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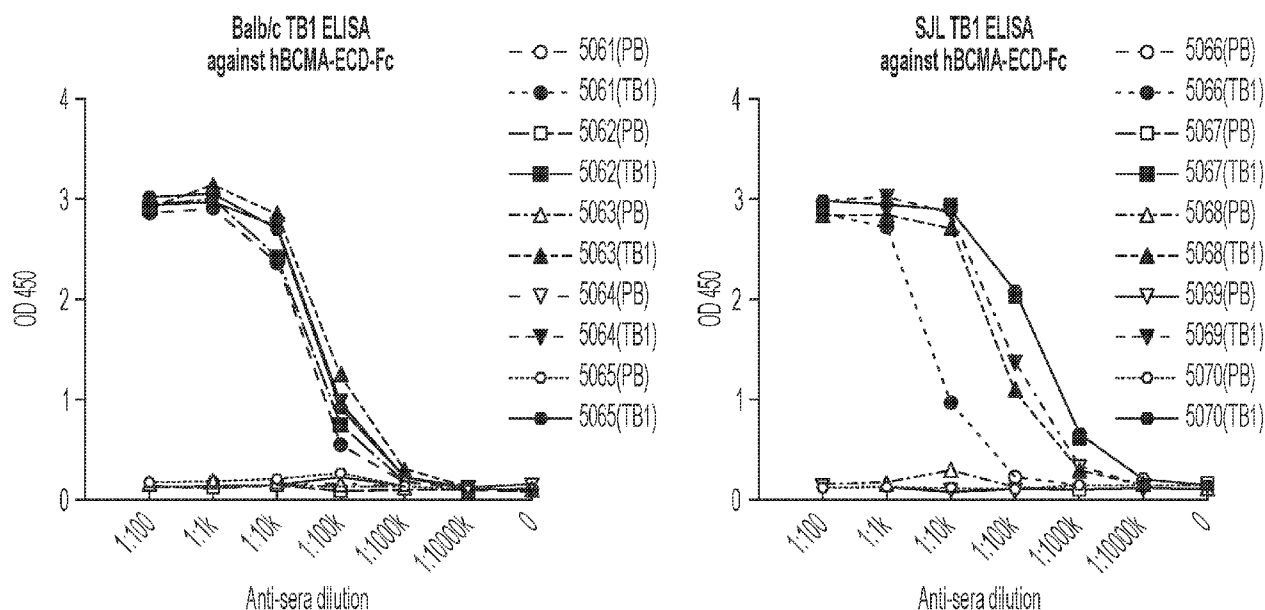


FIG. 1

(57) **Abstract:** Anti-BCMA antibodies and chimeric antigen receptors (CARs) are provided. Immune cells expressing the anti-BCMA CAR can be used to treat cancer. The anti-BCMA antibodies and CARs can recognize the extracellular domains of human BCMA. The anti-BCMA CAR T cells show specific cytotoxicity towards BCMA-positive target cells.

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ANTI-BCMA ANTIBODIES AND CHIMERIC ANTIGEN RECEPTORS

SEQUENCE LISTING

This application contains a Sequence Listing which has been filed electronically in
5 ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy,
created on May 7, 2021, is named 11299-009938-WO0_ST25.txt and is 91 KB in size.

TECHNICAL FIELD

The present invention relates to anti-BCMA antibodies and chimeric antigen receptors
10 (CARs), and preparation and applications thereof.

BACKGROUND

Multiple myeloma (MM) is the second most common hematological malignant tumor
next to non-Hodgkin's lymphoma. In recent years, although great progress has been made in
15 chemotherapy, proteasome inhibitors, immunomodulators (thalidomide derivatives) and
CD38 targeting antibodies, almost all patients will eventually relapse. Therefore, there is an
urgent need for new therapeutic regimens.

B-cell maturation antigen (BCMA), also known as a tumor necrosis factor receptor
superfamily member 17, is a membrane protein widely expressed on mature B cells. An
20 important feature of BCMA is that BCMA is highly expressed on all MM cells, and not
expressed in other normal tissues (except plasma cells). Therefore, BCMA has become a
popular target for many pharmaceutical companies and research institutions to treat relapsed
or refractory multiple myeloma (R/R MM patients).

At present, the immunotherapies developed for the BCMA target mainly fall into
25 three categories: chimeric antigen receptor T cell (CAR-T) therapy, bispecific antibodies
(BsAb) and antibody drug conjugates (ADC). A CAR-T (bb2121) jointly developed by
Celgene and Bluebird Bio, has entered the phase 3 clinical stage. The current bispecific
antibodies targeting BCMA have one end binding to BCMA, and the other end binding to a
CD3 T cell receptor on the surface of the T cell, thereby recruiting T cells to tumor cells
30 which then can kill the tumor cells. It was reported that the optimal dose of AMG-420
(Amgen) can reach 70% ORR when treating patients with R/R MM. In the aspect of ADC,
GSK-2857916 from GlaxoSmithKline (GSK) has been used in multiple clinical trials to treat
different types of MM patients. Among them, the key clinical trial for the treatment of R/R

MM patients as a 3/4-line therapy has obtained interim results. The results recently published in Blood Cancer Journal showed that the ORR of the patients treated with GSK-2857916 was 60%, the complete response rate (CRR) reached 15%, and the progression-free survival (PFS) reached 12 months.

5 Nevertheless, the therapies available for the treatment of R/R MM patients are still limited, and new drugs and methods for the treatment of R/R MM patients still need to be developed in this field.

SUMMARY

10 The present disclosure provides for an anti-BCMA antibody, or an antigen-binding portion thereof, comprising a light chain variable region (V_L) and a heavy chain variable region (V_H).

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

 The light chain variable region may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 76, 77 and 78, respectively, (ii) SEQ ID NOs: 82, 83 and 84, respectively, (iii) SEQ ID NOs: 88, 89 and 90, respectively, (iv)
20 SEQ ID NOs: 94, 95 and 96, respectively, (v) SEQ ID NOs: 100, 101 and 102, respectively, (vi) SEQ ID NOs: 106, 107 and 108, respectively, (vii) SEQ ID NOs: 112, 113 and 114, respectively, (viii) SEQ ID NOs: 118, 119 and 120, respectively, or (ix) SEQ ID NOs: 124, 125 and 126, respectively.

 The heavy chain variable region may comprise three complementarity
25 determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 79, 80 and 81, respectively, (ii) SEQ ID NOs: 85, 86 and 87, respectively, (iii) SEQ ID NOs: 91, 92 and 93, respectively, (iv) SEQ ID NOs: 97, 98 and 99, respectively, (v) SEQ ID NOs: 103, 104 and 105, respectively, (vi) SEQ ID NOs: 109, 110 and 111,
30 respectively, (vii) SEQ ID NOs: 115, 116 and 117, respectively, (viii) SEQ ID NOs: 121, 122 and 123, respectively, or (ix) SEQ ID NOs: 127, 128 and 129, respectively.

 The V_L and V_H may be as follows: (i) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 76, 77 and 78, respectively; the V_H

may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 79, 80 and 81, respectively; (ii) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 82, 83 and 84, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 85, 86 and 87, respectively; (iii) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 88, 89 and 90, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 91, 92 and 93, respectively; (iv) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 94, 95 and 96, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 97, 98 and 99, respectively; (v) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 100, 101 and 102, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 103, 104 and 105, respectively; (vi) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 106, 107 and 108, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 109, 110 and 111, respectively; (vii) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 112, 113 and 114, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino

acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 115, 116 and 117, respectively; (viii) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 118, 119 and 120, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 121, 122 and 123, respectively; or (ix) the V_L may comprise three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 124, 125 and 126, respectively; the V_H may comprise three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 127, 128 and 129, respectively.

The V_L and V_H may have amino acid sequences about 80% to about 100% identical to amino acid sequences set forth in (i) SEQ ID NO: 53 and SEQ ID NO: 54, respectively, (ii) SEQ ID NO: 55 and SEQ ID NO: 56, respectively, (iii) SEQ ID NO: 57 and SEQ ID NO: 58, respectively, (vi) SEQ ID NO: 59 and SEQ ID NO: 60, respectively, (v) SEQ ID NO: 61 and SEQ ID NO: 62, respectively, (vi) SEQ ID NO: 63 and SEQ ID NO: 64, respectively, (vii) SEQ ID NO: 65 and SEQ ID NO: 66, respectively, (viii) SEQ ID NO: 67 and SEQ ID NO: 68, respectively, or (ix) SEQ ID NO: 69 and SEQ ID NO: 70, respectively.

The V_L may comprise an amino acid sequence about 80% to about 100% identical to any one of the amino acid sequences set forth in SEQ ID NOs: 53, 55, 57, 59, 61, 63, 65, 67 and 69. The V_H may comprise an amino acid sequence about 80% to about 100% identical to any one of the amino acid sequences set forth in SEQ ID NOs: 54, 56, 58, 60, 62, 64, 66, 68 and 70.

The antibody or antigen-binding portion thereof may be (a) a whole immunoglobulin molecule; (b) an scFv; (c) a Fab fragment; (d) an F(ab')₂; or (e) a disulfide linked Fv.

The present antibody or antigen-binding portion thereof may comprise at least one constant domain selected from: a) an IgG constant domain; and (b) an IgA constant domain.

The present antibody or antigen-binding portion thereof may comprise at least one human constant domain.

The present disclosure provides for an antibody conjugate that comprises the present antibody or antigen-binding portion thereof, linked with a conjugate moiety. The conjugate moiety may be a detectable marker, a drug, a toxin, a cytokine, a radionuclide, an enzyme, a targeting moiety, and combinations thereof. In one embodiment, the
5 antibody conjugate is an antibody drug conjugate (ADC).

Also encompassed by the present disclosure is a composition comprising the present antibody or antigen-binding portion thereof, and a pharmaceutically acceptable carrier.

The present disclosure provides for a composition comprising the present CAR or
10 immune cells, and a pharmaceutically acceptable carrier.

The present disclosure provides for a nucleic acid encoding the present antibody or antigen-binding portion thereof (or encoding the CAR), a vector comprising the present nucleic acid, and a cell comprising the present vector.

In the CAR, the anti-BCMA antigen-binding region may be a single-chain
15 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,
- 20 (d) a co-stimulatory region, and
- (e) a cytoplasmic signaling domain.

The co-stimulatory region of the CAR may comprise 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,
25 or combinations thereof.

The cytoplasmic signaling domain of the CAR may comprise a cytoplasmic signaling domain of CD3 ζ .

The hinge region of the CAR may comprise a hinge region of Ig4, CD8, CD28, CD137, or combinations thereof.

The the transmembrane domain of the CAR may comprise a transmembrane
30 domain of CD8, CD28, CD3 ϵ , 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 CAR. The

immune cell may be a T cell, a natural killer (NK) cell, a natural killer T cell, a lymphoid progenitor cell, a hematopoietic stem cell, a stem cell, a macrophage, or a dendritic cell.

5 The present disclosure provides for a method of treating cancer. The method may comprise administering the present immune cell or composition 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.

10 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. In one embodiment, the immune cell is administered via intravenous infusion.

15 The immune cell may be allogeneic or autologous to the subject.

The subject may be a human or a mammal. The present antibodies, antigen-binding portions thereof, CARs, compositions and methods may be used in all vertebrates, e.g., mammals and non-mammals, including human, mice, rats, guinea pigs, hamsters, dogs, cats, cows, horses, goats, sheep, pigs, monkeys, apes, gorillas,
20 chimpanzees, rabbits, ducks, geese, chickens, amphibians, reptiles and other animals.

An object of the present disclosure is to provide a BCMA antibody, and preparation and application thereof.

25 In a first aspect of the present disclosure, a BCMA antibody is provided, wherein the antibody comprises heavy chain variable (V_H) regions encoded by nucleotide sequences shown in SEQ ID NO: 1, 3, 5, 7, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 26, 28, 30, 32, 34 and 37 and light chain variable (V_L) regions encoded by nucleotide sequences shown in SEQ ID NO: 2, 4, 6, 8, 13, 18, 23, 25, 27, 29, 31, 33, 35, 36 and 38.

Alternatively, the antibody comprises heavy chains with amino acid sequences as shown in SEQ ID NO: 39, 41, 43, 45, 47 and 49 and light chains with amino acid sequences as shown in SEQ ID NO: 40, 42, 44, 46, 48, 50 and 51.

Alternatively, the antibody comprises V_H regions with amino acid sequences as shown in SEQ ID NO: 54, 56, 58, 60, 62, 64, 66, 68 and 70 and V_L regions with amino acid sequences as shown in SEQ ID NO: 53, 55, 57, 59, 61, 63, 65, 67 and 69.

Any of the foregoing amino acid sequences may include a derivative sequence that optionally adds, deletes, modifies and/or substitutes at least one amino acid and can retain the binding affinity of BCMA.

In certain embodiments, the antibody comprises V_H regions and V_L regions encoded
5 by nucleotide sequences shown below:

Hybridoma No.	Nucleotide sequences encoding V _H regions	Nucleotide sequences encoding V _L regions
6G10-1D7 (CP01)	SEQ ID NO: 1	SEQ ID NO: 2
99B3G3 (CP02)	SEQ ID NO: 3	SEQ ID NO: 4
102A12H6	SEQ ID NO: 5	SEQ ID NO: 6
105C10F1(CP03)	SEQ ID NO: 7	SEQ ID NO: 8
107A11F1	SEQ ID NO: 9	SEQ ID NO: 13
	SEQ ID NO: 10	
	SEQ ID NO: 11	
	SEQ ID NO: 12	
107B11E1	SEQ ID NO: 14	SEQ ID NO: 18
	SEQ ID NO: 15	
	SEQ ID NO: 16	
	SEQ ID NO: 17	
107A9A4	SEQ ID NO: 19	SEQ ID NO: 23
	SEQ ID NO: 20	
	SEQ ID NO: 21	
	SEQ ID NO: 22	
113B3F12	SEQ ID NO: 24	SEQ ID NO: 25
100H2D12C6	SEQ ID NO: 3	SEQ ID NO: 4
109C5F3C1(CP06)	SEQ ID NO: 26	SEQ ID NO: 27
143D6F4(CP07)	SEQ ID NO: 28	SEQ ID NO: 29
151A9A4(CP08)	SEQ ID NO: 30	SEQ ID NO: 31
152D8E8(CP09)	SEQ ID NO: 32	SEQ ID NO: 33
107A11F1B7(CP04)	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107A9A4D2	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107B11E1D7(CP05)	SEQ ID NO: 37	SEQ ID NO: 38
97B8G8D12	SEQ ID NO: 3	SEQ ID NO: 4

In certain embodiments, the antibody is a murine antibody.

In certain embodiments, the antibody comprises heavy chains and light chains with amino acid sequences shown below:

Hybridoma No.	Amino acid sequences of heavy chains	Amino acid sequences of light chains
6G10-1D7 (CP01)	SEQ ID NO: 39	SEQ ID NO.:40
99B3G3(CP02)	SEQ ID NO: 41	SEQ ID NO: 42
105C10F1(CP03)	SEQ ID NO: 43	SEQ ID NO: 44
113B3F12	SEQ ID NO: 45	SEQ ID NO: 46
107B11E1D7(CP05)	SEQ ID NO: 47	SEQ ID NO: 48
107A9A4D2	SEQ ID NO: 49	SEQ ID NO: 50
		SEQ ID NO: 51

In certain embodiments, the antibody is a chimeric antibody.

In certain embodiments, the antibody comprises V_H regions and V_L regions with amino acid sequences shown below:

Antibody	Amino acid sequences of V _H regions	Amino acid sequences of V _L regions
CP01	SEQ ID NO: 54	SEQ ID NO.:53
CP02	SEQ ID NO: 56	SEQ ID NO: 55
CP03	SEQ ID NO: 58	SEQ ID NO: 57
CP04	SEQ ID NO: 60	SEQ ID NO: 59
CP05	SEQ ID NO: 62	SEQ ID NO: 61
CP06	SEQ ID NO: 64	SEQ ID NO: 63
CP07	SEQ ID NO: 66	SEQ ID NO: 65
CP08	SEQ ID NO: 68	SEQ ID NO: 67
CP09	SEQ ID NO: 70	SEQ ID NO: 69

5

In certain embodiments, the antibody is a single-chain antibody.

In certain embodiments, the antibody binds to a human BCMA protein and/or a machin BCMA protein.

10 In certain embodiments, the antibody binds to an extracellular domain of the BCMA protein.

In certain embodiments, the antibody does not bind to a tumor necrosis factor receptor superfamily 13B.

In certain embodiments, the antibody further comprises heavy chain constant regions and/or light chain constant regions.

15 In certain embodiments, the heavy chain constant regions are of human or mouse origin.

In certain embodiments, the heavy chain constant regions are heavy chain IgG1 constant regions of a human antibody.

In certain embodiments, the light chain constant regions are of human or mouse

origin.

In certain embodiments, the light chain constant regions are light chain kappa constant regions of a human antibody.

5 In certain embodiments, the number of the added, deleted, modified and/or substituted amino acids is 1 to 5 (e.g., 1 to 3, 1 to 2, or 1).

In certain embodiments, the derivative sequence that adds, deletes, modifies and/or substitutes at least one amino acid and can retain the binding affinity of BCMA is an amino acid sequence with at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of homology or sequence similarity.

10 In certain embodiments, the antibody is selected from animal-derived antibodies, chimeric antibodies, humanized antibodies, fully human antibodies, or combinations thereof.

In certain embodiments, the ratio of the immunogenicity Z1 of the chimeric antibodies in humans to the immunogenicity Z0 of non-chimeric antibodies (such as murine antibodies) in humans (Z1/Z0) is 0 to 0.5, 0 to 0.2, or 0 to 0.05 (e.g., 0.001 to 0.05).

15 In certain embodiments, the antibody is a partially or fully humanized or fully human monoclonal antibody.

In certain embodiments, the antibody is a double-chain antibody, or a single-chain antibody.

20 In certain embodiments, the antibody is an antibody full-length protein or an antigen-binding fragment.

In certain embodiments, the antibody is a bispecific antibody or a multispecific antibody.

In certain embodiments, the antibody is a monoclonal antibody or polyclonal antibody.

25 In a second aspect of the present disclosure, a recombinant protein is provided, which comprises:

- (i) The antibody described in the first aspect of the present disclosure; and
- (ii) An optional tag sequence for assisting expression and/or purification.

In certain embodiments, the tag sequence includes a 6xHis tag.

30 In certain embodiments, the recombinant protein (or polypeptide) comprises a fusion protein.

In certain embodiments, the recombinant protein is a monomer, dimer, or multimer.

In a third aspect of the present disclosure, a chimeric antigen receptor (CAR) fusion protein is provided, which from an N-terminal to a C-terminal, comprises:

- (i) scFv targeting BCMA,
- (ii) A transmembrane domain,
- (iii) At least one costimulatory domain, and
- (iv) An activation domain.

5 The scFv targeting BCMA comprises V_H regions with amino acid sequences as shown in SEQ ID NO: 54, 56, 58, 60, 62, 64, 66, 68 and 70 and V_L regions with amino acid sequences as shown in SEQ ID NO: 53, 55, 57, 59, 61, 63, 65, 67 and 69.

In certain embodiments, the scFv comprises V_H regions and V_L regions with amino acid sequences shown below:

Antibody	Amino acid sequences of V _H regions	Amino acid sequences of V _L regions
CP01	SEQ ID NO: 54	SEQ ID NO.:53
CP02	SEQ ID NO: 56	SEQ ID NO: 55
CP03	SEQ ID NO: 58	SEQ ID NO: 57
CP04	SEQ ID NO: 60	SEQ ID NO: 59
CP05	SEQ ID NO: 62	SEQ ID NO: 61
CP06	SEQ ID NO: 64	SEQ ID NO: 63
CP07	SEQ ID NO: 66	SEQ ID NO: 65
CP08	SEQ ID NO: 68	SEQ ID NO: 67
CP09	SEQ ID NO: 70	SEQ ID NO: 69.

10 In certain embodiments, the CAR fusion protein has a structure shown in the following Formula I:

L-scFv-H-TM-C-CD3ζ (I)

where,

15 Each “-” is independently a linking peptide or a peptide bond;

L is an optional signal peptide sequence;

scFv is scFv targeting BCMA;

H is an optional hinge region;

TM is a transmembrane domain;

20 C is a costimulatory signal molecule; and

CD3ζ is a cytoplasmic signal transduction sequence of CD3ζ.

In certain embodiments, the L is a signal peptide of a protein selected from the group consisting of: CD8, GM-CSF, CD4, CD137 or combinations thereof.

In certain embodiments, the L is a signal peptide derived from CD8.

25 In certain embodiments, the amino acid sequence of the signal peptide is shown in SEQ ID NO: 52.

In certain embodiments, the scFv has a structure as shown in the following Formula II or III:

VL-L1-VH (II)

VH-L2-VL (III)

- 5 where V_L is a light chain variable region;
 V_H is a heavy chain variable region;
 L1 and L2 are each independently a linking peptide.

In certain embodiments, the amino acid sequence of the linking peptide is as shown in SEQ ID NO: 71.

- 10 In certain embodiments, the H is a hinge region of a protein selected from the group consisting of: CD8, CD28, CD137, or combinations thereof. In certain embodiments, the H is a hinge region derived from CD8. In certain embodiments, the amino acid sequence of the hinge region is as shown in SEQ ID NO: 72.

- In certain embodiments, the TM is a transmembrane region of a protein selected from the group consisting of: CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or combinations thereof.

In certain embodiments, the TM includes a transmembrane region derived from CD8. In certain embodiments, the amino acid sequence of the transmembrane region is as shown in SEQ ID NO: 73.

- 20 In certain embodiments, the C is a costimulatory signal 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 combinations thereof. In certain embodiments, the C includes a costimulatory signal molecule derived from 4-1BB. In certain embodiments, the amino acid sequence of the costimulatory signal molecule is as shown in SEQ ID NO: 74.

In certain embodiments, the cytoplasmic signaling sequence of CD3 ζ is as shown in SEQ ID NO: 75.

In a fourth aspect of the present disclosure, a polynucleotide is provided, which encodes a polypeptide such as:

- 30 (1) The antibody as described in the first aspect of the present disclosure;
 (2) The recombinant protein as described in the second aspect of the present disclosure; and
 (3) The CAR fusion protein as described in the third aspect of the present disclosure.

In certain embodiments, the polynucleotides encoding the V_H regions of the antibody

are as shown in SEQ ID NO. 1, 3, 5, 7, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 26, 28, 30, 32, 34 and 37; and/or the polynucleotides encoding the V_L regions of the antibody are as shown in SEQ ID NO: 2, 4, 6, 8, 13, 18, 23, 25, 27, 29, 31, 33, 35, 36 and 38.

In certain embodiments, the polynucleotides encoding the V_H regions and the
5 polynucleotides encoding the V_L regions are shown below:

Hybridoma No.	Nucleotide sequences encoding V _H regions	Nucleotide sequences encoding V _L regions
6G10-1D7 (CP01)	SEQ ID NO: 1	SEQ ID NO.:2
99B3G3(CP02)	SEQ ID NO: 3	SEQ ID NO: 4
102A12H6	SEQ ID NO: 5	SEQ ID NO: 6
105C10F1(CP03)	SEQ ID NO: 7	SEQ ID NO: 8
107A11F1	SEQ ID NO: 9	SEQ ID NO: 13
	SEQ ID NO: 10	
	SEQ ID NO: 11	
	SEQ ID NO: 12	
107B11E1	SEQ ID NO: 14	SEQ ID NO: 18
	SEQ ID NO: 15	
	SEQ ID NO: 16	
	SEQ ID NO: 17	
107A9A4	SEQ ID NO: 19	SEQ ID NO: 23
	SEQ ID NO: 20	
	SEQ ID NO: 21	
	SEQ ID NO: 22	
113B3F12	SEQ ID NO: 24	SEQ ID NO: 25
100H2D12C6	SEQ ID NO: 3	SEQ ID NO: 4
109C5F3C1(CP06)	SEQ ID NO: 26	SEQ ID NO: 27
143D6F4(CP07)	SEQ ID NO: 28	SEQ ID NO: 29
151A9A4(CP08)	SEQ ID NO: 30	SEQ ID NO: 31
152D8E8(CP09)	SEQ ID NO: 32	SEQ ID NO: 33
107A11F1B7(CP04)	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107A9A4D2	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107B11E1D7(CP05)	SEQ ID NO: 37	SEQ ID NO: 38
97B8G8D12	SEQ ID NO: 3	SEQ ID NO: 4.

In a fifth aspect of the present disclosure, a vector is provided, which contains any of the polynucleotides in the fourth aspect of the present disclosure.

In certain embodiments, the vector includes a bacterial plasmid, a bacteriophage, a
10 yeast plasmid, a plant cell virus, a mammalian cell virus such as an adenovirus or a retrovirus,

or any other vector.

In certain embodiments, the vector includes a lentiviral vector.

In a sixth aspect of the present disclosure, a genetically engineered host cell is provided, which comprises the vector described in the fifth aspect of the present disclosure, or is integrated with an exogenous polynucleotide described in the fourth aspect of the present disclosure in the genome, or expresses the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, or the CAR fusion protein in the third aspect of the present disclosure.

In certain embodiments, the cell is an isolated cell, and/or a genetically engineered cell.

In certain embodiments, the immune cells are derived from humans or non-human mammals (such as mice).

In certain embodiments, the cells include T cells and NK cells.

In certain embodiments, the host cell is an engineered immune cell.

In certain embodiments, the engineered immune cell includes a T cell or an NK cell, such as, (i) a chimeric antigen receptor T cell (CAR-T cell); or (ii) a chimeric antigen receptor NK cell (CAR-NK cell).

In a seventh aspect of the present disclosure, an antibody conjugate is provided, which comprises:

(a) an antibody portion, which is selected from the group consisting of: the antibody as described in the first aspect of the present disclosure; and

(b) a conjugating portion conjugated to the antibody portion, which is selected from the group consisting of: detectable markers, drugs, toxins, cytokines, radionuclides, enzymes, or combinations thereof.

In certain embodiments, the antibody portion is conjugated to the conjugating portion via a chemical bond or a linker.

In certain embodiments, the antibody conjugate is an antibody drug conjugate.

In an eighth aspect of the present disclosure, a method for preparing an engineered cell is provided. The engineered cell expresses the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, or the CAR fusion protein described in the third aspect of the present disclosure. The following steps are comprised: transducing the polynucleotide described in the fourth aspect of the present disclosure or the vector described in the fifth aspect of the present disclosure into a host cell, thereby obtaining an engineered cell.

In certain embodiments, the method further comprises a step of detecting the function and effectiveness of the obtained engineered cell.

In a ninth aspect of the present disclosure, a pharmaceutical composition is provided, which comprises the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, the CAR fusion protein described in the third aspect of the present disclosure, the vector described in the fifth aspect of the present disclosure, the host cell described in the sixth aspect of the present disclosure, or the antibody conjugate described in the seventh aspect of the present disclosure, and a pharmaceutically acceptable carrier, diluent or excipient.

In certain embodiments, the pharmaceutical composition is a liquid preparation.

In certain embodiments, the pharmaceutical composition is an injection.

In certain embodiments, the pharmaceutical composition further comprises an anti-tumor second active ingredient, such as a second antibody or a chemotherapeutic agent.

In certain embodiments, the chemotherapeutic agent is docetaxel, carboplatin, or a combination thereof.

In the tenth aspect of the present disclosure, a use of an active ingredient is provided. The active ingredient is selected from the group consisting of: the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, the CAR fusion protein described in the third aspect of the present disclosure, the vector described in the fifth aspect of the present disclosure, the host cell described in the sixth aspect of the present disclosure, or the antibody conjugate described in the seventh aspect of the present disclosure, and is used for (a) preparing diagnostic reagents or kits; and/or (b) preparing drugs or preparations for preventing and/or treating cancers or tumors.

In certain embodiments, the tumor is a BCMA-positive tumor.

In certain embodiments, the tumors are hematological tumors, solid tumors, or combinations thereof.

In certain embodiments, the hematological tumor is acute myelocytic leukemia (AML), multiple myeloma (MM), chronic lymphocytic leukemia (CLL), acute lymphatic leukemia (ALL), diffuse large B cell lymphoma (DLBCL), or combinations thereof.

In certain embodiments, the solid tumor is gastric cancer, peritoneal metastasis of gastric cancer, liver cancer, kidney tumor, lung cancer, carcinoma of small intestine, bone cancer, prostate cancer, colorectal cancer, breast cancer, colon cancer, cervical cancer, ovarian cancer, lymphoma cancer, nasopharynx cancer, adrenal gland tumor, bladder tumor,

non-small cell lung cancer (NSCLC), brain glioma, endometrial cancer, testicular cancer, colorectal cancer, urinary tract tumor, thyroid cancer, or combinations thereof .

In certain embodiments, the tumor is multiple myeloma.

In certain embodiments, the diagnostic reagent is a test piece or a test plate.

5 In certain embodiments, the diagnostic reagent or kit is used for: (1) detecting BCMA proteins in the sample; (2) detecting endogenous BCMA proteins in tumor cells; and/or (3) detecting tumor cells expressing BCMA proteins.

10 In an eleventh aspect of the present disclosure, a method for *in vitro* detection (including diagnostic or non-diagnostic) of BCMA proteins in a sample is provided, which comprises steps of: (1) *in vitro*, contacting the sample with the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, or the antibody conjugate described in the seventh aspect of the present disclosure; and (2) detecting whether an antigen-antibody complex is formed, if yes, which means BCMA proteins exist in the sample.

15 In a twelfth aspect of the present disclosure, a test plate is provided, which comprises a substrate (support plate) and a test strip. The test strip comprises the antibody described in the first aspect of the present disclosure, the recombinant protein described in the second aspect of the present disclosure, or the antibody conjugate in the seventh aspect of the present disclosure, or combinations thereof.

20 In a thirteenth aspect of the present disclosure, a kit is provided, which may comprise: (1) a first container, which comprises the antibody described in the first aspect; and/or (2) a second container, which comprises a secondary antibody against the antibody described in the first aspect of the present disclosure.

25 The kit may comprise the test plate described in the twelfth aspect of the present disclosure.

30 In a fourteenth aspect of the present disclosure, a method for preparing a recombinant polypeptide is provided, which comprises steps of: (a) culturing the host cell described in the sixth aspect of the present disclosure under conditions suitable for expression; (b) isolating a recombinant polypeptide from the culture, the recombinant polypeptide being the antibody described in the first aspect of the present disclosure or the recombinant protein described in the second aspect of the present disclosure.

In a fifteenth aspect of the present disclosure, a method for treatment of a disease is provided. The method may comprise administering to a subject in need thereof an effective dose of the antibody described in the first aspect of the present disclosure, the recombinant

protein described in the second aspect of the present disclosure, the antibody conjugate described in the seventh aspect of the present disclosure, the host cell in the sixth aspect of the present disclosure or the pharmaceutical composition described in the ninth aspect of the present disclosure, or a combination thereof.

5 In certain embodiments, the disease is a BCMA-positive cancer/tumor.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows ELISA analysis on the binding titers of mouse serum to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc after the first booster immunization.

10 Fig. 2 shows flow cytometry analysis on the binding titers of mouse serum to K562-BCMA+ and K562 cells after the first booster immunization.

Fig. 3 shows ELISA analysis on the binding titers of mouse serum to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc after the second booster immunization.

15 Fig. 4 shows flow cytometry analysis on the binding titers of mouse serum to K562-BCMA+ and K562 cells after the second booster immunization.

Fig. 5 shows ELISA analysis on the binding titers of mouse serum to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc after the third booster immunization.

Fig. 6 shows flow cytometry analysis on the binding titers of mouse serum to L-BCMA+ and L cells before and after the third booster immunization.

20 Fig. 7 shows a hybridoma cell screening process (all the selected clones do not bind to NC-Fc).

Fig. 8 shows SDS-PAGE analysis on small-batch antibody production and purification.

Fig. 9 shows ELISA analysis on the binding ability of a hybridoma antibody to hBCMA-ECD-Fc.

25 Fig. 10 shows ELISA analysis on the binding ability of a hybridoma antibody to cynoBCMA-ECD-Fc.

Fig. 11 shows ELISA analysis on the binding ability of a hybridoma antibody to hTACI-ECD-Fc.

