thereof.

9. The CAR of claim 5, wherein the transmembrane domain comprises a transmembrane domain of CD8, CD28, CD3ε, CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or combinations thereof.

10. An immune cell expressing the CAR of claim 1.

11. The immune cell of claim 10, wherein the immune cell is a T cell or a natural killer (NK) cell.

12. A nucleic acid encoding the CAR of claim 1.

13. A vector comprising the nucleic acid of claim 12.

14. A method of treating cancer, the method comprising administering the immune cell of claim 10 to a subject in need thereof.

15. The method of claim 14, wherein the cancer is a hematologic cancer.

16. The method of claim 14, wherein the cancer is a plasma-cell malignancy.

17. The method of claim 14, wherein the cancer is a BCMA-positive malignancy.

18. The method of claim 14, wherein the cancer is multiple myeloma (MM), or plasma cell leukemia.

19. The method of claim 14, wherein the immune cell is administered by infusion, injection, transfusion, implantation, and/or transplantation.

20. The method of claim 14, wherein the immune cell is administered intravenously, subcutaneously, intradermally, intranodally, intratumorally, intramedullary, intramuscularly, or intraperitoneally.

21. The method of claim 14, wherein the immune cell is administered via intravenous infusion.

22. The method of claim 14, wherein the immune cell is allogeneic or autologous.

23. The method of claim 14, wherein the subject is a human.

24. A method for treating cancer, the method comprising administering the immune cell of claim 10 to a subject in need thereof, wherein the chimeric antigen receptor (CAR) generates an area under the curve (AUC) ranging from about 5.0e+05 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA in the blood of the subject in about 28 days after administration.

25. The method of claim 24, wherein the AUC ranges from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA in the blood of the subject in about 28 days after administration.

26. The method of claim 24, wherein the AUC ranges from about 5.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.3e+07 copies/gDNA in the blood of the subject in about 28 days after administration.

27. The method of claim 24, wherein the AUC ranges from about 7.0e+06 copies/μg genomic DNA (copies/gDNA) to about 1.0e+07 copies/gDNA in the blood of the subject in about 28 days after administration.

28. A method for treating cancer, the method comprising administering the immune cell of claim 10 to a subject in need thereof, wherein the chimeric antigen receptor (CAR) generates a maximum plasma concentration (C_{max}) ranging from about $5x10^4$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA in the blood of the subject.

29. The method of claim 28, wherein the C_{max} ranges from about $5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1.3x10^6$ copies/gDNA in the blood of the subject in about 28 days after administration.

30. The method of claim 28, wherein the C_{max} ranges from about $7.5x10^5$ copies/μg genomic DNA (copies/gDNA) to about $1x10^6$ copies/gDNA in the blood of the subject in about 28 days after administration.

31. The method of claim 28, wherein the CAR has a T_{max} ranging from about 12 days to about 25 days.

32. The method of claim 28, wherein the CAR has a T_{max} ranging from about 14 days to about 20 days.

33. The method of claim 28, wherein the CAR has a T_{max} ranging from about 6 days to about 22 days.

34. The CAR of claim 1, comprising an amino acid sequence about 80% to about 100% identical to the amino acid sequence set forth in SEQ ID NO: 59, SEQ ID NO: 61, or SEQ ID NO: 63.

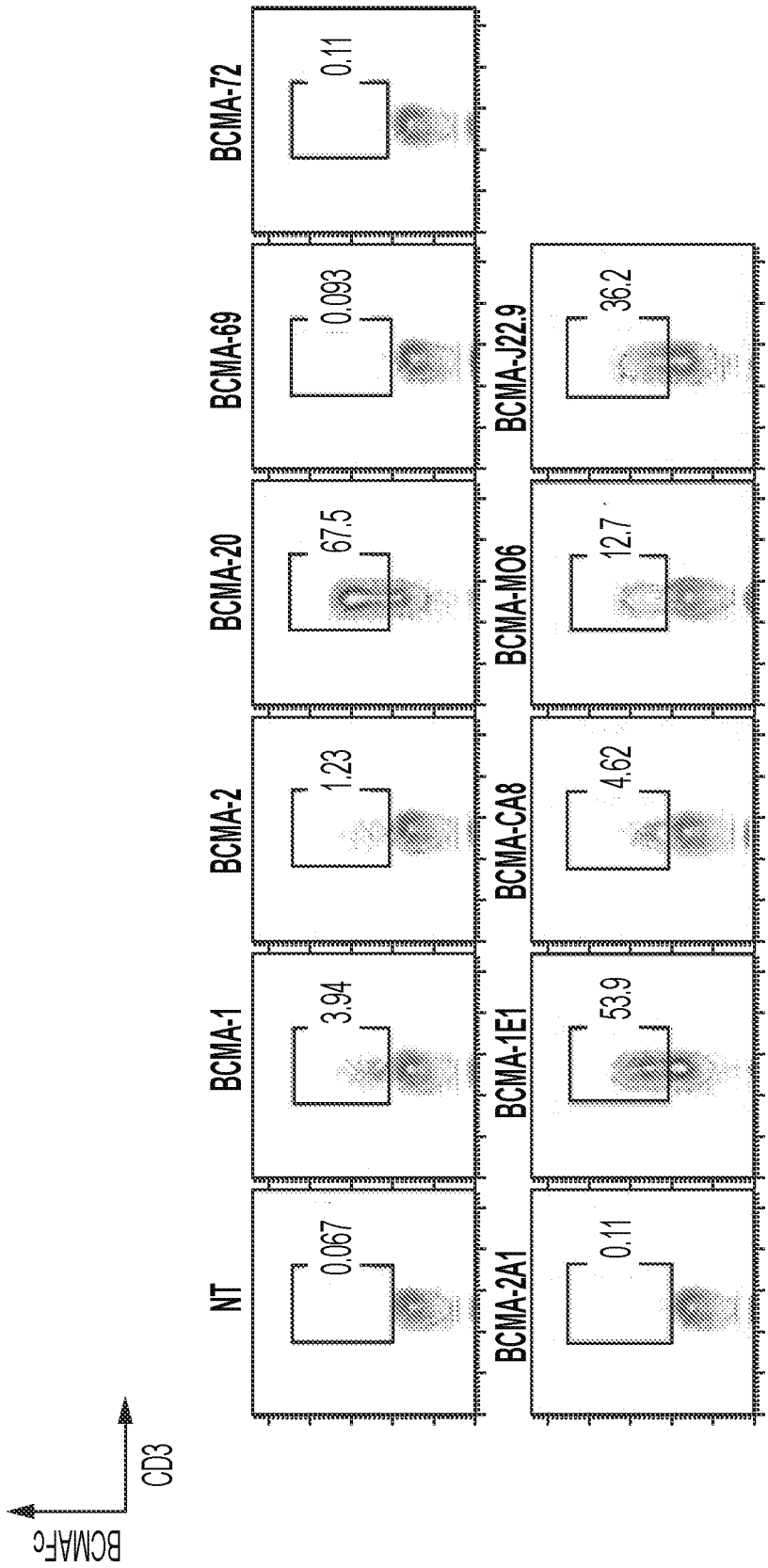

NT
0.067
BCMA-1
3.94
BCMA-2
1.23
BCMA-20
67.5
BCMA-69
0.093
BCMA-72
0.11
BCMA-2A1
0.11
BCMA-1E1
53.9
BCMA-CA8
4.62
BCMA-MO6
12.7
BCMA-J22.9
36.2
CD3
BCMAFc

FIG. 1A

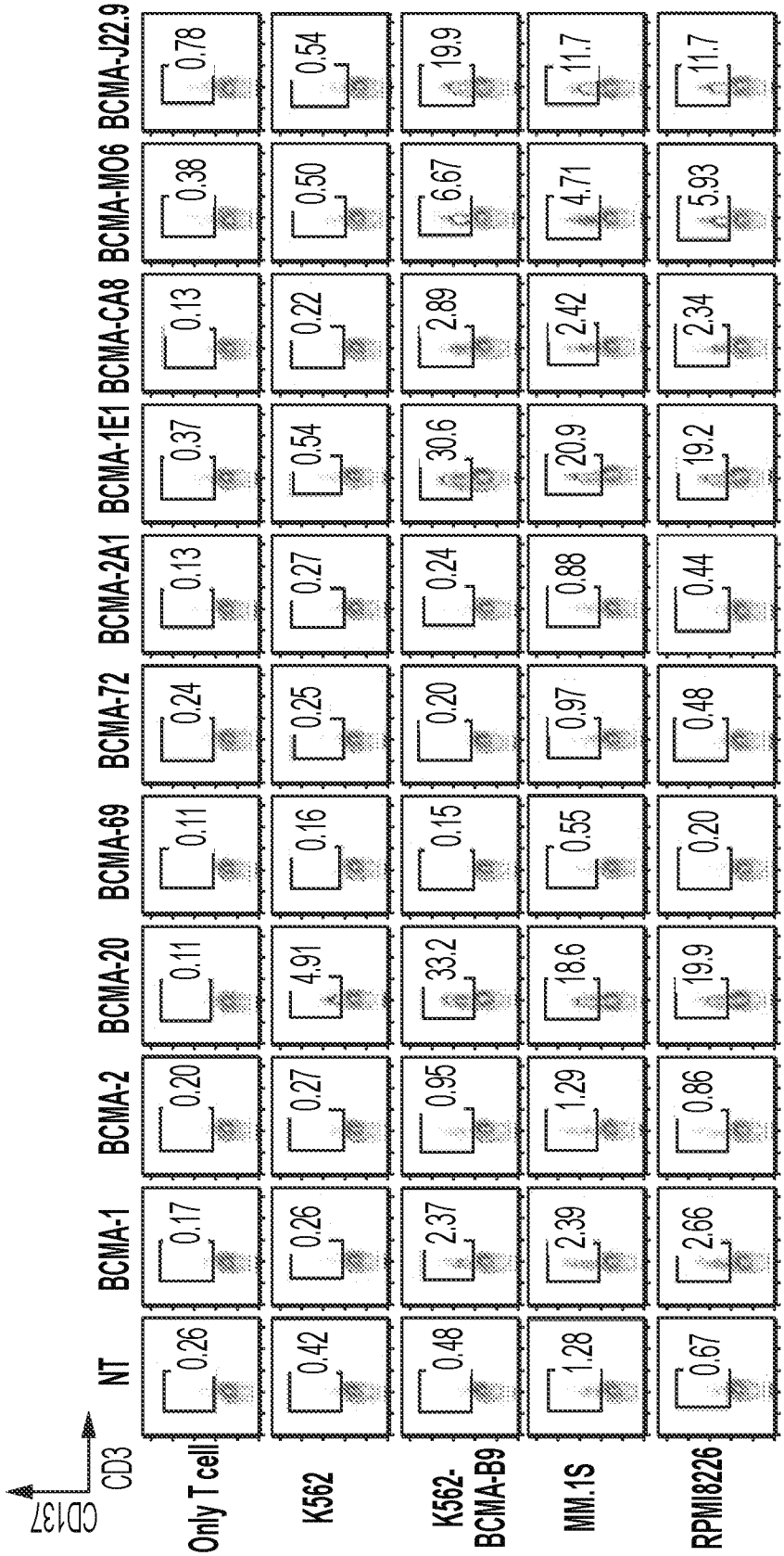

CD137
CD3
NT
BCMA-1
BCMA-2
BCMA-20
BCMA-69
BCMA-72
BCMA-2A1
BCMA-1E1
BCMA-CA8
BCMA-MO6
BCMA-J22.9
Only T cell
0.26 0.17 0.20 0.11 0.11 0.24 0.13 0.37 0.13 0.38 0.78
K562
0.42 0.26 0.27 4.91 0.16 0.25 0.27 0.54 0.22 0.50 0.54
K562-BCMA-B9
0.48 2.37 0.95 33.2 0.15 0.20 0.24 30.6 2.89 6.67 19.9
MM.1S
1.28 2.39 1.29 18.6 0.55 0.97 0.88 20.9 2.42 4.71 11.7
RPMI8226
0.67 2.66 0.86 19.9 0.20 0.48 0.44 19.2 2.34 5.93 11.7

FIG. 1B

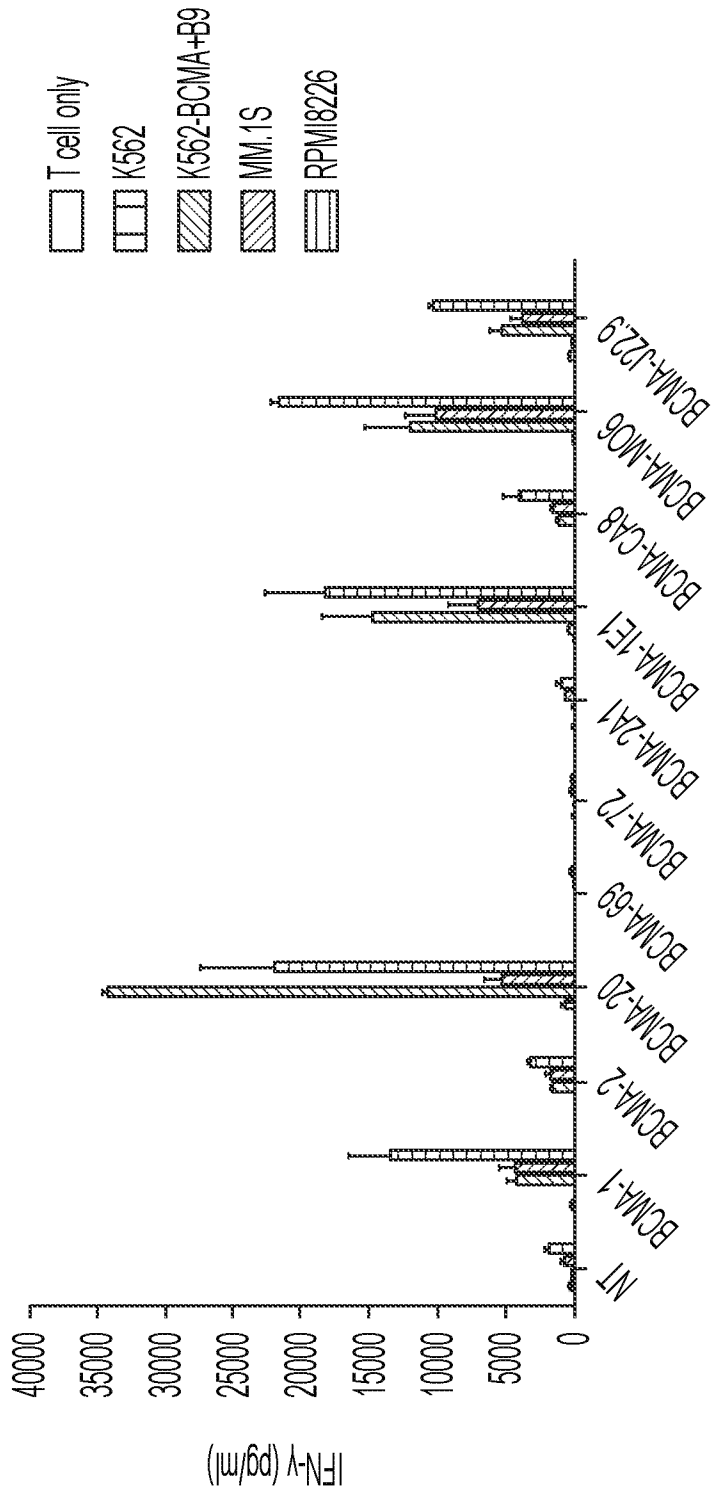

T cell only
K562
K562-BCMA+B9
MM.1S
RPMI8226
IFN-γ (pg/ml)
40000
35000
30000
25000
20000
15000
10000
5000
0
NT
BCMA-1
BCMA-2
BCMA-20
BCMA-69
BCMA-72
BCMA-241
BCMA-1E1
BCMA-CA8
BCMA-M06
BCMA-J229

FIG. 1C

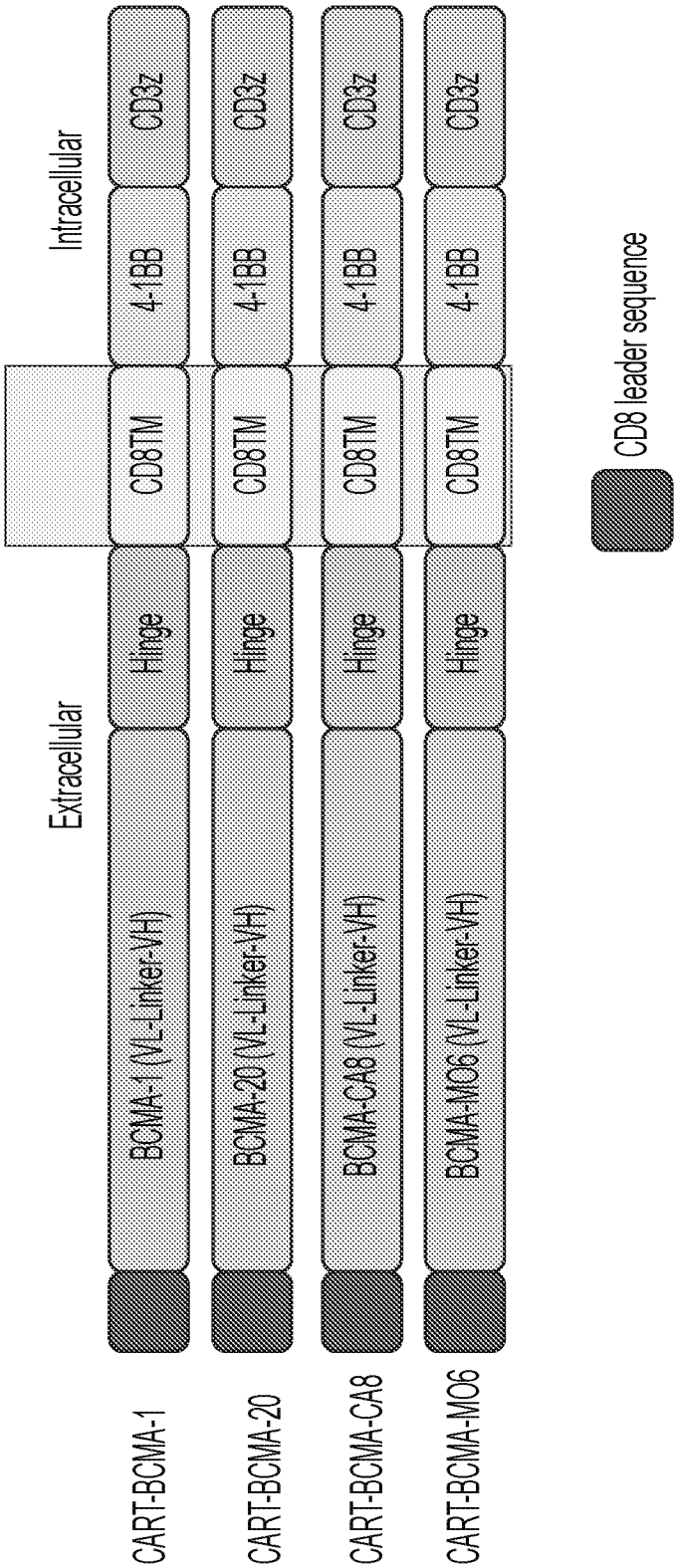
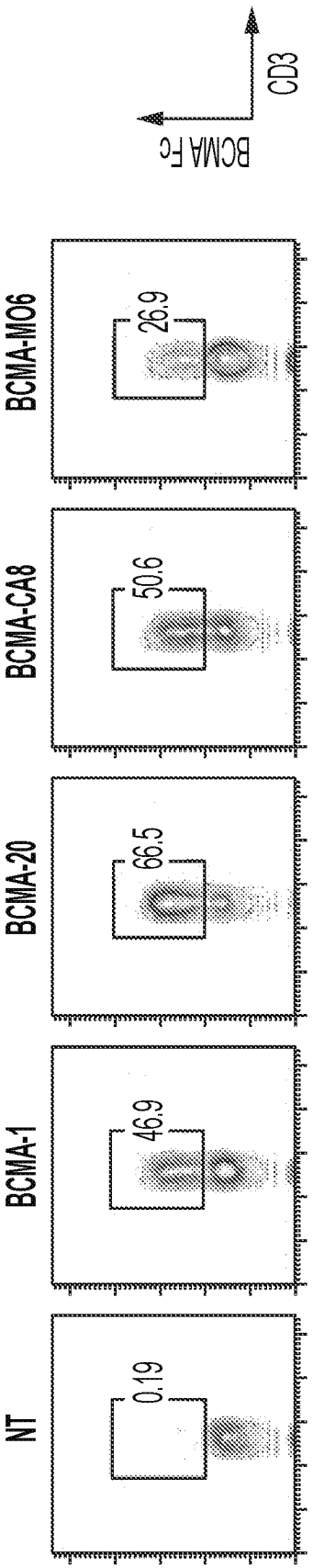

Extracellular
Intracellular
CART-BCMA-1
CART-BCMA-20
CART-BCMA-CA8
CART-BCMA-MO6
BCMA-1 (VL-Linker-VH)
BCMA-20 (VL-Linker-VH)
BCMA-CA8 (VL-Linker-VH)
BCMA-MO6 (VL-Linker-VH)
Hinge
CD8TM
4-1BB
CD3z
CD8 leader sequence

FIG. 2


NT
BCMA-1
BCMA-20
BCMA-CA8
BCMA-MO6
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46.9
66.5
50.6
26.9
BCMA Fc
CD3

FIG. 3A

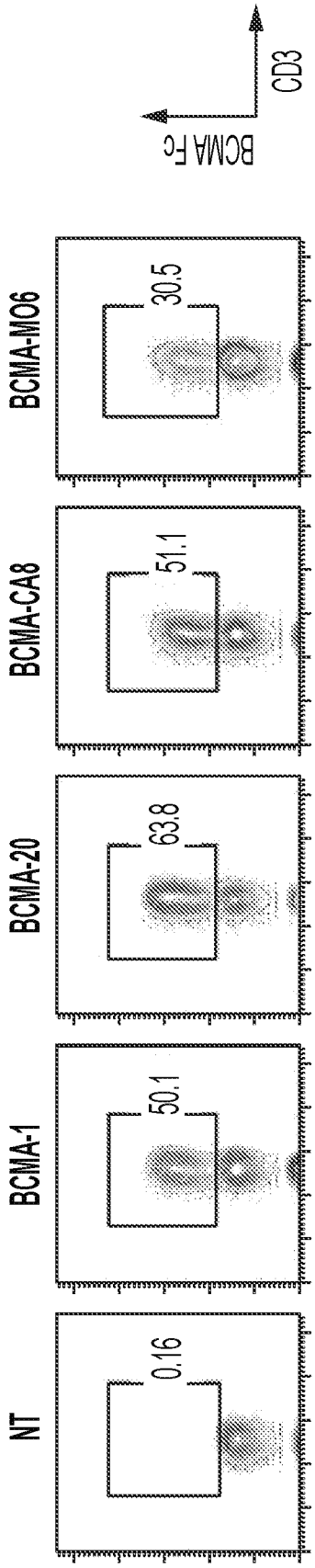
NT
BCMA-1
BCMA-20
BCMA-CA8
BCMA-MO6
0.16
50.1
63.8
51.1
30.5
BCMA Fc
CD3

FIG. 3B

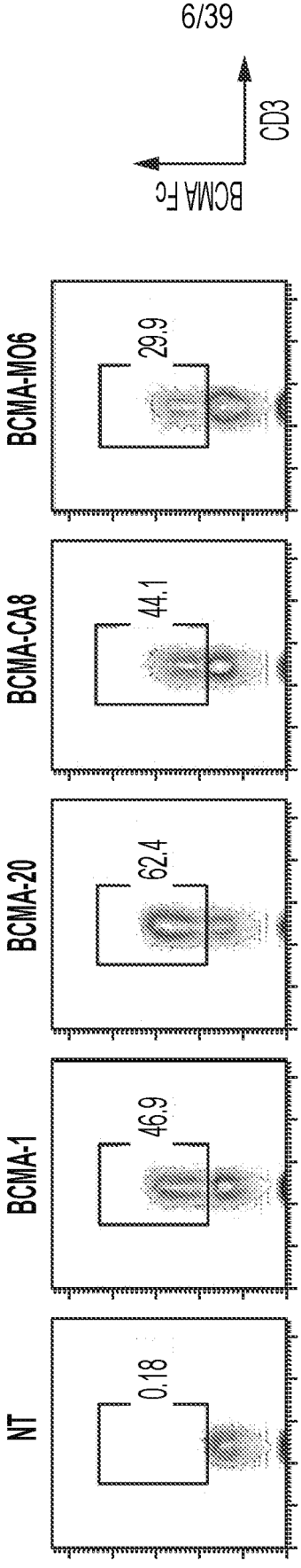
BCMA Fc
CD3
NT
0.18
BCMA-1
46.9
BCMA-20
62.4
BCMA-CA8
44.1
BCMA-MO6
29.9

FIG. 3C

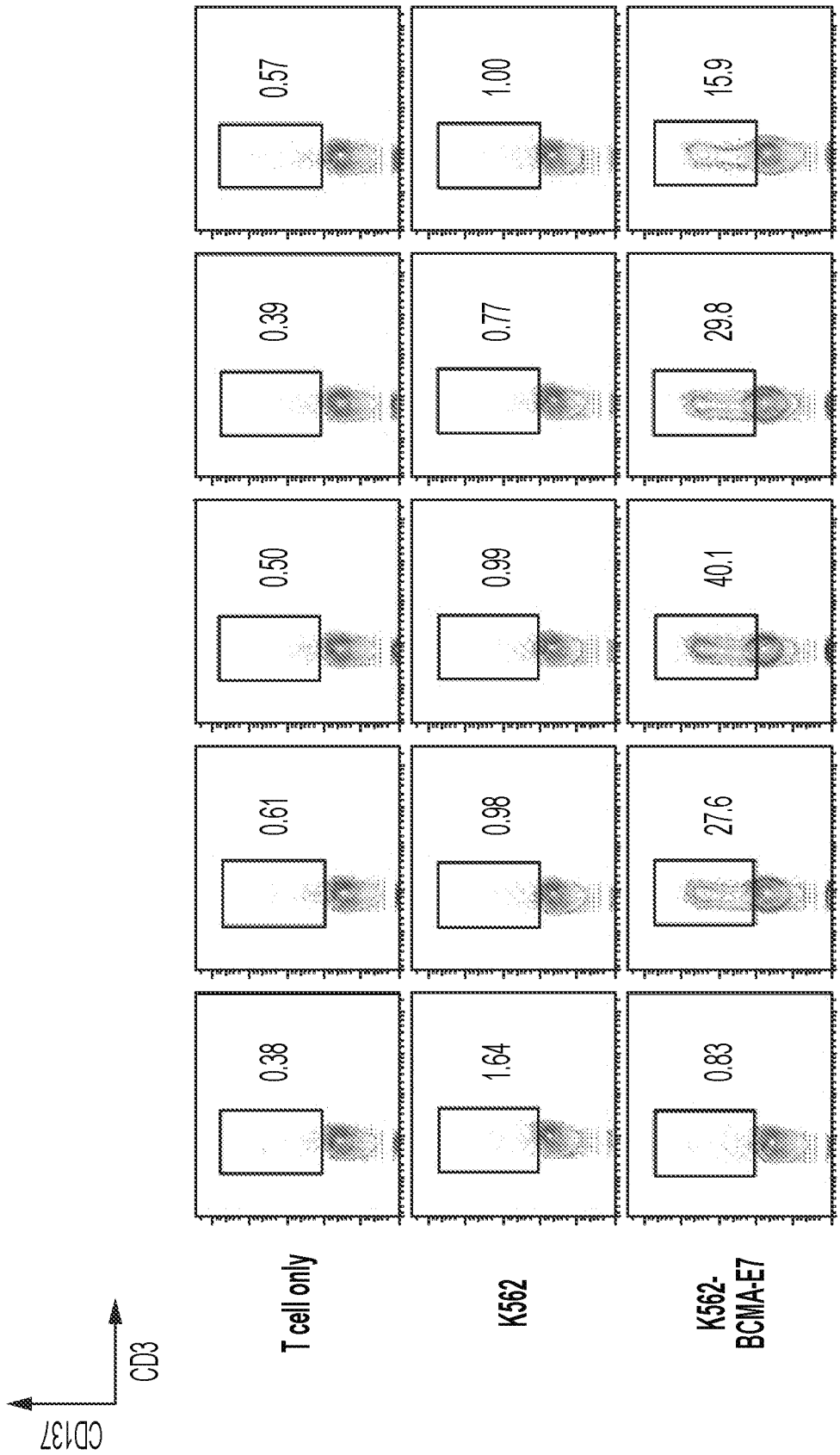
0.57
0.39
0.50
0.61
0.38
1.00
0.77
0.99
0.98
1.64
15.9
29.8
40.1
27.6
0.83
T cell only
K562
K562-BCMA-E7
CD3
CD137

FIG. 4A

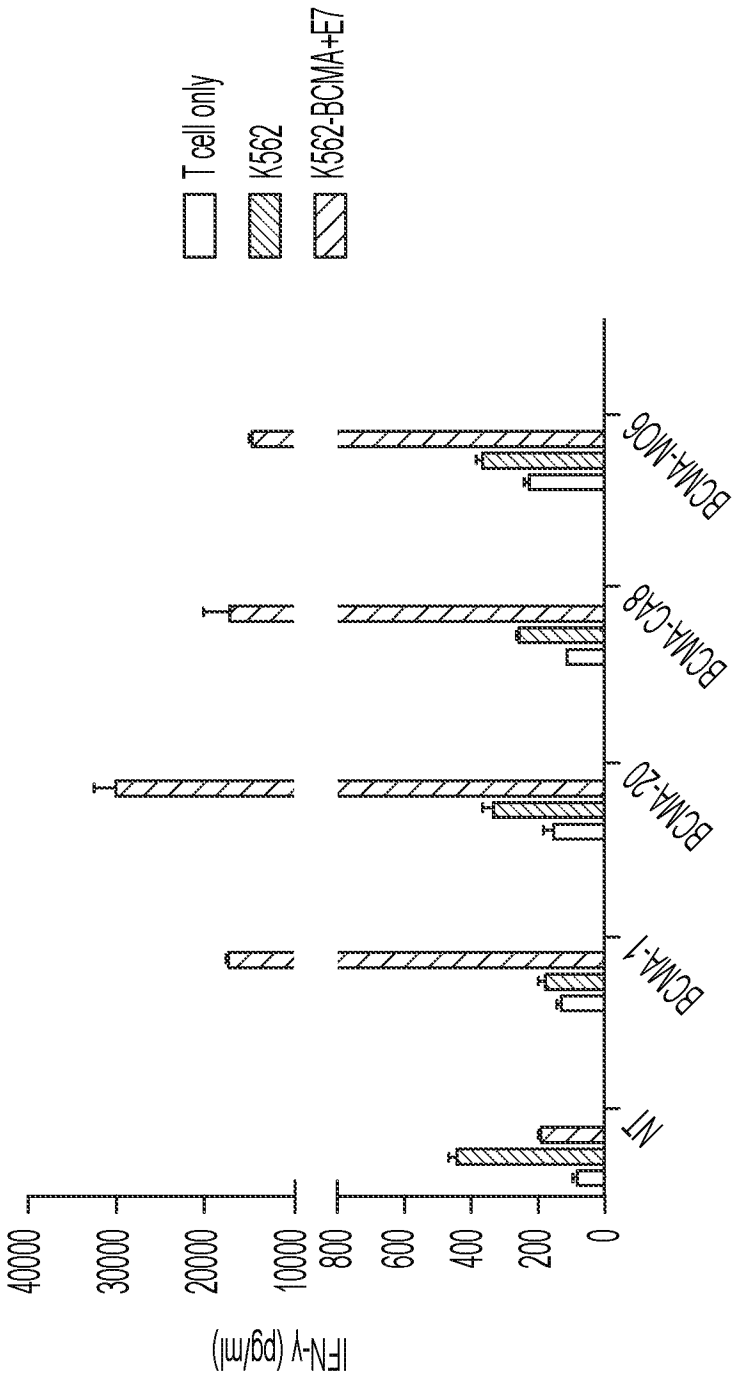
T cell only
K562
K562-BCMA+E7
IFN-γ (pg/ml)
40000
30000
20000
10000
800
600
400
200
0
NT
BCMA-1
BCMA-20
BCMA-CA8
BCMA-MO6

FIG. 4B

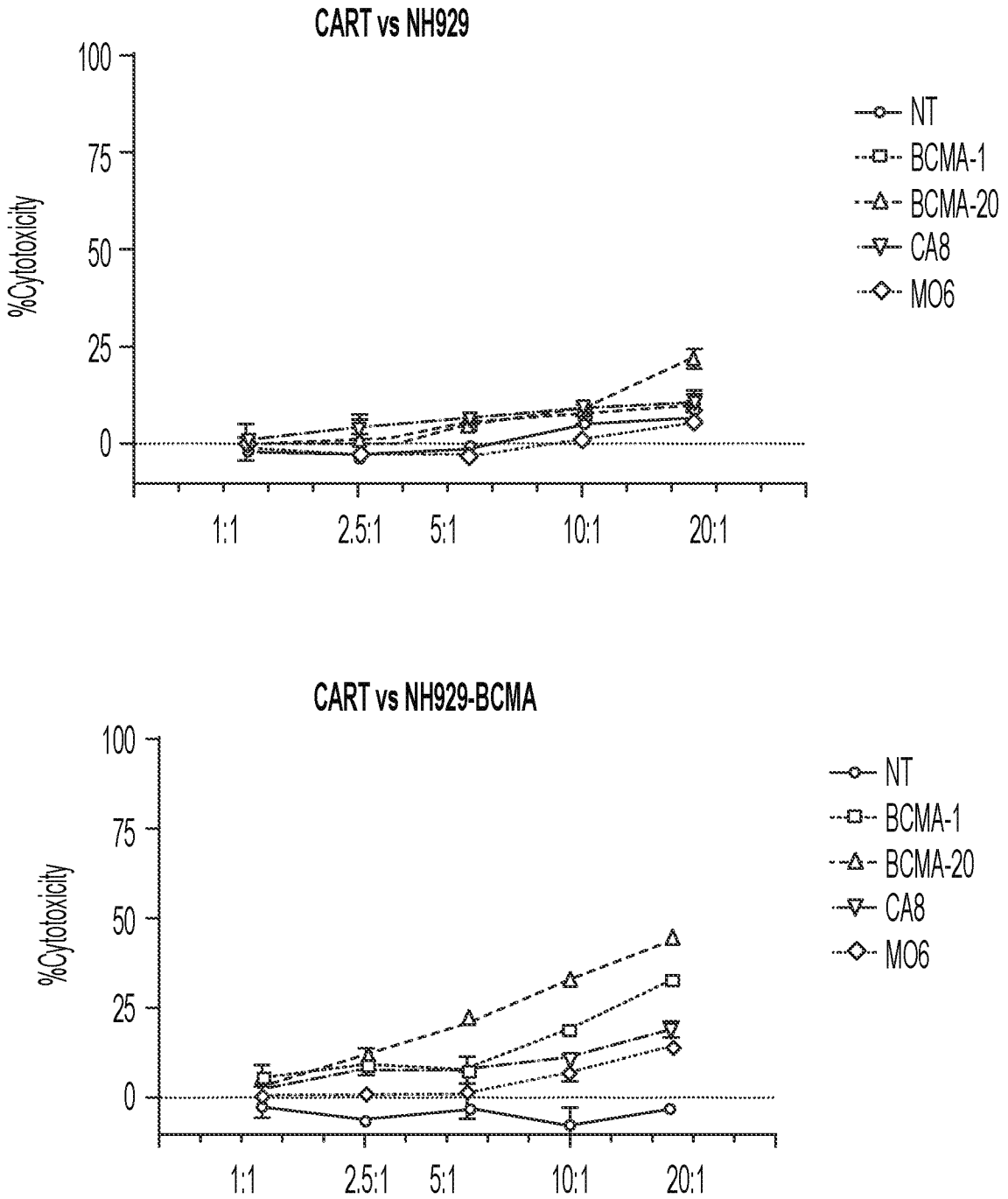
CART vs NH929
%Cytotoxicity
100
75
50
25
0
1:1
2.5:1
5:1
10:1
20:1
NT
BCMA-1
BCMA-20
CA8
MO6
CART vs NH929-BCMA
%Cytotoxicity
100
75
50
25
0
1:1
2.5:1
5:1
10:1
20:1
NT
BCMA-1
BCMA-20
CA8
MO6