30 Fig. 12 shows flow cytometry analysis on the binding ability of a hybridoma antibody to L-BCMA+ cells.

Fig. 13 shows flow cytometry analysis on the binding ability of a hybridoma antibody to L cells.

Fig. 14 shows flow cytometry analysis on the competitive binding of soluble BCMA to

mAb001.

Fig. 15 shows ELISA analysis on the binding activity of a chimeric antibody to hBCMA-ECD-Fc.

Fig. 16 shows flow cytometry analysis on the binding activity of a chimeric antibody to L-BCMA+ and L cells.

Fig. 17 shows the detection of the transfection efficiency of engineered T cells targeting a human BCMA chimeric antigen receptor. The recombinant human BCMA protein Fc fragment staining method identifies the expression level of a CAR gene-encoded protein on the cell membrane surface in the CART-BCMAs cells cultured for seven days.

Fig. 18 shows the expression level of CD137 on the T cell membrane surface detected by flow cytometry.

Fig. 19 shows the secretion level of IFN γ in the culture supernatant detected by the ELISA method.

Fig. 20 shows the RTCA real-time label-free cell analysis to detect the killing effect of CART-BCMAs on target cells. The human BCMA-positive A549-BCMA-1D6 tumor cell line, the monkey BCMA-positive A549-BCMA-M tumor cell line, and the BCMA-negative A549 tumor cell line are co-cultured in 200 μ l of CBMG-RC-09a medium, according to different effector target ratios for 8 h, and then the killing rate was calculated.

DETAILED DESCRIPTION

The present disclosure relates to anti-BCMA antibodies, antibody fragments (e.g., antigen-binding portions of the antibody) and chimeric antigen receptors that may be used in various therapeutic, prophylactic, diagnostic and other methods.

5 The antibodies, or antigen-binding portions thereof, include, but are not limited to, humanized antibodies, human antibodies, monoclonal antibodies, chimeric antibodies, polyclonal antibodies, recombinantly expressed antibodies, as well as antigen-binding portions of the foregoing. An antigen-binding portion of an antibody may include a portion of an antibody that specifically binds to BCMA.

10 The present disclosure provides methods of treating a disease such as cancer in a subject by administering to the subject the present antibody or antigen-binding portion thereof, or immune cells comprising the present chimeric antigen receptors, in an effective amount.

Also encompassed by the present disclosure is a method of blocking the function of
15 BCMA in a mammal comprising administering to the mammal a composition comprising the present antibodies, or antigen-binding portions thereof, or immune cells comprising the present chimeric antigen receptors.

Another method of the disclosure relates to inhibiting the growth and/or differentiation of cells expressing BCMA, comprising contacting the cells with the present
20 antibody or antigen-binding fragment, or immune cells comprising the present chimeric antigen receptors.

After extensive and in-depth research and mass screening, a number of anti-BCMA monoclonal antibodies were obtained. The present disclosure further provides the construction of chimeric antigen receptors targeting BCMA and a preparation method and
25 activity identification of T cells expressing the chimeric antigen receptors targeting BCMA. Specifically, the inventors successfully screened nine strains of hybridoma cells (6G10-1D7, 99B3G3, 105C10F1, 113B3F12, 109C5F3C1, 143D6F4, 151A9A4, 107B11E1D7 and 107A9A4D2), and the antibodies they secreted recognize soluble extracellular domains of human BCMA (e.g., on the cell membrane surface). The antibodies secreted by 6G10-1D7,
30 99B3G3, 109C5F3C1, 143D6F4, 151A9A4, 107B11E1D7 and 107A9A4D2 can also cross-recognize the soluble extracellular domains of machin BCMA molecules. Anti-BCMA chimeric antigen receptors (CARs) have also been constructed. These CARs have different reactivity to BCMA-positive target cells and have desirable specific cytotoxicity towards target cells.

The fusion protein (hBCMA-ECD-Fc) of human BCMA extracellular domain (Met1-Ala54) and human IgG1 Fc fragment (Pro100-Lys330) was used to immunize mice. The hybridoma technology was used to screen for monoclonal antibodies against human BCMA. The antibody must be able to cross-recognize human BCMA (cynoBCMA-ECD-Fc) and not recognize tumor necrosis factor receptor superfamily member 13B (TACI, which shares a common ligand with BCMA).

The present disclosure provides for an anti-BCMA antibody, or an antigen-binding portion thereof, comprising a light chain variable region (V_L) and a heavy chain variable region (V_H).

The present disclosure provides for 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).

In certain embodiments, the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) includes a light chain variable region comprising an amino acid sequence about 80% 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 NOs: 53, 55, 57, 59, 61, 63, 65, 67 and 69.

In certain embodiments, the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) includes a heavy chain variable region comprising an amino acid sequence about 80% 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 NOs: 54, 56, 58, 60, 62, 64, 66, 68 and 70.

In certain embodiments, the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) includes a light chain variable region (V_L) and a heavy chain variable region (V_H), where the V_L and V_H comprise/have amino acid sequences about 80% 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 amino acid sequences set forth in (i) SEQ ID NO: 53 and SEQ ID NO: 54, respectively, (ii) SEQ ID NO: 55 and SEQ ID NO: 56, respectively, (iii) SEQ ID NO: 57 and SEQ ID NO: 58, respectively, (vi) SEQ ID NO: 59 and SEQ ID NO: 60, respectively, (v) SEQ ID NO: 61 and SEQ ID NO: 62, respectively, (vi) SEQ ID NO: 63 and SEQ ID NO: 64, respectively, (vii) SEQ ID NO: 65 and SEQ ID NO: 66, respectively, (viii) SEQ ID NO: 67 and SEQ ID NO: 68, respectively, or (ix) SEQ ID NO: 69 and SEQ ID NO: 70, respectively.

A light chain variable region of the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) can comprise one, two, or three complementarity determining regions (CDRs) that are about 80% 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 sequences set forth in (i) SEQ ID NOs: 76, 77 and 78, respectively, (ii) SEQ ID NOs: 82, 83 and 84, respectively, (iii) SEQ ID NOs: 88, 89 and 90, respectively, (iv) SEQ ID NOs: 94, 95 and 96, respectively, (v) SEQ ID NOs: 100, 101 and 102, respectively, (vi) SEQ ID NOs: 106, 107 and 108, respectively, (vii) SEQ ID NOs: 112, 113 and 114, respectively, (viii) SEQ ID NOs: 118, 119 and 120, respectively, or (ix) SEQ ID NOs: 124, 125 and 126, respectively.

A heavy chain variable region of the anti-BCMA antigen-binding region (or the

anti-BCMA antibody, or an antigen-binding portion thereof) can comprise one, two, or three complementarity determining regions (CDRs) that are about 80% 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%,
5 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
10 sequences set forth in (i) SEQ ID NOs: 79, 80 and 81, respectively, (ii) SEQ ID NOs: 85, 86 and 87, respectively, (iii) SEQ ID NOs: 91, 92 and 93, respectively, (iv) SEQ ID NOs: 97, 98 and 99, respectively, (v) SEQ ID NOs: 103, 104 and 105, respectively, (vi) SEQ ID NOs: 109, 110 and 111, respectively, (vii) SEQ ID NOs: 115, 116 and 117, respectively, (viii) SEQ ID NOs: 121, 122 and 123, respectively, or (ix) SEQ ID NOs:
15 127, 128 and 129, respectively.

In certain embodiments, a light chain variable region of the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) comprises three CDRs (CDR1, CDR2 and CDR3) that are identical to the amino acid sequences set forth in (i) SEQ ID NOs: 76, 77 and 78, respectively, (ii) SEQ ID
20 NOs: 82, 83 and 84, respectively, (iii) SEQ ID NOs: 88, 89 and 90, respectively, (iv) SEQ ID NOs: 94, 95 and 96, respectively, (v) SEQ ID NOs: 100, 101 and 102, respectively, (vi) SEQ ID NOs: 106, 107 and 108, respectively, (vii) SEQ ID NOs: 112, 113 and 114, respectively, (viii) SEQ ID NOs: 118, 119 and 120, respectively, or (ix) SEQ ID NOs: 124, 125 and 126, respectively; and a heavy chain variable region of the
25 anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) includes three CDRs (CDR1, CDR2 and CDR3) that are identical to the amino acid sequences set forth in (i) SEQ ID NOs: 79, 80 and 81, respectively, (ii) SEQ ID NOs: 85, 86 and 87, respectively, (iii) SEQ ID NOs: 91, 92 and 93, respectively, (iv) SEQ ID NOs: 97, 98 and 99, respectively, (v) SEQ ID NOs: 103, 104 and 105,
30 respectively, (vi) SEQ ID NOs: 109, 110 and 111, respectively, (vii) SEQ ID NOs: 115, 116 and 117, respectively, (viii) SEQ ID NOs: 121, 122 and 123, respectively, or (ix) SEQ ID NOs: 127, 128 and 129, respectively.

In certain embodiments, the anti-BCMA antigen-binding region (or the anti-BCMA antibody, or an antigen-binding portion thereof) comprises a light chain variable region (V_L) and a heavy chain variable region (V_H), where,

(i) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 76, 77 and 78, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 79, 80 and 81, respectively;

(ii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 82, 83 and 84, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 85, 86 and 87, respectively;

(iii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 88, 89 and 90, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 91, 92 and 93, respectively;

(iv) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 94, 95 and 96, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100%, at least or about 70%, at least or about 75%, at least or about 80%, at least or
5 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
10 about 97%, at least or about 98%, at least or about 99%, or about 100%, identical to the amino acid sequences set forth in SEQ ID NOs: 97, 98 and 99, respectively;

(v) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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
15 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%,
20 or about 100%, identical to the amino acid sequences set forth in SEQ ID NOs: 100, 101 and 102, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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
25 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
30 amino acid sequences set forth in SEQ ID NOs: 103, 104 and 105, respectively;

(vi) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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%,
5 or about 100%, identical to the amino acid sequences set forth in SEQ ID NOs: 106, 107 and 108, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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
10 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
15 amino acid sequences set forth in SEQ ID NOs: 109, 110 and 111, respectively;

(vii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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%,
20 or about 100%, identical to the amino acid sequences set forth in SEQ ID NOs: 112, 113 and 114, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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
25 amino acid sequences set forth in SEQ ID NOs: 115, 116 and 117, respectively;

(viii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 118, 119 and 120, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 121, 122 and 123, respectively; or

(ix) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 124, 125 and 126, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% 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 sequences set forth in SEQ ID NOs: 127, 128 and 129, respectively.

5 In certain embodiments, the CDR, V_H and/or V_L have sequence variations. For example, the CDR, V_H or V_L, in which 1, 2, 3, 4, 5, 6, 7 or 8 residues, or less than 20%, less than 30%, or less than about 40%, of total residues in the CDR, V_H or V_L, are substituted or deleted can be present in an antibody (or antigen-binding portion thereof) or CAR that binds BCMA.

10 Also within the scope of the disclosure are antibodies or antigen-binding portions thereof, or CAR, in which specific amino acids have been substituted, deleted or added. These alternations do not have a substantial effect on the peptide's biological properties such as binding activity. For example, antibodies or antigen-binding portions thereof, or CAR, may have amino acid substitutions in the framework region, such as to improve
15 binding to the antigen. In another example, a selected, small number of acceptor framework residues can be replaced by the corresponding donor amino acids. The donor framework can be a mature or germline human antibody framework sequence or a consensus sequence. Guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., Science, 247: 1306-1310 (1990).
20 Cunningham et al., Science, 244: 1081-1085 (1989). Ausubel (ed.), Current Protocols in Molecular Biology, John Wiley and Sons, Inc. (1994). T. Maniatis, E. F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor laboratory, Cold Spring Harbor, N.Y. (1989). Pearson, Methods Mol. Biol. 243:307-31 (1994).
Gonnet et al., Science 256:1443-45 (1992).

25 The present peptides may be the functionally active variant of antibodies or antigen-binding portions thereof, or CAR, disclosed herein, e.g., with less than about 30%, about 25%, about 20%, about 15%, about 10%, about 5% or about 1% amino acid residues substituted or deleted but retain essentially the same immunological properties including, but not limited to, binding to BCMA.

30 The antibodies or antigen-binding portions thereof, or CAR, may also include variants, analogs, orthologs, homologs and derivatives of peptides, that exhibit a biological activity, e.g., binding of BCMA. The peptides may contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified

amino acids from mammalian systems etc.), peptides with substituted linkages, as well as other modifications known in the art.

The antibody, or antigen-binding portion thereof, can be derivatized or linked to another functional molecule. For example, an antibody, or antigen-binding portion thereof, can be functionally linked (by chemical coupling, genetic fusion, noncovalent interaction, etc.) to one or more other molecular entities, such as another antibody, a detectable agent, an immunosuppressant, a cytotoxic agent, a pharmaceutical agent, a protein or peptide that can mediate association with another molecule (such as a streptavidin core region or a polyhistidine tag), amino acid linkers, signal sequences, immunogenic carriers, or ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and staphylococcal protein A. Cytotoxic agents may include radioactive isotopes, chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant, or animal origin, and fragments thereof. Such cytotoxic agents can be coupled to the antibodies, or antigen-binding portion thereof, of the present disclosure using standard procedures, and used, for example, to treat a patient indicated for therapy with the antibody.

One type of derivatized protein is produced by crosslinking two or more proteins (of the same type or of different types). Suitable crosslinkers include those that are heterobifunctional, having two distinct reactive groups separated by an appropriate spacer (e.g., m-maleimidobenzoyl-N-hydroxysuccinimide ester) or homobifunctional (e.g., disuccinimidyl suberate). Useful detectable agents with which a protein can be derivatized (or labeled) include fluorescent agents, various enzymes, prosthetic groups, luminescent materials, bioluminescent materials, and radioactive materials.

Non-limiting, exemplary fluorescent detectable agents include fluorescein, fluorescein isothiocyanate, rhodamine, and phycoerythrin. A protein or antibody can also be derivatized with detectable enzymes, such as alkaline phosphatase, horseradish peroxidase, beta-galactosidase, acetylcholinesterase, glucose oxidase and the like. A protein can also be derivatized with a prosthetic group (e.g., streptavidin/biotin and avidin/biotin).

The antibodies can be full-length or can include a fragment (or fragments) of the antibody having an antigen-binding portion, including, but not limited to, Fab, F(ab')₂, Fab', F(ab)', Fv, single chain Fv (scFv), bivalent scFv (bi-scFv), trivalent scFv (tri-scFv), Fd, dAb fragment (e.g., Ward et al., Nature, 341:544-546 (1989)), an isolated CDR, diabodies, triabodies, tetrabodies, linear antibodies, single-chain antibody

molecules, and multispecific antibodies formed from antibody fragments. Single chain antibodies produced by joining antibody fragments using recombinant methods, or a synthetic linker, are also encompassed by the present disclosure. Bird et al. Science, 1988, 242:423-426. Huston et al., Proc. Natl. Acad. Sci. USA, 1988, 85:5879-5883.

5 The present antibody or antigen-binding portion thereof may comprise at least one constant domain, such as, (a) an IgG constant domain; (b) an IgA constant domain, etc.

10 All antibody isotypes are encompassed by the present disclosure, including IgG (e.g., IgG1, IgG2, IgG3, IgG4), IgM, IgA (IgA1, IgA2), IgD or IgE. The antibodies or antigen-binding portions thereof may be mammalian (e.g., mouse, human) antibodies or antigen-binding portions thereof. The light chains of the antibody may be of kappa or lambda type.

15 The antibodies or antigen-binding portions thereof of the present disclosure may be monospecific, bi-specific or multi-specific. Multi-specific or bi-specific antibodies or fragments thereof may be specific for different epitopes of one target polypeptide (e.g., BCMA) or may contain antigen-binding domains specific for more than one target polypeptide (e.g., antigen-binding domains specific for BCMA and another antigen). In one embodiment, a multispecific antibody or antigen-binding portion thereof comprises at least two different variable domains, wherein each variable domain is capable of

20 specifically binding to a separate antigen or to a different epitope on the same antigen. Tutt et al., 1991, J. Immunol. 147:60-69. Kufer et al., 2004, Trends Biotechnol.

22:238-244. The present antibodies can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion,

25 noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second binding specificity. For example, the present disclosure includes bi-specific antibodies wherein one arm of an immunoglobulin is specific for BCMA, and the other arm of the immunoglobulin is specific for a second therapeutic target or is

30 conjugated to a therapeutic moiety as described herein.

 The antibodies or antigen-binding portions thereof described herein are useful as affinity purification agents. In this process, the antibodies or fragments thereof are immobilized on a solid phase such as Protein A resin, using methods well known in the art.

The present anti-BCMA antibodies or antigen-binding portions thereof are also useful in diagnostic assays to detect and/or quantify BCMA protein, for example, detecting BCMA expression in specific cells, tissues, or serum.

The antibodies or antigen-binding portions thereof described herein may be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. See, e.g., Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp. 147-158 (CRC Press, Inc. 1987).

Antibody

The term “antibody” or “immunoglobulin” may mean a heterotetrameric glycoprotein of about 150,000 daltons with the same structural characteristics, which comprises two identical light chains (L) and two identical heavy chains (H). Each light chain is linked to a heavy chain by means of a covalent disulfide bond, and the number of disulfide bonds between the heavy chains of different immunoglobulin isotypes is different. Each heavy chain and light chain also have regularly spaced intrachain disulfide bonds. Each heavy chain has a variable region (VH) at one end, followed by a plurality of constant regions. Each light chain has a variable region (VL) at one end and a constant region at the other end; the constant region of the light chain is opposite to the first constant region of the heavy chain, and the variable region of the light chain is opposite to the variable region of the heavy chain. Special amino acid residues form interfaces between the variable regions of the light and heavy chains.

The term “variable” may mean that certain parts of the variable regions of the antibody are different in sequence, which forms the binding and specificity of various specific antibodies to specific antigens thereof. Nevertheless, the variability is not uniformly distributed in the variable regions of the entire antibody and is concentrated in three fragments of the complementarity determining regions (CDR) or hypervariable regions in the light chain and heavy chain variable regions. The more conserved parts of the variable regions are called framework regions (FRs). The variable regions of the natural heavy chains and light chains each contain four FRs, which are roughly in a β -folded configuration and are linked by three CDRs, which form an adapter ring. In some cases, a partial β -folded structure can be formed. The CDRs in each chain are closely joined together by means of the FRs and form antigen binding sites of the antibody together with the CDRs of another chain (see Kabat et al., NIH Publ.No. 91-3242, Volume I, pages 647-669 (1991)). Constant regions do not directly participate in the binding of antibodies to antigens, but they exhibit different

effector functions, such as participating in antibody-dependent cytotoxicity of the antibody.

The “light chains” of vertebrate antibodies (immunoglobulins) can be classified into one of two distinct categories (called κ and λ) based on the amino acid sequences in their constant regions. According to the amino acid sequences of heavy chain constant regions of immunoglobulins, the immunoglobulins can be classified into different types. There are mainly five types of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, some of which can be further divided into subclasses (isotypes), such as IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. The heavy chain constant regions corresponding to different types of immunoglobulins are called α , δ , ϵ , γ and μ , respectively. The subunit structures and three-dimensional configurations of different types of immunoglobulins are well known to those skilled in the art.

Generally, the antigen-binding properties of an antibody can be described by 3 specific regions located in the heavy chain and light chain variable regions, which are called variable regions (CDRs) and space this fragment into four framework regions (FRs). The amino acid sequences of the four FRs are relatively conservative and do not directly participate in the binding reaction. These CDRs form a circular structure and are close to each other in the space structure by means of the β -folds formed by the FRs among the CDRs. The CDRs on the heavy chains and the corresponding CDRs on the light chain constitute antigen binding sites of the antibody. The amino acid sequences of the same type of antibody can be compared to determine which amino acids constitute the FRs or CDRs.

The present disclosure not only includes a complete antibody, but also includes immunologically active antibody fragments or fusion proteins formed by the antibody and other sequences. Therefore, the present disclosure also includes fragments, derivatives and analogs of the antibody.

In the present disclosure, antibodies include murine, chimeric, humanized or fully human antibodies prepared by technologies well known to those skilled in the art. Recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprise a human portion and a non-human portion, can be obtained through standard DNA recombination techniques, and are all useful antibodies. A chimeric antibody is a molecule in which different parts are derived from different animal species, such as a chimeric antibody with variable regions of a mouse-derived monoclonal antibody, and constant regions of a human-derived immunoglobulin (see U.S. patent 4,816,567 and U.S. patent 4,816,397 for example, incorporated herein by reference in their entirety). A humanized antibody may refer

to an antibody molecule derived from non-human species and comprising one or more complementarity determining regions (CDRs) derived from non-human species and framework regions derived from human immunoglobulin molecules (see U.S. patent 5,585,089, incorporated herein by reference in its entirety). These chimeric and humanized monoclonal antibodies can be prepared using DNA recombination techniques well known in the art.

In the present disclosure, antibodies can be monospecific, bispecific, trispecific, or multispecific.

In the present disclosure, the antibody also includes its conservative variants, which means that compared with the amino acid sequences of the antibody provided by the present disclosure, at most 10, at most 8, at most 5, or at most 3 amino acids are substituted by amino acids with similar properties to form polypeptides. For example, the conservative variant polypeptides may be produced by amino acid substitutions according to Table A.

Table A

Initial residue	Representative substitution	Exemplary substitution
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Lys; Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro; Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe	Leu
Leu (L)	Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Leu; Val; Ile; Ala; Tyr	Leu
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala	Leu

Anti-BCMA antibody

The present disclosure provides an antibody against BCMA and with high specificity

and high affinity, which comprises heavy chains and light chains, the heavy chains contain amino acid sequences of V_H regions, and the light chains contain amino acid sequences of V_L regions.

- In certain embodiments, the antibody comprises V_H regions and V_L regions encoded by nucleotide sequences shown below:

Hybridoma No.	Nucleotide sequences encoding V _H regions	Nucleotide sequences encoding V _L regions
6G10-1D7 (CP01)	SEQ ID NO: 1	SEQ ID NO: 2
99B3G3(CP02)	SEQ ID NO: 3	SEQ ID NO: 4
102A12H6	SEQ ID NO: 5	SEQ ID NO: 6
105C10F1(CP03)	SEQ ID NO: 7	SEQ ID NO: 8
107A11F1	SEQ ID NO: 9	SEQ ID NO: 13
	SEQ ID NO: 10	
	SEQ ID NO: 11	
	SEQ ID NO: 12	
107B11E1	SEQ ID NO: 14	SEQ ID NO: 18
	SEQ ID NO: 15	
	SEQ ID NO: 16	
	SEQ ID NO: 17	
107A9A4	SEQ ID NO: 19	SEQ ID NO: 23
	SEQ ID NO: 20	
	SEQ ID NO: 21	
	SEQ ID NO: 22	
113B3F12	SEQ ID NO: 24	SEQ ID NO: 25
100H2D12C6	SEQ ID NO: 3	SEQ ID NO: 4
109C5F3C1(CP06)	SEQ ID NO: 26	SEQ ID NO: 27
143D6F4(CP07)	SEQ ID NO: 28	SEQ ID NO: 29
151A9A4(CP08)	SEQ ID NO: 30	SEQ ID NO: 31
152D8E8(CP09)	SEQ ID NO: 32	SEQ ID NO: 33
107A11F1B7(CP04)	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107A9A4D2	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107B11E1D7(CP05)	SEQ ID NO: 37	SEQ ID NO: 38
97B8G8D12	SEQ ID NO: 3	SEQ ID NO: 4

In certain embodiments, the antibody is a murine antibody.

In certain embodiments, the antibody comprises heavy chains and light chains with amino acid sequences shown below:

Hybridoma No.	Amino acid sequences of heavy chains	Amino acid sequences of light chains
6G10-1D7 (CP01)	SEQ ID NO: 39	SEQ ID NO.:40
99B3G3(CP02)	SEQ ID NO: 41	SEQ ID NO: 42
105C10F1(CP03)	SEQ ID NO: 43	SEQ ID NO: 44
113B3F12	SEQ ID NO: 45	SEQ ID NO: 46
107B11E1D7(CP05)	SEQ ID NO: 47	SEQ ID NO: 48
107A9A4D2	SEQ ID NO: 49	SEQ ID NO: 50
		SEQ ID NO: 51

In certain embodiments, the antibody is a chimeric antibody.

In certain embodiments, the antibody comprises V_H regions and V_L regions with amino acid sequences shown below:

Antibody	Amino acid sequences of V _H regions	Amino acid sequences of V _L regions
CP01	SEQ ID NO: 54	SEQ ID NO:53
CP02	SEQ ID NO: 56	SEQ ID NO: 55
CP03	SEQ ID NO: 58	SEQ ID NO: 57
CP04	SEQ ID NO: 60	SEQ ID NO: 59
CP05	SEQ ID NO: 62	SEQ ID NO: 61
CP06	SEQ ID NO: 64	SEQ ID NO: 63
CP07	SEQ ID NO: 66	SEQ ID NO: 65
CP08	SEQ ID NO: 68	SEQ ID NO: 67
CP09	SEQ ID NO: 70	SEQ ID NO: 69

5

The CDR sequences of antibodies CP01-CP09 are shown below.

Name	CDR	SEQ ID No:	Sequence
CP01 VL		53	DIVMTQSQRFMSTSVGDRVSITCKASQSVGTAVAWY QQTPGQFPKLLIYSTSNRYTGVPDRFTGSGSGTDFTLT ISNMQSEDLADYFCQQYSTYPLTFGSGTKLELK
	CDR-L1	76	KASQSVGTAVA
	CDR-L2	77	STSNRYT
	CDR-L3	78	QQYSTYPLT
CP01 VH		54	EVQLQQSGPELVKPGASMKISCKASDYSFTDYIMTW VKQSHGKNLEWIGLINPYNGGTTYNQKFKDKATFTV DKSSTTAYMDLLSLTSEDSAVYYCARRGITTDYYTM DYWGQGTSVTVSS
	CDR-H1	79	DYIMT
	CDR-H2	80	LINPYNGGTTYNQKFKD
	CDR-H3	81	RGITTDYYTMDY
CP02		55	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSIQKN

VL			YLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSG TDFTLTISVVQAEDLADYFCQQHYSSPLTFGAGTKLEL K
	CDR-L1	82	KSSQSLLNSSIQKNYLA
	CDR-L2	83	FASTRES
	CDR-L3	84	QQHYSSPLT
CP02 VH		56	EVQLQQSGPVLVKPGASVKMSCASGYTFTDLYMN WVKQSHGKSLEWIGVINPYNGGTSYNQKFKAKATLT VDKSSITAYMELNSLTSEDSAVYYCARGDSIYVMDY WGQGTSVTVSS
	CDR-H1	85	DLYMN
	CDR-H2	86	VINPYNGGTSYNQKFKA
	CDR-H3	87	GDSIYVMDY
CP03 VL		57	DIVMTSPSQKFMSTSVGDRVSVTCKASQNVGTNVAWY QQKPGQSPKALIYSASYRYSQVDPDRFTGSGSGTDFTL TISNVQSEDLAEYFCQHYNSYPFTFGSGTKLEIK
	CDR-L1	88	KASQNVGTNVA
	CDR-L2	89	SASYRYS
	CDR-L3	90	QHYNSYPFT
CP03 VH		58	EVKLLQSGGGLVQPGGSLKLSAASGIDFSRYWMSW VRRAPGKGLEWIGEINPDSSTINYAPSLKDKFIISRDA AKNTLYLQMSKVRSEDTALYYCATLYDYDGDYAM DYWGQGTSTVTVSS
	CDR-H1	91	RYWMS
	CDR-H2	92	EINPDSSTINYAPSLKD
	CDR-H3	93	LYDYDGDYAMDY
CP04 VL		59	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSIQKN YLAWYQQKPGQSPKLLIYFASTRESGVPDRFIGSGSG TDFTLTISVVQAEDLADYFCQQHYSTPLTFGAGTKLEL K
	CDR-L1	94	KSSQSLLNSSIQKNYLA
	CDR-L2	95	FASTRES
	CDR-L3	96	QQHYSTPLT
CP04 VH		60	EVQLQQSGPVLVKPGASVKMSCASGYTFTDLYMN WLKQSHGKRLEWIGVINPYNGGTSYNQKFKGKATLT VDKSSSTAYMDLNSLTSEDSAVYYCARGDSIYVMDY WGQGTSTFTVSS
	CDR-H1	97	DLYMN
	CDR-H2	98	VINPYNGGTSYNQKFKG
	CDR-H3	99	GDSIYVMDY
CP05 VL		61	ENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQ QKSSTSPKLWIYDTSKLSSGVPGRFSGSGSGKSYSLTI SSMEAEDVATYYCFQGSGYPLFTFGSGTKLEIK

	CDR-L1	100	SASSSVSYM
	CDR-L2	101	DTSKLSS
	CDR-L3	102	FQSGGYPLFT
CP05 VH		62	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMN WLKQSHGKRLEWIGVINPYNGGTSYNQKFKGKATLT VDKSSSTAYMDLNSLTSEDSAVYYCARGDSIYVMDY WGQGTSTVSS
	CDR-H1	103	DLYMN
	CDR-H2	104	VINPYNGGTSYNQKFKG
	CDR-H3	105	GDSIYVMDY
CP06 VL		63	DIVMTQSPSSLALSVGQKVTMSCKSSQSLLDNSNQKH YLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSG TDFTLTISVQAEDLADYFCQQHYTAPLTFGAGTKLA LK
	CDR-L1	106	KSSQSLLDNSNQKHYLA
	CDR-L2	107	FASTRES
	CDR-L3	108	QQHYTAPLT
CP06 VH		64	EVQLQQSGPVLVKPGASVKMSCKVSGYTFTDYMN WVKQSHGKSLEWIGVITPYNGANRYNQKFKGKATLT VDKSSSTAYMEVSSLTSEDSAVYYCARGDSIYVMDY WGQGTSVIVSS
	CDR-H1	109	DYMN
	CDR-H2	110	VITPYNGANRYNQKFKG
	CDR-H3	111	GDSIYVMDY
CP07 VL		65	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSIQKN YLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSG TDFTLTISVQAEDLADYFCQQHYSTPLTFGGGKLEL K
	CDR-L1	112	KSSQSLLNSSIQKNYLA
	CDR-L2	113	FASTRES
	CDR-L3	114	QQHYSTPLT
CP07 VH		66	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYSLNW VKQSHGKSLEWIGVVNPYNGGTSHNQKFKGKATLTV DKSSSTAYMELNSLTSEDSAVYYCARPDSIYVMDYW GQGTSTVTVSS
	CDR-H1	115	DYSLN
	CDR-H2	116	VVNPYNGGTSHNQKFKG
	CDR-H3	117	PDSIYVMDY
CP08 VL		67	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSNIQKN YLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSG TDFTLTISVQAEDLADYFCQQHYSTPLTFGAGTKLEL K
	CDR-L1	118	KSSQSLLNSNIQKNYLA

	CDR-L2	119	FASTRES
	CDR-L3	120	QQHYSTPLT
CP08 VH		68	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYSLNW VKQSHGKSLEWIGVVPNYPYNGGTTYNQKFKGKATLTV DKSSSTAYMELNSLTSEDSAVYYCARPDSIYVMDSW GQGTSVTVSS
	CDR-H1	121	DYSLN
	CDR-H2	122	VVNPYNGGTTYNQKFKG
	CDR-H3	123	PDSIYVMDS
CP09 VL		69	DIKMTQSPSSMYVSLGERVTITCKASQDINRNLSWFQ QKPGKSPKTLIYRANRLVDGVPLRFSGSGSGQDYSLTI SSLEYEDMGIYYCLQYDEFPRTFGGGGTKLEIK
	CDR-L1	124	KASQDINRNLS
	CDR-L2	125	RANRLVD
	CDR-L3	126	LQYDEFPRT
CP09 VH		70	QVTLKESGPGILQSSQTLSTCSFSGFSLNTSGMGVN WIRQSSGKDLEWLAHIYWNDDKRYNPSLKSRLTISKD TSRNQVFLRITSVDATDTATYFCCRSRLSFDYWGHGT TLTVSS
	CDR-H1	127	TSGMGVN
	CDR-H2	128	HIYWNDDKRYNPSLKS
	CDR-H3	129	SRLSFDY

In certain embodiments, the antibody is a single-chain antibody.

In certain embodiments, any of the foregoing amino acid sequences also includes a derivative sequence that optionally adds, deletes, modifies and/or substitutes at least one amino acid and can retain the binding affinity of BCMA.

In certain embodiments, the sequence formed by addition, deletion, modification and/or substitution of at least one amino acid sequence may have a homology of at least 80%, at least 85%, at least 90%, or at least 95% of amino acid sequences. The number of the added, deleted, modified and/or substituted amino acid residues can be 1 to 7, 1 to 5, 1 to 3, or 1 to 2.

The antibody provided by the present disclosure can be a double-chain or single-chain antibody, and can be selected from animal-derived antibodies, chimeric antibodies and humanized antibodies, a human-animal chimeric antibody, or a fully humanized antibody.

The antibody derivatives provided by the present disclosure can be single-chain antibodies and/or antibody fragments, such as: Fab, Fab', (Fab')₂ or other antibody derivatives known in the art and any one or more of IgA, IgD, IgE, IgG and IgM antibodies or antibodies of other subtypes.

Among them, the animal may be a mammal, such as a mouse.

The antibody provided by the present disclosure can be a chimeric antibody, humanized antibody, or CDR-grafted and/or -modified antibody that targets human BCMA.

Specifically, in the embodiments of the present application, four rounds of hybridoma cell fusion were carried out. A total of 14 hybridoma cells (6G10-1D7, 99B3G3, 102A12H6, 107A11F1, 107A9A4, 107B11E1, 100H2D12C6, 105C10F1, 113B3F12, 109C5F3C1, 97B8G8D12, 143D6F4, 151A9A4 and 152D8E8) were selected for antibody production and purification in small batches. Among them, 13 of the 14 clones (except 97B8G8D12) all successfully generated corresponding antibodies. Except 152D8E8 (CP09), the remaining 12 hybridoma antibodies all could bind to the soluble extracellular domains of human BCMA molecules. Except 105C10F1(CP03), 152D8E8(CP09) and 113B3F12, the remaining 10 hybridoma antibodies all could cross-recognize the soluble extracellular domains of human BCMA molecules. Except 102A12H6 and 152D8E8 (CP09), the remaining 11 hybridoma antibodies all could recognize the extracellular domains of human BCMA molecules on the cell surface.

17 strains of hybridoma cells in total were sequenced for antibody variable regions. 12 strains of the hybridoma cells were monoclonal according to the sequencing: 6G10-1D7, 99B3G3, 102A12H6, 100H2D12C6, 105C10F1, 113B3F12, 109C5F3C1, 97B8G8D12, 143D6F4, 151A9A4, 152D8E8 and 107B11E1D7, of which 99B3G3, 100H2D12C6 and 97B8G8D12 had the same sequence in the antibody variable regions. Five strains of the hybridoma cells were polyclonal according to the sequencing: 107A11F1, 107A9A4, 107B11E1, 107A9A4D2 and 107A11F1B7, of which 107A11F1, 107A9A4 and 107B11E1 each had four heavy chains and a light chain; and 107A9A4D2 and 107A11F1B7 each had a heavy chain and two light chains, and had the same sequence. Five strains of monoclonal hybridoma cells (6G10-1D7, 99B3G3, 105C10F1, 113B3F12 and 107B11E1D7) and a strain of polyclonal hybridoma cell (107A9A4D2) were selected for chimeric antibody expression. Among them, 107A9A4D2VH was paired and expressed with 107A9A4D2VL-1 and 107A9A4D2VL-2, respectively. The detection results of ELISA and flow cytometry showed that the chimeric antibodies of the hybridomas 6G10-1D7, 99B3G3, 105C10F1 and 107B11E1D7 all bound to the soluble extracellular domains of human BCMA molecules on the cell surface. The chimeric antibodies formed by pairing of the heavy chain 107A9A4D2VH and the light chain 107A9A4D2VL-2 of the hybridoma 107A9A4D2 all bound to the soluble extracellular domains of the human BCMA molecules on the cell surface. The chimeric antibodies formed by pairing of 107A9A4D2VH and 107A9A4D2VL-1 did not

bind to the soluble extracellular domains of the human BCMA molecules on the cell surface.

Antibody preparation

The sequence of the DNA molecule of the antibody or its fragments provided by the present disclosure can be obtained by conventional techniques, such as PCR amplification or
5 genomic library screening. In addition, the coding sequences of the light chains and the heavy chains may also be fused together to form a single-chain antibody.

Once relevant sequences are obtained, the relevant sequences can be obtained in large batches by recombination. Generally, the relevant sequences are obtained by cloning the relevant sequences into vectors, then transferring the relevant sequences into cells, and then
10 isolating the relevant sequences from the proliferated host cells by conventional methods.

In addition, artificial synthesis methods can be used to synthesize the relevant sequences, especially when the fragment length is short. Generally, a fragment with a long sequence can be obtained by synthesizing a plurality of small fragments first and then linking the small fragments.

At present, a DNA sequence encoding the antibody (or fragment or derivative thereof) provided by the present disclosure can be obtained completely through chemical synthesis. The DNA sequence can then be introduced into various existing DNA molecules (or such as vectors) and cells known in the art. In addition, mutations can be introduced into the protein sequences of the present disclosure by chemical synthesis.
15

The present disclosure also relates to vectors containing the foregoing appropriate DNA sequences and appropriate promoters or control sequences. These vectors can be used to transform appropriate host cells so that they can express proteins.
20

The host cells can be prokaryotic cells, such as bacterial cells; or lower eukaryotic cells, such as yeast cells; or higher eukaryotic cells, such as mammalian cells. The animal cells may include (but are not limited to): CHO-S and HEK-293 cells.
25

Normally, the obtained host cells are cultured and transformed under the conditions suitable for expression of the antibody provided by the present disclosure. Then conventional immunoglobulin purification steps, such as protein A-Sepharose, hydroxyapatite chromatography, gel electrophoresis, dialysis, ionization exchange chromatography, hydrophobic chromatography, molecular sieve chromatography or affinity chromatography
30 and other conventional isolation and purification methods well known to those skilled in the art, are used for purification to obtain the antibody provided by the present disclosure.

The obtained monoclonal antibody can be identified by conventional means. For example, the binding specificity of the monoclonal antibody can be determined by

immunoprecipitation or in vitro binding test (such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA)). The binding affinity of the monoclonal antibody, for example, can be determined by the Scatchard analysis of Munson et al., *Anal. Biochem.*, 107:220 (1980).

5 The antibody provided by the present disclosure may be expressed in a cell, or on a cell membrane, or secreted out of a cell. If necessary, a recombinant protein can be isolated and purified through various isolation methods by employing the physical, chemical, and other properties of the recombinant protein. These methods are well known to those skilled in the art. Examples of these methods include, but are not limited to: conventional renaturation
10 treatment, treatment with a protein precipitation agent (salting-out method), centrifugation, osmotic bacteriostasis, ultrasonic treatment, ultracentrifugation, molecular sieve chromatography (gel filtration), adsorption chromatography, ion exchange chromatography, high performance liquid chromatography (HPLC) and various other liquid chromatography techniques and combinations of these methods.

15 **Antibody-drug conjugate (ADC)**

The present disclosure further provides an antibody-drug conjugate (ADC) based on the antibody provided by the present disclosure.

Typically, the ADC comprises the antibody and an effector molecule, and the antibody is conjugated, e.g., chemically conjugated, to the effector molecule. The effector molecule
20 may be a drug with therapeutic activity. Further, the effector molecule may be one or more of toxic proteins, chemotherapeutics, small-molecule drugs or radionuclides.

The antibody provided by the present disclosure and the effector molecule may be conjugated by means of a coupling agent. Examples of the coupling agent include one or more of non-selective coupling agents, coupling agents using a carboxyl group, peptide
25 chains, and coupling agents using a disulfide bond. The non-selective coupling agent refers to a compound that makes the effector molecule and the antibody form a covalent bond, such as glutaraldehyde. The coupling agents using a carboxyl group can be any one or more of cis-aconitic anhydride coupling agents (e.g., cis-aconitic anhydride) and acyl hydrazone coupling agents (the coupling site is acyl hydrazone).

30 Some residues on the antibody (e.g., Cys or Lys) may be used to link a variety of functional groups, including imaging reagents (e.g., chromophoric groups and fluorescent groups), diagnostic reagents (e.g., MRI contrast agents and radioisotopes), stabilizers (e.g., glycol polymers) and therapeutic agents. The antibody can be conjugated to a functional agent to form an antibody-functional agent conjugate. Functional agents (e.g., drugs,

detection reagents and stabilizers) may be conjugated (covalently linked) to the antibody. The functional agent may be linked to the antibody directly or indirectly by means of a linker.

An antibody can be conjugated to a drug to form an antibody drug conjugate (ADC). Typically, the ADC comprises a linker located between the drug and the antibody. The linker
5 can be a degradable or a non-degradable linker. The degradable linker is typically easily degraded in the intracellular environment, for example, the linker is degraded at the target site, so that the drug is released from the antibody. Suitable degradable linkers include, for example, enzymatically degraded linkers, which include peptidyl-containing linkers that can be degraded by intracellular proteases (e.g., lysosomal proteases or endosomal proteases), or
10 sugar linkers, for example, glucuronide-containing linkers that can be degraded by glucosidase. The peptidyl linkers may include, for example, dipeptides, such as valine-citrulline, phenylalanine-lysine or valine-alanine. Other suitable degradable linkers include, for example, pH-sensitive linkers (e.g., linkers that are hydrolyzed when the pH is less than 5.5, such as hydrazone linkers) and linkers that will be degraded under reducing
15 conditions (e.g., disulfide bond linkers). A non-degradable linker typically releases a drug under the condition that the antibody is hydrolyzed by protease.

Before linking the antibody, the linker may have an active reactive group that can react with some amino acid residues where the linking is achieved through the active reactive group. Sulfhydryl-specific active reactive groups include: for example, maleimide
20 compounds, halogenated amides (e.g., iodinated, brominated, or chlorinated); halogenated esters (e.g., iodinated, brominated, or chlorinated); halogenated methyl ketones (e.g., iodinated, brominated, or chlorinated), benzyl halides (e.g., iodinated, brominated, or chlorinated); vinyl sulfone, and pyridyl disulfide; mercury derivatives such as 3,6-di-(mercury methyl) dioxane, with the counter ion being acetate, chloride ion or nitrate;
25 and poly(methylene dimethyl sulfide ether) thiosulfonate. The linker may include, for example, maleimide linked to the antibody by thiosuccinimide.

The drug can be any drug, which is cytotoxic, inhibits cell growth or is immunosuppressive. In an implementation manner, a linker links an antibody and a drug, and the drug has a functional group that can form a bond with the linker. For example, the drug
30 may have an amino group, a carboxyl group, a sulfhydryl group, a hydroxyl group, or a keto group that can form a bond with the linker. In the case where the drug is directly linked to the linker, the drug has a reactive active group before being linked to the antibody.

Useful drug categories include, for example, anti-tubulin drugs, DNA minor groove binders, DNA replication inhibitors, alkylating reagents, antibiotics, folate antagonists,

antimetabolites, chemotherapy sensitizers, topoisomerase inhibitors and Vinca alkaloids. Examples of particularly useful cytotoxic drugs include, for example, DNA minor groove binders, DNA alkylating reagents and tubulin inhibitors. Typical cytotoxic drugs include, for example, auristatins, camptothecins, duocarmycins, etoposides, maytansines and
5 maytansinoids compounds (e.g., DM1 and DM4), taxanes, benzodiazepines or benzodiazepine containing drugs (e.g., pyrrolidine [1,4] benzodiazepine (PBDs), indolinobenzodiazepines and oxazolidinobenzodiazepines) and vinca alkaloids.

The drug-linker may be used to form ADC in a simple step. In other implementation manners, bifunctional linker compounds can be used to form ADCs in a two-step or
10 multi-step process. For example, a cysteine residue reacts with the reactive part of the linker in the first step, and in the subsequent step, the functional group on the linker reacts with the drug, thereby forming an ADC.

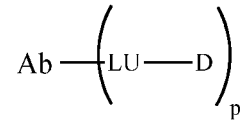
Generally, a functional group on the linker is selected to facilitate the specific reaction with an appropriate reactive group on the drug portion. As a non-limiting example, the
15 azide-based portion can be used to specifically react with the reactive alkynyl group on the drug portion. The drug is covalently bound to the linker through the 1,3-dipolar cycloaddition between the azide and the alkynyl group. Other useful functional groups include, for example, ketones and aldehydes (suitable for reacting with hydrazides and alkoxyamines), phosphines (suitable for reacting with azides); isocyanates and isothiocyanates (suitable for reacting with
20 amines and alcohols); and activated esters, such as N-hydroxysuccinimide ester (suitable for reacting with amines and alcohols). These and other linking strategies, such as those described in "Bioconjugate Techniques," Second Edition (Elsevier), are well known to those skilled in the art. Those skilled in the art can understand that, for the selective reaction between the drug portion and the linker, when reactive functional groups in a complementary
25 pair are selected, each member of the complementary pair can be used in both the linker and the drug.

The present disclosure further provides a method for preparing an ADC, which may further comprise binding an antibody to a drug-linker compound under conditions sufficient to form an antibody-drug conjugate (ADC).

30 In some implementation manners, the method provided by the present disclosure comprises binding an antibody to a bifunctional linker compound under conditions sufficient to form an antibody-linker conjugate. In these implementation manners, the method provided by the present disclosure further comprises binding the antibody linker conjugate to the drug portion under conditions sufficient to covalently link the drug portion to the antibody by

means of a linker.

In some implementation manners, the antibody-drug conjugate ADC is as shown in the following molecular formula:



5 where, Ab is an antibody, LU is a linker, D is a drug, and the subscript p is a value selected from 1 to 8.

Chimeric antigen receptor (CAR)

The chimeric antigen receptor (CAR) provided by the present disclosure may comprise an extracellular domain, a transmembrane domain and an intracellular domain. The
10 extracellular domain may comprise a target-specific binding element (also known as an antigen binding domain). The intracellular domain may comprise a costimulatory signaling region and a ζ chain portion. The costimulatory signaling region may refer to a part of the intracellular domain that comprises costimulatory molecules. The co-stimulatory molecules are cell surface molecules required for effective response of lymphocytes to antigens, rather
15 than antigen receptors or ligands thereof.

A linker may 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. The term “linker” may refer to any oligopeptide or polypeptide that functions to link the transmembrane domain to the extracellular domain or cytoplasmic domain of the
20 polypeptide chain. The linker may comprise 0 to 300 amino acids, 2 to 100 amino acids, or 3 to 50 amino acids.

In certain embodiments, the extracellular domain of the CAR includes an antigen-binding domain targeting BCMA. When the CAR is expressed in T cells, antigen recognition can be performed based on the antigen binding specificity. When the T cells bind
25 to antigens associated therewith, the T cells will affect the tumor cells, such as causing the tumor cells not to grow, or resulting in tumor cell death, which can reduce or eliminate the patient's tumor burden.

The antigen binding domain may be fused with one or more intracellular domains from the costimulatory molecule and the ζ chain. In one embodiment, the antigen binding domain
30 is fused with the intracellular domain formed by combination of the 4-1BB signaling domain and the CD3 ζ signal domain.

The terms “antigen-binding domains” and “single-chain antibody fragments” may refer

to Fab fragments, Fab' fragments, F(ab')₂ fragments, or single Fv fragments, which have antigen-binding activity. The Fv antibody comprises antibody VH regions and VL regions, but no constant regions, and has the smallest antibody fragment of all antigen binding sites. Generally, the Fv antibody further comprises a polypeptide linker between the VH and VL domains, and can form a structure required for antigen binding. The antigen binding domain is generally a scFv (single-chain variable fragment). The size of the scFv is generally 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 specifically recognizes BCMA.

For hinge regions and transmembrane regions (transmembrane domains), a CAR may be designed to include transmembrane domains fused to the extracellular domains of the CAR. In an implementation manner, a transmembrane domain that is naturally associated with one of the domains in the CAR is used. In some examples, modification can be performed by selecting transmembrane domains or replacing amino acids to avoid binding such domains to the transmembrane domains of the same or different surface membrane proteins, thereby minimizing interaction with other members of the receptor complex.

The intracellular domains in the CAR may include 4-1BB signaling domains and CD3ζ signaling domains.

Based on the light chains and heavy chains of the 9 antibodies obtained through screening in the present disclosure, 18 chimeric antigen receptors (CARs) were constructed. These CARs have different reactivities to BCMA-positive target cells and have a desirable specific killing ability to the target cells. Specifically, the foregoing nine antibodies comprise V_H regions and V_L regions with amino acid sequences shown below:

Antibody	Amino acid sequences of V _H regions	Amino acid sequences of V _L regions
CP01	SEQ ID NO: 54	SEQ ID NO.:53
CP02	SEQ ID NO: 56	SEQ ID NO: 55
CP03	SEQ ID NO: 58	SEQ ID NO: 57
CP04	SEQ ID NO: 60	SEQ ID NO: 59
CP05	SEQ ID NO: 62	SEQ ID NO: 61
CP06	SEQ ID NO: 64	SEQ ID NO: 63
CP07	SEQ ID NO: 66	SEQ ID NO: 65
CP08	SEQ ID NO: 68	SEQ ID NO: 67
CP09	SEQ ID NO: 70	SEQ ID NO: 69

In certain embodiments, the gene structure of a CAR may comprise a leader sequence (signal peptide), an antigen recognition sequence, a linker region, a transmembrane region, a costimulatory factor signal region, and a CD3zeta signaling region, and the linking sequence

is as follows:

[CD8 LS]-[VL-Linker-VH]-[hinge-CD8TM]-[4-1BB]-[CD3zeta] or
[CD8 LS]-[VH-Linker-VL]-[hinge-CD8TM]-[4-1BB]-[CD3zeta].

The present disclosure has identified the correlation between the expression time and
5 expression intensity of different CAR structures on the cell membrane surface after virus
infection, and then identified the differences in the easiness of expression of different CAR
structural proteins. This finding indicates a difference between the expression level of the
CAR protein on the membrane surface and the persistence of *in vivo* activity of CART under
the same infection conditions of different CAR structures.

10 **Vector**

The nucleic acid sequences encoding desired molecules can be obtained using
recombinant methods known in the art, such as, for example, by screening a library from cells
expressing the gene, by obtaining the gene from a vector known to include the gene, or by
using standard techniques to isolate the gene directly from the cells and tissues that contain
15 the gene. Optionally, the gene of interest can be synthesized and produced

The present disclosure also provides a vector into which an expression cassette
provided by the present disclosure is inserted. Vectors derived from retroviruses such as
lentiviruses are suitable vehicles to achieve long-term gene transfer because they allow
long-term, stable integration of transgenes and propagation of the transgenes in daughter cells.
20 Lentiviral vectors have advantages over vectors derived from oncogenic retroviruses such as
murine leukemia viruses, because they can transduce non-proliferating cells, such as
hepatocytes. They also have the advantage of low immunogenicity.

The expression cassettes or nucleic acid sequences in the present disclosure may be
operably linked to promoters and incorporated into expression vectors in general. The vectors
25 are suitable for replication and integration of eukaryotic cells. A typical cloning vector
comprises a transcription and translation terminator, an initial sequence and a promoter that
can be used to regulate the expression of expected nucleic acid sequences.

The expression constructs may also use standard gene delivery protocols for nucleic
acid immunization and a gene therapy. The method of gene delivery is known in the art. See,
30 for example, U.S. patents 5,399,346, 5,580,859 and 5,589,466. In certain embodiments, the
present disclosure provides a gene therapy vector.

The nucleic acid can be cloned into many types of vectors. For example, the nucleic
acid can be cloned into such vectors, which include, but are not limited to, plasmids,
phagemids, phage derivatives, animal viruses, and cosmids. Specific vectors of interest

include expression vectors, replication vectors, probe generation vectors, and sequencing vectors.

Further, the expression vectors can be provided to cells in the form of viral vectors. The viral vector technology is well known in the art and is described in, for example, Sambrook et al. (2001, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York) and other virology and molecular biology manuals. Viruses that can be used as vectors include, but are not limited to, retroviruses, adenoviruses, adeno-associated viruses, herpes viruses, and lentiviruses. Generally, a suitable vector comprises an origin of replication that functions in at least one organism, a promoter sequence, a convenient restriction enzyme site, and one or more selectable markers (e.g., WO01/96584; WO01/29058; and U.S. patent 6,326,193).

Many virus-based systems have been developed for transferring genes into mammalian cells. For example, retroviruses provide a convenient platform for gene delivery systems. Techniques known in the art can be used to insert selected genes into vectors and package the selected genes into retroviral particles. The recombinant virus can then be isolated and delivered to target cells in vivo or ex vivo. Many retroviral systems are known in the art. In some implementation manners, adenoviral vectors are used. Many adenoviral vectors are known in the art. In an implementation manner, lentiviral vectors are used.

Additional promoter elements, such as enhancers, can regulate the frequency of transcription initiation. Generally, they are located in the 30-110bp region upstream of the start site, although it has recently been shown that many promoters also contain functional elements downstream of the start site. The spacing between promoter elements is often flexible in order to maintain the promoter function when the elements are inverted or moved relative to one another. In a thymidine kinase (tk) promoter, the spacing between promoter elements can be increased by 50 bp before the activity begins to decrease. Depending on the promoter, it appears that individual elements can act cooperatively or independently to initiate transcription.

An example of a suitable promoter is an immediate early cytomegalovirus (CMV) promoter sequence. The promoter sequence is a strong constitutive promoter sequence capable of driving high-level expression of any polynucleotide sequence operably linked to the promoter sequence. Another example of a suitable promoter is an elongation growth factor -1 α (EF-1 α). Nevertheless, other constitutive promoter sequences can be used, too, including but not limited to simian virus 40 (SV40) early promoters, mouse mammary tumor viruses (MMTV), human immunodeficiency virus (HIV) long terminal repeat (LTR)

promoters, MoMuLV promoters, avian leukemia virus promoters, Epstein-Barr virus immediate early promoters, Rous sarcoma virus promoters, and human gene promoters, such as but not limited to actin promoters, myosin promoters, heme promoters and creatine kinase promoters. Inducible promoters are also considered as part of the present disclosure. The use
5 of an inducible promoter provides a molecular switch that can turn on the expression of a polynucleotide sequence operably linked to the inducible promoter when such expression is expected, or turn off the expression when such expression is unexpected. Examples of inducible promoters include, but are not limited to, metallothionein promoters, glucocorticoid promoters, progesterone promoters and tetracycline promoters.

10 In order to evaluate the expression of a CAR polypeptide or part thereof, an expression vector introduced into a cell may also contain either or both of a selectable marker gene or a reporter gene, so as to identify and select expression cells from the transfected or infected cell population searched by means of viral vectors. In other aspects, the selectable marker can be carried on a single fragment of DNA and used in a co-transfection procedure. The flanks of
15 both the selectable marker and reporter gene may have appropriate regulatory sequences so as to be expressed in the host cell. Useful selectable markers include, for example, antibiotics resistance genes, such as neo, etc.

Reporter genes may be used to identify potentially transfected cells and to evaluate the functionality of regulatory sequences. Generally, the reporter genes are the following genes:
20 they are not present in recipient organisms or tissues or are expressed by the recipient organisms or tissues, and encode polypeptides whose expression is clearly indicated by some easily detectable properties such as enzyme activity. After DNA has been introduced into a receptor cell, the expression of the reporter genes is determined at an appropriate time. Suitable reporter genes may include genes encoding luciferase, β -galactosidase,
25 chloramphenicol acetyltransferase, secreted alkaline phosphatase or green fluorescent protein (e.g., Ui-Tei et al., 2000, FEBS Letters, 479:79 -82). Suitable expression systems are well known and can be prepared using known techniques or obtained commercially. Generally, a construct with a minimum of 5 flanking regions that shows the highest level of reporter gene expression is identified as a promoter. Such a promoter region can be linked to a reporter
30 gene and used to evaluate the ability of a reagent to regulate the promoter-driven transcription.

Methods for introducing genes into cells and expressing genes into cells are known in the art. In the content of an expression vector, the vector can be easily introduced into a host cell by any method in the art, for example, mammal, bacteria, yeast or insect cells. For

example, the expression vector can be transferred into the host cell by physical, chemical or biological means.

The physical methods for introducing polynucleotides into host cells include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, etc. Methods for producing cells that comprise 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 introducing polynucleotides into host cells is calcium phosphate transfection.

Biological methods for introducing polynucleotides of interest into host cells include the use of DNA and RNA vectors. Viral vectors, especially retroviral vectors, have become the most widely used methods for inserting genes into mammalian cells such as human cells. Other viral vectors can be derived from lentiviruses, poxviruses, herpes simplex viruses I, adenoviruses, adeno-associated viruses, etc. See, for example, U.S. patents 5,350,674 and 5,585,362.

Chemical means for introducing polynucleotides into host cells include colloidal dispersion systems, such as macromolecular complexes, nanocapsules, microspheres, and beads; and lipid-based systems, including oil-in-water emulsions, micelles, mixed micelles, and liposomes. Exemplary colloidal systems used as delivery vehicles in vitro and in vivo are liposomes (e.g., artificial membrane vesicles).

In the case of using a non-viral delivery system, an exemplary delivery tool is a liposome. The use of a lipid preparation is considered to introduce nucleic acids into host cells (in vitro, ex vivo or in vivo). On the other hand, the nucleic acids can be associated with lipids. Lipid-associated nucleic acids can be encapsulated in the aqueous interior of liposomes, dispersed in the lipid bilayer of liposomes, and attached to liposomes via linking molecules associated with both liposomes and oligonucleotides, trapped in liposomes, complexed with liposomes, dispersed in a solution containing lipids, mixed with lipids, combined with lipids, contained in lipids as a suspension, contained in micelles or complexed with micelles, or associated with lipids by other methods. The lipids, lipids/DNA or lipids/expression vectors associated with the composition are not limited to any specific structure in the solution. For example, they can exist in a bilayer structure, as micelles or have a “collapsed” structure. They can also simply be dispersed in a solution, possibly forming aggregates in uneven sizes or shapes. Lipids are fatty substances and can occur naturally or be synthesized. For example, lipids include fat droplets, which naturally occur in cytoplasm and in compounds containing long-chain aliphatic hydrocarbons and their

derivatives such as fatty acids, alcohols, amines, amino alcohols and aldehydes.

In certain embodiments, the vector is a lentiviral vector.

Therapeutic applications of CAR T

The present disclosure includes therapeutic applications using cells (e.g., T cells) transduced with a lentiviral vector (LV) encoding the expression cassette of the present disclosure. The transduced T cells can target BCMA, a marker of tumor cells, synergetically activate T cells and give rise to immune responses of the T cells, thereby significantly improving the killing efficiency of the T cells to tumor cells.

Therefore, the present disclosure further provides a method for stimulating T cell-mediated immune responses to mammalian target cell populations or tissues, which comprises the step of administering the CAR-T cells of the present disclosure to the mammal.

In an implementation manner, the present disclosure includes a cell therapy that isolates the patient's autologous T cells (or heterologous donors), activates and genetically modifies them to produce CAR-T cells, and then injects them into the same patient. In this way, the probability of suffering from graft-versus-host diseases is extremely low, and the antigen is recognized by T cells in a non-MHC-restricted manner. Further, one CAR-T can treat all cancers that express the antigen. Not like an antibody therapy, CAR-T cells can be replicated in vivo, producing long-term persistence that can lead to sustained tumor control.

In an implementation manner, the CAR-T cells provided by the present disclosure can undergo a stable expansion of T cells in vivo for a continuously extendable length of time. Further, the CAR-mediated immune response can be part of an adoptive immunotherapy step, in which CAR-modified T cells induce an immune response specific to the antigen-binding domain in the CAR. For example, CAR-T cells against BCMA arouse a specific immune response against cells that express BCMA.

Although the data disclosed herein specifically disclose a lentiviral vector comprising anti-BCMA scFv, a hinge, a transmembrane region, and 4-1BB and CD3 ζ signaling domains, the present disclosure should be construed as including any number of changes in each of the components of the construct.

Treatable cancers include tumors that have not been vascularized or substantially have not been vascularized, as well as vascularized tumors. Cancers may include non-solid tumors (such as hematological tumors, such as leukemia and lymphoma) or may include solid tumors. The types of cancers treated with the CAR, antibody, or an antigen-binding portion thereof, provided by the present disclosure include but are not limited to carcinoma, blastoma and sarcoma, and some leukemia or lymphoid malignancies, benign and malignant tumors such as

sarcoma, carcinoma and melanoma, also include adult tumors/cancers and pediatric tumors/cancers.

Hematological cancers are cancers of blood or bone marrow. Examples of hematological (or hematogenic) cancers include leukemia, including acute leukemia (such as acute lymphoblastic leukemia, acute myeloblastic leukemia, acute myelogenous leukemia, and myeloblastic, promyelocytic, myelomonocytic, monocytic erythrocytic leukemia), chronic leukemia (such as chronic myeloblastic (granulocytic) leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia), polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma (painless and high-grade form), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia and myelodysplasia.

A solid tumor is an abnormal mass of tissue that generally does not contain a cyst or fluid area. Solid tumors can be benign or malignant. Different types of solid tumors are named after the types of cells that form the solid tumors (such as sarcoma, carcinoma and lymphoma). Examples of solid tumors such as sarcoma and carcinoma include fibrosarcoma, myxosarcoma, liposarcoma, mesothelioma, lymphoid malignancy, pancreatic cancer and ovarian cancer.

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

For ex vivo immunization, at least one of the following items occurs in vitro before the cells are administered into the mammal: i) amplifying cells, ii) introducing the nucleic acids that encode CARs into the cells, and/or iii) cryopreserving the cells.

Ex vivo procedures are well known in the art and will be more fully discussed below. In brief, cells are isolated from a mammal (preferably a human) and genetically modified (i.e., transduced or transfected in vitro) with the vectors expressing the CARs disclosed herein. The CAR-modified cells can be administered to mammalian recipients to provide therapeutic benefits. The mammalian recipients can be humans, and the CAR-modified cells can be autologous relative to the recipients. Optionally, the cells can be allogeneic, syngeneic or xenogeneic relative to the recipients.

In addition to using cell-based vaccines for ex vivo immunization, the present disclosure also provides compositions and methods for in vivo immunization to cause immune responses against antigens in patients.

The present disclosure provides a method for treating tumors, which comprises administering to a subject in need thereof a therapeutically effective dose of the

CAR-modified T cells provided by the present disclosure.

The CAR-modified T cells provided by the present disclosure can be administered alone or administered as a pharmaceutical composition in combination with a diluent and/or other components such as IL-2, IL-17 or other cytokines or cell populations. In brief, the pharmaceutical composition provided by the present disclosure may comprise a target cell population as described herein, combined with one or more of pharmaceutically or physiologically acceptable vectors, diluents or excipients. Such composition may comprise a buffer solution such as neutral buffer saline and sulfate buffer; carbohydrates such as glucose, mannose, sucrose, dextran and mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxides); and preservatives. The composition may be suitable for intravenous administration.

The pharmaceutical composition provided by the present disclosure can be administered in a manner suitable for the disease to be treated (or prevented). The number and frequency of administrations will be determined by factors such as the patient's condition, and the type and severity of the patient's disease - although an appropriate dose can be determined by clinical trials.

When “immunologically effective dose,” “anti-tumor effective dose,” “tumor-suppressive effective dose” or “therapeutic dose” is indicated, the precise dose of the composition to be administered can be determined by the physician, who considers the age, weight, tumor size, degree of infection or metastasis and individual difference of disease in the patient (subject). It may generally be indicated that the pharmaceutical composition comprising the T cells described herein can be administered at a dose of 10^4 to 10^9 cells/kg of body weight, or at a dose of 10^5 to 10^6 cells/kg of body weight (including all integer values within those ranges). The T cell composition may also be administered multiple times at these doses. Cells can be administered by using well-known injection techniques in immunotherapy (see, for example, Rosenberg et al., New Eng. J. of Med. 319:1676, 1988). The optimal dose and therapeutic regimen for a specific patient can be easily determined by those skilled in the medical field by monitoring the patient's signs of disease and thus adjusting the treatment.