FIG. 5

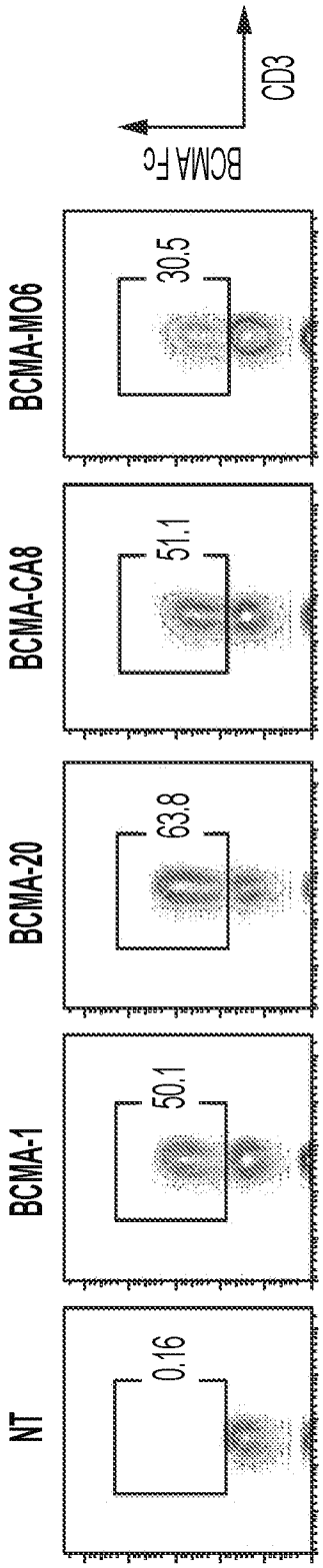
BCMA Fc
CD3
NT
0.16
BCMA-1
50.1
BCMA-20
63.8
BCMA-CA8
51.1
BCMA-MO6
30.5

FIG. 6A

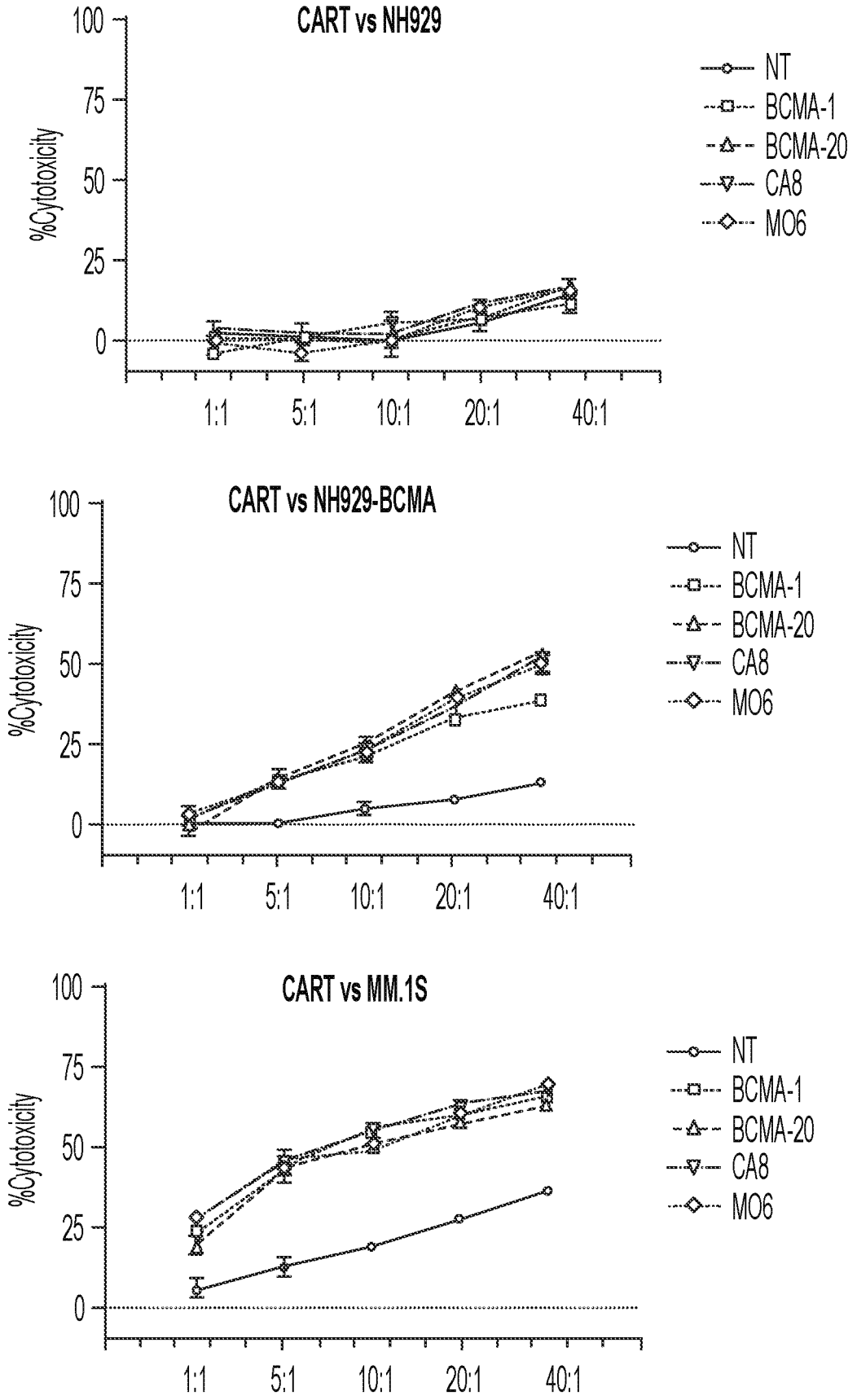
CART vs NH929
%Cytotoxicity
100
75
50
25
0
1:1
5:1
10:1
20:1
40:1
NT
BCMA-1
BCMA-20
CA8
MO6
CART vs NH929-BCMA
%Cytotoxicity
100
75
50
25
0
1:1
5:1
10:1
20:1
40:1
NT
BCMA-1
BCMA-20
CA8
MO6
CART vs MM.1S
%Cytotoxicity
100
75
50
25
0
1:1
5:1
10:1
20:1
40:1
NT
BCMA-1
BCMA-20
CA8
MO6

FIG. 6B

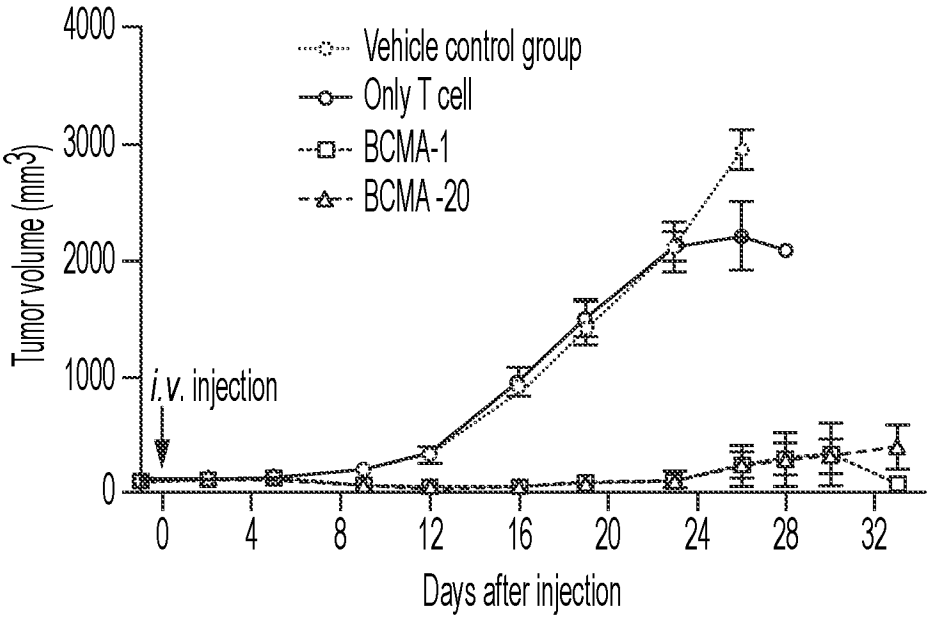
4000
3000
2000
1000
0
Tumor volume (mm3)
i.v. injection
Vehicle control group
Only T cell
BCMA-1
BCMA -20
0
4
8
12
16
20
24
28
32
Days after injection

FIG. 7A

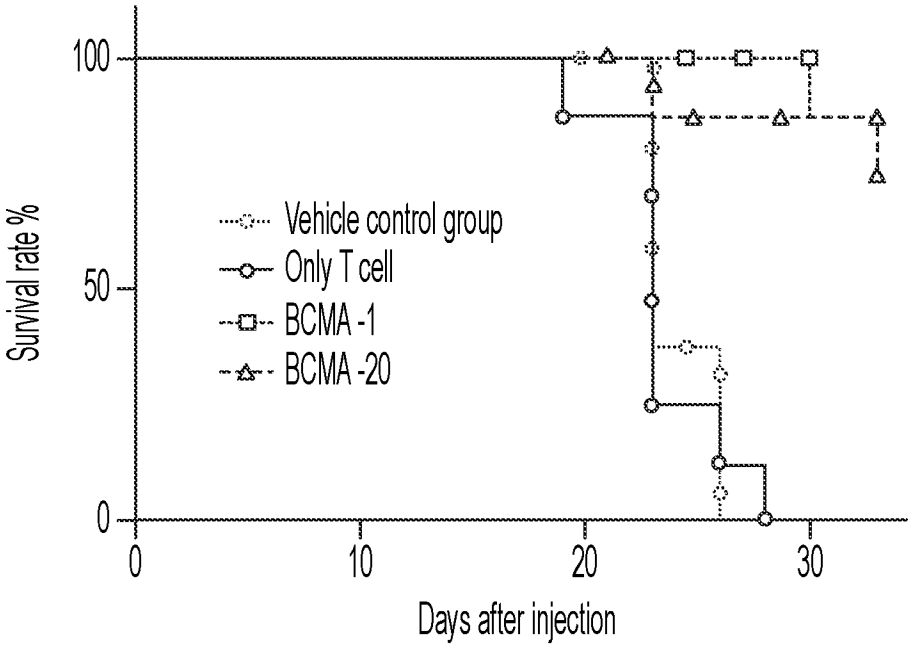
100
50
0
Survival rate %
Vehicle control group
Only T cell
BCMA -1
BCMA -20
0
10
20
30
Days after injection

FIG. 7B

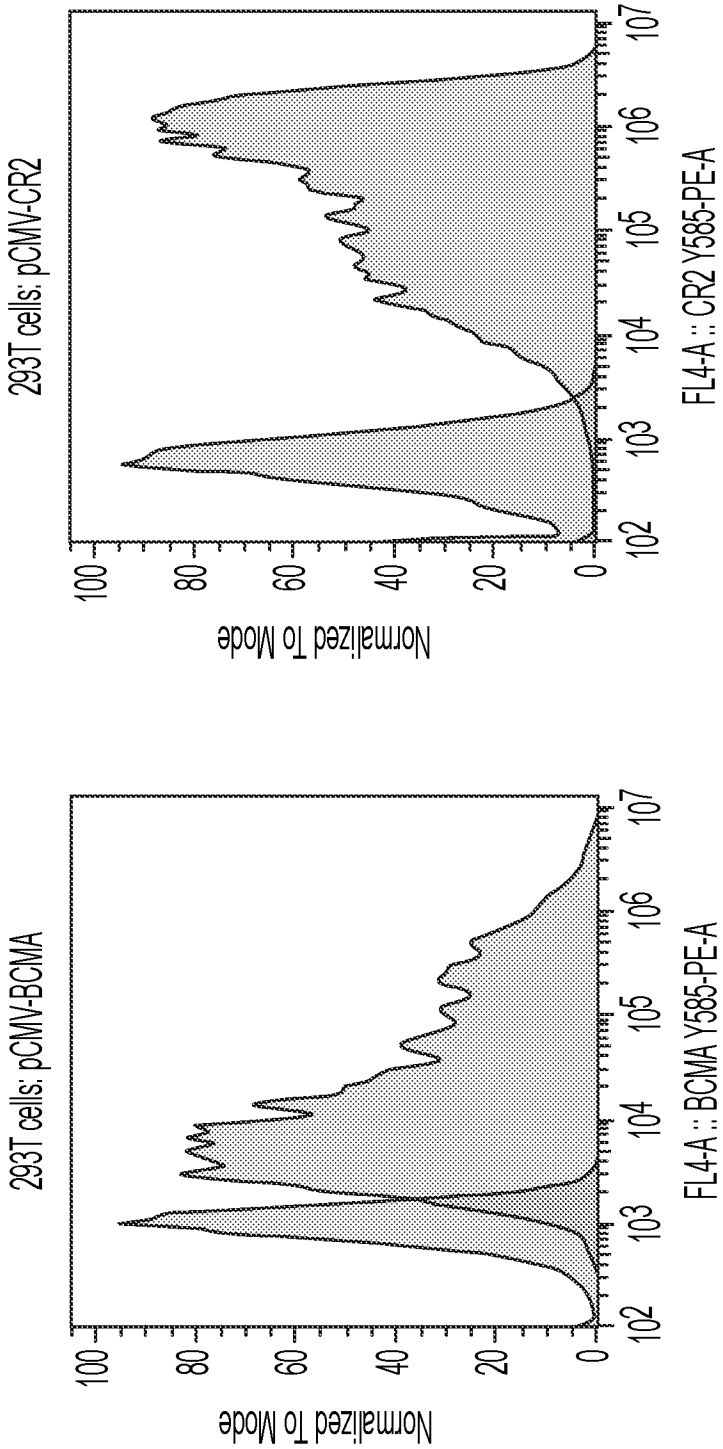
293T cells: pCMV-CR2
Normalized To Mode
100
80
60
40
20
0
10^2
10^3
10^4
10^5
10^6
10^7
FL4-A :: CR2 Y585-PE-A
293T cells: pCMV-BCMA
Normalized To Mode
FL4-A :: BCMA Y585-PE-A

FIG. 8

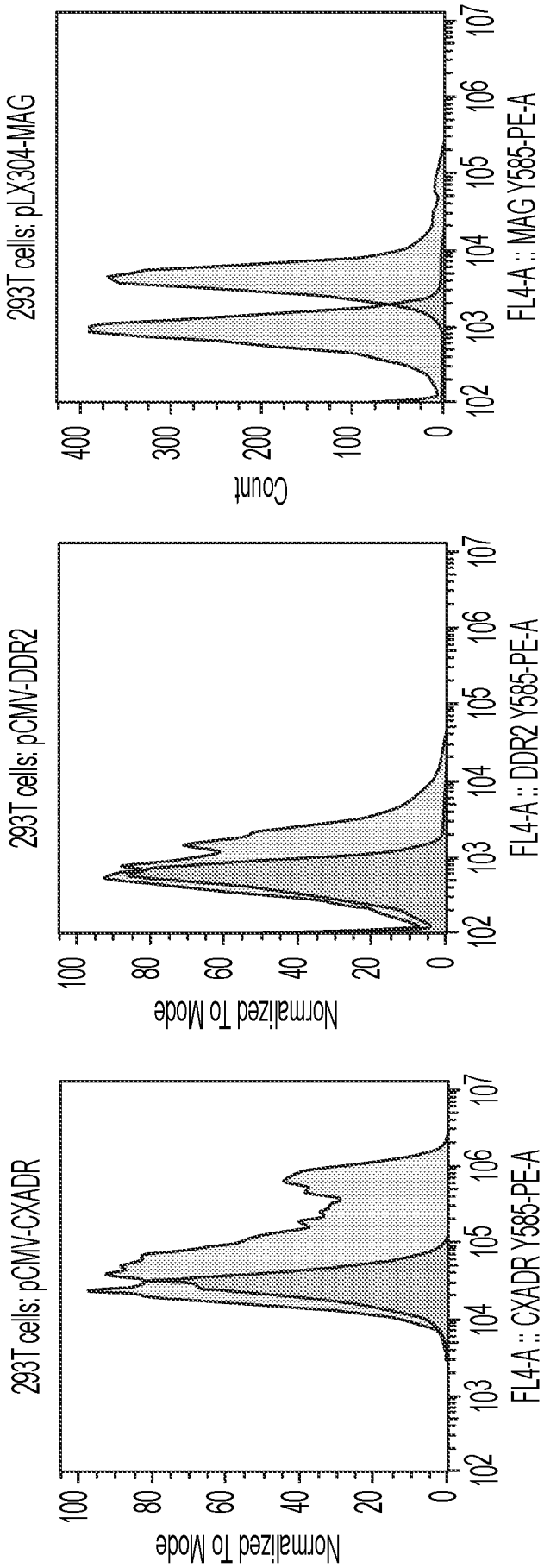

FIG. 8 CONTINUED

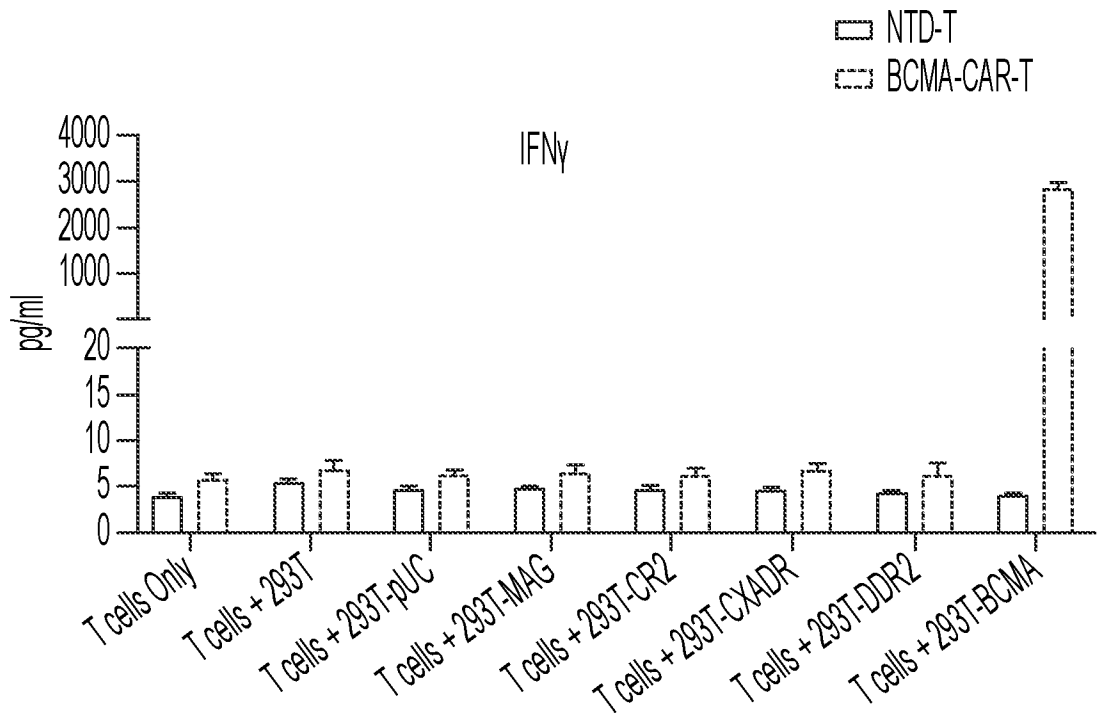
NTD-T
BCMA-CAR-T
IFNγ
pg/ml
4000
3000
2000
1000
20
15
10
5
0
T cells Only
T cells + 293T
T cells + 293T-pUC
T cells + 293T-MAG
T cells + 293T-CR2
T cells + 293T-CXADR
T cells + 293T-DDR2
T cells + 293T-BCMA