The administration of the composition by the subject can be carried out in any convenient manner, including by spraying, injection, swallowing, infusion, implantation or transplantation. The composition described herein can be administered to the patient

subcutaneously, intracutaneously, intratumorally, intranodally, intraspinally or intramuscularly, or by intravenous injection (i.v.), or intraperitoneally. In an implementation manner, the T cell composition provided by the present disclosure is administered to the patient by intradermal or subcutaneous injection. In certain embodiments, the T cell
5 composition is administered by intravenous injection (i.v.). The T cell composition may be directly injected into a tumor, lymph node or infection position.

In certain embodiments, cells activated and expanded using the methods described herein or other methods known in the art to expand T cells to a therapeutic level are administered to the patient in combination with any number of relevant treatment forms (e.g.,
10 before, at the same time or after). The treatment forms include but are not limited to treatment with the following reagents: The reagents include, for example, an antiviral therapy, cidofovir and interleukin-2, cytarabine (also known as ARA-C) or natalizumab for MS patients or erfazumab monoclonal treatment for psoriasis patients or other treatments for PML patients. In a further implementation manner, the T cells provided by the present disclosure can be
15 used in combination with the following: chemotherapy, radiation, immunosuppressors, such as cyclosporine, azathioprine, methotrexate, mycophenolate and FK506, antibodies or other immunotherapeutics. In certain embodiments, the cell composition provided by the present disclosure is administered to the patient in combination with bone marrow transplantation, chemotherapeutic agents such as fludarabine, an external beam radiotherapy (XRT),
20 cyclophosphamide (e.g., before, at the same time or after). For example, the subject can undergo the standard treatment of high-dose chemotherapy followed by peripheral blood stem cell transplantation. In certain embodiments, after the transplantation, the subject receives an injection of expanded immune cells according to the present disclosure. In certain embodiments, the expanded cells are administered before or after a surgery.

The foregoing therapeutic dose administered to the patient will vary with the precise
25 nature of the condition being treated and the receiver of the treatment. The dosage ratio of human administration can be implemented according to the practice accepted in the art. Generally, 1×10^6 to 1×10^{10} modified T cells (e.g., CAR-T20 cells) can be administered to the patient by venous re-transfusion per treatment or per course of treatment.

30 **CART preparation**

The present disclosure provides CAR-T cells, as well as a pharmaceutically acceptable carrier, diluent or excipient. In an implementation manner, the preparation is a liquid preparation. In one embodiment, the preparation is an injection. In one embodiment, the concentration of the CAR-T cells in the preparation is 1×10^3 to 1×10^8 cells/ml, or 1×10^4 to

1×10⁷ cells/ml.

In certain embodiments, the preparation may comprise a buffer solution such as neutral buffer saline and sulfate buffer saline; carbohydrates such as glucose, mannose, sucrose, dextran and mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; 5 chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. The preparation may be suitable for intravenous administration.

Pharmaceutical composition

The present disclosure further provides a composition. In certain embodiments, the composition is a pharmaceutical composition, which contains the foregoing antibody or 10 active fragments thereof, fusion proteins thereof, ADCs thereof or corresponding CAR-T cells, and a pharmaceutically acceptable carrier. Generally, these substances can be prepared in a non-toxic, inert and pharmaceutically acceptable aqueous carrier medium, with pH of about 5 to 8, or about 6 to 8, although the pH value may vary with the nature of the prepared substances and the diseases to be treated. The prepared pharmaceutical composition can be 15 administered by conventional routes, including (but not limited to): intratumoral, intraperitoneal, intravenous, or topical administration.

The antibody described in the present disclosure can also be used in a cell therapy for intracellular expression of nucleotide sequences. For example, the antibody is used in a chimeric antigen receptor T cell immunotherapy (CAR-T).

20 The pharmaceutical composition provided by the present disclosure can be directly used to bind TF protein molecules, and thus can be used to prevent and treat tumors and other diseases. In addition, other therapeutic agents can also be used at the same time.

The pharmaceutical composition provided by the present disclosure contains a safe and effective dose (e.g., 0.001-99 wt%, 0.01-90 wt%, or 0.1-80 wt%) of the foregoing 25 monoclonal antibody provided by the present disclosure (or conjugate thereof) and a pharmaceutical acceptable carrier or excipient. Such carriers include (but are not limited to): saline, buffer solutions, glucose, water, glycerol, ethanol, and combinations thereof. The pharmaceutical preparation should match the way of administration. The pharmaceutical composition provided by the present disclosure can be prepared in the form of injections, for 30 example, from physiological saline or an aqueous solution containing glucose and other adjuvants by conventional methods. The pharmaceutical composition such as an injection or a solution should be manufactured under sterile conditions. The dosage of the active ingredient is a therapeutically effective dose, for example, about 1 mg/kg of body weight to about 5 mg/kg of body weight per day. In addition, the polypeptide provided by the present

disclosure may also be used together with other therapeutic agents.

The use of a pharmaceutical composition is to administer a safe and effective dose of an immunoconjugate to a mammal, where the safe and effective dose is generally at least about 10 mg/kg of body weight, and in most cases, it does not exceed about 50 mg/kg of body weight. For example, the dose is about 10 mg/kg of body weight to about 20 mg/kg of body weight. Of course, the specific dose should also consider factors such as the route of administration and the patient's health status, which are all within the skills of skilled physicians.

Detection purposes and kits

The antibodies or conjugates thereof provided by the present disclosure can be used in detection applications, for example, used to detect samples, thereby providing diagnostic information.

The specimens (samples) may include cells, tissue samples, and biopsy specimens. The term "biopsy" may include all types of biopsy known to those skilled in the art. Therefore, the biopsy may include, for example, a tumor resection sample, and a tissue sample prepared by an endoscopic method or a puncture or needle biopsy of an organ.

The samples may include fixed or preserved cell or tissue samples.

The present disclosure further provides a kit containing the antibody (or fragment thereof), or CAR, of the present disclosure. In an embodiment, the kit further comprises a container, an operating manual, a buffer agent, etc. In an embodiment, the antibody can be attached to a test plate.

The present disclosure further provides a use of the antibody. For example, the antibody is used to prepare a diagnostic preparation or a drug for preventing and/or treating the BCMA-positive cancer/tumor.

The antibodies provided by the present disclosure may recognize soluble extracellular domains of human BCMA molecules on the cell membrane surface. Some antibodies can also cross-recognize the soluble extracellular domains of machin BCMA molecules.

The CAR-T cells provided by the present disclosure do not recognize tumor necrosis factor receptor superfamily member 13B.

The CAR-T cells provided by the present disclosure have desirable specific cytotoxicity toward BCMA-positive target cells.

The following examples of specific aspects for carrying out the present disclosure are offered for illustrative purposes only, and are not intended to limit the scope of The present disclosure in any way.

General materials and methods

The materials and methods used in the Examples are as follows:

1 Sources of cells and mice

K562-BCMA⁺: K562-BCMA-B22D8 (provided by Cellular Biomedicine Group)

5 K562 (ATCC; provided by Cellular Biomedicine Group)

L-BCMA⁺: L-BCMA-1E6-A4 (provided by Cellular Biomedicine Group)

L Cells (mouse fibroblast, ATCC: cat. CRL-2648TM; lot, 63903687; provided by Cellular Biomedicine Group)

Sp2/0-Ag14 cell (ATCC; provided by ChemPartner)

10 Balb/c mice (Shanghai Slac)

SJL mice (Shanghai Slac)

2 Main reagents

Table 1 Reagents

Name	Manufacturer	Goods No.	Batch No.
hBCMA-ECD-Fc	ChemPartner	---	171030004
cynoBCMA-ECD-Fc	ChemPartner	---	171030003
Recombinant hFc fusion protein control (NC-Fc)	ChemPartner	---	---
Recombinant human TACI/TNFRSF13B Fc chimeric protein, CF (hTACI-ECD-Fc)	R&D Systems	174-TC	EFN0417051
Tool antibody (tAb, anti-hBCMA)	Biolegend	357502	B206531
mIgG	Invitrogen	026502	1623974A

3 Main laboratory instruments

Table 2 Laboratory instruments

Name	Manufacturer	Model
Microplate reader	Molecular Devices	Plus 384
ELISA microplate washer	BioTek	ELx406UCWS
Centrifuge	Eppendorf	5810R
Flow cytometer	BD	FACSVerse

4 Experimental design

4.1 Mouse immunization and serum titer detection

Five Balb/c mice and five SJL mice were divided into two groups and immunized with

hBCMA-ECD-Fc according to Table 3. As shown in Table 4, booster immunization should be performed at least twice after the first immunization (the third booster immunization uses K562-BCMA⁺ cells). After immunization, ELISA and FACS were used to detect the titer of mouse serum. After the serum titer met the requirements (ELISA reaches 1:10,000 dilution or FACS reaches 1:1,000 dilution), hybridoma cell fusion screening was performed.

Table 3 Mouse immunization groups

Animal Species	Qty	Immunization Method	Reference Number
Balb/c mouse	5	Intraperitoneal injection	5061, 5062, 5063, 5064, 5065
SJL mouse	5	Intraperitoneal injection	5066, 5067, 5068, 5069, 5070

Table 4 Immunization strategy

Day 0	Draw blood before immunization (PB, 15-30 μ l of serum/mouse) The first immunization: hBCMA-ECD-Fc, 50 μ g/mouse (CFA adjuvant)
Day 14	Booster immunization: hBCMA-ECD-Fc, 25 μ g/mouse (IFA adjuvant)
Day 21	Draw blood from mice (TB1, 15-30 μ l of serum/mouse)
Day 22	Detect serum titer by ELISA/FACS
Day 35	Booster immunization: hBCMA-ECD-Fc, 25 μ g/mouse (IFA adjuvant)
Day 42	Draw blood from mice (TB2, 15-30 μ l of serum/mouse)
Day 43	Detect serum titer by ELISA/FACS
Day 56	Pre-fusion immunization: hBCMA-ECD-Fc, 25 μ g/mouse (IFA adjuvant)
Day 60	Electro-fusion of hybridoma cells

4.2 Screening of hybridoma cell strains

4.2.1 Fusion of hybridoma cells

Through FACS detection, the mouse with the highest serum titer (Balb/c and SJL each one) was determined, and the spleen and lymph node lymphocytes and Sp2/0-Ag14 cells were fused by the electrofusion method to obtain hybridoma cells.

4.2.2 Monoclonal screening of hybridoma cells

After red blood cell lysis, the fusion cells of each mouse were spread on 96-well plates, 2.5×10^6 cells per plate, 20 plates in total. Primary screening was carried out after 10 days: the binding ability of the medium supernatant to hBCMA-ECD-Fc protein was detected by ELISA, and the clones with a positive test result were transferred to a 24-well plate for multiplication culture.

For the cells after multiplication culture, ELISA was used to detect the binding ability of the medium supernatant to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc, and FACS was

used to detect the binding ability of the medium supernatant to L-BCMA⁺ cells (secondary screening). In the end, the clones with strong binding to L-BCMA⁺ cells were selected to conduct subclonal screening.

4.2.3 Subclonal screening of hybridoma cells

The monoclonal cells obtained in 4.2.2 were spread on two 96-well plates, the ELISA and FACS screening processes in 4.2.2 were repeated and the in the end, subclonal cell strains were obtained. The target clones were transferred to culture bottles for multiplication culture, a seed bank was established and 4 to 6 units of cells under each strain were cryopreserved ($0.5-1 \times 10^7$ cells/unit).

4.3 Production and purification of hybridoma antibodies

Monoclonal cells that bind to both human and machin BCMA were selected for small-batch trial production. Cells were cultured in 250 to 500 ml cell culture shake flasks, and the produced antibodies were purified by Protein A affinity column and treated with endotoxin removal in sequence, and 3 to 5 mg of antibodies were obtained for characteristic analysis.

4.4 Identification of purified hybridoma antibodies

Antibody identification includes the following three points:

- a) Analysis of the binding specificity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and hTACI-ECD-Fc (ELISA)
- b) Analysis of the binding ability to L cells and L-BCMA⁺ cells (FACS)
- c) Analysis of the competitive binding to soluble BCMA (FACS)

4.5 Sequencing of antibody variable regions

Extract the RNA of the hybridoma cell of the target clone, reversely transcribe the RNA into cDNA, amplify the antibody VH/VL gene fragments by PCR, and sequence to obtain the gene sequences of the antibody variable regions of the target clone.

4.6 Expression identification of chimeric antibodies

Clone the antibody VH regions obtained from sequencing to an IgG1, κ recombinant antibody heavy chain expression vector and clone the VL regions to an IgG1, κ recombinant antibody light chain expression vector to construct expression plasmids of a chimeric antibody, and meanwhile use the two plasmids to transfect HEK 293T cells. Collect the supernatant of the culture after culturing for three days. Determine the binding abilities of the supernatant to hBCMA-ECD-Fc(ELISA) and L-BCMA⁺ cells (FACS).

Example 1 Mouse immunization and serum titer detection

Mouse immunization was performed. Three booster immunizations and four fusions were conducted. As shown in Table 5, the first two booster immunizations used hBCMA-ECD-Fc to immunize mice, and then F0109 and F0227 were fused. The third booster immunization used K562-BCMA⁺ cells to immunize mice and then F0508 and F0614 were fused.

Table 5 Timetable of mouse immunization and fusion

Strain	Mouse #	Prime	1 st boost	bleed 1	2 nd boost	bleed 2	3 rd boost	bleed 3	Final boost	Fusion	Note
Balb/c	5061	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	3/20/2018	3/27/2018	6/11/2018	6/14/2018	F0614
	5062	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	1/5/2018	X	dead after final boost
	5063	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	2/23/2018	2/27/2018	F0227
	5064	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	3/20/2018	3/27/2018	5/4/2018	5/8/2018	F0508
	5065	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	1/5/2018	1/9/2018	F0109
SJL	5066	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	3/20/2018	3/27/2018	6/11/2018	6/14/2018	F0614
	5067	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	1/5/2018	1/9/2018	F0109
	5068	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	2/23/2018	2/27/2018	F0227
	5069	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	3/20/2018	3/27/2018	5/4/2018	5/8/2018	F0508
	5070	11/7/2017	11/21/2017	11/28/2017	12/12/2017	12/19/2017	X	X	2/23/2018	X	dead after final boost
Immunosource:			hBCMA-ECD-Fc			K562BCMA ⁺ cell line					

The results of ELISA analysis of mouse serum titers after the first booster immunization are shown in Figure 1. After the first booster immunization using hBCMA-ECD-Fc, ELISA detected that the sera of the 10 mice at a dilution of 1:10k all had a binding ability to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc, of which the titer of SJL #5066 was relatively low and the remaining nine mice had similar titers.

The FACS detection results are as shown in Figure 2. Except JL #5066, the sera of the remaining mice at a dilution of 1:1,000 all had a strong binding ability to K562-BCMA⁺.

The results of ELISA analysis of mouse serum titers after the second booster

immunization are shown in Figure 3. After the second booster immunization using hBCMA-ECD-Fc, ELISA detected that the sera of the 10 mice at a dilution of 1:10k all had a desirable binding ability to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc and had similar titers.

The FACS detection results are as shown in Figure 4. The sera of the ten mice at a dilution of 1:1,000 all bound to K562-BCMA⁺. In the two groups of mice, Balb/c #5062 and SJL #5067 had the highest titers.

Because mouse Balb/c #5062 died before fusion and after immunization, mice Balb/c #5065 and SJL #5067 were selected to conduct the first fusion F0109. Because mouse SJL#5070 died before fusion and after immunization, mice Balb/c #5063 and SJL #5068 were selected to conduct the second fusion F0227 (this fusion did not obtain positive clones when screened).

As F0109 only generated one clone and F0227 did not generate a positive clone, K562-BCMA⁺ cells were used to conduct the third booster immunization. Mouse serum (TB2-2) was taken before immunization and mouse serum (TB3) was taken after one week of immunization.

The ELISA analysis results of mouse titers after the third booster immunization are as shown in Figure 5. The sera of four mice at a dilution of 1:10k all had a desirable binding ability to hBCMA-ECD-Fc and cynoBCMA-ECD-Fc before and after immunization and had similar titers.

The FACS detection results are as shown in Figure 6. The sera of four mice at a dilution of 1:1,000 all bound to L-BCMA⁺ cells. In the two mouse groups, Balb/c #5064 and SJL #5069 had the highest titers.

After the third booster immunization, Balb/c #5064 and SJL #5069 were selected to conduct the third fusion F0508, and Balb/c #5061 and SJL #5066 were selected to conduct the fourth fusion F0614.

Example 2 Screening of hybridoma cell strains

2.1 Screening of fusion F0109 hybridoma cells

The cells after electrofusion were spread on 40 96-well plates. Among them, Balb/c #5065 was spread on plates #1 to #20, and SJL #5067 was spread on plates #21 to #40. Primary screening: ELISA detected the binding ability of the medium supernatant to hBCMA-ECD-Fc, a negative control group was NC-Fc, the set threshold value was Dvalue > 0.8 and meanwhile OD450(hBCMA ECD-Fc) - OD450(hFc) > 0.5, and 68 clones in total were obtained. After multiplication culture, secondary screening was conducted, 6G10 of

Balb/c #5065 had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and K562-BCMA⁺ cells; 34D1 of SJL #5067 had a good binding affinity to K562-BCMA⁺ cells. These two clones were selected as parent clones to conduct subclonal screening.

The monoclonals 6G10-1D7 and 6G10-1H2 and hybrid clones 6G10-1B11 and 6G10-1D3 derived from Balb/c #5065 and obtained from subclonal screening had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and K562-BCMA⁺; and the subclonal 34D1-2H2 derived from SJL #5067 had a strong binding affinity to hBCMA-ECD-Fc and K562-BCMA⁺. The five clones were selected and cryopreserved. Clone 6G10-1D7 was selected to conduct antibody production in small batches.

2.2 Screening of fusion F0227 hybridoma cells

From subclonal screening of fusion F0227, no positive clones that could bind to hBCMA-ECD-Fc and L-BCMA⁺ cells were obtained.

2.3 Screening of fusion F0508 hybridoma cells

The cells after electrofusion were spread on 40 96-well plates. Among them, Balb/c #5064 was spread on plates #81 to #100 and SJL #5069 was spread on plates #101 to #120. Primary screening: ELISA detected the binding affinity of the medium supernatant to hBCMA-ECD-Fc, a negative control group was NC-Fc, the set threshold value was Dvalue $\geq$ 2, and 79 clones in total were obtained. After multiplication culture, secondary screening was conducted, and the obtained 19 clones (109C5, 107A11, 107B11, 116H6, 102G2, 102A12, 111F11, 107A9, 111D5, 105F9, 114C6, 97B8, 97C4, 104H4, 115G7, 116A9, 100H2, 99B3 and 110A11) all had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ cells; the obtained 4 clones (120D6, 120A10, 105C10 and 113B3) all had a strong binding affinity to hBCMA-ECD-Fc and L-BCMA⁺ cells, and these 23 clones were used as parent clones to conduct subclonal screening, as shown in Figure 7.

Each parent clone was spread on a 96-well plate to conduct subclonal screening. In primary screening, the subclonals of six clones 105F9, 111F11, 120D6, 104H4, 115G7 and 110A11 were all negative; 120A10 had a subclonal, which was negative in ELISA, while other clones were all negative. When 120A10 was screened before subcloning, it did not have cross-reactivity with machin BCMA, so this clone did not undergo secondary screening. The 96-well plates spread with the foregoing clones were cultured for two more days. Then ELISA screening was performed once again, and the screening result was still negative. Therefore, the subclonal screening of these seven parent clones was stopped.

The remaining 16 parent clones underwent secondary screening. Five subclones, 99B3G3, 102A12H6, 107A11F1, 107A9A4 and 107B11E1, obtained from screening all had

a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ cells and did not bind to NC-Fc. Two subclones, 105C10F1 and 113B3F12, both had a strong binding affinity to hBCMA-ECD-Fc and L-BCMA⁺, and did not bind to cynoBCMA-ECD-Fc, NC-Fc. The foregoing seven subclones were selected to produce antibodies in small batches.

5 In addition, the four clones 97B8G8, 100H2D12, 109C5F3 and 114C6C8 were not monoclonal according to the microscopic examination and underwent the second round of subcloning. The results of the second round of primary subclonal screening are as follows. 114C6C8 did not generate a positive subclone, so this clone was no longer retained. Clones 97B8G8D12, 97B8G8E6, 97B8G8F7, 97B8G8G2, 100H2D12B10, 100H2D12C6,
10 100H2D12D5, 100H2D12H3, 109C5F3C1, 109C5F3D2, 109C5F3D4 and 109C5F3H3 were selected to undergo secondary screening. The results indicate that two obtained clones 100H2D12C6 and 109C5F3C1 both had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ cells and did not bind to NC-Fc. A clone that was generated, 97B8G8D12, had a strong binding affinity to hBCMA-ECD-Fc and
15 cynoBCMA-ECD-Fc, and had a weak binding affinity to L-BCMA⁺ cells. The foregoing three clones were selected to conduct antibody production in small batches.

As most of the subclones derived from clones 116A9, 111D5 and 116H6 had strong binding affinity to NC-hFc, FACS was used to screen all the subclones from the foregoing three clones: those from 116A9 were all negative clones; those from 116H6C10 were positive
20 clones, but had strong binding affinity to NC-hFc; 10 subclones were selected from 111D5 to conduct secondary screening, and all the subclones had strong binding affinity to NC-hFc. Therefore, clones 116A9, 111D5 and 116H6, and subclones thereof were no longer retained.

Clones 97C4F2, 102G2B5, 102G2D1 and 102G2F3 did not bind to L-BCMA⁺ cells, so they were no longer retained, either.

25 The sequencing results indicate that 107A11F1, 107B11E1 and 107A9A4 each had four heavy chains and a light chain, these three clones underwent the second round of subclonal screening. The results indicate that subclones 107A9A4D2, 107A11F1B7 and 107B11E1D7 of 107A11F1 had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ cells. These three clones were selected for sequencing; and subclones
30 107A9A4B2, 107A9A4D8, 107A9A4E9, 107A11F1C5, 107A11F1E6, 107A11F1E7, 107B11E1A8, 107B11E1B10 and 107B11E1C11 were cryopreserved.

2.4 Screening of fusion F0614 hybridoma cells

The cells after electrofusion were spread on 40 96-well plates. Among them, Balb/c #5061 was spread on plates #121 to #140, and SJL #5066 was spread on plates #141 to #160.

ELISA was used in the primary screening to detect the binding affinity of the medium supernatant to hBCMA-ECD-Fc, with the set threshold value being $D_{value} \geq 0.8$. 33 clones in total were obtained. After multiplication culture, a secondary screening was conducted. Five obtained clones (151A9, 156E11, 149H4, 143D6 and 154B8) all had a binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ and did not bind to NC-Fc. One obtained clone (152D8) had a strong binding affinity to hBCMA-ECD-Fc and L-BCMA⁺ and did not bind to NC-Fc. These six clones were selected as parent clones to conduct subclonal screening.

Each parent clone was spread on a 96-well plate to conduct subclonal screening. The subclones of three clones 156E11, 149H4 and 154B8 were all negative, so no subcloning of these three parent clones underwent the secondary screening.

Subclones were selected from the remaining three parent clones to conduct the secondary screening. The results indicate that the three subclones, 143D6F4, 151A9A4 and 152D8E8, all had a strong binding affinity to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and L-BCMA⁺ and did not bind to NC-Fc. These three subclones were selected for antibody production in small batches. 143D6D8 and 151A9F1 were cryopreserved.

2.5 Summary of hybridoma cell screening results

As shown in Figure 7, four rounds of hybridoma cell fusion were conducted. After subclonal screening, 14 strains of hybridoma cells (6G10-1D7, 99B3G3, 102A12H6, 107A11F1, 107A9A4, 107B11E1, 100H2D12C6, 105C10F1, 113B3F12, 109C5F3C1, 97B8G8D12, 143D6F4, 151A9A4 and 152D8E8) were selected to undergo small-batch hybridoma antibody production and purification as well as sequencing of antibody variable regions.

The sequencing results indicate that the sequences of the antibody variable regions of 100H2D12C6 and 97B8G8D12 were the same as those of 99B3G3. 107A11F1, 107A9A4 and 107B11E1 were not monoclonal. These three hybridoma cells underwent the second round of subcloning. 107A9A4D2, 107A11F1B7 and 107B11E1D7 were selected to undergo sequencing of antibody variable regions. The antibody variable regions of 107A9A4D2 and 107A11F1B7 had the same sequence and each had a heavy chain and two light chains. The screening data of the foregoing hybridoma supernants are as shown in Table 6.

Table 6 Screening results of hybridoma cell supernants

Clone	ELISA (OD450 nm)			FACS (MFI)	
	hBCMA-ECD-Fc	cynoBCMA-ECD-Fc	NC-Fc	BCMA ⁺	BCMA ⁻

				cells	cells
6G10-1D7	2.9	1.95	0.08	3882.8	104.9
99B3G3	3.68	3.65	0.14	1929.4	106.1
102A12H6	3.6	3.53	0.12	762.2	105.4
105C10F1	3.42	0.18	0.1	1958.2	104.9
107A11F1	3.63	3.65	0.1	4997.3	102.6
107B11E1	3.56	3.61	0.09	3521.4	105.9
107A9A4	3.33	3.61	0.09	2655.8	101.8
113B3F12	3.9	0.18	0.14	3888.1	102.5
100H2D12C6	3.37	3.48	0.13	1142.5	96.1
109C5F3C1	3.57	3.41	0.57	2891.9	101.1
143D6F4	3.26	3.4	0.2	1507.9	114.5
151A9A4	3.34	3.4	0.24	2915.3	103.9
152D8E8	3.35	3.31	0.23	1184.7	103.9
97B8G8D12	3.06	3.37	0.13	357.5	95.8
107A9A4D2	3.5093	3.583	0.4596	4645.2	97.5
107A11F1B7	3.5267	3.5005	0.4413	5181	114.9
107B11E1D7	2.9167	3.5361	0.4431	3513.9	128.1

Example 3 Production and purification of hybridoma antibodies

14 hybridoma cells in total were selected for antibody production in small batches. Among them, 97B8G8D12 did not produce antibodies. The remaining 13 clones all successfully generated corresponding antibodies, as shown in Table 7. SDS-PAGE results indicate that pure antibodies were obtained from purification, as shown in Figure 8.

Table 7 Information about small-batch production and purification of antibodies

Antibody No.	Clone	Subtype	conc (mg/ml)	Total amount (mg)	Animal origin
mAb001	6G10-1D7	IgG1, κ	0.847	5.929	Balb/c #5065
mAb002	99B3G3	IgG1, κ	0.847	7.1995	Balb/c #5064
mAb003	102A12H6	IgG1, κ	0.686	6.517	SJL #5069

mAb004	105C10F1	IgG2b, κ	0.861	10.332	SJL #5069
mAb005	107A11F1	IgG2b, κ	1.139	14.2375	SJL #5069
mAb006	107B11E1	IgG1, κ	0.993	11.4195	SJL #5069
mAb007	107A9A4	IgG2b, κ	2.248	30.348	SJL #5069
mAb008	113B3F12	IgG2b, κ	0.832	10.4	SJL #5069
mAb009	100H2D12C 6	IgG1, κ	0.453	2.9445	Balb/c #5064
mAb010	109C5F3C1	IgG2c, κ	0.73	5.11	SJL #5069
mAb011	143D6F4	IgG2b, κ	0.73	10.95	SJL #5066
mAb012	151A9A4	IgG2b, κ	0.569	5.69	SJL #5066
mAb013	152D8E8	IgG1, κ	0.058	0.29	SJL #5066

Example 4 Identification of purified hybridoma antibodies

1.0 μ g/ml hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and hTACI-ECD-Fc were spread on plates to detect the specificity of hybridoma antibodies by ELISA.

- 5 ELISA analysis results are shown in Figures 9-11. Purified hybridoma antibody mAb001(6G10-1D7) could bind to the extracellular domains of human BCMA, but had a weak binding affinity to the extracellular domains of machin BCMA. mAb001(6G10-1D7) bound to the extracellular domain of machin BCMA molecules only at a high concentration. mAb013(152D8E) did not bind to the extracellular domains of human BCMA and machin
- 10 BCMA. mAb004(105C10F1) and mAb008(13B3F12) could bind to the extracellular domains of human BCMA, but could not recognize the extracellular domains of machin BCMA. All other purified hybridoma antibodies could bind to the extracellular domains of human BCMA and machin BCMA. None of the hybridoma antibodies recognized hTACI-ECD-Fc. The EC50 for the binding of each antibody to hBCMA-ECD-Fc, cynoBCMA-ECD-Fc and
- 15 hTACI-ECD-Fc is shown in Table 8.

Table 8 Analysis of binding specificity of hybridoma antibodies

Antibody No.	Clone	Subtype	EC50 (nM)		
			hBCMA-ECD-Fc	cynoBCMA-ECD-Fc	hTACI-ECD-Fc
mAb001	6G10-1D7	IgG1, κ	0.034	Low binding	No binding

mAb002	99B3G3	IgG1, κ	0.032	0.23	No binding
mAb003	102A12H6	IgG1, κ	0.058	0.062	No binding
mAb004	105C10F1	IgG2b, κ	0.038	No binding	No binding
mAb005	107A11F1	IgG2b, κ	0.134	0.144	No binding
mAb006	107B11E1	IgG1, κ	0.029	0.019	No binding
mAb007	107A9A4	IgG2b, κ	0.21	0.17	No binding
mAb008	113B3F12	IgG2b, κ	0.15	No binding	No binding
mAb009	100H2D12C6	IgG1, κ	0.033	0.033	No binding
mAb010	109C5F3C1	IgG2c, κ	0.18	0.18	No binding
mAb011	143D6F4	IgG2b, κ	0.15	0.17	No binding
mAb012	151A9A4	IgG2b, κ	0.17	0.15	No binding
mAb013	152D8E8	IgG1, κ	No binding	No binding	No binding

The detection results of flow cytometry are as shown in Figures 12-13. Except mAb003 and mAb013, the remaining 11 hybridoma antibodies all had a desirable binding affinity to L-BCMA⁺ cells and did not have non-specific binding to L cells.

- 5 The analysis results of the competitive binding of hybridoma antibodies to soluble BCMA are as shown in Figure 14. When the concentration of hBCMA-ECD-Fc was greater than 240 ng/ml, the binding of K562-BCMA⁺ cells to mAb001 (final concentration EC80: 1 μ g/ml) could be competitively inhibited, with IC₅₀ being 731 ng/ml and the corresponding molar ratio 1.7 : 1. When BCMA concentration of K562-BCMA⁺ medium supernatant was
- 10 grater than 120 ng/ml, the binding of K562-BCMA⁺ cells to mAb001 (final concentration EC80: 1 μ g/ml) could be competitively inhibited, with IC₅₀ being 466 ng/ml, and the corresponding molar ratio 10.4:1.

Example 5 Sequencing of antibody variable regions

- 15 17 strains of hybridoma cells in total underwent sequencing of antibody variable regions. The sequencing results indicate that 12 strains of hybridoma cells were monoclonal: 6G10-1D7(CP01), 99B3G3(CP02), 102A12H6, 100H2D12C6, 105C10F1(CP03), 113B3F12, 109C5F3C1(CP06), 97B8G8D12, 143D6F4(CP07), 151A9A4(CP08), 152D8E8(CP09) and 107B11E1D7(CP05). 99B3G3(CP02), 100H2D12C6 and 97B8G8D12 had the same
- 20 sequence of the antibody variable regions. 5 strains of hybridoma cells were polyclonal: 107A11F1, 107A9A4, 107B11E1, 107A9A4D2 and 107A11F1B7 (CP04). 107A11F1,

107A9A4 and 107B11E1 each had four heavy chains and one light chain. 107A9A4D2 and 107A11F1B7(CP04) each had one heavy chain and two light chains with the same sequences.

Table 9 shows the sequences of the antibody variable regions.

5 **Table 9** Nucleotide sequences encoding antibody variable regions

Hybridoma No.	Nucleotide sequence encoding V _H regions	Nucleotide sequence encoding V _L regions
6G10-1D7 (CP01)	SEQ ID NO: 1	SEQ ID NO.:2
99B3G3(CP02)	SEQ ID NO: 3	SEQ ID NO: 4
102A12H6	SEQ ID NO: 5	SEQ ID NO: 6
105C10F1(CP03)	SEQ ID NO: 7	SEQ ID NO: 8
107A11F1	SEQ ID NO: 9	SEQ ID NO: 13
	SEQ ID NO: 10	
	SEQ ID NO: 11	
	SEQ ID NO: 12	
107B11E1	SEQ ID NO: 14	SEQ ID NO: 18
	SEQ ID NO: 15	
	SEQ ID NO: 16	
	SEQ ID NO: 17	
107A9A4	SEQ ID NO: 19	SEQ ID NO: 23
	SEQ ID NO: 20	
	SEQ ID NO: 21	
	SEQ ID NO: 22	
113B3F12	SEQ ID NO: 24	SEQ ID NO: 25
100H2D12C6	SEQ ID NO: 3	SEQ ID NO: 4
109C5F3C1(CP06)	SEQ ID NO: 26	SEQ ID NO: 27
143D6F4(CP07)	SEQ ID NO: 28	SEQ ID NO: 29
151A9A4(CP08)	SEQ ID NO: 30	SEQ ID NO: 31
152D8E8(CP09)	SEQ ID NO: 32	SEQ ID NO: 33
107A11F1B7(CP04)	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36

107A9A4D2	SEQ ID NO: 34	SEQ ID NO: 35
		SEQ ID NO: 36
107B11E1D7(CP05)	SEQ ID NO: 37	SEQ ID NO: 38
97B8G8D12	SEQ ID NO: 3	SEQ ID NO: 4

Example 6 Expression and identification of chimeric antibodies

The antibody V_H regions obtained from sequencing were cloned to an IgG1, κ recombinant antibody heavy chain expression vector, and the V_L regions were cloned to an IgG1, κ recombinant antibody light chain expression vector to construct expression plasmids of chimeric antibodies. Five strains of monoclonal hybridoma cells (6G10-1D7, 99B3G3, 105C10F1, 113B3F12 and 107B11E1D7) and one strain of polyclonal hybridoma cells (107A9A4D2) were selected for expression of chimeric antibodies. Among them, 107A9A4D2VH was paired with 107A9A4D2VL-1 and 107A9A4D2VL-2, respectively for expression. The heavy and light chain sequences of the recombinantly expressed chimeric antibodies are as follows (the underlined parts are the antibody variable region sequences):

1. Hybridoma 6G10-1D7

>6G10-1D7VH heavy chain (SEQ ID NO: 39; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVQLQQSGPELVKPGASMKISCKASDYSFTDYIMTWV
 15 KQSHGKNLEWIGLINPYNGGTTYNQKFKDKATFTVDKSSTTAYMDLLSLTSEDSAV
YYCARRGITTDYYTMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
 KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
 KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
 20 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
 ALHNHYTQKSLSLSPGK

>6G10-1D7VL light chain (SEQ ID NO: 40):

MDMRVPAQLLGLLLLWFPGSRCDIVMTQSQRFMSTSVGDRVSITCKASQSVGTAVA
 25 WYQQTPGQFPKLLIYSTSNRYTGVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQY
STYPLTFGSGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
 VDNALQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSPVT
 KSFNRGEC

2. Hybridoma 99B3G3

>99B3G3VH heavy chain (SEQ ID NO: 41; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNW
VKQSHGKSLEWIGVINPYNGGTSYNQKFKAKATLTVDKSSITAYMELNSLTSEDSAV
 5 YYCARGDSIYVMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP
 SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVTV
 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
 10 IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
 HNHYTQKSLSLSPGK

>99B3G3VL light chain (SEQ ID NO: 42; V_L is underlined):

MDMRVPAQLLGLLLLWFPGRCDIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSIQ
 15 KNYLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADY
FCQQHYSSPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREA
 KVQWKVDNALQSGNSQESVTEQDSKDSSTLSKADYEKHKVYACEVTHQ
 GLSSPVTKSFNRGEC

20 3. Hybridoma 105C10F1

>105C10F1VH heavy chain (SEQ ID NO: 43; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVKLLQSGGGLVQPGGSLKLSCAASGIDFSRYWMSWV
RRAPGKGLEWIGEINPDSSTINYAPSLKDKFISRDAAKNTLYLQMSKVRSEDTALYY
CATLYYDYDGDYAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
 25 KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
 KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
 30 ALHNHYTQKSLSLSPGK

>105C10F1VL light chain (SEQ ID NO: 44; V_L is underlined):

MDMRVPAQLLGLLLLWFPGRCDIVMTPSQKFMSTSVGDRVSVTCKASQNVGTNV
AWYQQKPGQSPKALIYSASYRYSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQH

YNSYPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC

5 4. Hybridoma 113B3F12

>113B3F12VH heavy chain (SEQ ID NO: 45; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNW
VKQSHGKSLEWIGVINPYNGGTDYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSA
YYCARRRESYGTSYQGAYFDSWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAA
 10 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
 CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT
 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNKKEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
 KGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
 15 VMHEALHNHYTQKSLSLSPGK

>113B3F12VL light chain (SEQ ID NO: 46; V_L is underlined):

MDMRVPAQLLGLLLLWFGSRCDIQMTQTSSLSASLGDRVTISCRASQDISNYLNW
YQKQPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLISDLEQEDIATYFCQQVITL
 20 PWTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
 NALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
 FNRGEC

5. Hybridoma 107B11E1D7

25 >107B11E1D7VH heavy chain (SEQ ID NO: 47; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNW
LKQSHGKRLEWIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMDLNSLTSEDSA
YYCARGDSIYVMDYWGQGSFTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVK
 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
 30 PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
 LHNHYTQKSLSLSPGK

>107B11E1D7VL light chain (SEQ ID NO: 48; V_L is underlined):

MDMRVPAQLLGLLLLWFPGRSCENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHW
 YQKSSTSPKLWIYDTSKLSSGVPGRFSGSGSGKSYSLTISSMEAEDVATYYCFQGSG
 5 YPLFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
 DNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

6. Hybridoma 107A9A4D2

10 >107A9A4D2VH heavy chain (SEQ ID NO: 49; V_H is underlined):

MEFGLSWLFLVAILKGVQCEVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNW
 LKQSHGKRLEWIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMDLNSLTSEDSA
 VYYCARGDSIYVMDYWGQGTSTFTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
 15 PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
 DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEA
 LHNHYTQKSLSLSPGK

20

>107A9A4D2VL-1 light chain (SEQ ID NO: 50; V_L is underlined):

MDMRVPAQLLGLLLLWFPGRSCENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHW
 YQKSSTSPKLWIYDTSKLSSGVPGRFSGSGSGKSYSLTISSMEAEDVATYYCFQGSG
 YPLFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
 25 DNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

>107A9A4D2VL-2 light chain (SEQ ID NO: 51; V_L is underlined):

MDMRVPAQLLGLLLLWFPGRSCDIVMTQSPSSLAMSVGQKVTMCKSSQSLNSSIQ
 30 KNYLAWYQQKPGQSPKLLIYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYF
 CQQHYSTPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
 VQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGL
 SSPVTKSFNRGEC

Example 7 Expression identification of chimeric antibodies

The results of ELISA analysis on the expression identification of chimeric antibodies are shown in Figure 15. The results of flow cytometry detection are shown in Figure 16. The chimeric antibodies of hybridoma 6G10-1D7, 99B3G3, 105C10F1 and 107B11E1D7 bound to the soluble extracellular domains of human BCMA molecules on the cell surface. The chimeric antibodies formed by pairing of the heavy chain 107A9A4D2VH and the light chain 107A9A4D2VL-2 of the hybridoma 107A9A4D2 all bound to the soluble extracellular domains of human BCMA molecules on the cell surface. The chimeric antibodies formed by pairing of 107A9A4D2VH and 107A9A4D2VL-1 did not bind to the soluble extracellular domains of human BCMA molecules on the cell surface. See Table 10 for detailed data.

Table 10 Detection results of the supernants of the chimeric antibodies

Clone	Elisa (OD450 nm)	FACS (MFI)	
	hBCMA-ECD-Fc	L-BCMA ⁺	L
6G10-1D7	2.35	3467.5	31
99B3G3	2.3	2180	31
105C10F1	2.39	1801	32
113B3F12	0.09	37.5	32
107A9A4D2VH/VL-1	0.13	42.5	36
107A9A4D2VH/VL-2	2.45	525	35
107B11E1D7	2.38	565.5	34

Example 8 Construction of lentiviral expression vectors containing a CAR structure

The light chains and heavy chains of the nine antibodies obtained from the foregoing screening shown in Table 11 were used to construct 18 chimeric antigen receptors (CARs). The structure of a CAR comprises a signal peptide (leader sequence), an antigen-binding region, a linker region, a transmembrane domain, a costimulatory region, and a cytoplasmic signaling domain (e.g., a cytoplasmic signaling domain of CD3zeta), and the hinge region is as follows:

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

Table 11 Chimeric antigen receptors constructed by using the VL and VH of the antibodies

Clones	Re-named	VL-Linker-VH	VH-Linker-VL
6G10-1D7	CP01	BCMA-CP01	BCMA-CP01R
99B3G3	CP02	BCMA-CP02	BCMA-CP02R
105C10F1	CP03	BCMA-CP03	BCMA-CP03R
107A11F1B7	CP04	BCMA-CP04	BCMA-CP04R
107B11E1D7	CP05	BCMA-CP05	BCMA-CP05R
109C5F3C1	CP06	BCMA-CP06	BCMA-CP06R
143D6F4	CP07	BCMA-CP07	BCMA-CP07R
151A9A4	CP08	BCMA-CP08	BCMA-CP08R
152D8E8	CP09	BCMA-CP09	BCMA-CP09R

Based on the sequences of the CARs constructed above, expression vectors were constructed through full-length DNA synthesis and cloning. The selected expression vectors were pWPT lentiviral vectors, and the cloning sites were BamH I and Sal I sites. The specific sequence of each CAR is as follows:

(1) The leader sequence (signal peptide) was the leader sequence of CD8 antigen: MALPVTALLLPLALLLHAARP (SEQ ID NO: 52)

(2) Single-chain variable region light chain (VL) sequence derived from BCMA-CP01 antibody:

DIVMTQSQRFMSTSVGDRVSITCKASQSVGTAVAWYQQTPGQFPKLLIYSTSNR
YTGVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYSTYPLTFGSGTKLELK (SEQ
ID NO: 53)

(3) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP01 antibody:

EVQLQQSGPELVKPGASMKISCKASDYSFTDYIMTWVKQSHGKNLEWIGLINPY
NGGTTYNQKFKDKATFTVDKSSTTAYMDLLSLTSEDSAVYYCARRGITTDYITMDY
WGQGTSTVTVSS (SEQ ID NO: 54)

(4) Single-chain variable region light chain (VL) sequence derived from BCMA-CP02 antibody:

DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSIQKNYLAWYQQKPGQSPKLL
VYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQQHYSSPLTFGAGTKLE
LK (SEQ ID NO: 55)

(5) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP02 antibody:

EVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNWVKQSHGKSLEWIGVIN
 PYNGGTSYNQKFKAKATLTVDKSSITAYMELNSLTSEDSAVYYCARGDSIYVMDYW
 5 GQGTSVTVSS (SEQ ID NO: 56)

(6) Single-chain variable region light chain (VL) sequence derived from BCMA-CP03 antibody:

DIVMTPSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASY
 RYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQHYNSYPFTFGSGTKLEIK (SEQ
 10 ID NO: 57)

(7) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP03 antibody:

EVKLLQSGGGLVQPGGSLKLSCAASGIDFSRYWMSWVRRAPGKGLEWIGEINP
 DSSTINYAPSLKDKFIISRDAAKNTLYLQMSKVRSEDTALYYCATLYDYDGDYAM
 15 DYWGQGTSTVTVSS (SEQ ID NO: 58)

(8) Single-chain variable region light chain (VL) sequence derived from BCMA-CP04 antibody:

DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSIQKNYLAWYQQKPGQSPKLLI
 YFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQQHYSTPLTFGAGTKLEL
 20 K (SEQ ID NO: 59)

(9) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP04 antibody:

EVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNWLKQSHGKRLEWIGVIN
 PYNGGTSYNQKFKGKATLTVDKSSSTAYMDLNSLTSEDSAVYYCARGDSIYVMDY
 25 WGQGTSTVTVSS (SEQ ID NO: 60)

(10) Single-chain variable region light chain (VL) sequence derived from BCMA-CP05 antibody:

ENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWIYDTSKLS
 SGVPGRFSGSGSGKSYSLTISSMEAEDVATYYCFQGSGLYPLFTFGSGTKLEIK (SEQ ID
 30 NO: 61)

(11) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP05 antibody:

EVQLQQSGPVLVKPGASVKMSCKASGYTFTDLYMNWLKQSHGKRLEWIGVIN
 PYNGGTSYNQKFKGKATLTVDKSSSTAYMDLNSLTSEDSAVYYCARGDSIYVMDY

WGQGTSFTVSS (SEQ ID NO: 62)

(12) Single-chain variable region light chain (VL) sequence derived from BCMA-CP06 antibody:

DIVMTQSPSSLALSVGQKVTMSCKSSQSLLDNSNQKHYLA
 5 WYQQKPGQSPKLL
 VYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQ
 QHYTAPLTFGAGTKLA
 LK (SEQ ID NO: 63)

(13) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP06 antibody:

EVQLQQSGPVLVKPGASVKMSCKVSGYTFTDYMNWVKQSHGKSLEWIGVIT
 10 PYNGANRYNQKFKGKATLTVDKSSSTAYMEVSSLTSEDSAVYYCARGDSIYVMDY
 WGQGTSVIVSS (SEQ ID NO: 64)

(14) Single-chain variable region light chain (VL) sequence derived from BCMA-CP07 antibody:

DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSIQKNYLA
 15 WYQQKPGQSPKLL
 VYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQ
 QHYSTPLTFGGGTKLE
 LK (SEQ ID NO: 65)

(15) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP07 antibody:

EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYSLNWVKQSHGKSLEWIGVVN
 20 PYNGGTSHNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARPDSIYVMDYW
 GQGTSVTVSS (SEQ ID NO: 66)

(16) Single-chain variable region light chain (VL) sequence derived from BCMA-CP08 antibody:

DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSNIQKNYLA
 25 WYQQKPGQSPKLL
 VYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQ
 QHYSTPLTFGAGTKLE
 LK (SEQ ID NO: 67)

(17) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP08 antibody:

EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYSLNWVKQSHGKSLEWIGVVN
 30 PYNGGTTYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARPDSIYVMDSW
 GQGTSVTVSS (SEQ ID NO: 68)

(18) Single-chain variable region light chain (VL) sequence derived from BCMA-CP09 antibody:

DIKMTQSPSSMYVSLGERVTITCKASQDINRNLWVWFQQKPGKSPKTLIYRANRL

VDGVPLRFSGSGSGQDYSLTISSEYEDMGIYYCLQYDEFPRTFGGGKLEIK (SEQ ID NO: 69)

(19) Single-chain variable region heavy chain (VH) sequence derived from BCMA-CP09 antibody:

5 QVTLKESGPGILQSSQTLSTCSFSGFSLNTSGMGVNWIRQSSGKDLEWLAHIY
WNDDKRYNPSLKSRLTISKDTSRNQVFLRITSVDATDTATYFCCSRSLSFQYWGHT
TLTVSS (SEQ ID NO: 70)

(20) Linker sequence between the heavy chains and light chains in the single-chain variable regions of BCMA-CP01/R, 02/R, 03/R, 04/R, 05/R, 06/R, 07/R, 08/R and 09/R is as
10 follows:

GGGGSGGGSGGGGS (SEQ ID NO: 71)

(21) Sequence of the hinge region (and linker region):

FVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD
(SEQ ID NO: 72)

15 (22) Sequence of a transmembrane domain, which is a CD8 (CD8TM) transmembrane domain:

IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 73)

(23) Sequence of an intracellular signaling motif from 4-1BB in the co-stimulatory region:

20 KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 74)

(24) Sequence of an immunoreceptor tyrosine-based activation motif (ITAM) from TCR complex in the cytoplasmic signaling region of CD3 zeta:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPQR
RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH
25 MQALPPR (SEQ ID NO: 75)

Example 9 Preparation of CAR-T cells

(1) Healthy human venous blood was taken and isolation by the density gradient centrifugation was performed to obtain mononuclear cells (PBMCs).

30 (2) On Day 0, PBMCs were inoculated into cell culture flasks coated in advance with a 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 CBMG-RC-09a cell medium containing 1% human albumin. Recombinant human interleukin 2 (CBMG-RC-05b) at a final concentration of 1000 U/mL was added. The

medium was cultured in a CO₂ incubator at 37 °C and saturated humidity of 5%.

(3) On Day 1, the supernatant of the cultured PBMCs was slowly removed, fresh CBMG-RC-09a cell medium containing 1% human albumin was added. Recombinant human interleukin 2 (CBMG-RC-05b) was added to the medium to a final concentration of 1000 U/mL. The cells continued to be cultured in a CO₂ incubator at 37 °C and saturated humidity of 5%.

(4) On Day 3, fresh culture medium, concentrated and purified CAR-BCMAs lentiviruses, protamine sulfate (12 µg/ml), and CBMG-RC-05b at a final concentration of 1000 U/mL were added. After transduction in a 37°C, 5% CO₂ incubator for 12 hours, the culture solution was discarded, fresh medium was added, and culturing was continued in the 37°C, 5% CO₂ incubator.

(5) From Day 6 on, CART-BCMAs cells were used for desired activity tests.

Example 10 Detection of the integration rates of CAR genes in T cell genomes and the expression levels of proteins encoded by the CAR genes on the membrane surface

Using 0.5×10⁶ CART-BCMAs cells cultured for 7 days in Example 9, after staining of recombinant human BCMA protein Fc fragment, the expression levels of CAR-BCMA proteins on the T cell membrane surface were analyzed on a flow cytometer.

The results are shown in Figure 17. Except that BCMA-CP01, CP09, and CP09R, the three CAR-T lentiviruses, did not have a transfection rate, the other 15 BCMA-CP CAR-T cells all had a relatively high T cell surface expression of CAR after seven days of transduction. 6C and 8C were positive controls.

Example 11 Detection of CART-BCMAs *in vitro* activation ability

The CART-BCMAs cells cultured for seven days in Example 9 were used to detect proteins CD137 and IFN γ , the cell activation level indicators. 1×10⁵ CART-BCMA cells cultured for seven days were cultured with human BCMA-positive A549-BCMA-1D6, MM.1S, RPMI822 6 tumor cell line, monkey BCMA-positive A549-BCMA-M, BCMA-negative A549 tumor cell line or addition-free tumor cells, respectively, in 200 µl of CBMG-RC-09a medium at a ratio of 1:1 for 18 h. Then the expression level of CD137 on the T cell membrane surface was detected by flow cytometry, and the secretion level of IFN γ in the culture supernatant was detected by ELISA.

The results are as shown in Figures 18 and 19. BCMA-CP01R, CP03 and CP03R showed a high-specificity IFN- γ release ability and CD137 activation-specific up-regulation

expression to A549-BCMA-1D6 cells only. BCMA-CP02/R, CP04/R and CP05/R showed a high-specificity IFN- γ release ability and CD137 activation-specific up-regulation expression to both A549-BCMA-1D6 and A549-BCMA-M cells.

5 **Example 12 Detection of cytotoxicity of CART-BCMAs cells towards target cells**

RTCA (real-time cellular analysis) was performed to detect the cytotoxicity of the CART cells (BCMA-CP01/R - 05/R) cultured for 14 days and the CART cells (BCMA-CP06/R - 09/R) cultured for 12 days in Example 9 towards target cells. After they were co-cultured with BCMA-negative cells (A549), human BCMA-positive self-constructed cells A549-BCMA-1D6, or monkey BCMA-positive self-constructed cells A549-BCMA-M at the ratios shown in Figure 4 in 200 μ l of CBMG-RC-09a medium, respectively for 8 h, the cytotoxicities of the CART cells towards each target cell were analyzed.

The results are shown in Figure 20. BCMA-CP01R, CP03 and CP03R had strong cytotoxicity towards A549-BCMA-1D6. BCMA-CP02/R, 04/R and 05/R had strong cytotoxicity towards A549-BCMA-1D6 and A549-BCMA-M cells and did not have a significant killing effect on negative target cells A549. The untransduced control group (NT) also did not have a significant killing effect on the target cells.

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.

What is claimed is:

1. An anti-BCMA antibody, or an antigen-binding portion thereof, comprising a light chain variable region (V_L) and a heavy chain variable region (V_H),

5 wherein the light chain variable region comprises three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 76, 77 and 78, respectively, (ii) SEQ ID NOs: 82, 83 and 84, respectively, (iii) SEQ ID NOs: 88, 89 and 90, respectively, (iv) SEQ ID NOs: 94, 95 and 96, respectively, (v) SEQ ID NOs: 100, 101 and 102, respectively, (vi) SEQ ID NOs: 106, 107 and 108, respectively, (vii) SEQ ID NOs: 112, 113 and 114, respectively, (viii) SEQ ID NOs: 118, 119 and 120, respectively, or (ix) SEQ ID NOs: 124, 125 and 126, respectively; and

 wherein the heavy chain variable region comprises three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences
15 about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 79, 80 and 81, respectively, (ii) SEQ ID NOs: 85, 86 and 87, respectively, (iii) SEQ ID NOs: 91, 92 and 93, respectively, (iv) SEQ ID NOs: 97, 98 and 99, respectively, (v) SEQ ID NOs: 103, 104 and 105, respectively, (vi) SEQ ID NOs: 109, 110 and 111, respectively, (vii) SEQ ID NOs: 115, 116 and 117, respectively, (viii) SEQ ID NOs: 121, 122 and 123, respectively, or (ix) SEQ ID NOs: 127, 128 and 129, respectively.

2. An anti-BCMA antibody, or an antigen-binding portion thereof, comprising a light chain variable region (V_L) and a heavy chain variable region (V_H),

25 (i) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 76, 77 and 78, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 79, 80 and 81, respectively;

30 (ii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 82, 83 and 84, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences

about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 85, 86 and 87, respectively;

(iii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 88, 89 and 90, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 91, 92 and 93, respectively;

(iv) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 94, 95 and 96, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 97, 98 and 99, respectively;

(v) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 100, 101 and 102, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 103, 104 and 105, respectively;

(vi) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 106, 107 and 108, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 109, 110 and 111, respectively;

(vii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 112, 113 and 114, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 115, 116 and 117, respectively;

(viii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth

in SEQ ID NOs: 118, 119 and 120, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 121, 122 and 123, respectively; or

5 (ix) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 124, 125 and 126, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs:
10 127, 128 and 129, respectively.

3. The antibody or antigen-binding portion thereof of claims 1 or 2, wherein the V_L and V_H have amino acid sequences about 80% to about 100% identical to amino acid sequences set forth in (i) SEQ ID NO: 53 and SEQ ID NO: 54, respectively, (ii) SEQ ID
15 NO: 55 and SEQ ID NO: 56, respectively, (iii) SEQ ID NO: 57 and SEQ ID NO: 58, respectively, (vi) SEQ ID NO: 59 and SEQ ID NO: 60, respectively, (v) SEQ ID NO: 61 and SEQ ID NO: 62, respectively, (vi) SEQ ID NO: 63 and SEQ ID NO: 64, respectively, (vii) SEQ ID NO: 65 and SEQ ID NO: 66, respectively, (viii) SEQ ID NO: 67 and SEQ ID NO: 68, respectively, or (ix) SEQ ID NO: 69 and SEQ ID NO: 70,
20 respectively.

4. The antibody or antigen-binding portion thereof of claims 1 or 2, wherein the V_L comprises an amino acid sequence about 80% to about 100% identical to any one of the amino acid sequences set forth in SEQ ID NOs: 53, 55, 57, 59, 61, 63, 65, 67 and 69,
25 and wherein the V_H comprises an amino acid sequence about 80% to about 100% identical to any one of the amino acid sequences set forth in SEQ ID NOs: 54, 56, 58, 60, 62, 64, 66, 68 and 70.

5. The antibody or antigen-binding portion thereof of any of claims 1-4, wherein the
30 antibody or antigen-binding portion thereof is selected from the group consisting of: (a) a whole immunoglobulin molecule; (b) an scFv; (c) a Fab fragment; (d) an F(ab')₂; and (e) a disulfide linked Fv.

6. An antibody conjugate, comprising the antibody or antigen-binding portion thereof of any of claims 1-4, linked with a conjugate moiety selected from the group consisting of a detectable marker, a drug, a toxin, a cytokine, a radionuclide, an enzyme, a targeting moiety, and combinations thereof.

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7. The antibody conjugate of claim 6, which is an antibody drug conjugate (ADC).

8. A composition comprising the antibody or antigen-binding portion thereof of any of claims 1-4, and a pharmaceutically acceptable carrier.

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9. A nucleic acid encoding the antibody or antigen-binding portion thereof of any of claims 1-4.

10. A vector comprising the nucleic acid of claim 9.

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11. A cell comprising the vector of claim 10.

12. 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),

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wherein the light chain variable region comprises three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 76, 77 and 78, respectively, (ii) SEQ ID NOs: 82, 83 and 84, respectively, (iii) SEQ ID NOs: 88, 89 and 90, respectively, (iv) SEQ ID NOs: 94, 95 and 96, respectively, (v) SEQ ID NOs: 100, 101 and 102, respectively, (vi) SEQ ID NOs: 106, 107 and 108, respectively, (vii) SEQ ID NOs: 112, 113 and 114, respectively, (viii) SEQ ID NOs: 118, 119 and 120, respectively, or (ix) SEQ ID NOs: 124, 125 and 126, respectively; and

25

wherein the heavy chain variable region comprises three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in (i) SEQ ID NOs: 79, 80 and 81, respectively, (ii) SEQ ID NOs: 85, 86 and 87, respectively, (iii) SEQ ID NOs: 91, 92 and 93, respectively, (iv) SEQ ID NOs: 97, 98 and 99, respectively, (v) SEQ ID NOs: 103, 104 and 105, respectively, (vi) SEQ ID NOs: 109, 110 and 111,

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respectively, (vii) SEQ ID NOs: 115, 116 and 117, respectively, (viii) SEQ ID NOs: 121, 122 and 123, respectively, or (ix) SEQ ID NOs: 127, 128 and 129, respectively.

13. A chimeric antigen receptor (CAR), comprising an anti-BCMA antigen-binding
5 region which comprises a light chain variable region (V_L) and a heavy chain variable region (V_H),

(i) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid
sequences about 80% to about 100% identical to the amino acid sequences set forth in
SEQ ID NOs: 76, 77 and 78, respectively; the V_H comprising three complementarity
10 determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences
about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs:
79, 80 and 81, respectively;

(ii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid
sequences about 80% to about 100% identical to the amino acid sequences set forth in
15 SEQ ID NOs: 82, 83 and 84, respectively; the V_H comprising three complementarity
determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences
about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs:
85, 86 and 87, respectively;

(iii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid
20 sequences about 80% to about 100% identical to the amino acid sequences set forth in
SEQ ID NOs: 88, 89 and 90, respectively; the V_H comprising three complementarity
determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences
about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs:
91, 92 and 93, respectively;

(iv) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid
25 sequences about 80% to about 100% identical to the amino acid sequences set forth in
SEQ ID NOs: 94, 95 and 96, respectively; the V_H comprising three complementarity
determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences
about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs:
30 97, 98 and 99, respectively;

(v) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid
sequences about 80% to about 100% identical to the amino acid sequences set forth in
SEQ ID NOs: 100, 101 and 102, respectively; the V_H comprising three complementarity
determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences

about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 103, 104 and 105, respectively;

(vi) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 106, 107 and 108, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 109, 110 and 111, respectively;

(vii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 112, 113 and 114, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 115, 116 and 117, respectively;

(viii) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 118, 119 and 120, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 121, 122 and 123, respectively; or

(ix) the V_L comprising three CDRs, CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 124, 125 and 126, respectively; the V_H comprising three complementarity determining regions (CDRs), CDR1, CDR2 and CDR3, having amino acid sequences about 80% to about 100% identical to the amino acid sequences set forth in SEQ ID NOs: 127, 128 and 129, respectively.

14. The CAR of claims 12 or 13, wherein the V_L and V_H have amino acid sequences about 80% to about 100% identical to amino acid sequences set forth in (i) SEQ ID NO: 53 and SEQ ID NO: 54, respectively, (ii) SEQ ID NO: 55 and SEQ ID NO: 56, respectively, (iii) SEQ ID NO: 57 and SEQ ID NO: 58, respectively, (iv) SEQ ID NO: 59 and SEQ ID NO: 60, respectively, (v) SEQ ID NO: 61 and SEQ ID NO: 62, respectively, (vi) SEQ ID NO: 63 and SEQ ID NO: 64, respectively, (vii) SEQ ID NO: 65 and SEQ ID NO: 66, respectively, (viii) SEQ ID NO: 67 and SEQ ID NO: 68,

respectively, or (ix) SEQ ID NO: 69 and SEQ ID NO: 70, respectively.

15. The CAR of any of claims 12-14, wherein the anti-BCMA antigen-binding region is a single-chain variable fragment (scFv) that specifically binds BCMA.

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16. The CAR of any of claims 12-15, wherein the CAR further comprises one or more of the following:

- (a) a signal peptide,
- (b) a hinge region,
- 10 (c) a transmembrane domain,
- (d) a co-stimulatory region, and
- (e) a cytoplasmic signaling domain.

17. The CAR of claim 16, 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.

18. The CAR of claim 16, wherein the cytoplasmic signaling domain comprises a cytoplasmic signaling domain of CD3 ζ .

19. The CAR of claim 16, wherein the hinge region comprises a hinge region of Ig4, CD8, CD28, CD137, or combinations thereof.

20. The CAR of claim 16, wherein the transmembrane domain comprises a transmembrane domain of CD8, CD28, CD3 ϵ , CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or combinations thereof.

21. An immune cell expressing the CAR of any of claims 12-15.

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22. The immune cell of claim 21, wherein the immune cell is a T cell, a natural killer (NK) cell, a natural killer T cell, a lymphoid progenitor cell, a hematopoietic stem cell, a stem cell, a macrophage, or a dendritic cell.

23. A nucleic acid encoding the CAR of any of claims 12-15.

24. A vector comprising the nucleic acid of claim 23.

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25. A method of treating cancer, the method comprising administering the immune cell of claim 21 to a subject in need thereof.

26. The method of claim 25, wherein the cancer is a hematologic cancer.

10

27. The method of claim 25, wherein the cancer is a plasma-cell malignancy.

28. The method of claim 25, wherein the cancer is a BCMA-positive malignancy.

15

29. The method of claim 25, wherein the cancer is multiple myeloma (MM), or plasma cell leukemia.

30. The method of claim 25, wherein the immune cell is administered by infusion, injection, transfusion, implantation, and/or transplantation.

20

31. The method of claim 25, wherein the immune cell is administered intravenously, subcutaneously, intradermally, intranodally, intratumorally, intramedullary, intramuscularly, or intraperitoneally.