FIG. 9A

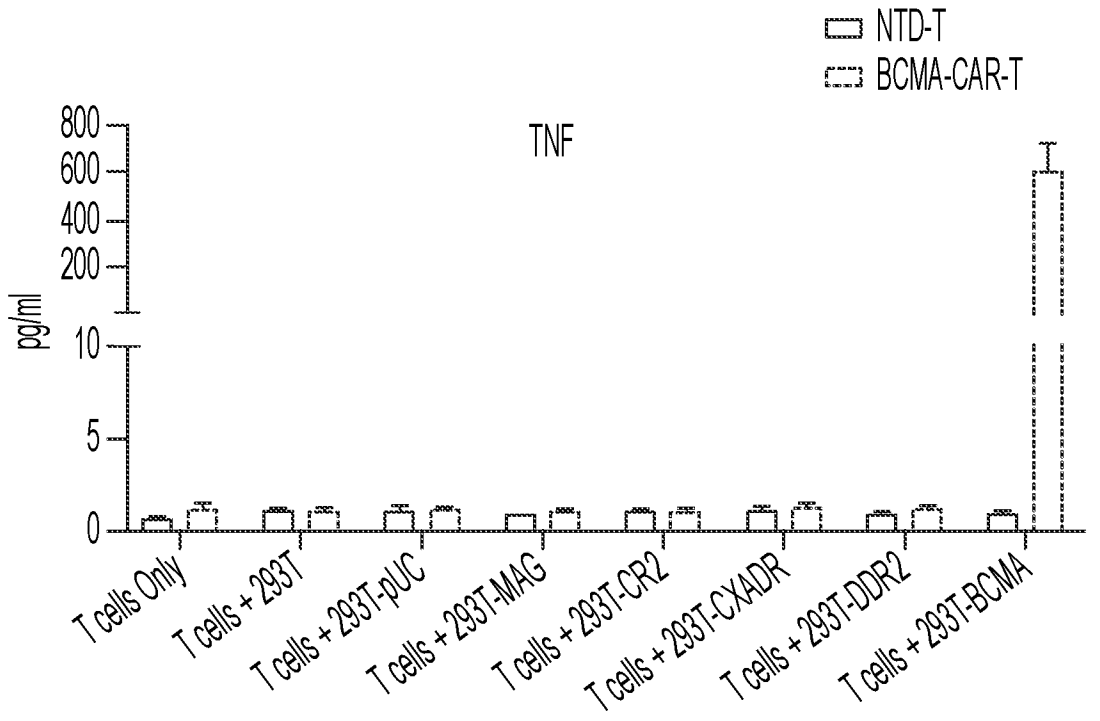
NTD-T
BCMA-CAR-T
TNF
pg/ml
800
600
400
200
10
5
0
T cells Only
T cells + 293T
T cells + 293T-pUC
T cells + 293T-MAG
T cells + 293T-CR2
T cells + 293T-CXADR
T cells + 293T-DDR2
T cells + 293T-BCMA

FIG. 9B

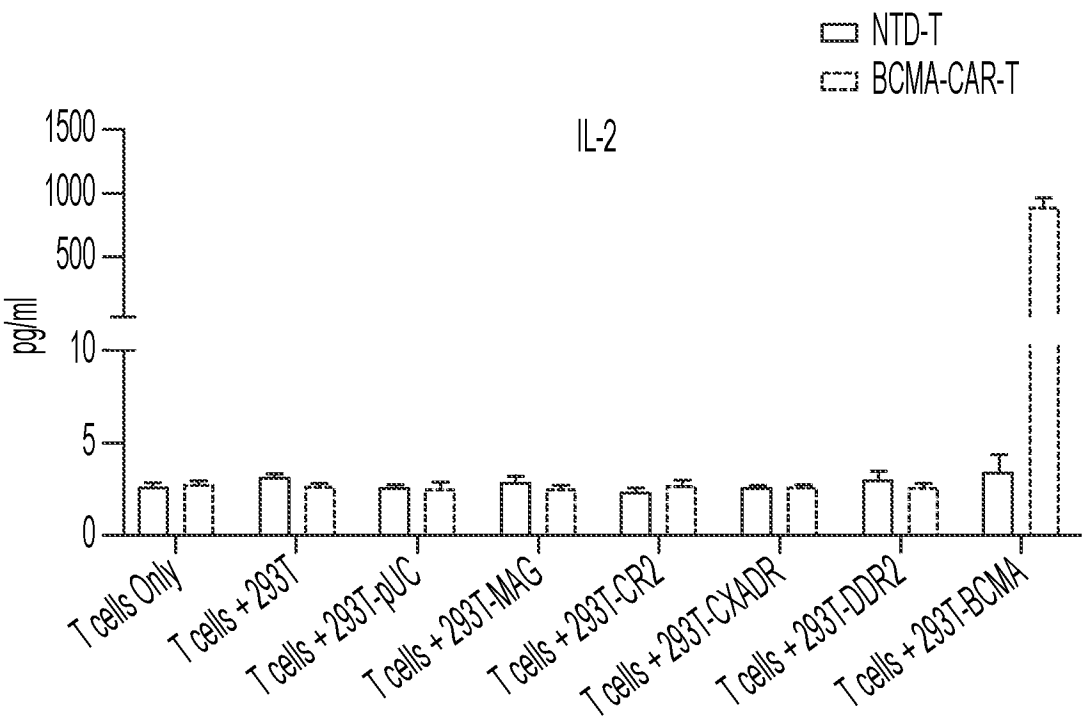
NTD-T
BCMA-CAR-T
IL-2
pg/ml
1500
1000
500
10
5
0
T cells Only
T cells + 293T
T cells + 293T-pUC
T cells + 293T-MAG
T cells + 293T-CR2
T cells + 293T-CXADR
T cells + 293T-DDR2
T cells + 293T-BCMA

FIG. 9C

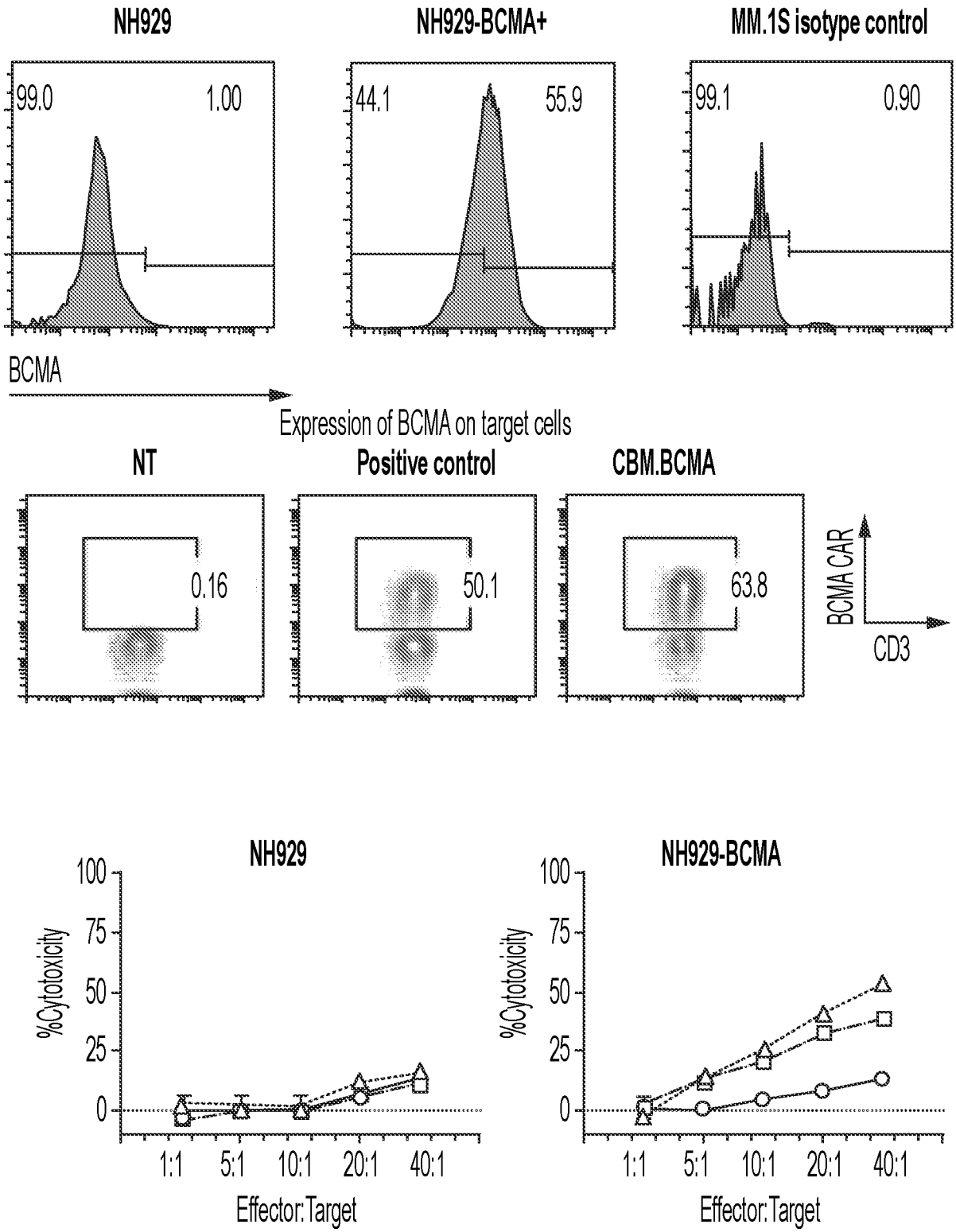
NH929
NH929-BCMA+
MM.1S isotype control
99.0
1.00
44.1
55.9
99.1
0.90
BCMA
Expression of BCMA on target cells
NT
Positive control
CBM.BCMA
0.16
50.1
63.8
BCMA CAR
CD3
NH929
NH929-BCMA
%Cytotoxicity
100
75
50
25
0
1:1
5:1
10:1
20:1
40:1
Effector:Target

FIG. 10

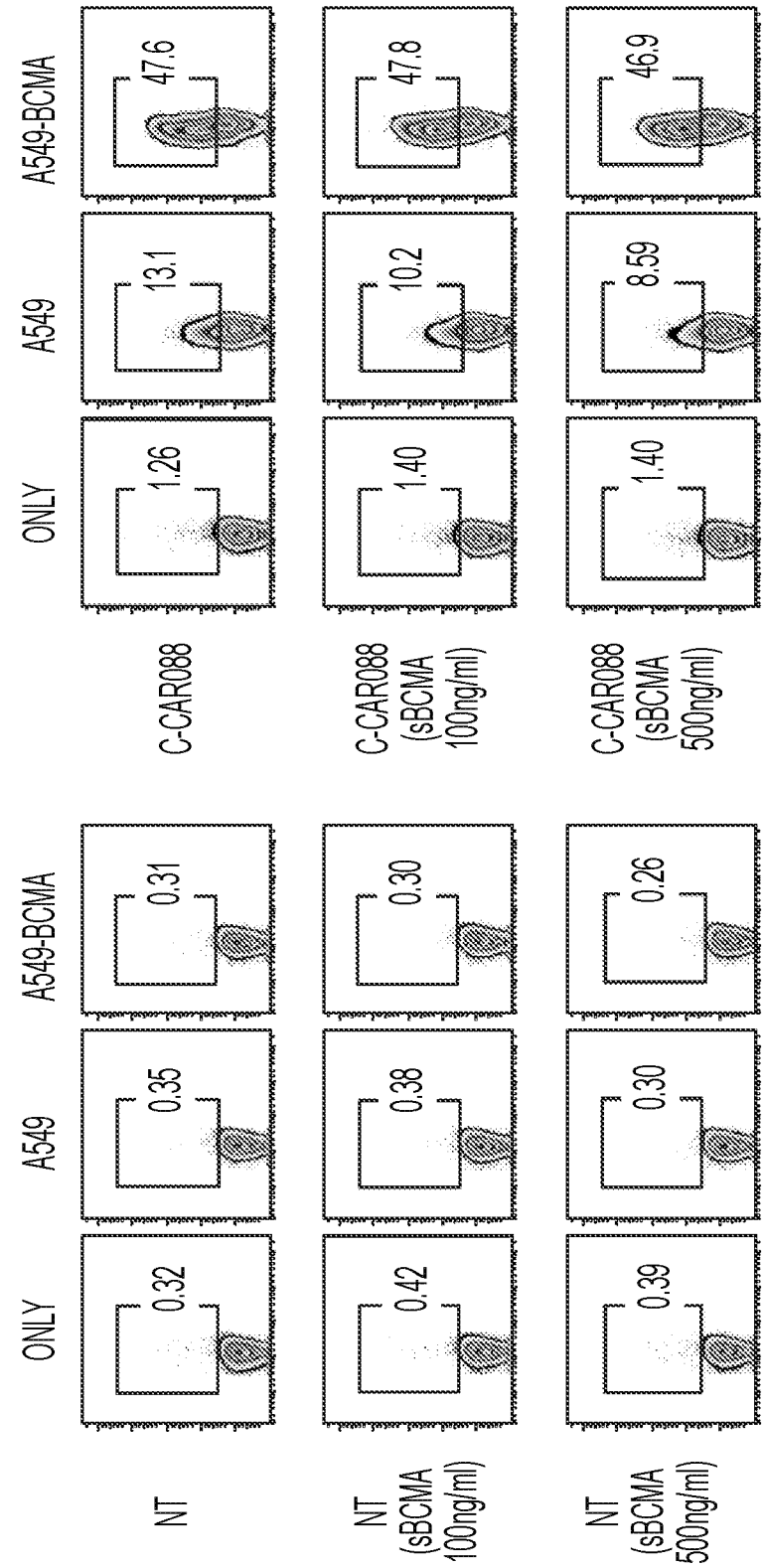
ONLY
A549
A549-BCMA
C-CAR088
C-CAR088 (sBCMA 100ng/ml)
C-CAR088 (sBCMA 500ng/ml)
NT
NT (sBCMA 100ng/ml)
NT (sBCMA 500ng/ml)
0.32
0.35
0.31
0.42
0.38
0.30
0.39
0.30
0.26
1.26
13.1
47.6
1.40
10.2
47.8
1.40
8.59
46.9
CD137
CD3