25

32. The method of claim 25, wherein the immune cell is administered via intravenous infusion.

33. The method of claim 25, wherein the immune cell is allogeneic or autologous.

30

34. The method of claim 25, wherein the subject is a human.

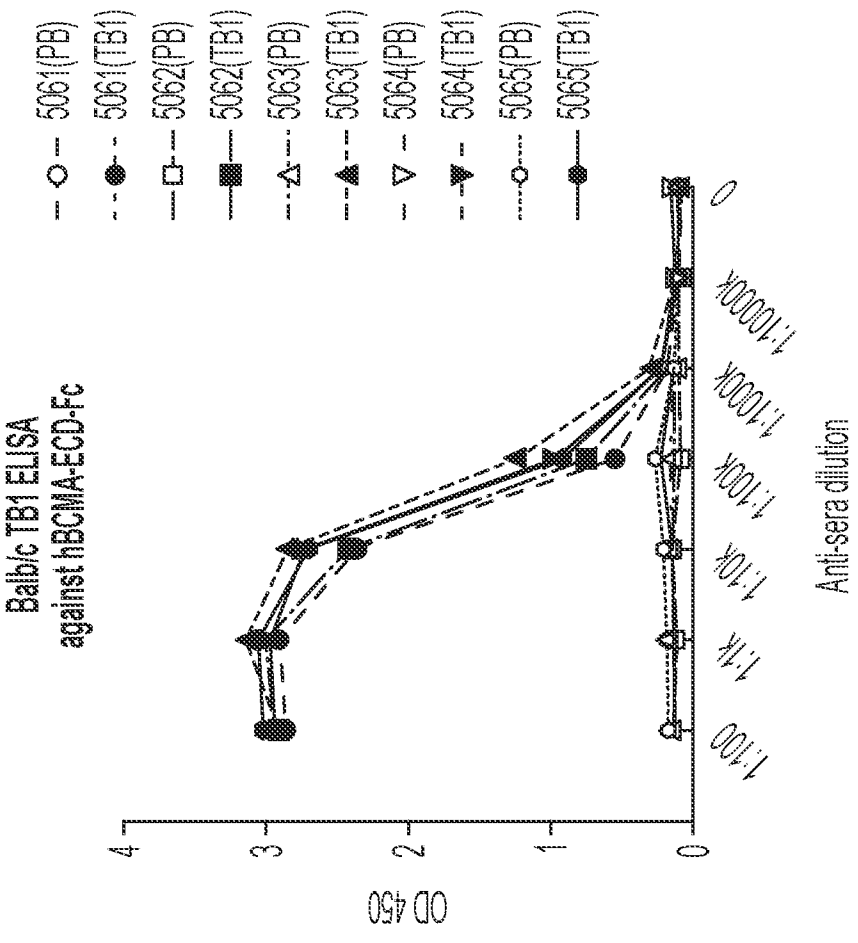
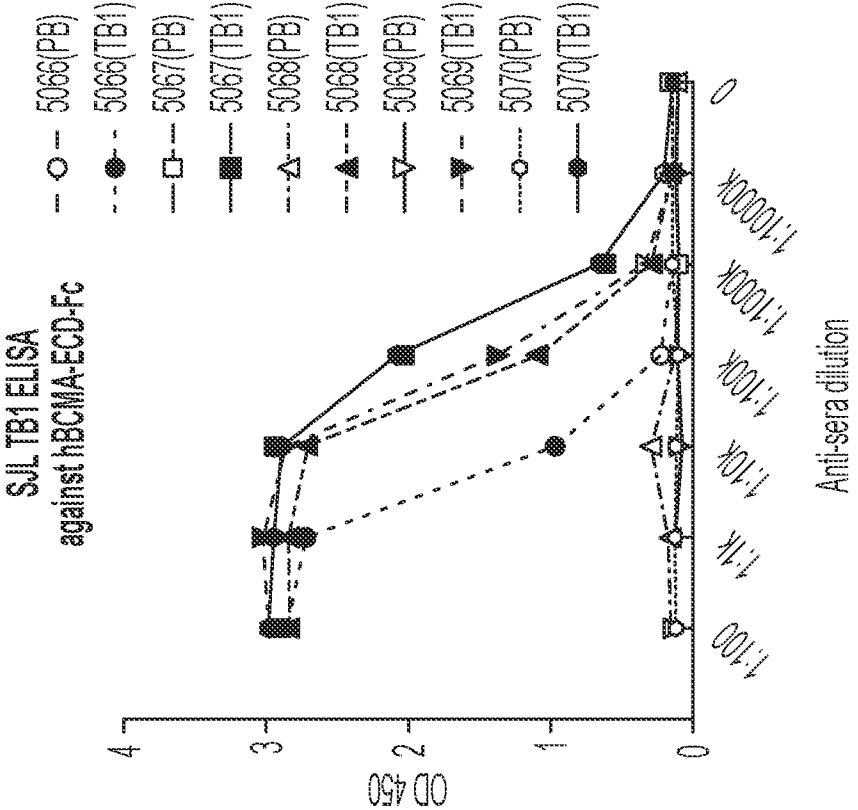


FIG. 1

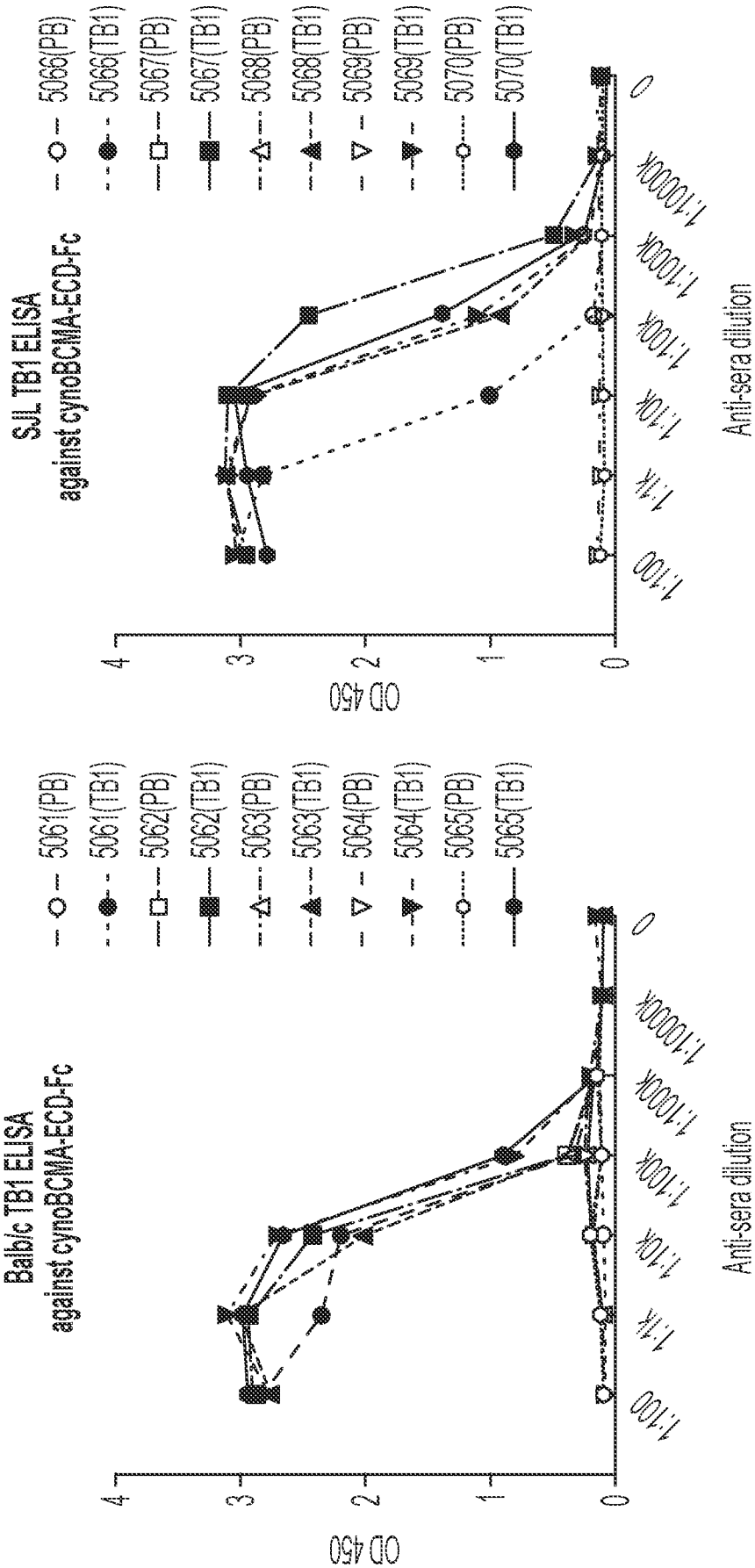
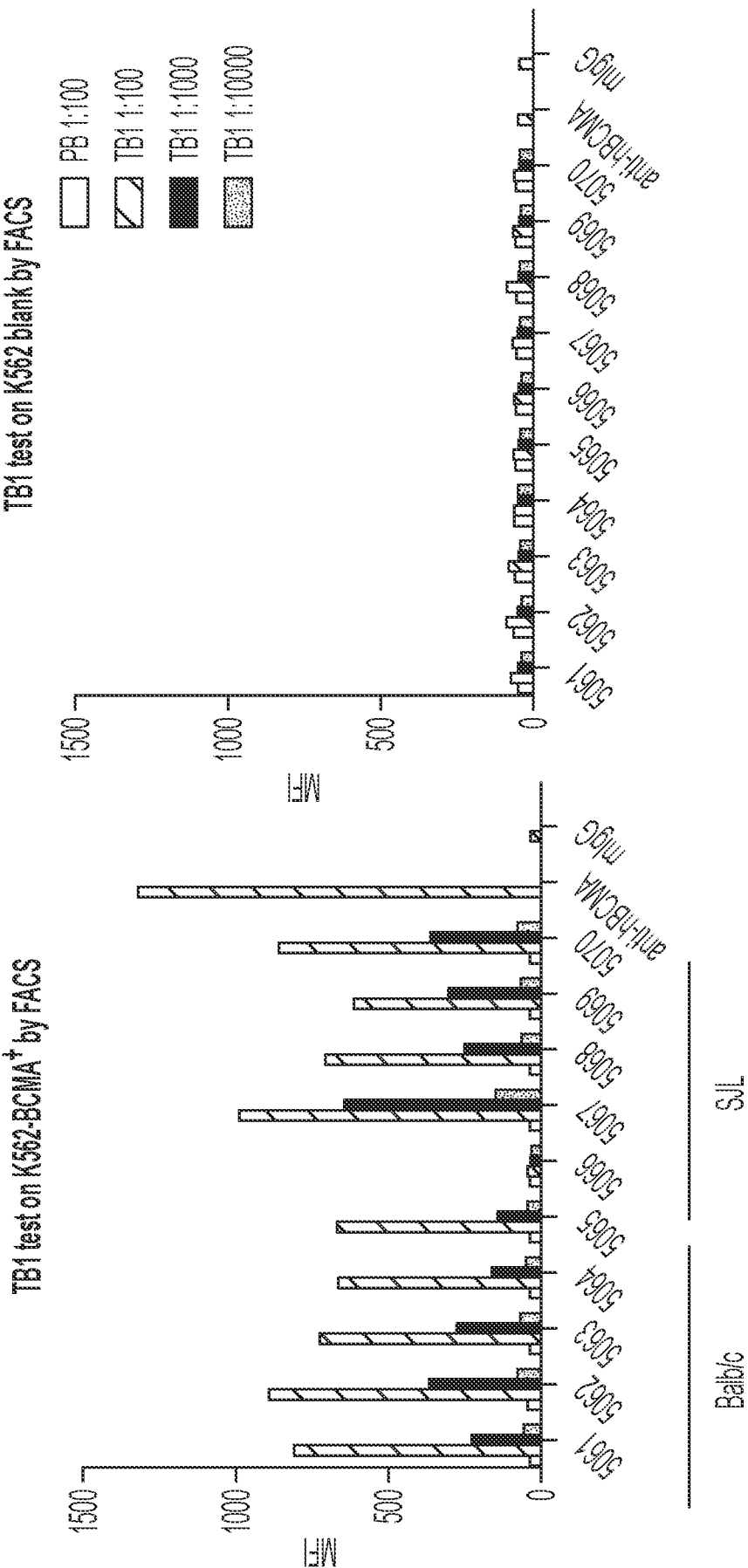


FIG. 1 CONT.

3/52



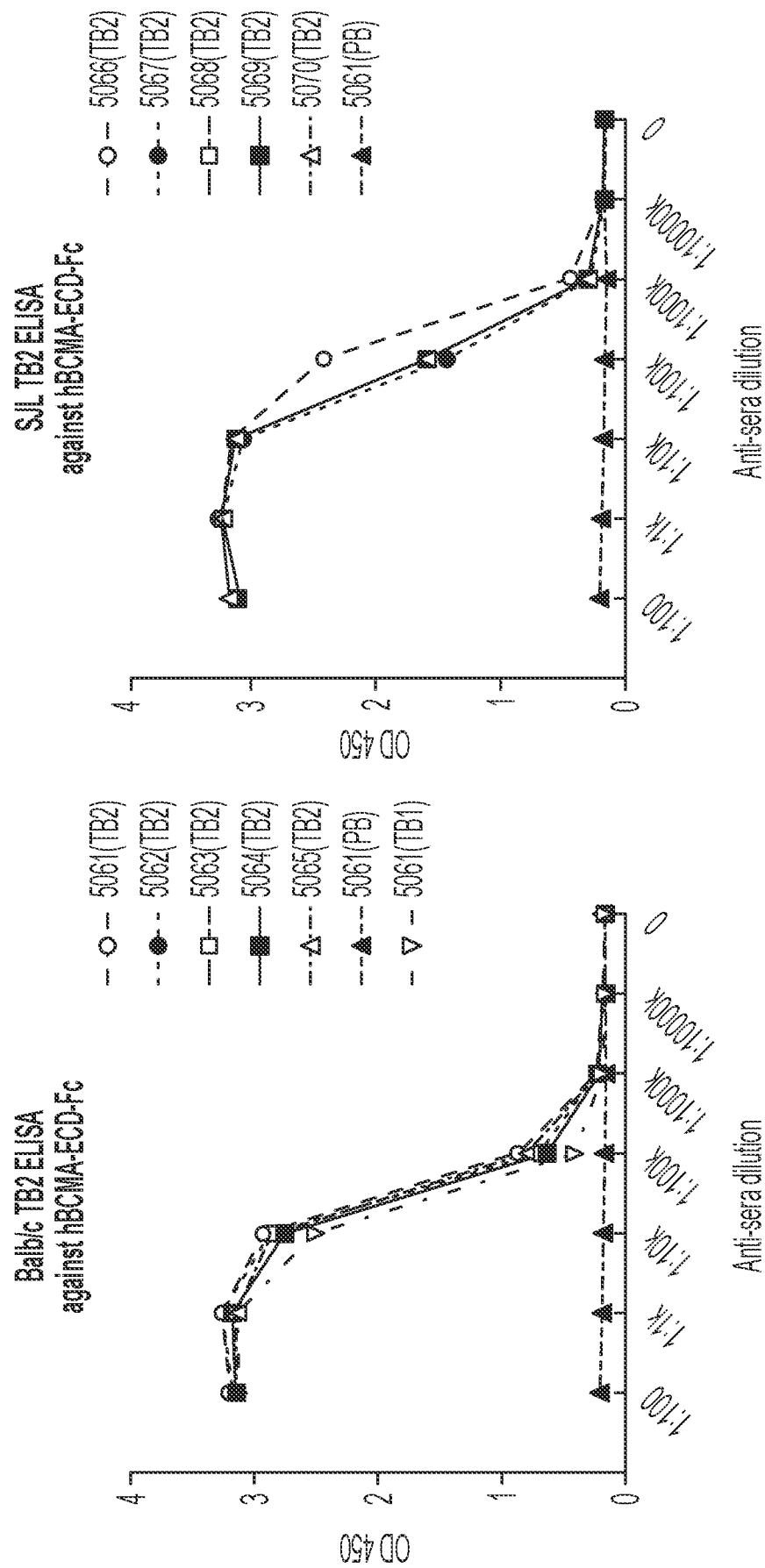


FIG. 3

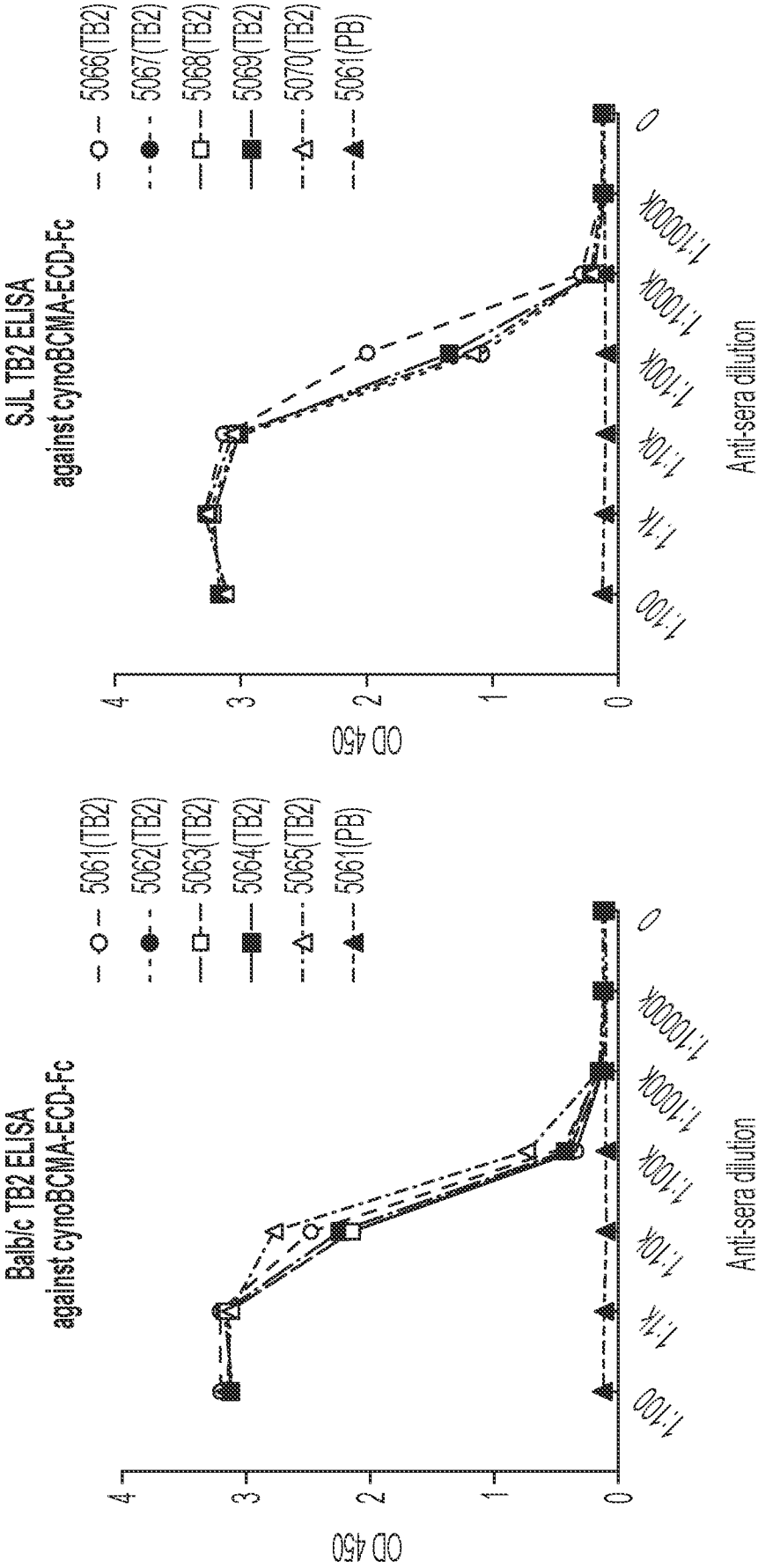


FIG. 3 CONT.

6/52

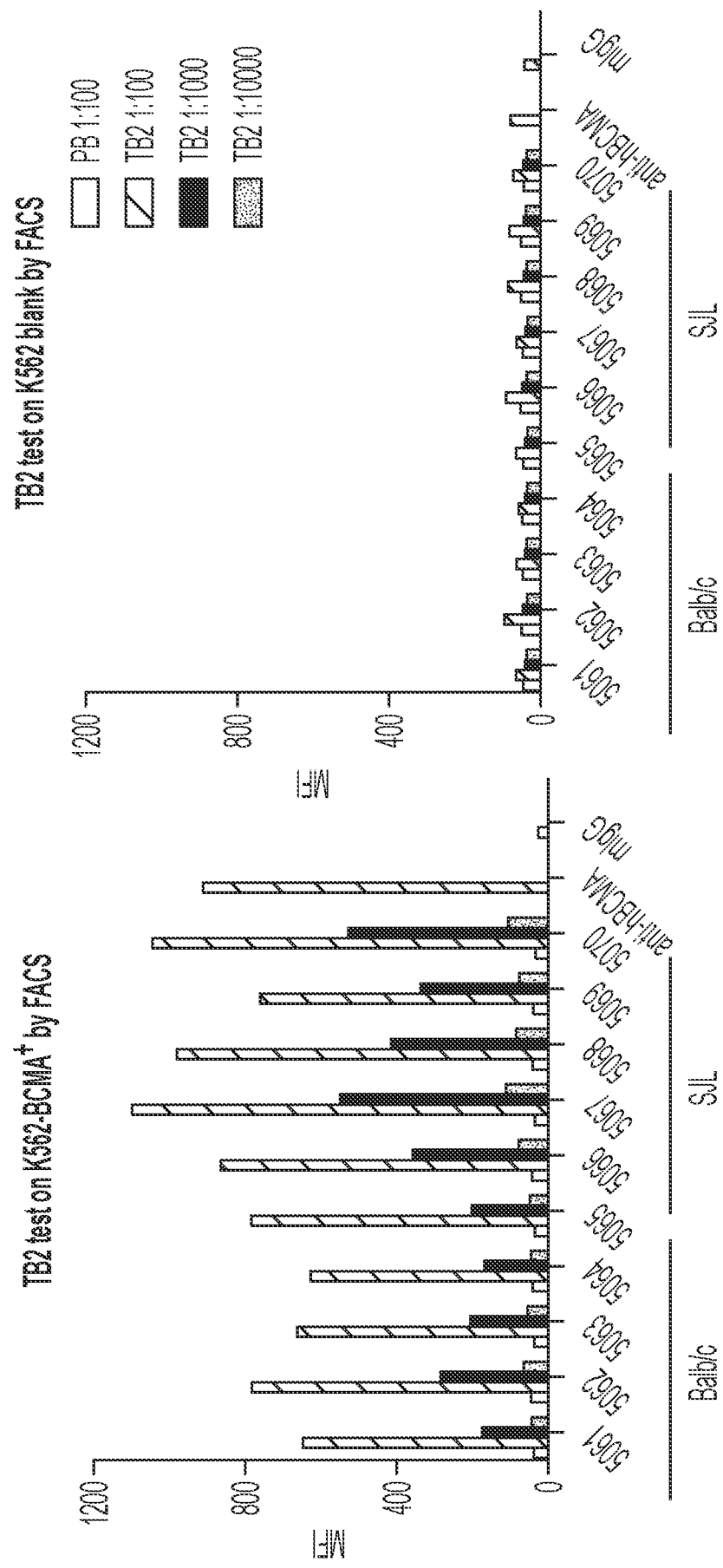


FIG. 4

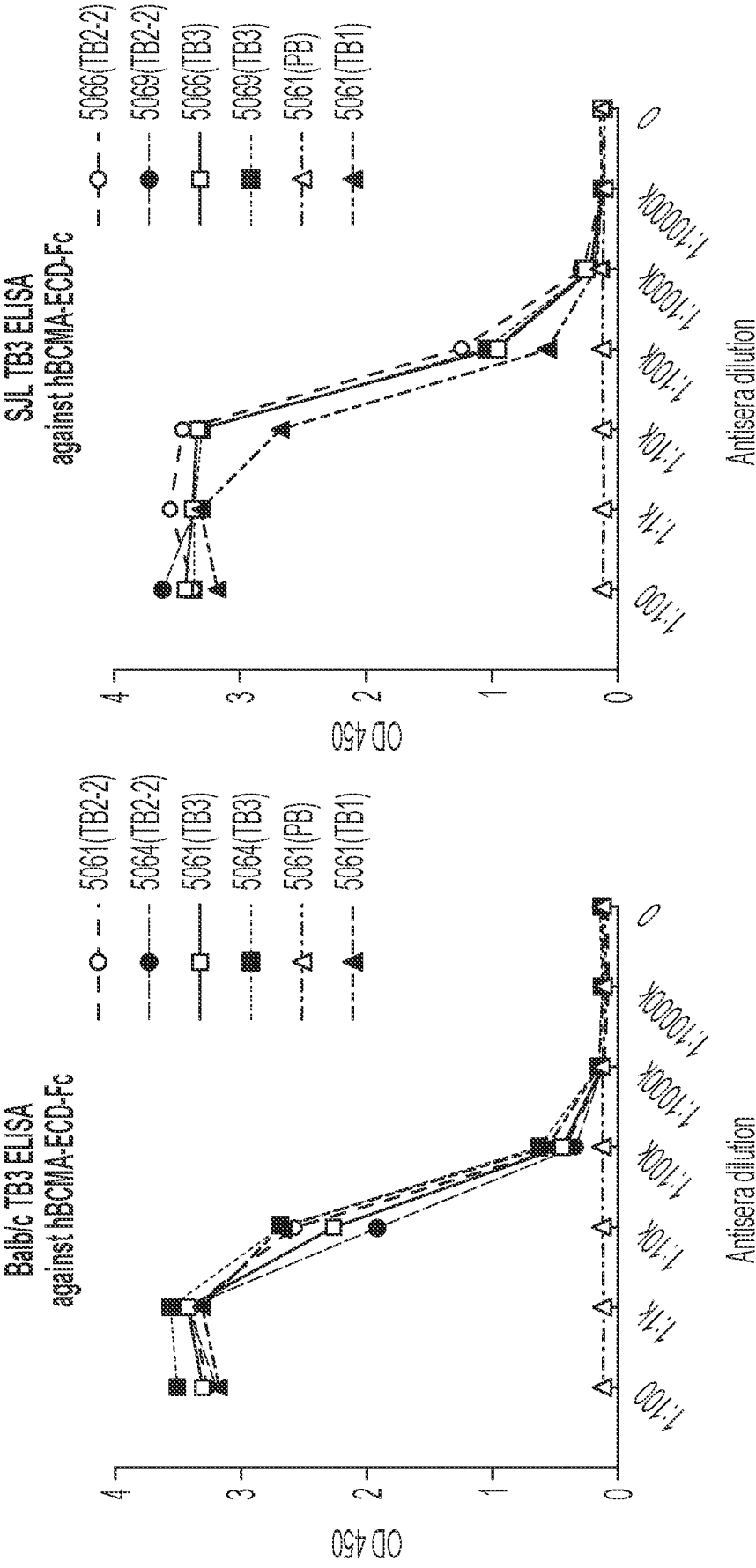


FIG. 5

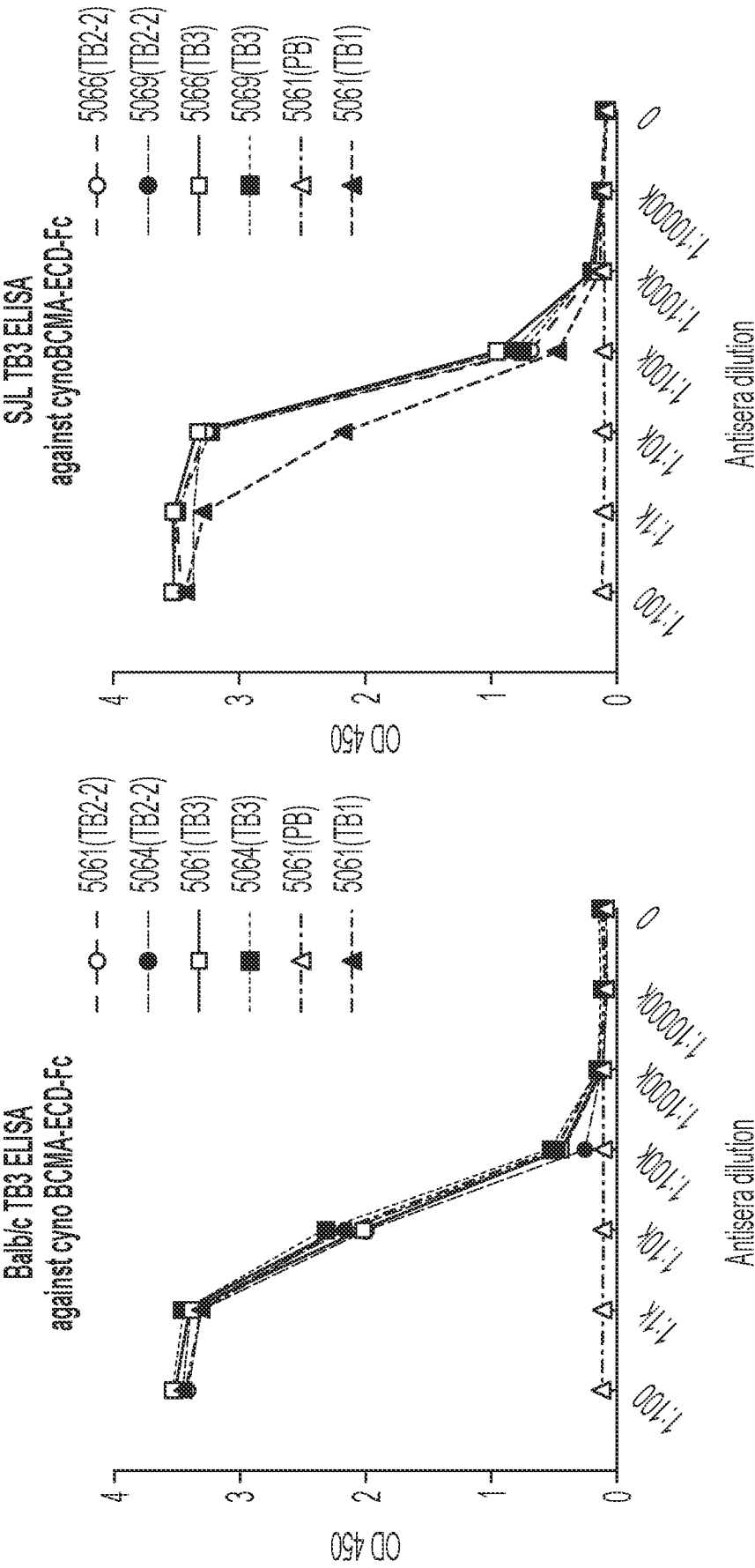


FIG. 5 CONT.

9/52

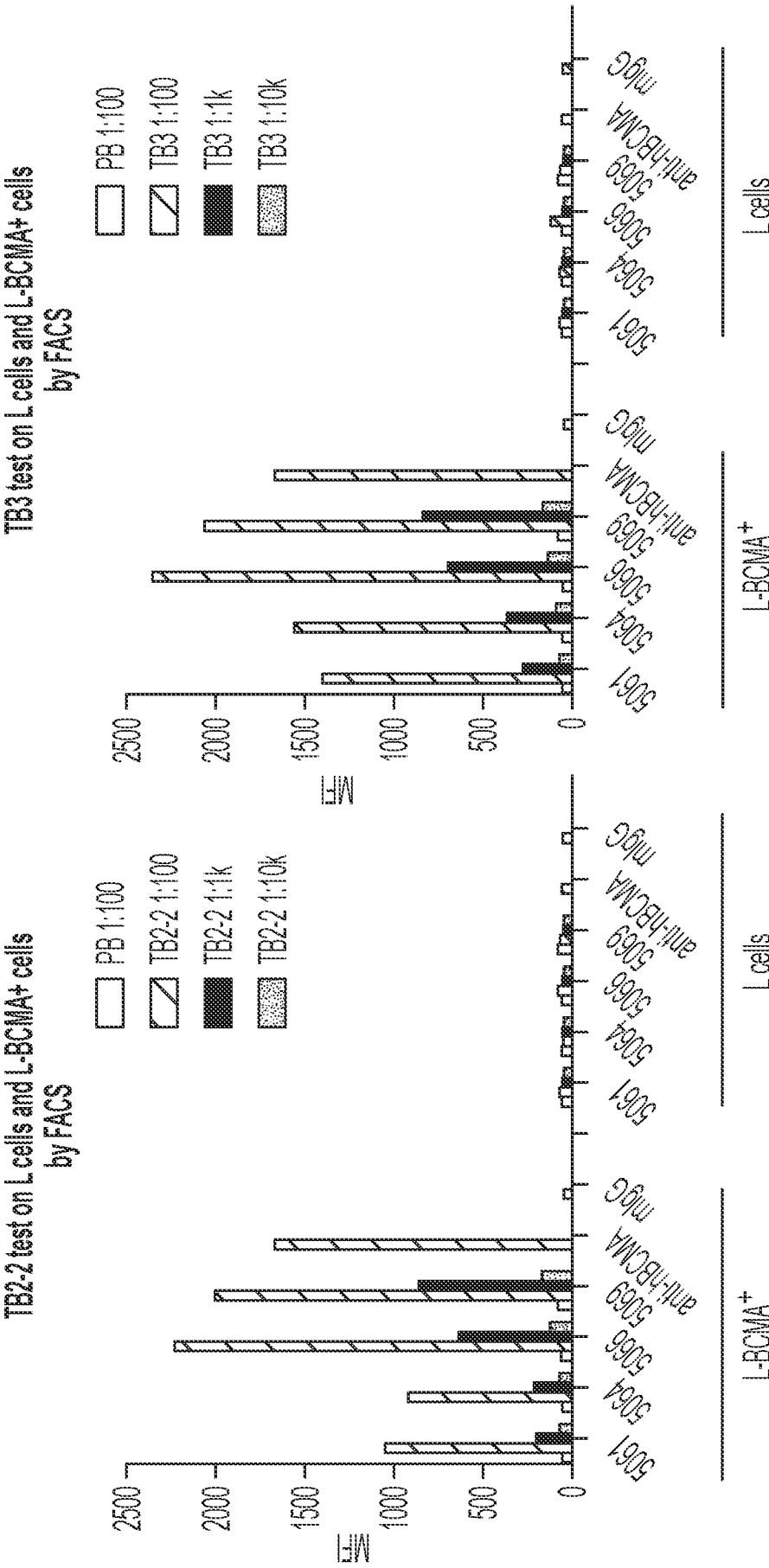


FIG. 6

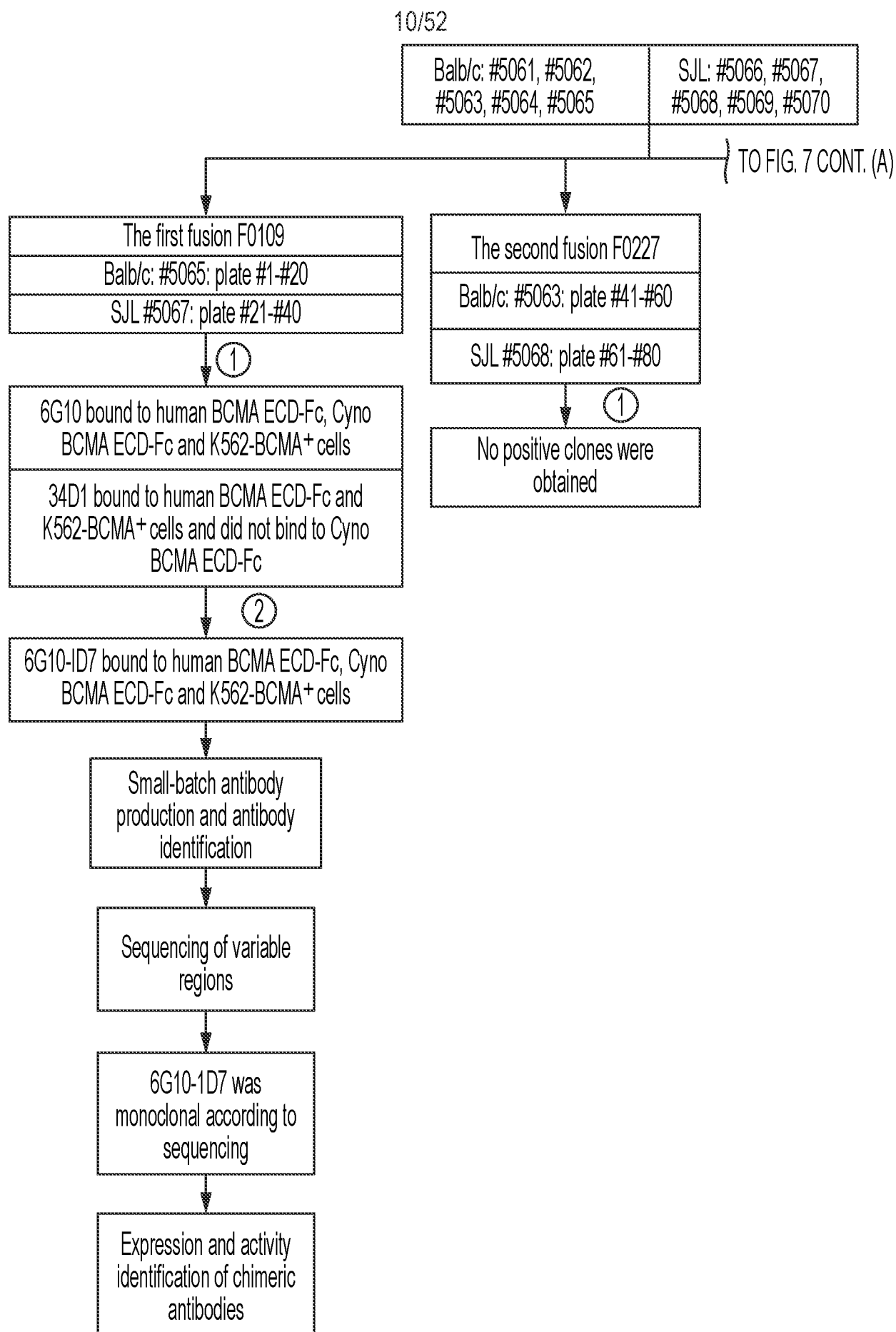


FIG. 7

FROM TO FIG.7 CONT. (A) } TO FIG. 7 CONT. (B)

The third fusion F0508
Balb/c: #5064; plate #81 #100
SJL #5069; plate #101 #120

①

109C5, 107A11, 107B11, 116H6, 102G2, 102A12, 111F11, 107A9, 111D5, 105F9, 114C6, 97B8, 97C4, 104H4, 115G7, 116A9, 100H2, 99B3, 110A11 bound to human BCMA ECD-Fc; Cyno BCMA ECD-Fc and L-BCMA⁺ cells

120D6, 120A10, 105C10, 113B3 bound to human BCMA ECD-Fc and L-BCMA⁺ cells;
and, did not bind to Cyno BCMA ECD-Fc

②

99B3G3, 102A12H6, 107A11F1, 107A9A4, 107B11E1 bound to human BCMA ECD-Fc; Cyno BCMA ECD-Fc and L-BCMA⁺ cells

Small-batch antibody
production and antibody
identification

Sequencing of variable
regions

TO FIG. 7 CONT. (C)

97B8G8, 100H2D12, 109C5F3 and 114C6C8 were not
monoclonal according to microscopic examination

②

100H2D12C6, 109C5F3C1 and 97B8G8D12 bound to human
BCMA ECD-Fc; Cyno BCMA ECD-Fc and L-BCMA⁺ cells

Small-batch antibody production and antibody identification

Sequencing of variable regions

The variable region sequences of 100H2D12C6 and
97B8G8D12 were same as those of 99B3G3; 109C5F3C1
was monoclonal according to sequencing

105C10F1 and 113B3F12 bound to human
BCMA ECD-Fc and L-BCMA⁺ cells; and
did not bind to Cyno BCMA ECD-Fc

Small-batch antibody production and antibody identification

Sequencing of variable regions

105C10F1 and 113B3F12 were monoclonal according
to sequencing

Expression and activity
identification of chimeric antibodies

11/52

FIG. 7 CONT.

12/52

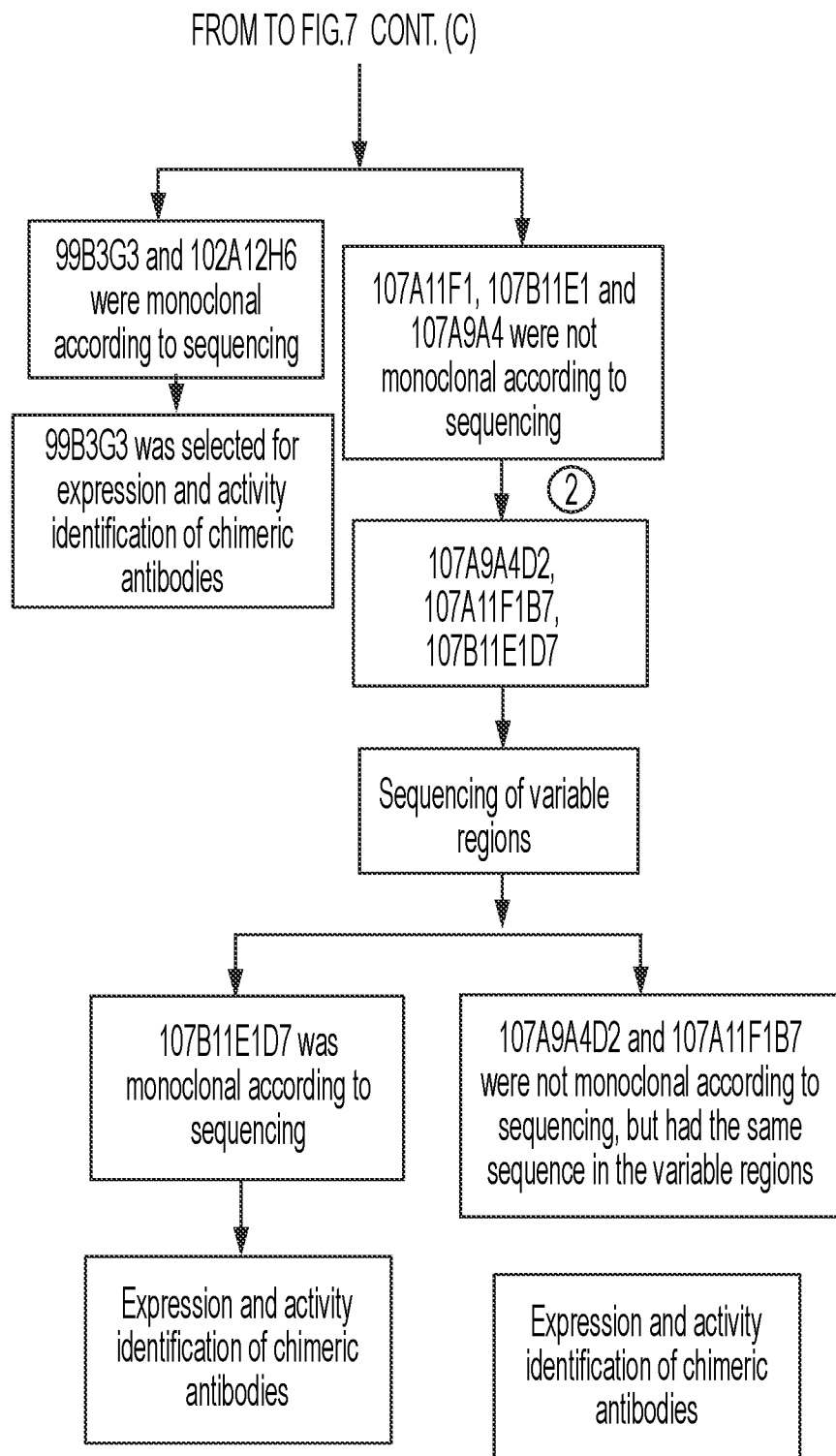


FIG. 7 CONT.

13/52

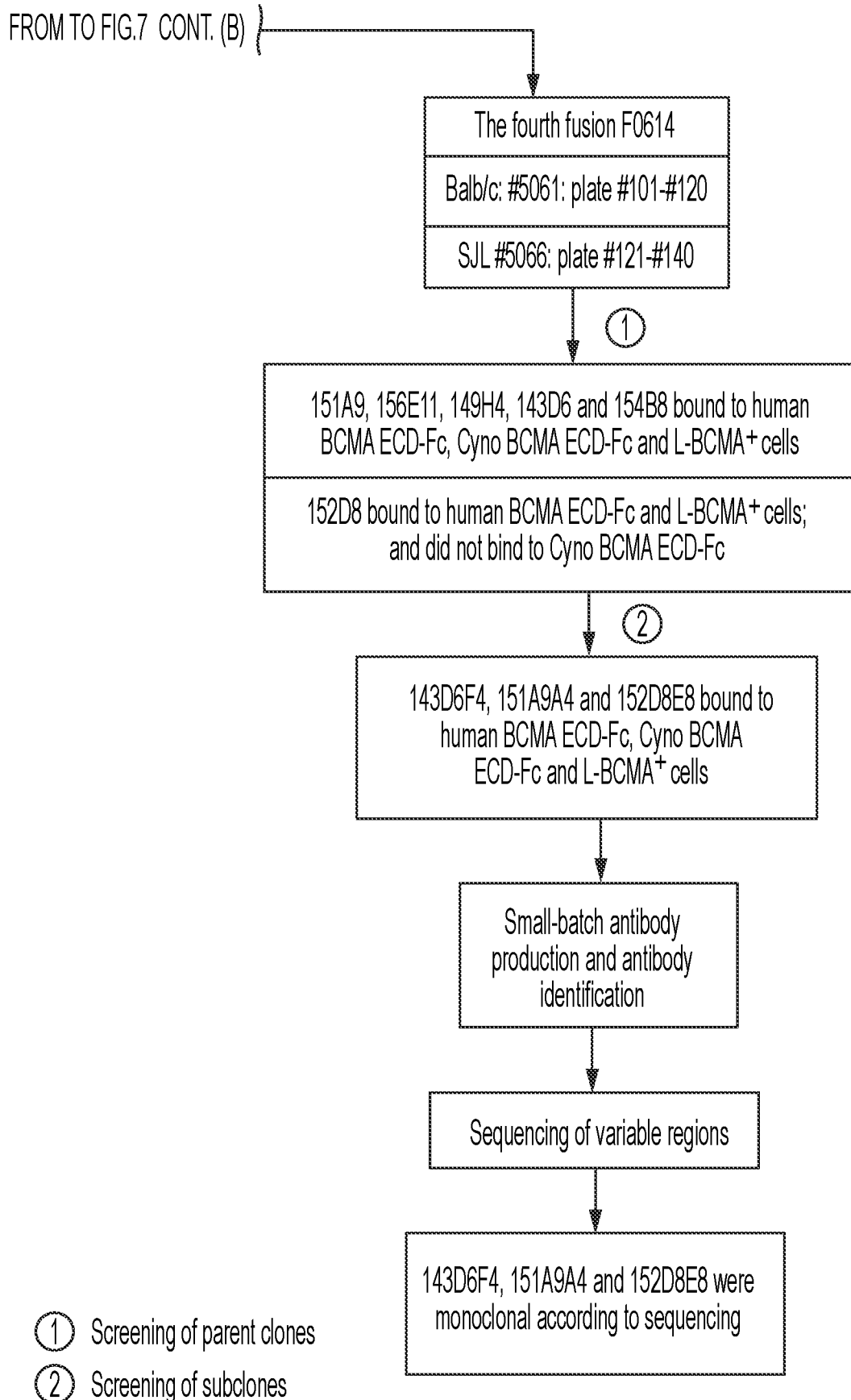


FIG. 7 CONT.

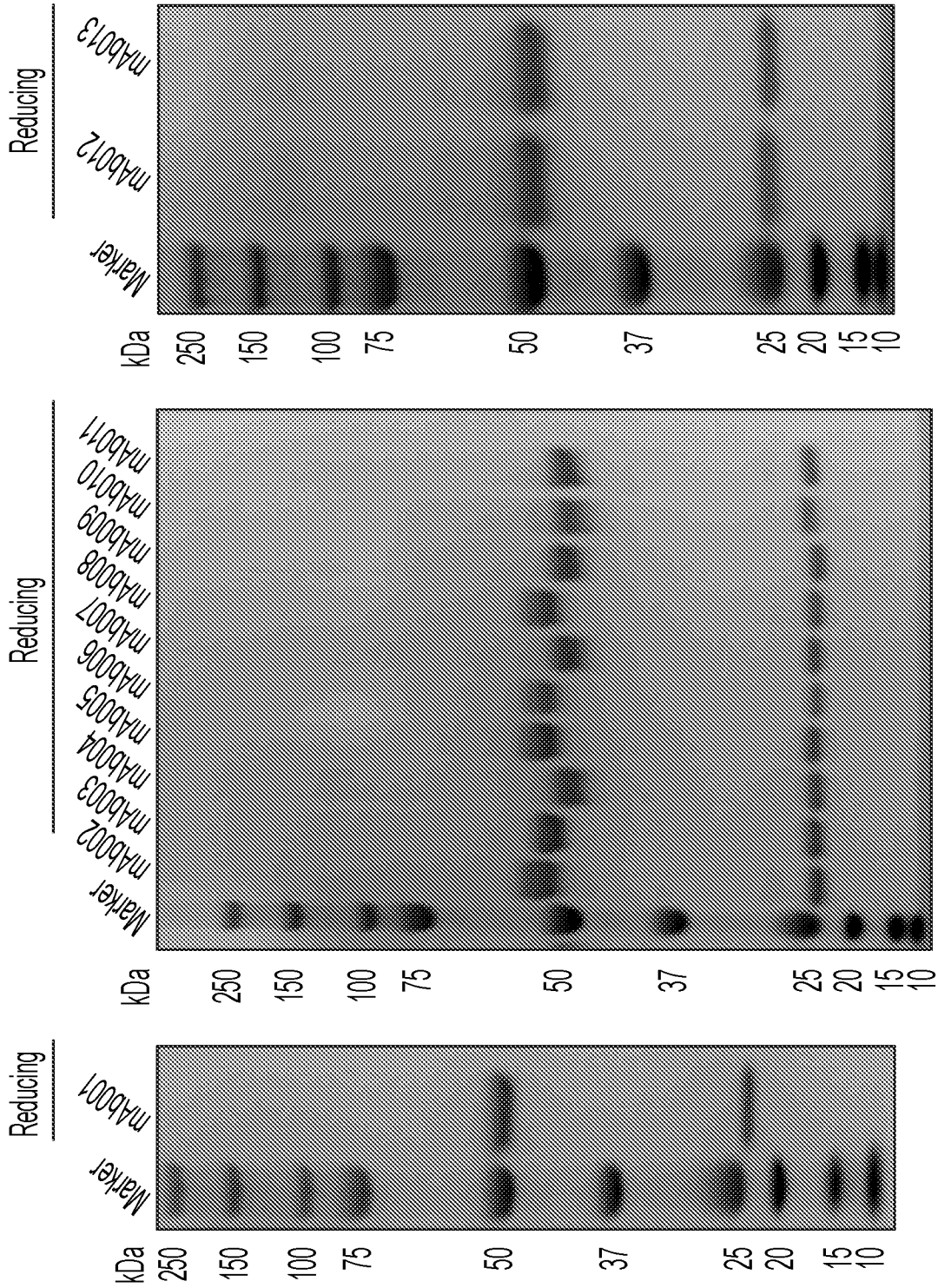


FIG. 8

	EC50
mAb001	0.03389
mAb002	0.03194
mAb003	0.05809
mAb004	0.03804
mAb005	0.1341
mAb006	0.02926
mAb007	0.2061
mAb008	0.1548
mgG	
anti-hBCMA	0.2735

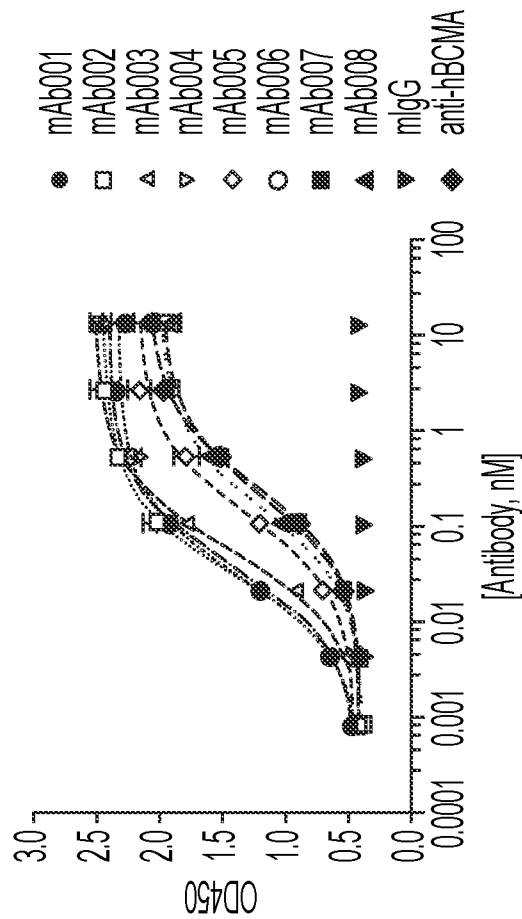


FIG. 9

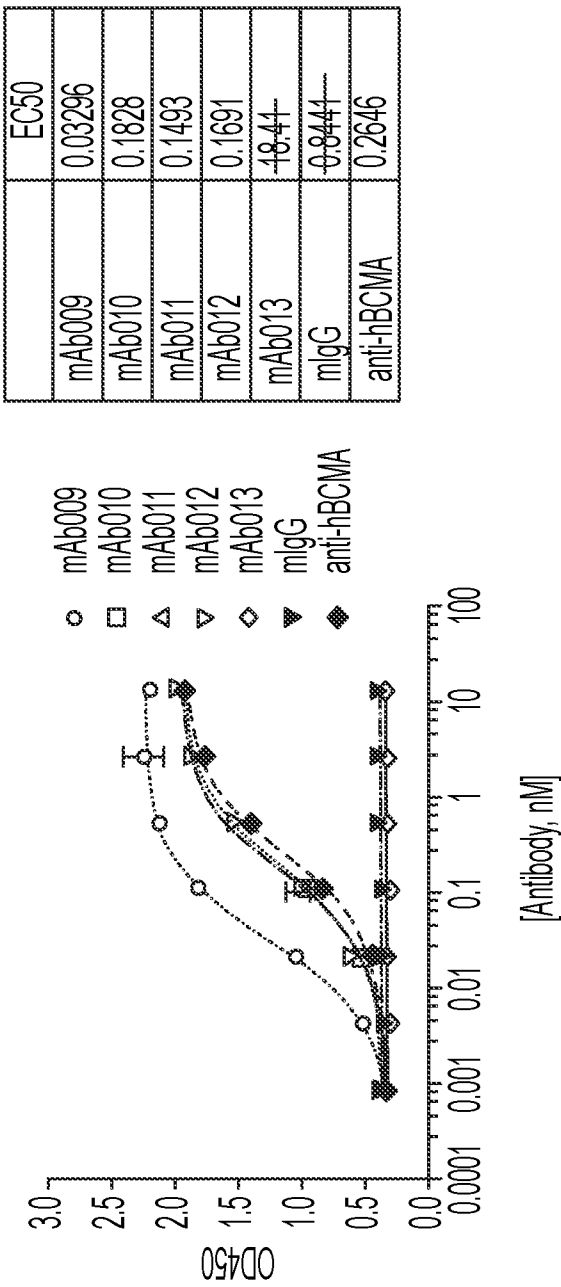


FIG. 9 CONT.

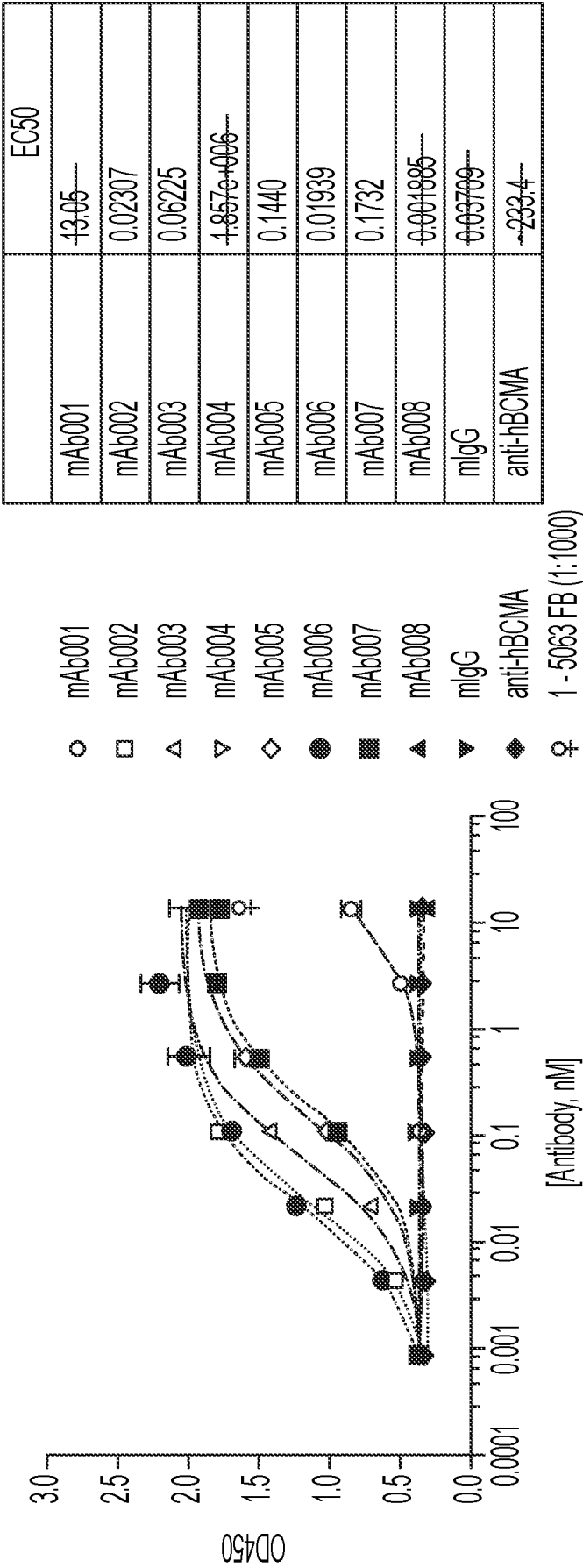


FIG. 10

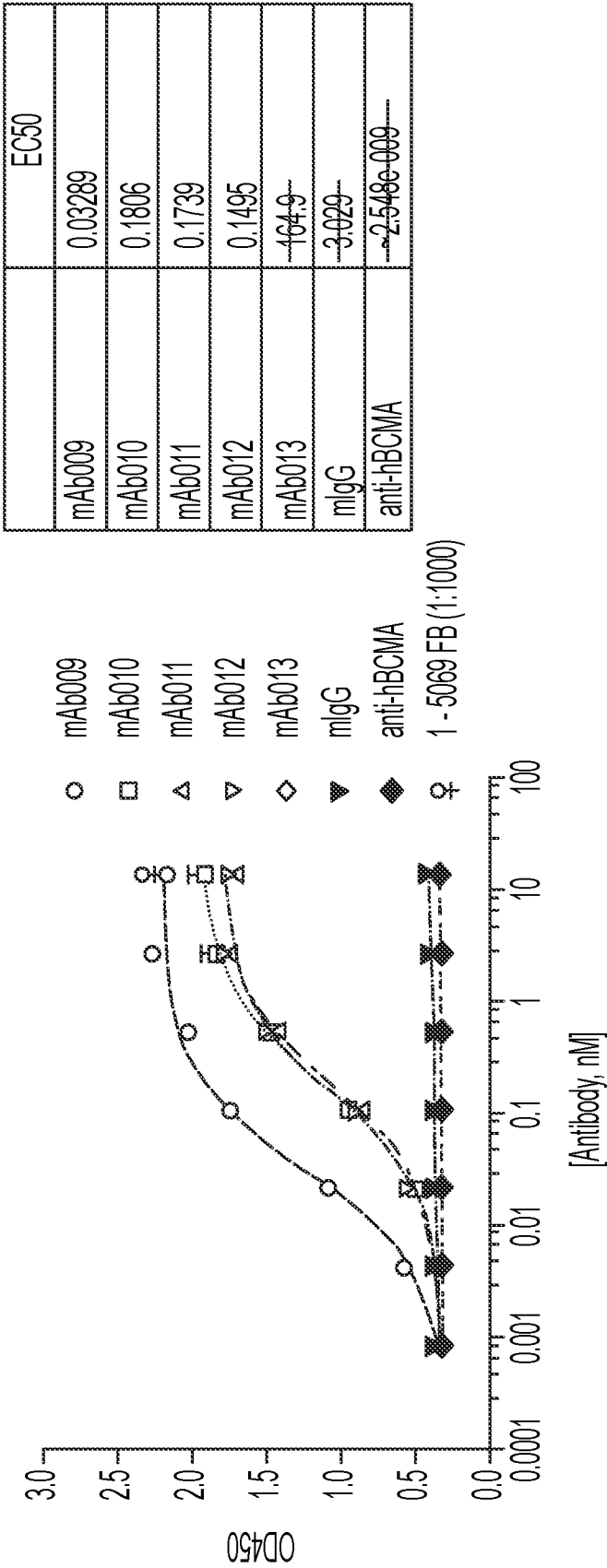


FIG. 10 CONT.

	EC50
mAb001	~~0.1266~~
mAb002	~~78.35~~
mAb003	~~0.006461~~
mAb004	~~0.0003199~~
mAb005	~~0.004793~~
mAb006	~~15844~~
mAb007	~~28208~~
mAb008	~~25476~~
mlgG	~~492860~~
anti-hTACI	0.04574

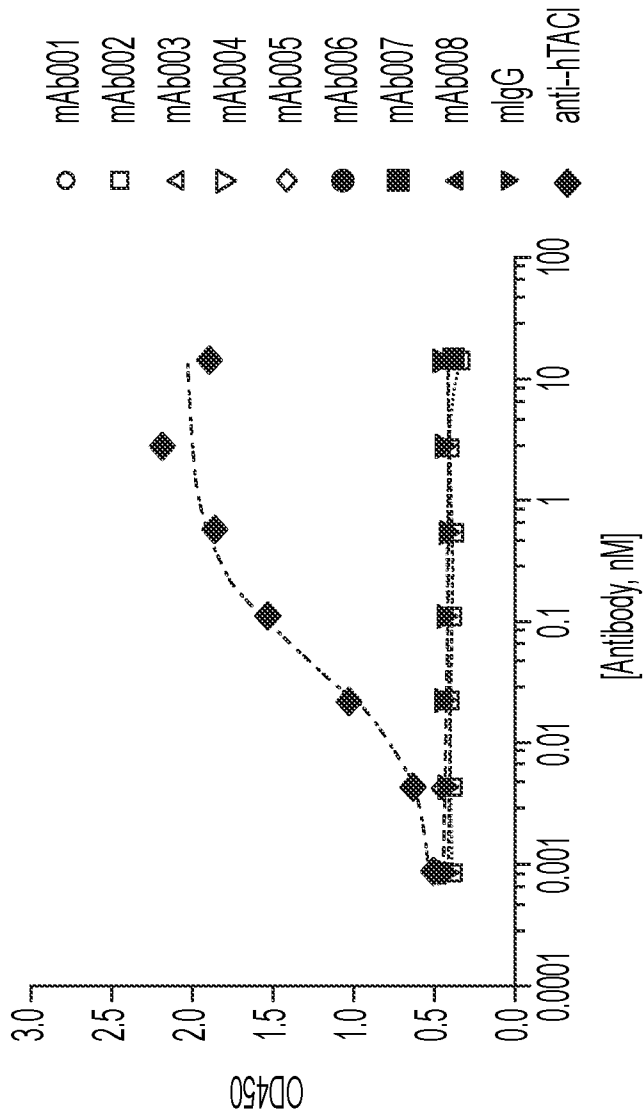


FIG. 11

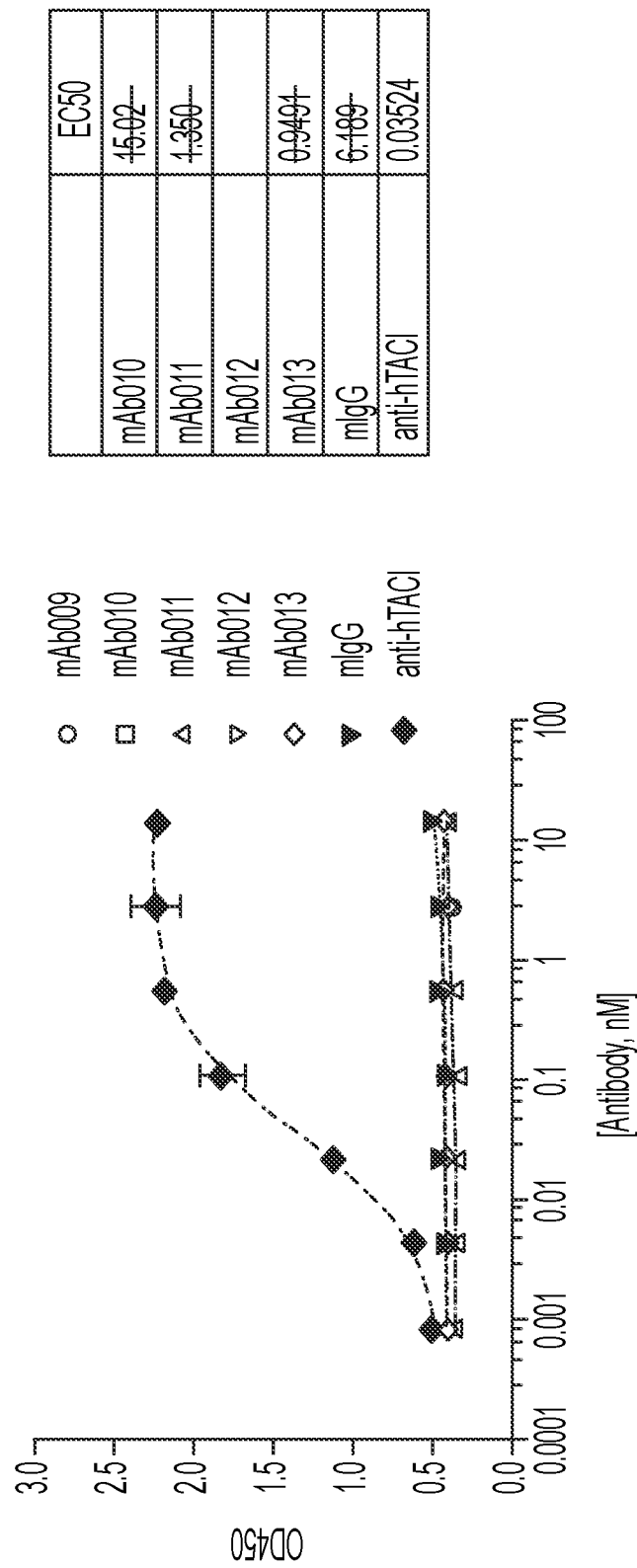


FIG. 11 CONT.