FIG. 11

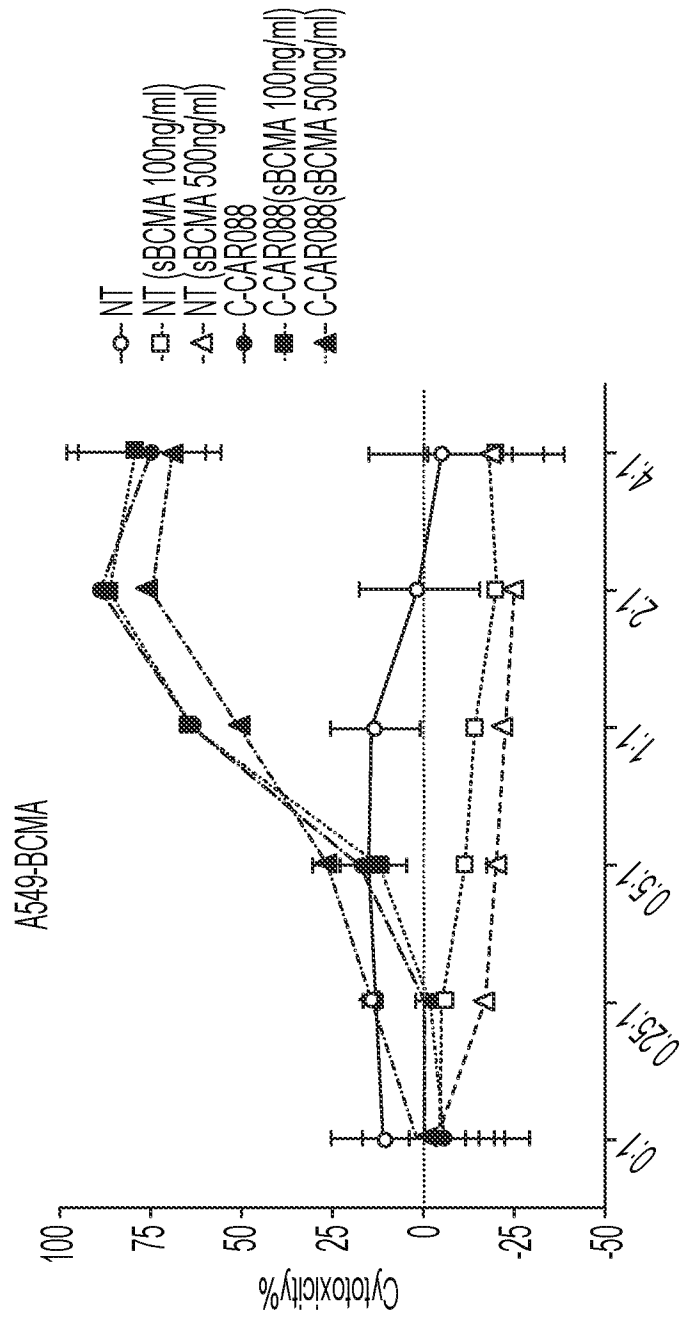

FIG. 11 CONTINUED

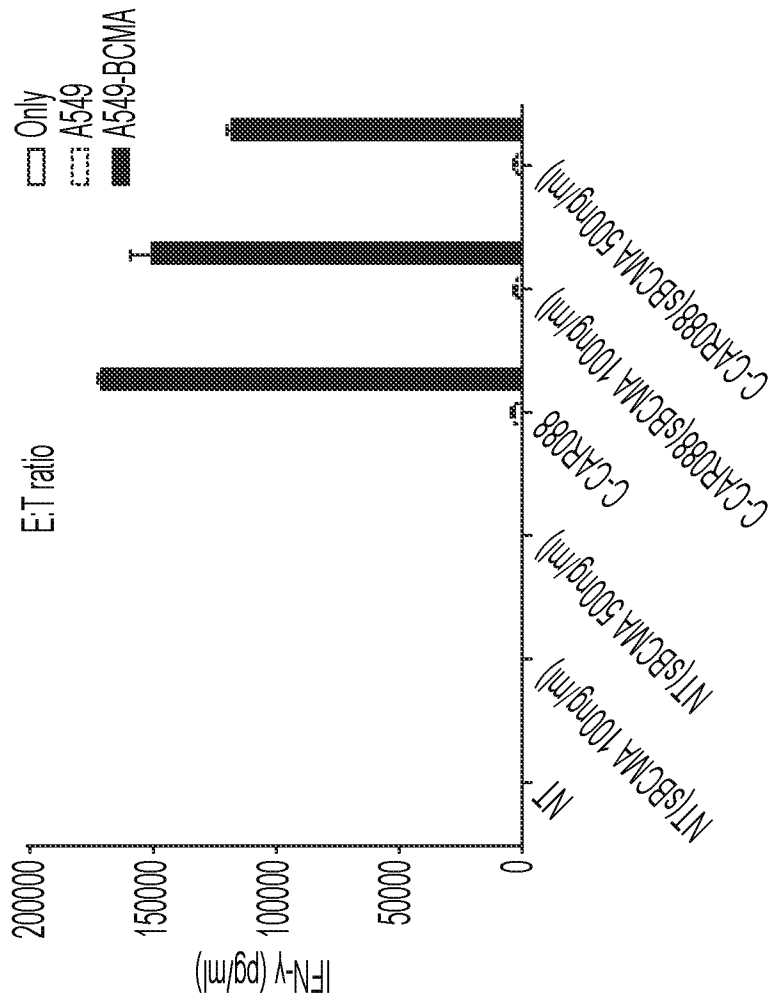

FIG. 11 CONTINUED

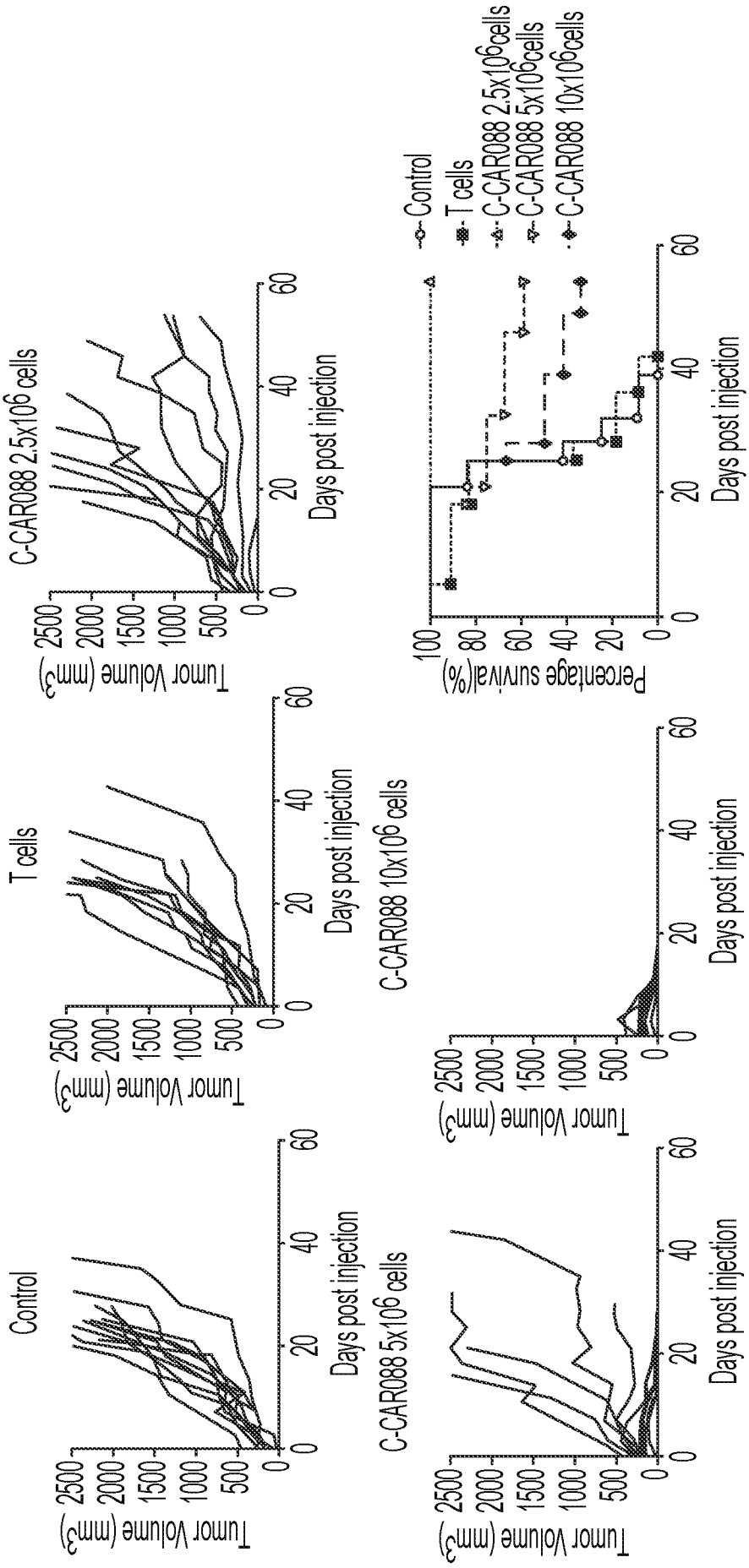
Control
T cells
C-CAR088 2.5x10^6 cells
C-CAR088 5x10^6 cells
C-CAR088 10x10^6 cells
Tumor Volume (mm^3)
Days post injection
Percentage survival(%)

FIG. 12

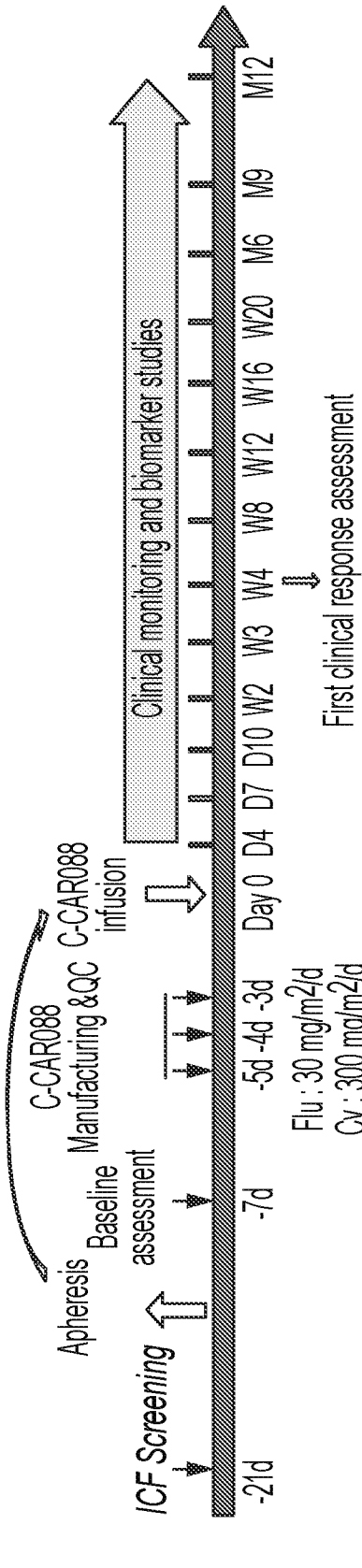
ICF Screening
Apheresis
C-CAR088 Manufacturing &QC
Baseline assessment
C-CAR088 infusion
Clinical monitoring and biomarker studies
-21d
-7d
-5d -4d -3d
Day 0 D4 D7 D10 W2 W3 W4 W8 W12 W16 W20 M6 M9 M12
Flu : 30 mg/m2/d
Cy : 300 mg/m2/d
3+3 Dose Escalation
First clinical response assessment
1x10^6/kg
3x10^6/kg
6x10^6/kg
9x10^6/kg(TBD)

FIG. 13

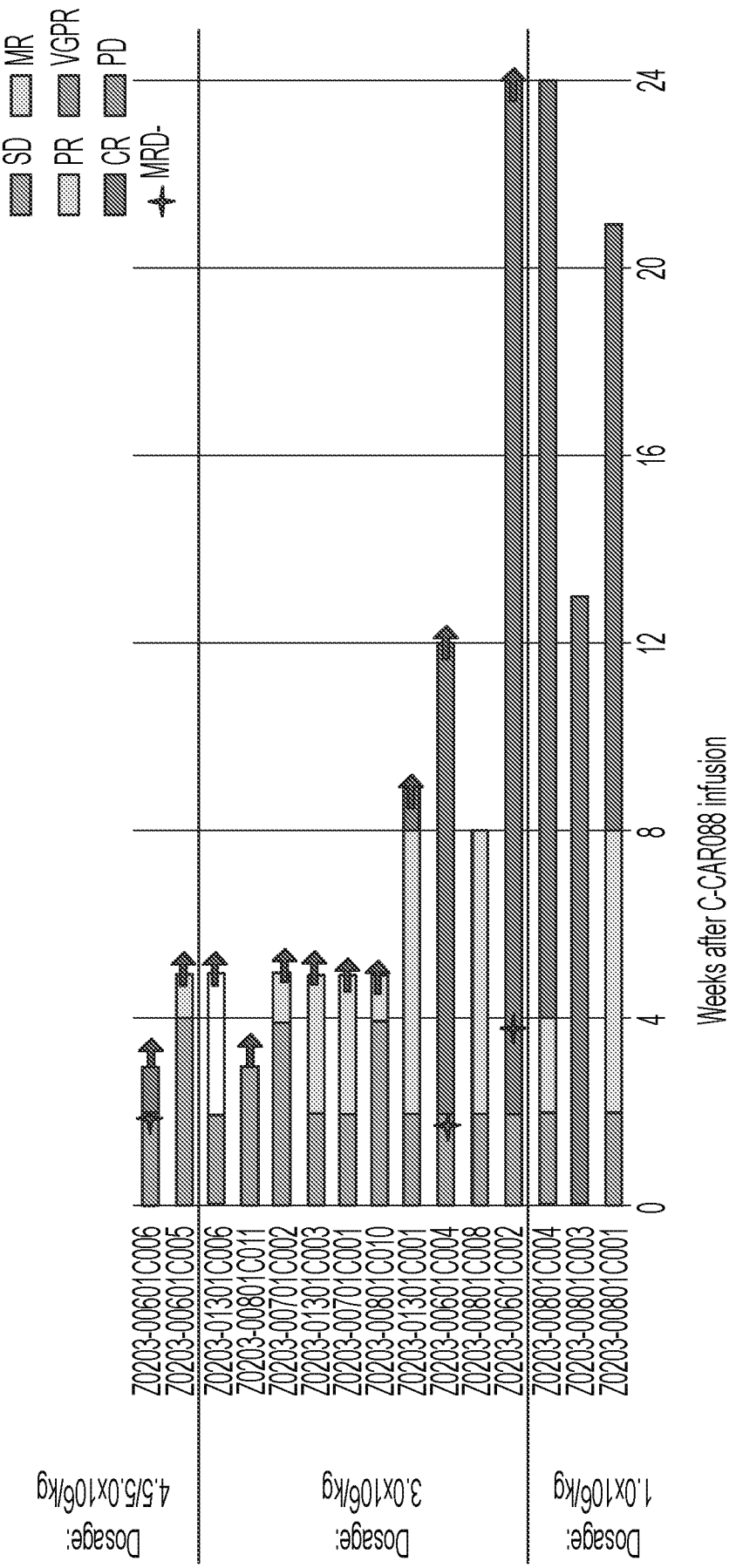
SD
MR
PR
VGPR
CR
PD
MRD-
0
4
8
12
16
20
24
Weeks after C-CAR088 infusion
Z0203-00601C006
Z0203-00601C005
Z0203-01301C006
Z0203-00801C011
Z0203-00701C002
Z0203-01301C003
Z0203-00701C001
Z0203-00801C010
Z0203-01301C001
Z0203-00601C004
Z0203-00801C008
Z0203-00601C002
Z0203-00801C004
Z0203-00801C003
Z0203-00801C001
Dosage:
4.5/5.0x10^6/kg
Dosage:
3.0x10^6/kg
Dosage:
1.0x10^6/kg

FIG. 14

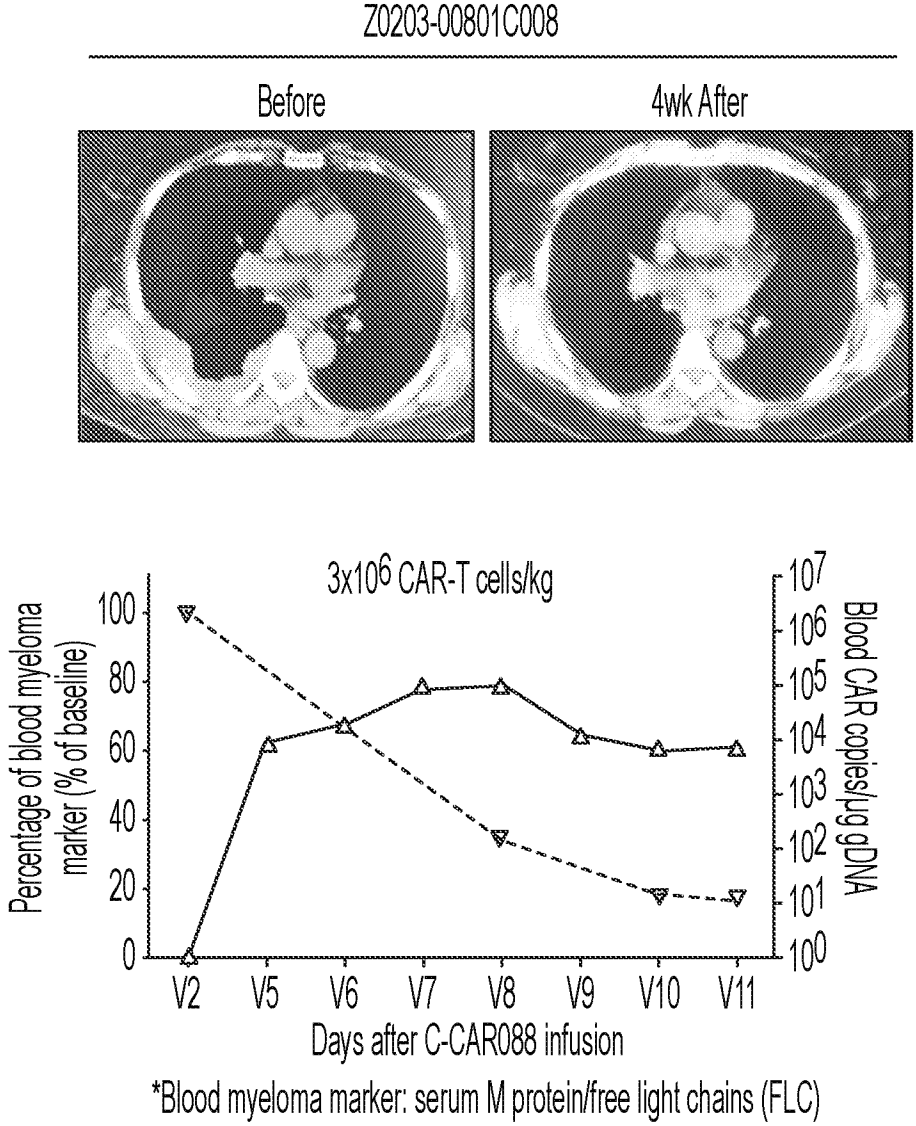
Z0203-00801C008
Before
4wk After
3x10^6 CAR-T cells/kg
Percentage of blood myeloma marker (% of baseline)
Blood CAR copies/μg gDNA
0
20
40
60
80
100
10^0
10^1
10^2
10^3
10^4
10^5
10^6
10^7
V2
V5
V6
V7
V8
V9
V10
V11
Days after C-CAR088 infusion
*Blood myeloma marker: serum M protein/free light chains (FLC)

FIG. 15

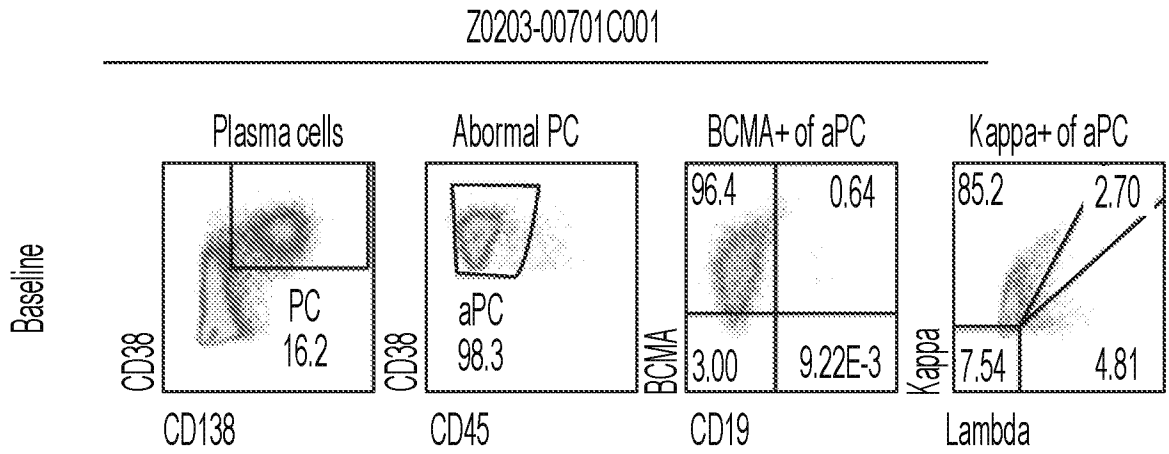

FIG. 16A

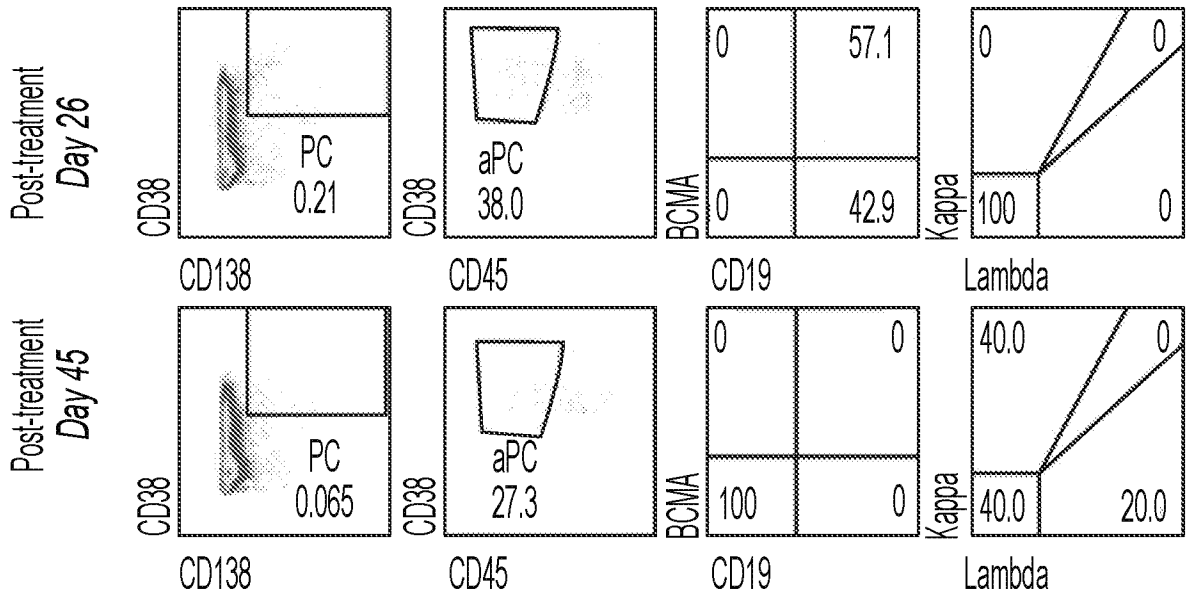

FIG. 16B

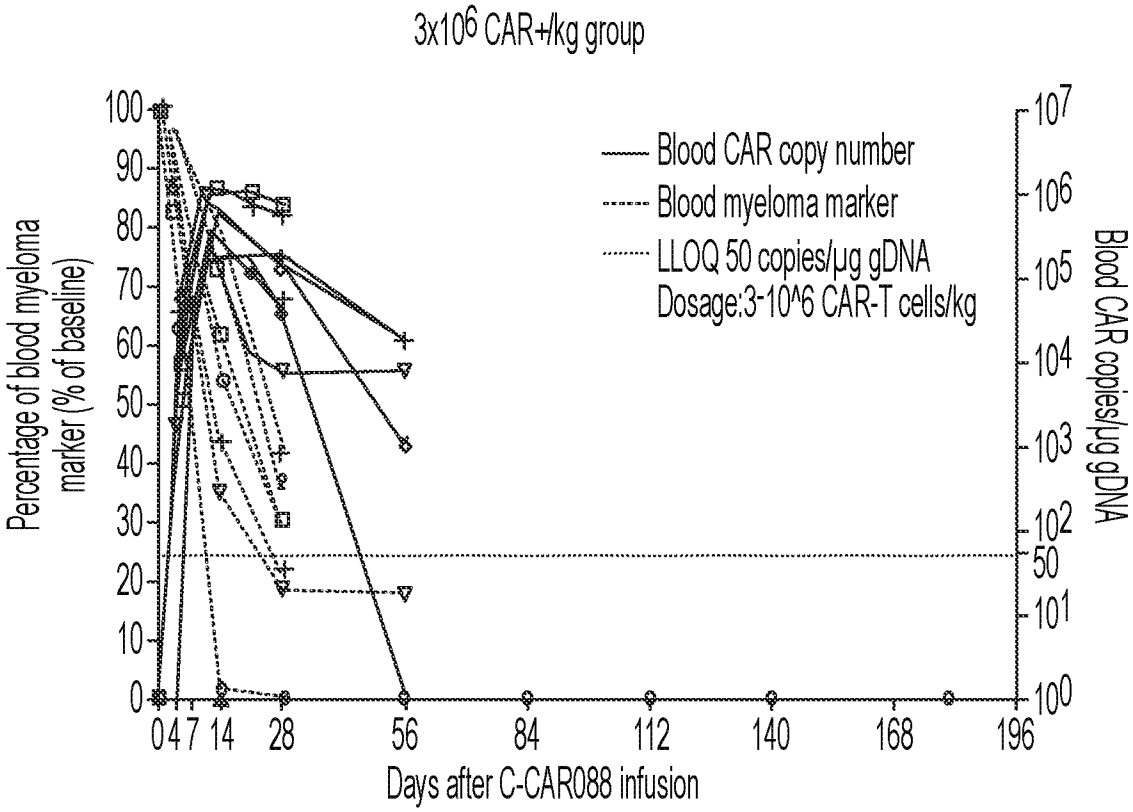
3x10^6 CAR+/kg group
Blood CAR copy number
Blood myeloma marker
LLOQ 50 copies/µg gDNA
Dosage:3-10^6 CAR-T cells/kg
Percentage of blood myeloma marker (% of baseline)
Blood CAR copies/µg gDNA
Days after C-CAR088 infusion
0 4 7 14 28 56 84 112 140 168 196
0 10 20 30 40 50 60 70 80 90 100
10^0 10^1 50 10^2 10^3 10^4 10^5 10^6 10^7

FIG. 17

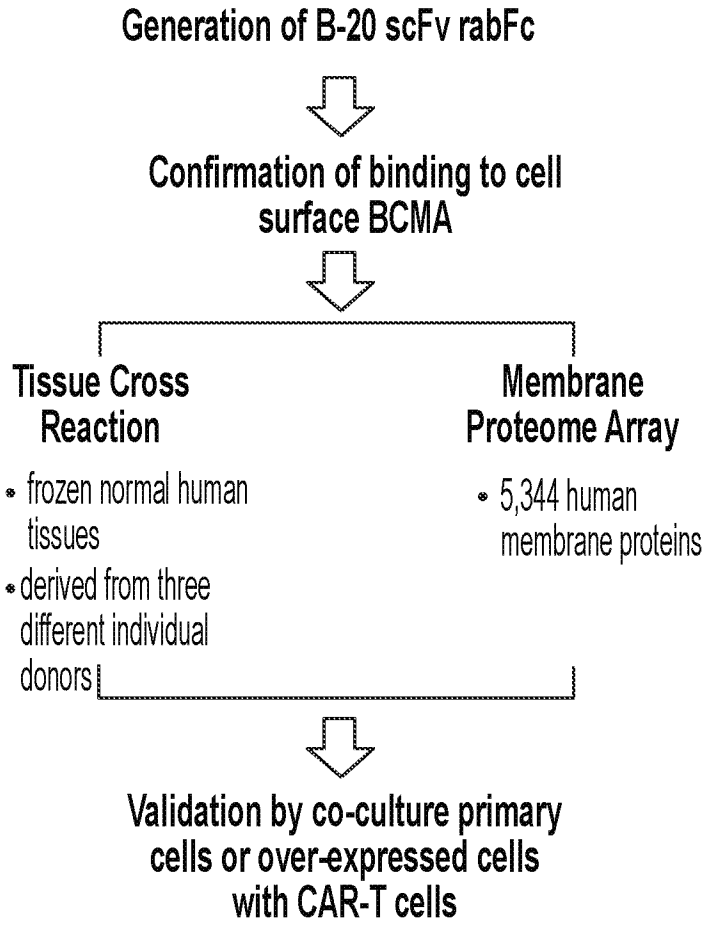

FIG. 18A

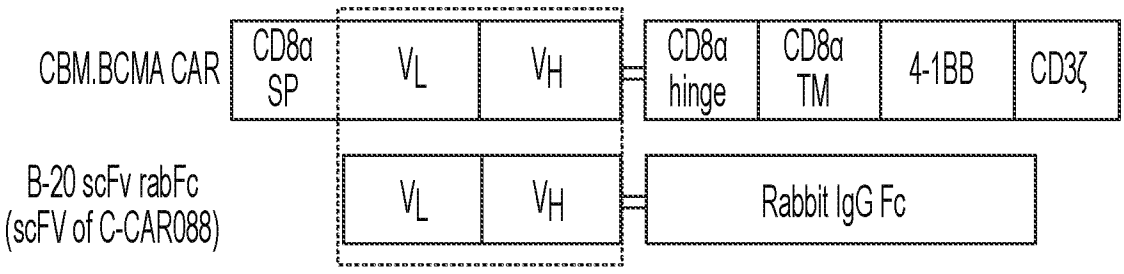

FIG. 18B

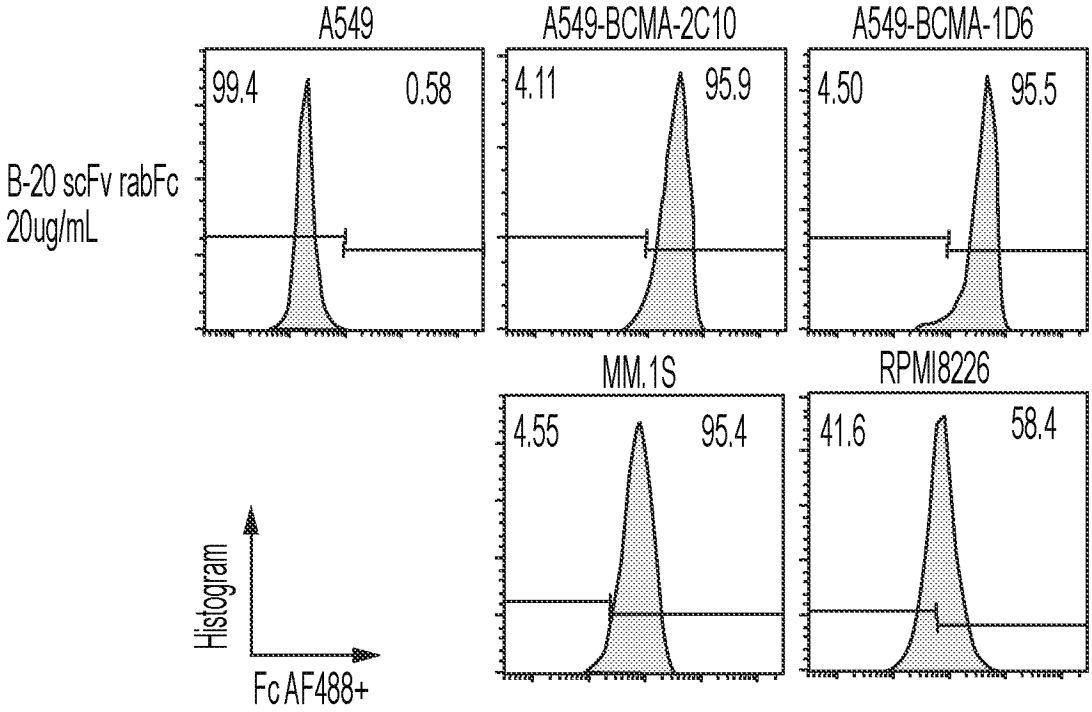

FIG. 18C

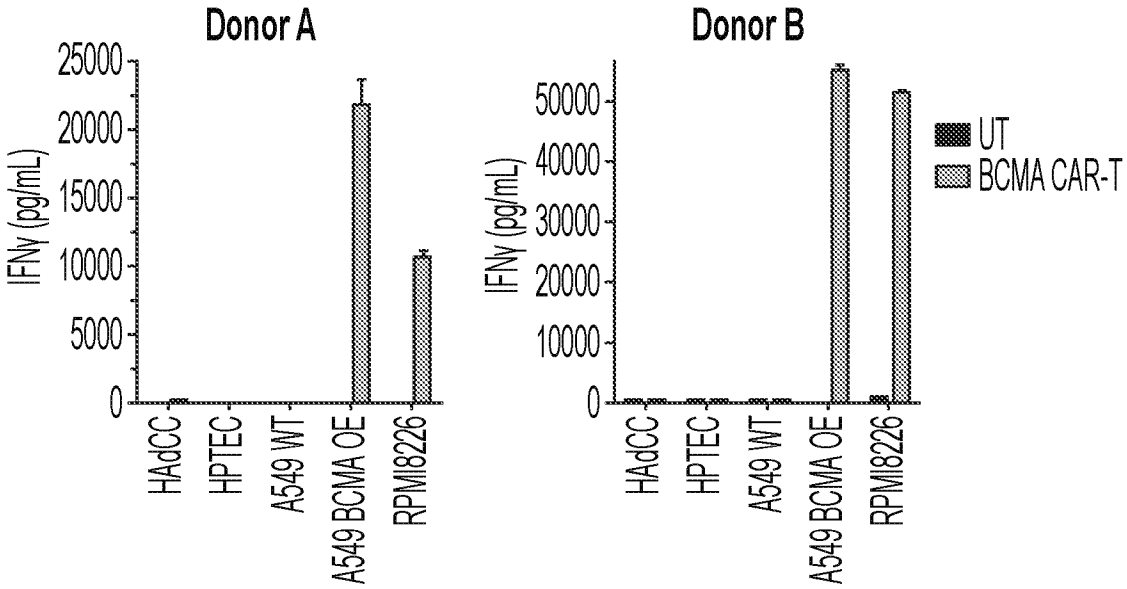

FIG. 19A

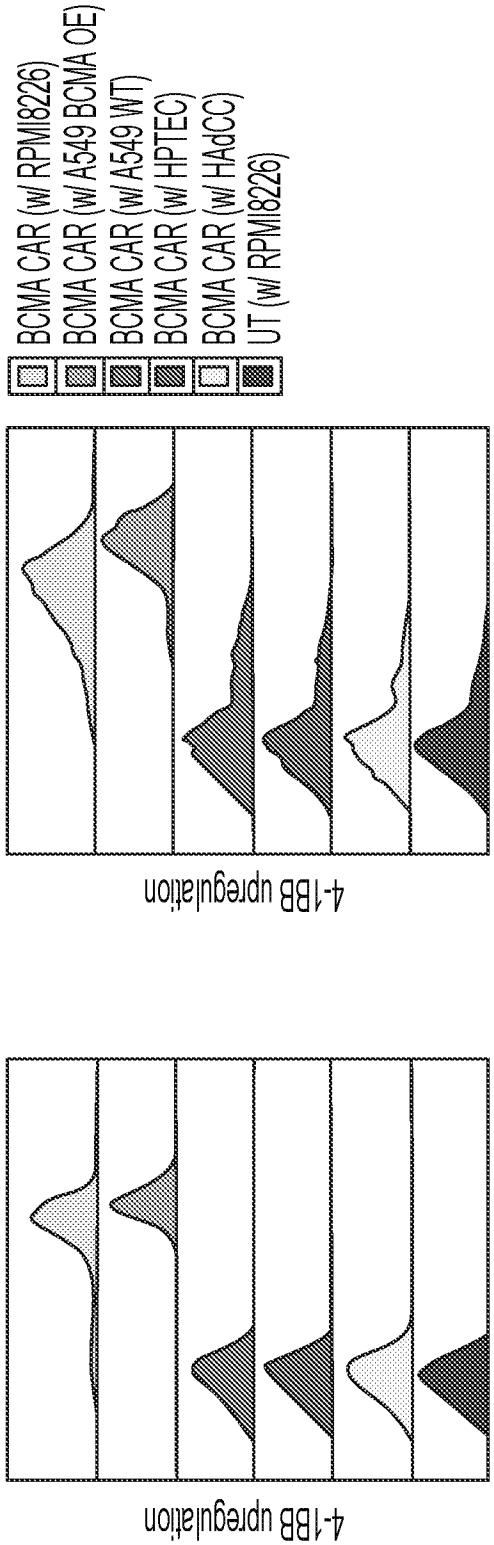
BCMA CAR (w/ RPMI8226)
BCMA CAR (w/ A549 BCMA OE)
BCMA CAR (w/ A549 WT)
BCMA CAR (w/ HPTEC)
BCMA CAR (w/ HAdCC)
UT (w/ RPMI8226)
4-1BB upregulation
4-1BB upregulation

FIG. 19B

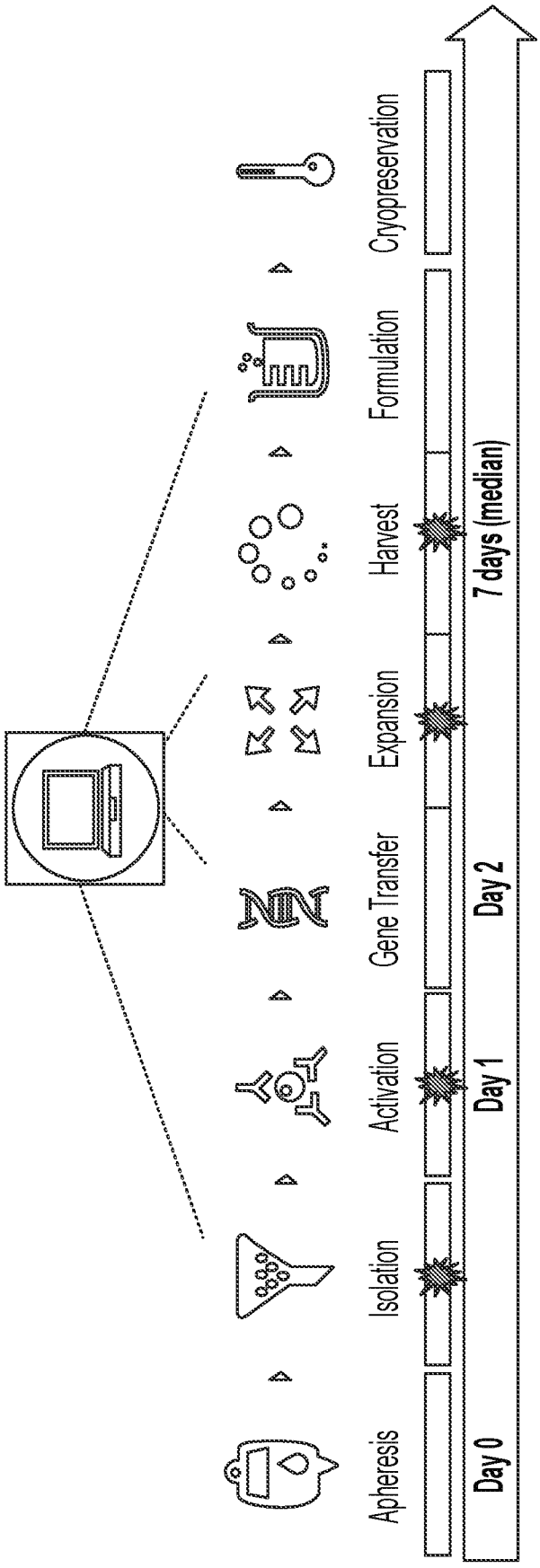
Apheresis
Isolation
Activation
Gene Transfer
Expansion
Harvest
Formulation
Cryopresevation
Day 0
Day 1
Day 2
7 days (median)

FIG. 20

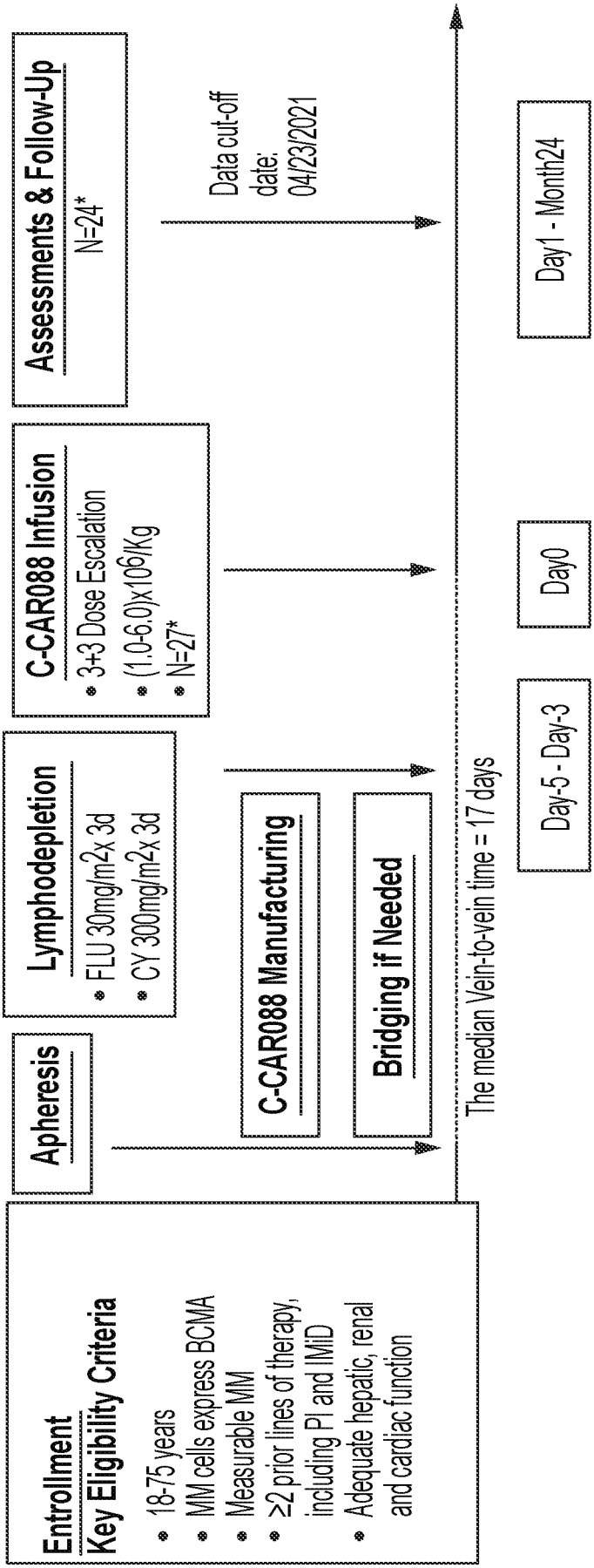
Entrollment
Key Eligibility Criteria
18-75 years
MM cells express BCMA
Measurable MM
≥2 prior lines of therapy, including PI and IMiD
Adequate hepatic, renal and cardiac function
Apheresis
Lymphodepletion
FLU 30mg/m2x 3d
CY 300mg/m2x 3d
C-CAR088 Manufacturing
Bridging if Needed
C-CAR088 Infusion
3+3 Dose Escalation
(1.0-6.0)x10^6/Kg
N=27*
Assessments & Follow-Up
N=24*
Data cut-off date: 04/23/2021
The median Vein-to-vein time = 17 days
Day-5 - Day-3
Day0
Day1 - Month24

FIG. 21

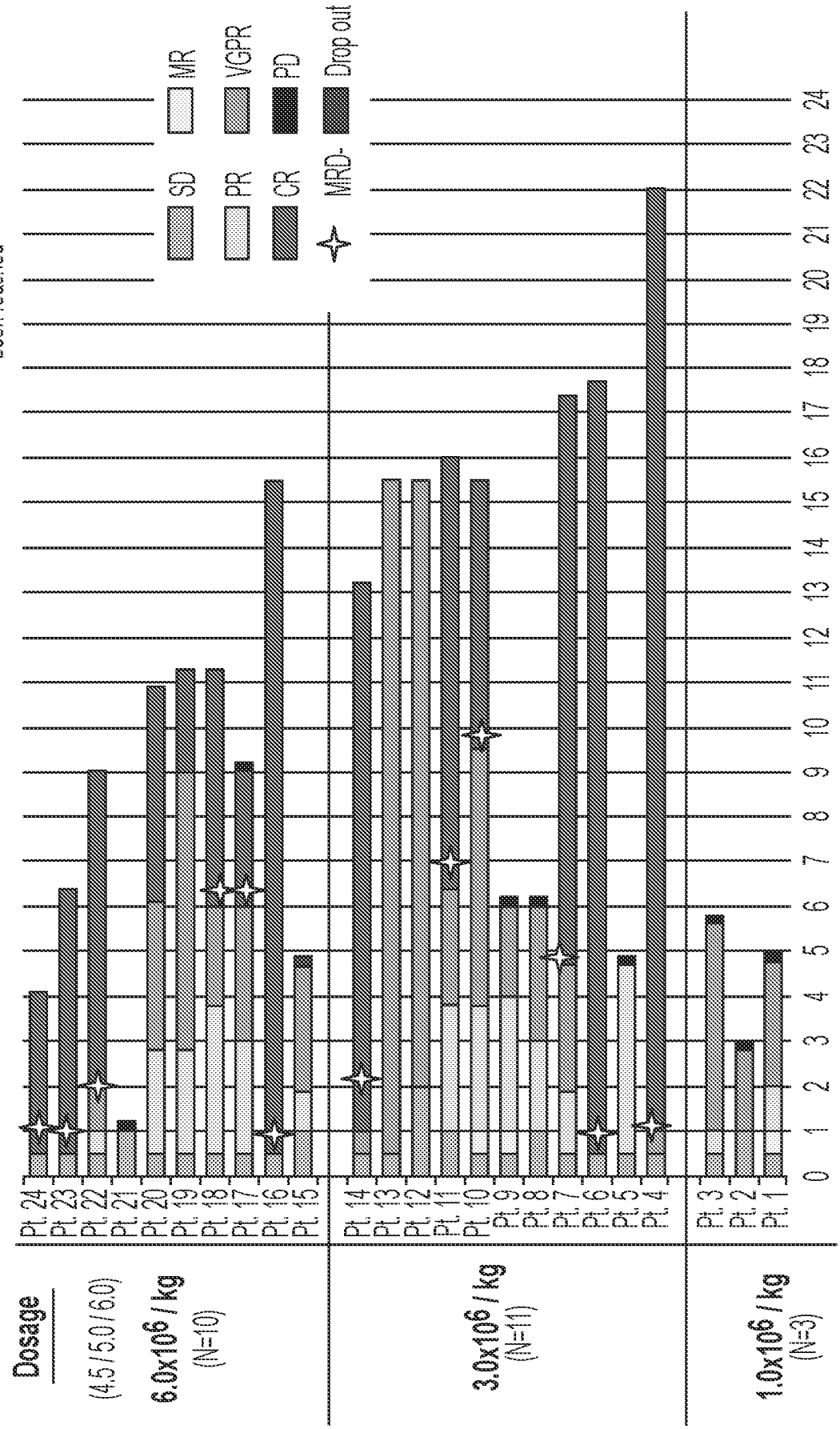
96% ORR, CR rate: 67% (14/21) in two higher dose cohorts
Median F/U: 11.1 months (range:1~21.5), Median DOR had not been reached
SD
MR
PR
VGPR
CR
PD
MRD-
Drop out
Dosage
(4.5/5.0/6.0)
6.0x10^6 / kg
(N=10)
3.0x10^6 / kg
(N=11)
1.0x10^6 / kg
(N=3)
Pt. 24
Pt. 23
Pt. 22
Pt. 21
Pt. 20
Pt. 19
Pt. 18
Pt. 17
Pt. 16
Pt. 15
Pt. 14
Pt. 13
Pt. 12
Pt. 11
Pt. 10
Pt. 9
Pt. 8
Pt. 7
Pt. 6
Pt. 5
Pt. 4
Pt. 3
Pt. 2
Pt. 1
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
Months after C-CAR088 infusion

FIG. 22

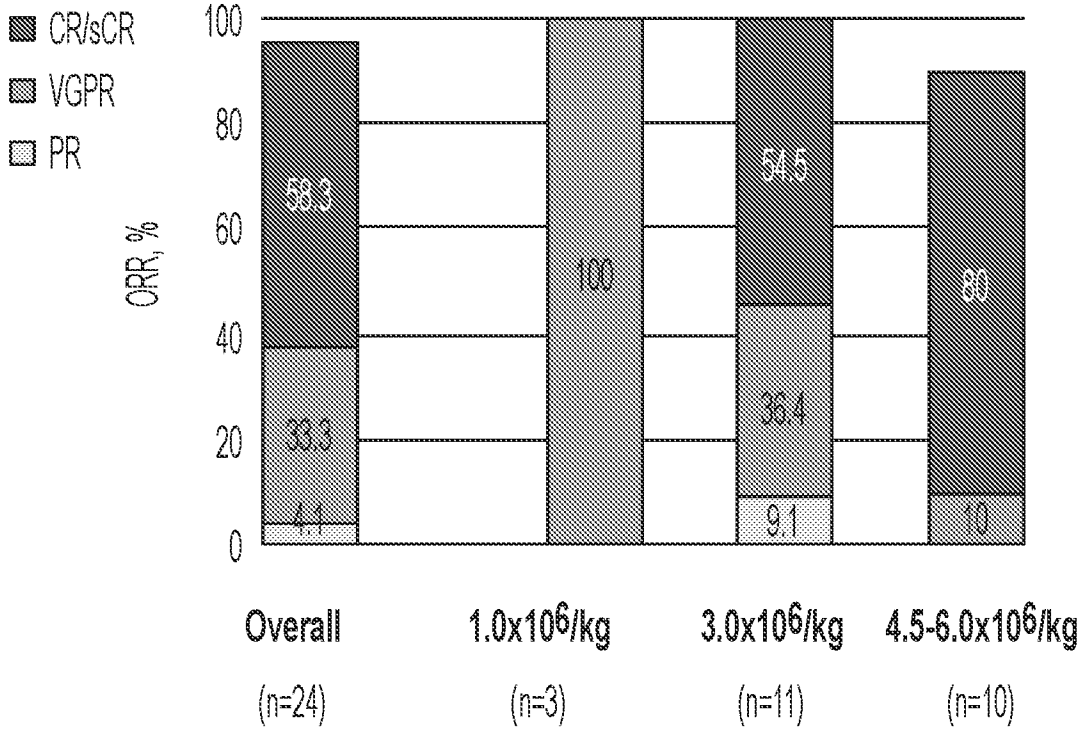
CR/sCR
VGPR
PR
ORR, %
100
80
60
40
20
0
58.3
33.3
4.1
100
54.5
36.4
9.1
80
10
Overall
(n=24)
1.0x10^6/kg
(n=3)
3.0x10^6/kg
(n=11)
4.5-6.0x10^6/kg
(n=10)

FIG. 23

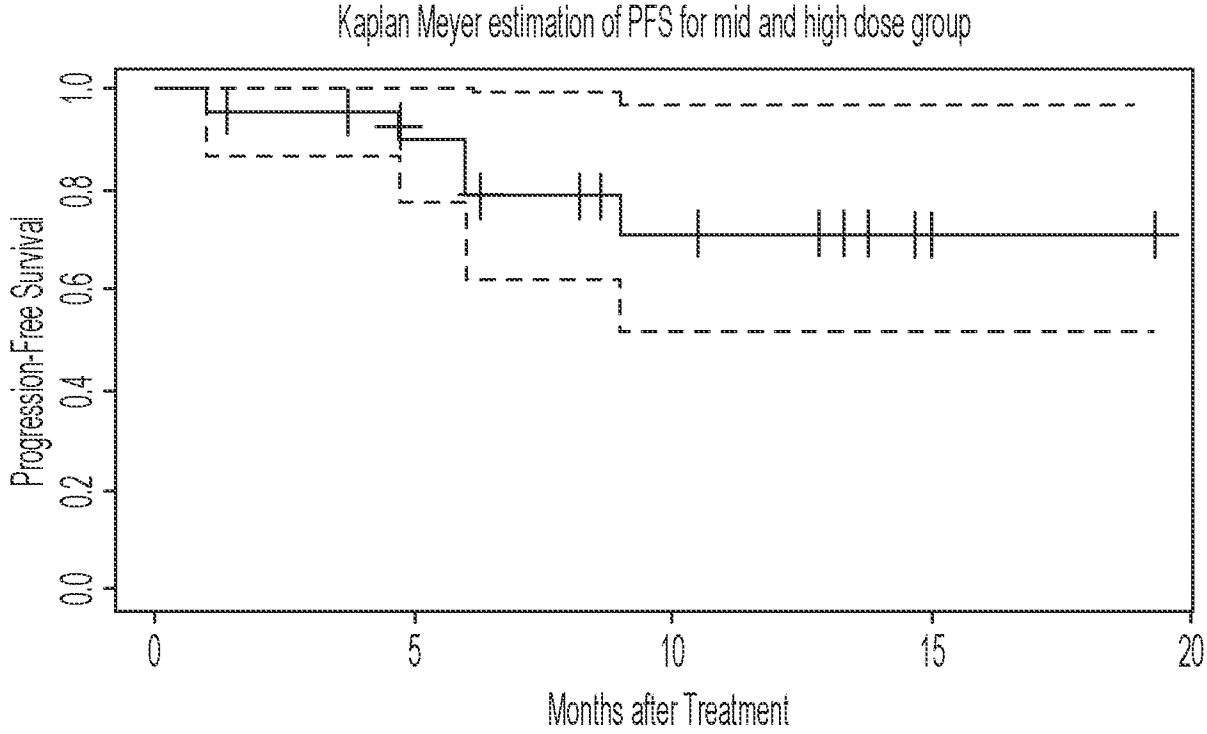
Kaplan Meyer estimation of PFS for mid and high dose group
Progression-Free Survival
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20
Months after Treatment

FIG. 24

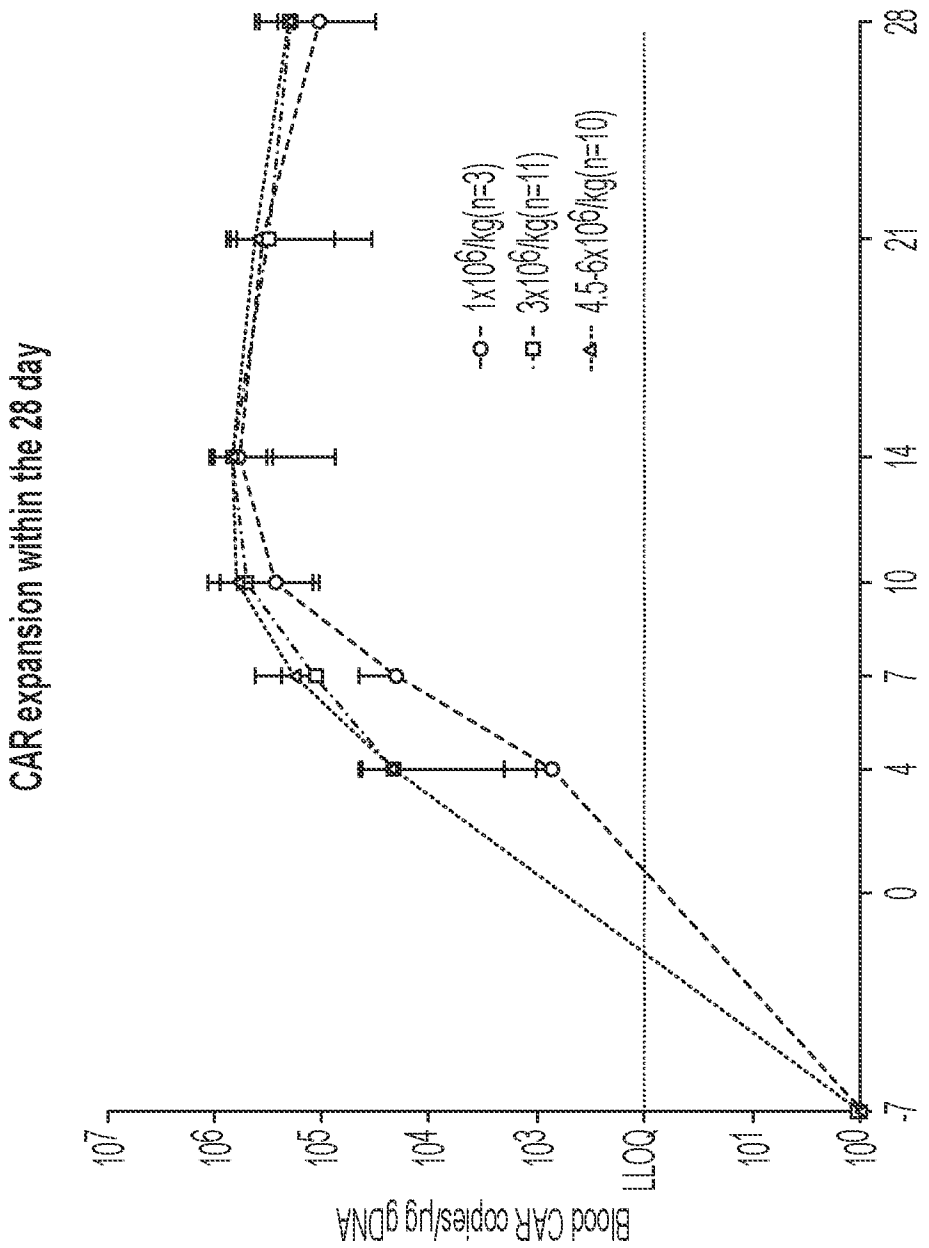
CAR expansion within the 28 day
Blood CAR copies/µg gDNA
LLOQ
Days after C-CAR088 infusion
1x10⁶/kg(n=3)
3x10⁶/kg(n=11)
4.5-6x10⁶/kg(n=10)

FIG. 25A

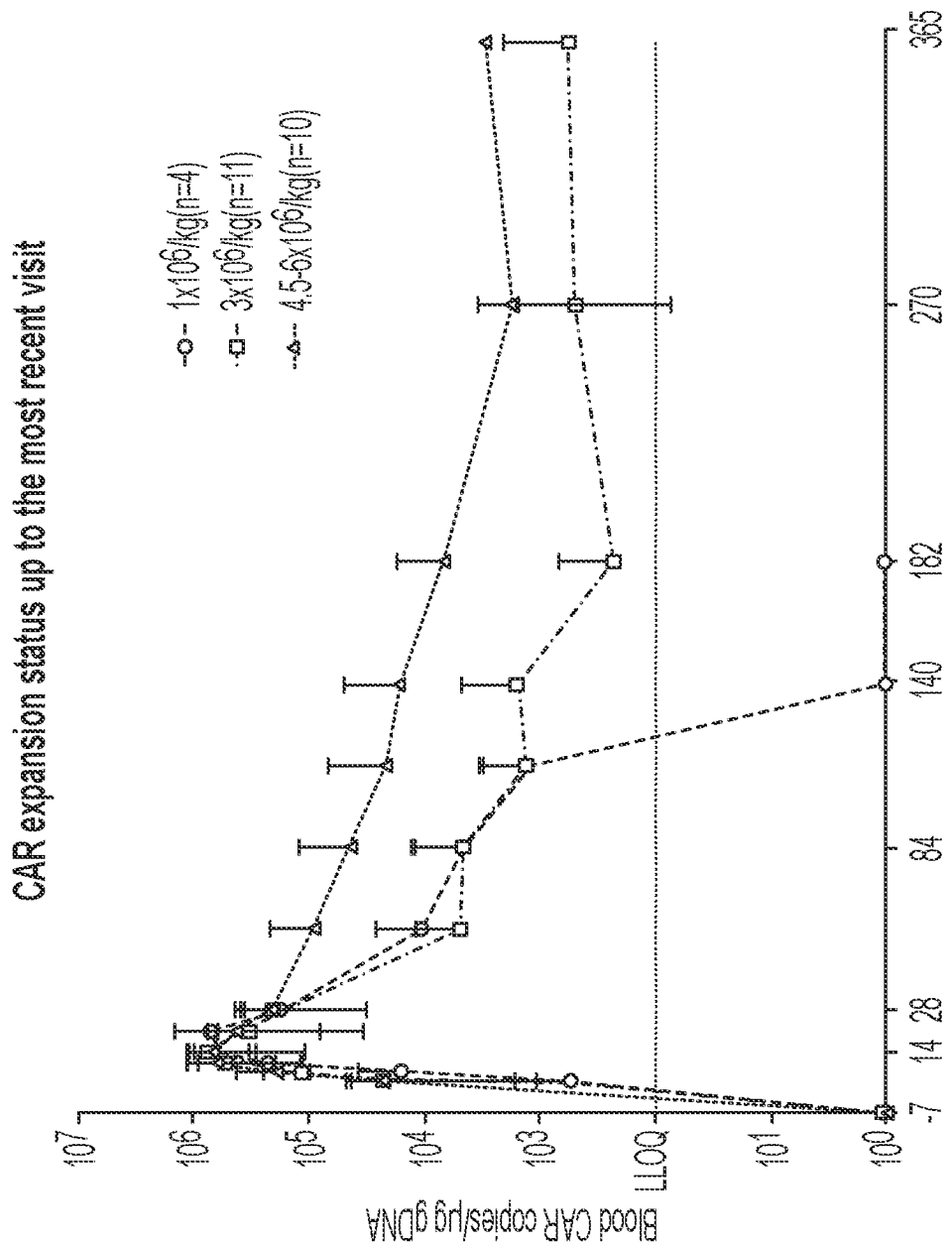
CAR expansion status up to the most recent visit
1x10^6/kg(n=4)
3x10^6/kg(n=11)
4.5-6x10^6/kg(n=10)
Blood CAR copies/µg gDNA
LLOQ
Days after C-CAR088 infusion

FIG. 25B

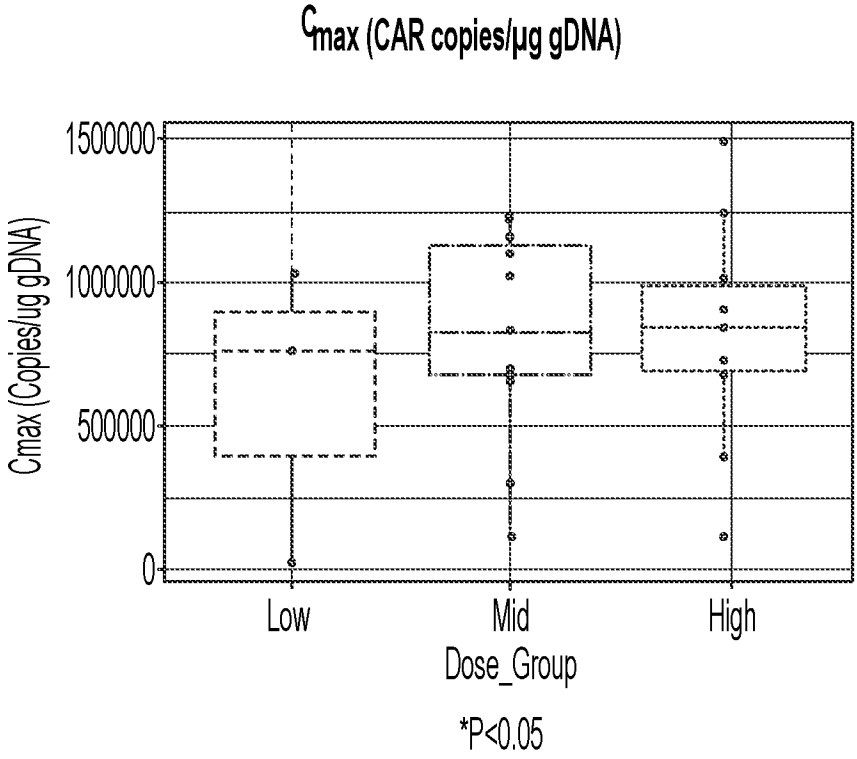
Cmax (CAR copies/µg gDNA)
1500000
1000000
500000
0
Cmax (Copies/ug gDNA)
Low
Mid
High
Dose_Group
*P<0.05

FIG. 25C

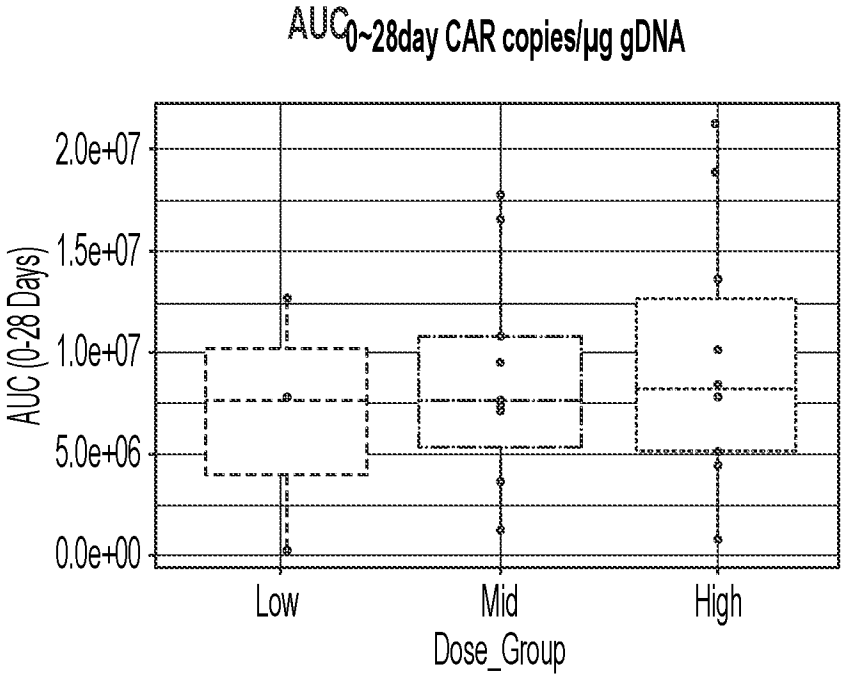
AUC0~28day CAR copies/µg gDNA
2.0e+07
1.5e+07
1.0e+07
5.0e+06
0.0e+00
AUC (0-28 Days)
Low
Mid
High
Dose_Group

FIG. 25D

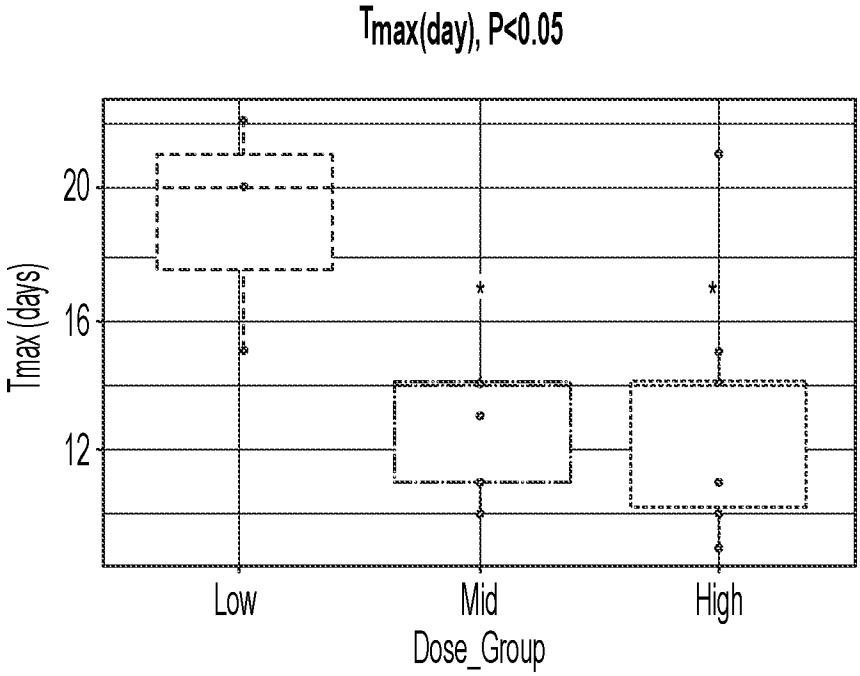

FIG. 25E

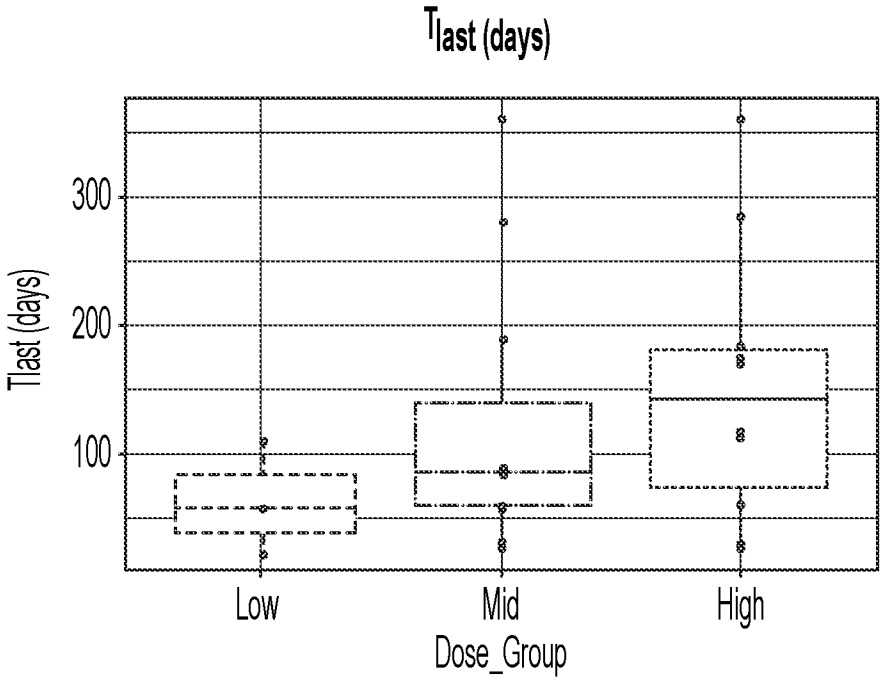

FIG. 25F

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/61410

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07K 19/00, A61K 35/17, C12N 15/62 (2022.01)

CPC - A61K 35/17, A61K 38/00, C07K 16/2878, C07K 19/00, C12N 15/62, C12N 5/0638, C07K 2319/02, C12N 2510/00

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

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

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

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 2019/196713 A1 (CELLULAR BIOMEDICINE GROUP HK LIMITED) 17 October 2019 (17.10.2019) Claim 1, Claim 3, Claim 4, Claim 5, Claim 6, Claim 8, pg 3, ln 21-22, pg 3, ln 25-27, pg 4, ln 30-32, pg 7, ln 18-25,	1-10, 12-13 ---- 11, 34
Y	WO 2019/232503 A1 (UNIVERSITY OF SOUTHERN CALIFORNIA) 05 December 2019 (05.12.2019) abstract, para [0008], [00140], Table 7, SEQ ID NO: 4359	11, 34

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

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
21 March 2022	MAR 30 2022
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Kari Rodriquez Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/61410

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. [X] forming part of the international application as filed:

      [X] in the form of an Annex C/ST.25 text file.

      [ ] on paper or in the form of an image file.

   b. [ ] furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. [ ] furnished subsequent to the international filing date for the purposes of international search only:

      [ ] in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      [ ] on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. [ ] In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/61410

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

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

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

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

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

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

This International Searching Authority found multiple inventions in this international application, as follows:

- see extra sheet for Box No. III Observations where unity of invention is lacking -

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-13, 34 limited to SEQ ID NOs: 1, 2, 17, 19, 21, 24, 26, 28 and 59

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/61410

Continuation of:
Box No. III. Observations where unity of invention is lackin

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

Groups I+: Claims 1-13, 34, drawn to a chimeric antigen receptor (CAR), comprising: an anti-BCMA antigen-binding region. The composition will be searched to the extent that the anti-BCMA encompasses LCDR1-3 of SEQ ID NOs: 17, 19 and 21, respectively; HCDR1-3 of SEQ ID NOs: 24, 26 and 28, respectively; VL SEQ ID NO: 1 and VH SEQ ID NO: 2; and the CAR encompasses SEQ ID NO: 59. It is believed that claims 1-13, 34 encompass this first named invention, and thus these claims will be searched without fee to the extent that they encompass SEQ ID NOs: 1, 2, 17, 19, 21, 24, 26, 28 and 59. Additional CAR(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected CAR(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be a CAR encompassing LCDR1-3 of SEQ ID NOs: 31, 33 and 35, respectively; HCDR1-3 of SEQ ID NOs: 38, 40 and 42, respectively; VL SEQ ID NO: 3 and VH SEQ ID NO: 4; and the CAR encompassing SEQ ID NO: 61 (Claims 1-13, 34).

Group II: claims 14-33, drawn to a method for treating cancer.

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

Groups I+ include the special technical feature of a composition which differs from the special technical feature of a method, as disclosed by Group II.

No technical features are shared between the amino acid sequences of Groups I+ and, accordingly, these groups lack unity a priori.

Additionally, even if Groups I+ and II were considered to share the technical features of including: a chimeric antigen receptor (CAR), comprising: an anti-BCMA antigen-binding region, these shared technical features are previously disclosed by WO 2019/196713 A1 to Cellular Biomedicine Group HK Limited (hereinafter "CBGHK").

CBGHK teaches (instant claim 1) a chimeric antigen receptor (CAR), comprising: an anti-BCMA antigen-binding region (Claim 1 (translation), A chimeric antigen receptor characterized in that the antigen binding domain of the chimeric antigen receptor is an antibody single chain variable region sequence that targets the extracellular region of BCMA.) which comprises a light chain variable region (VL) and a heavy chain variable region (VH), VL comprising three complementarity determining regions (CDRs), LCDR1, LCDR2 and LCDR3, VH comprising three CDRs, HCDR1, HCDR2 and HCDR3 (Claim 3, (translation) wherein the structure of the antigen-binding domain is as shown in the following formula I: VL -VH (I).; pg 7, ln 18-25, (translation, pg 8, first para) Each VH and VL contains three CDRs and four Frs, arranged from the amino terminus to the carboxy terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.).

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

Groups I+ and II therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.