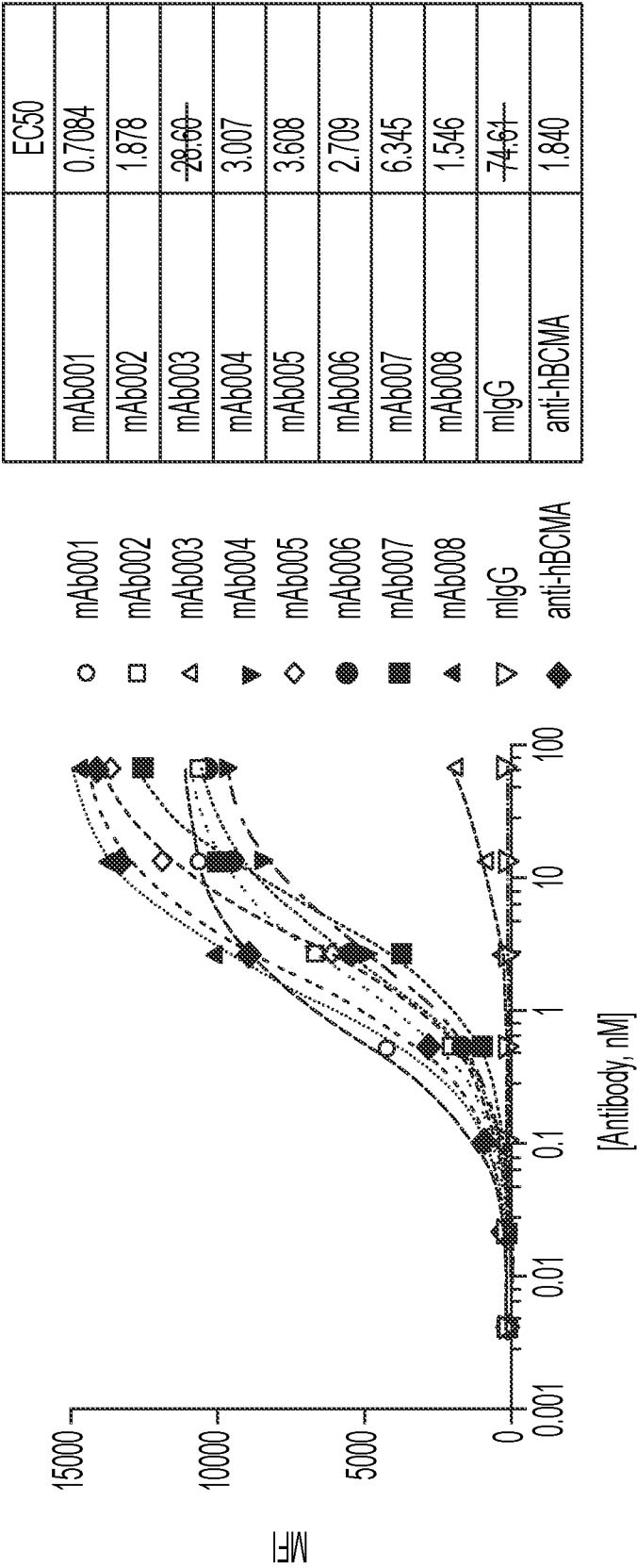


FIG. 12

	EC50
mAb009	3.190
mAb010	3.042
mAb011	4.854
mAb012	5.802
mAb013	1.474e-007
anti-hBCMA	2.484
mlgG	45.75

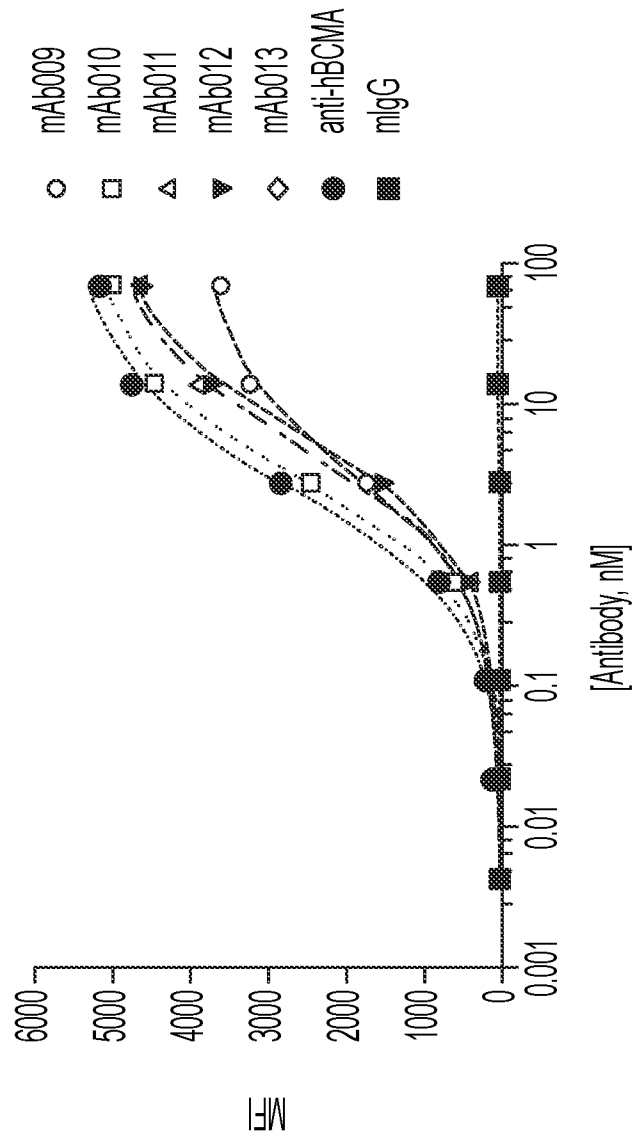


FIG. 12 CONT.

	EC50
mAb001	0.2527
mAb002	1.989
mAb003	44960
mAb004	2.089e+006
mAb005	
mAb006	0.003007
mAb007	0.02591
mAb008	0.4556
mlgG	48.80
anti-hBCMA	2373



FIG. 13

	EC50
mAb009	73.56
mAb010	5.254e+006
mAb011	4.527
mAb012	2.092e+006
mAb013	
anti-hBCMA	0.000000
mlgG	0.0004735

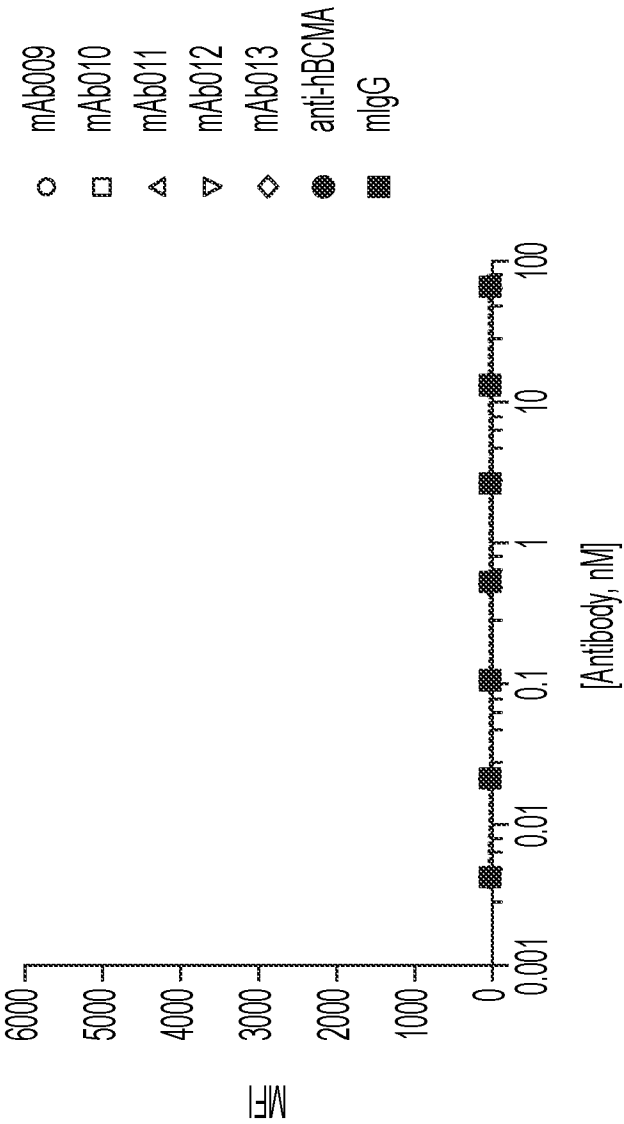
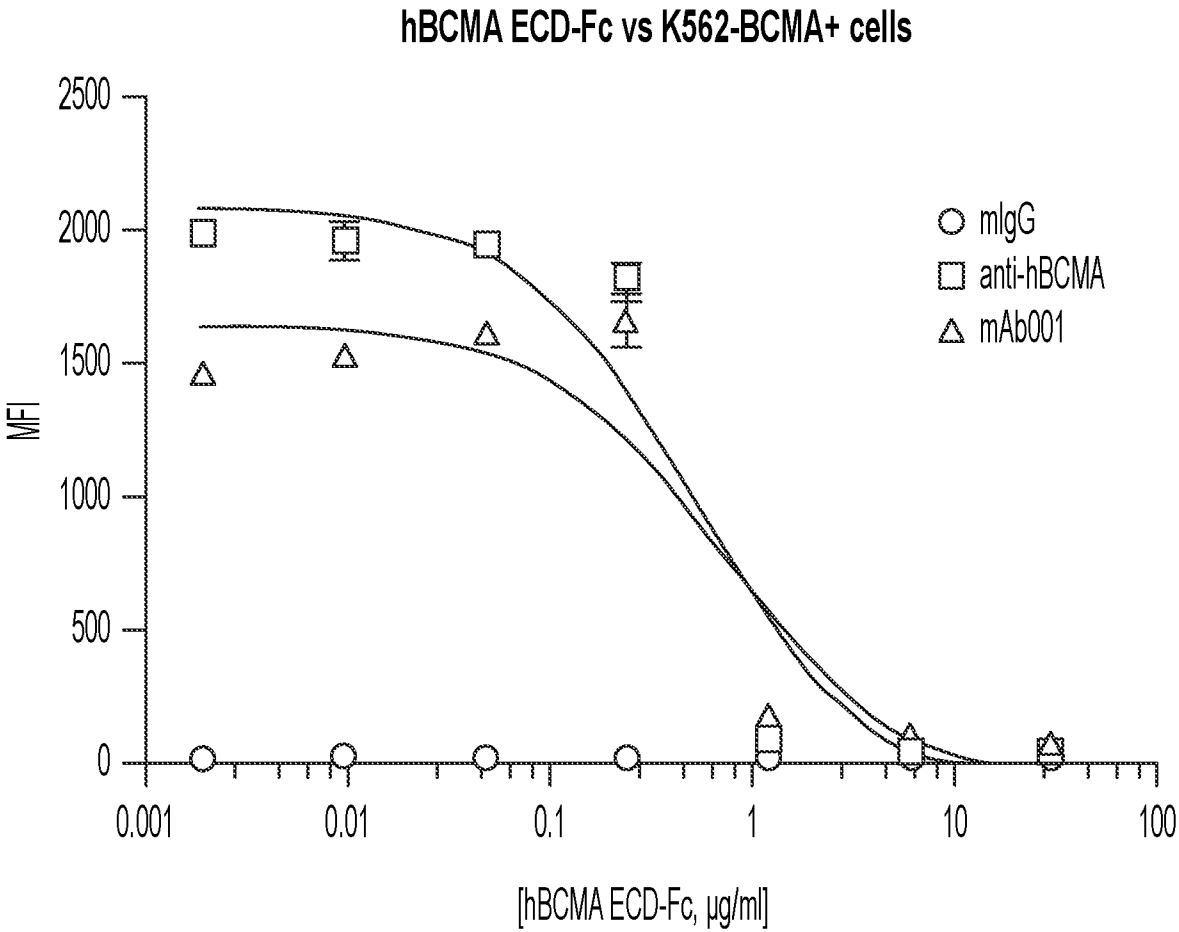


FIG. 13 CONT.



	anti-hBCMA	mAb001
IC50	0.5314	0.7312

FIG. 14

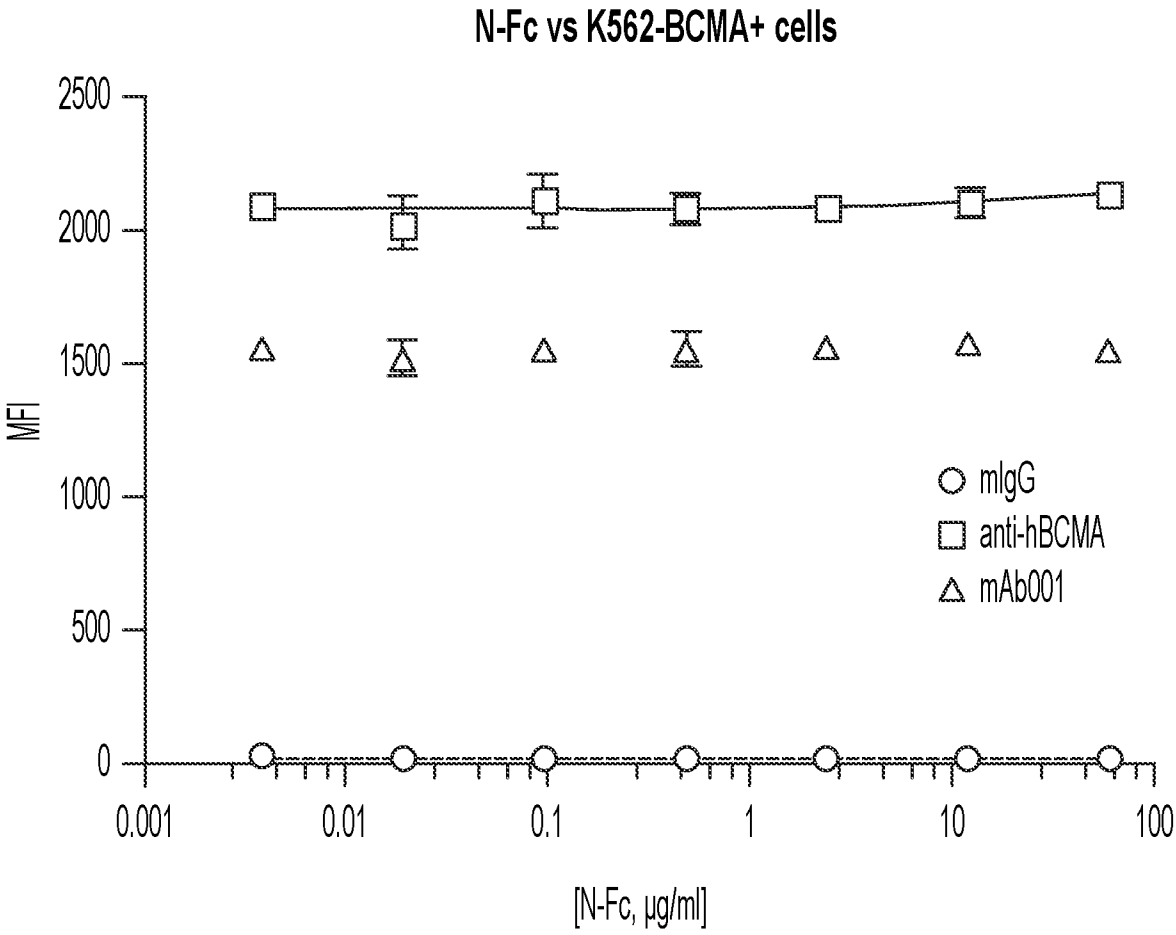


FIG. 14 CONT.

27/52

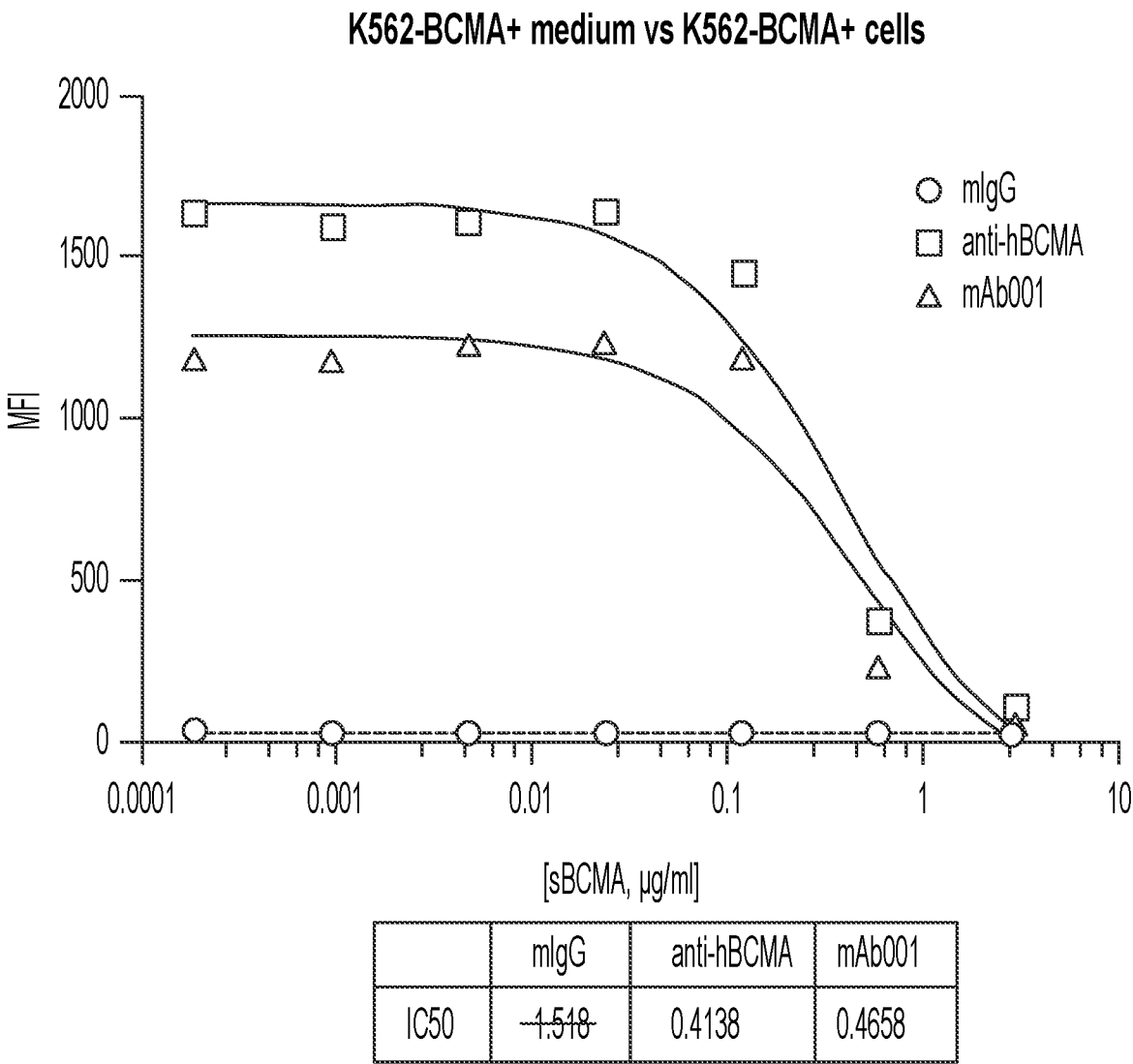


FIG. 14 CONT.

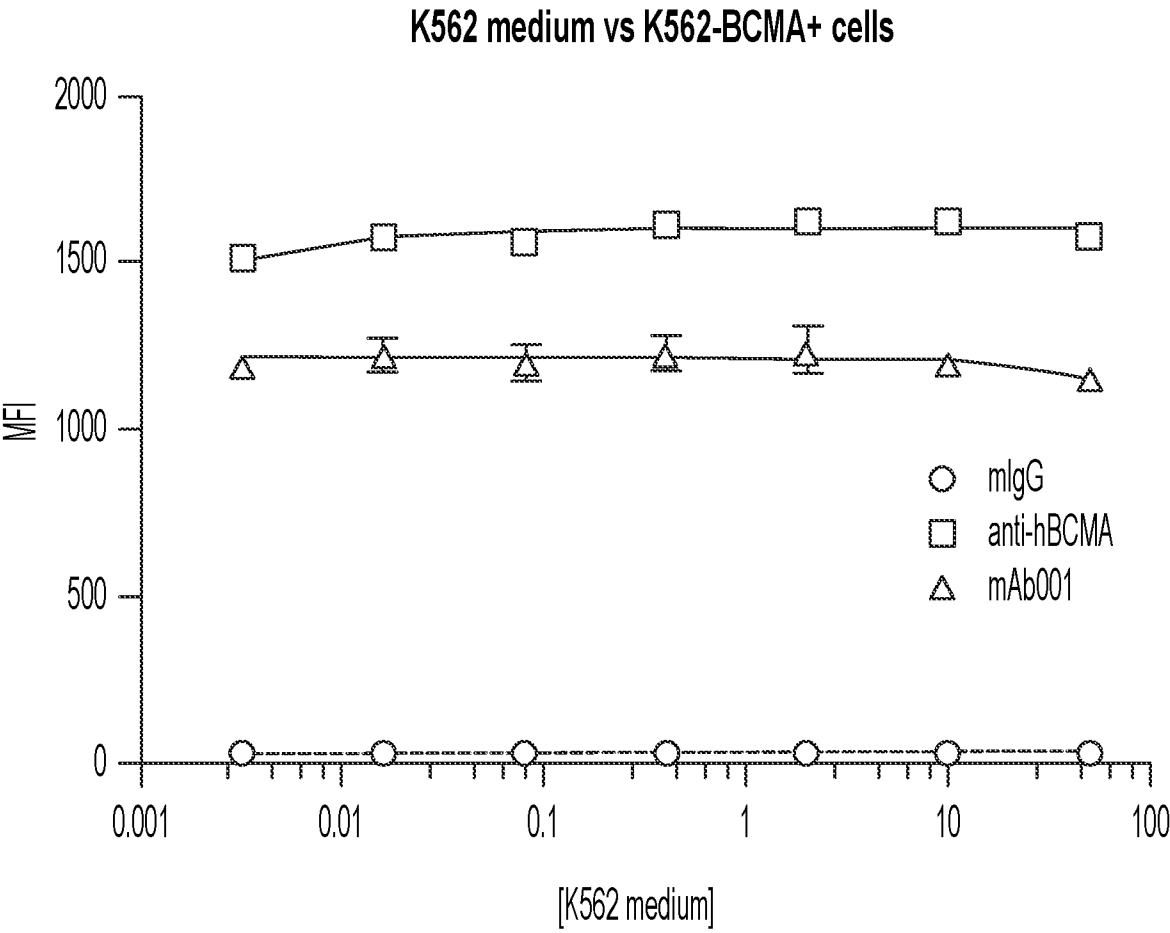


FIG. 14 CONT.

29/52

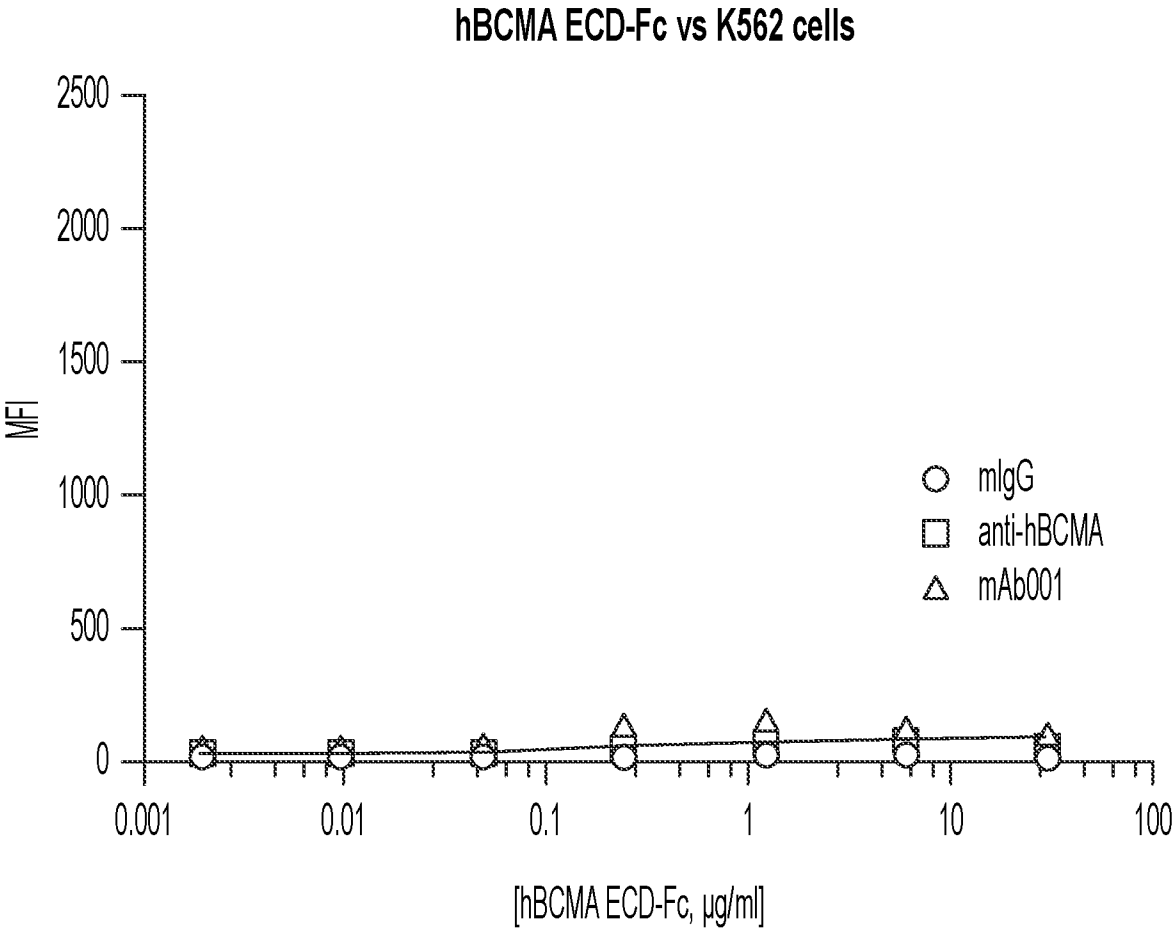


FIG. 14 CONT.

30/52

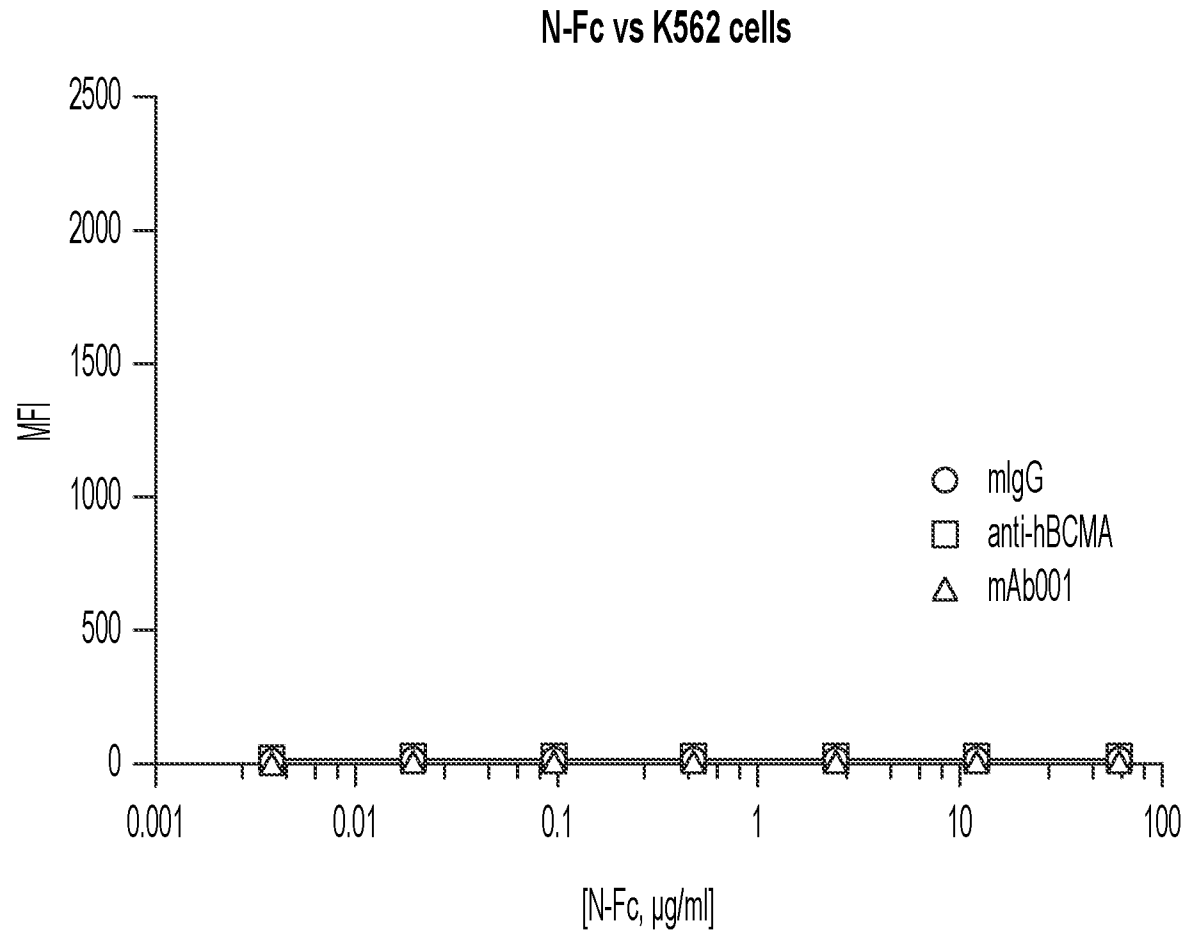


FIG. 14 CONT.

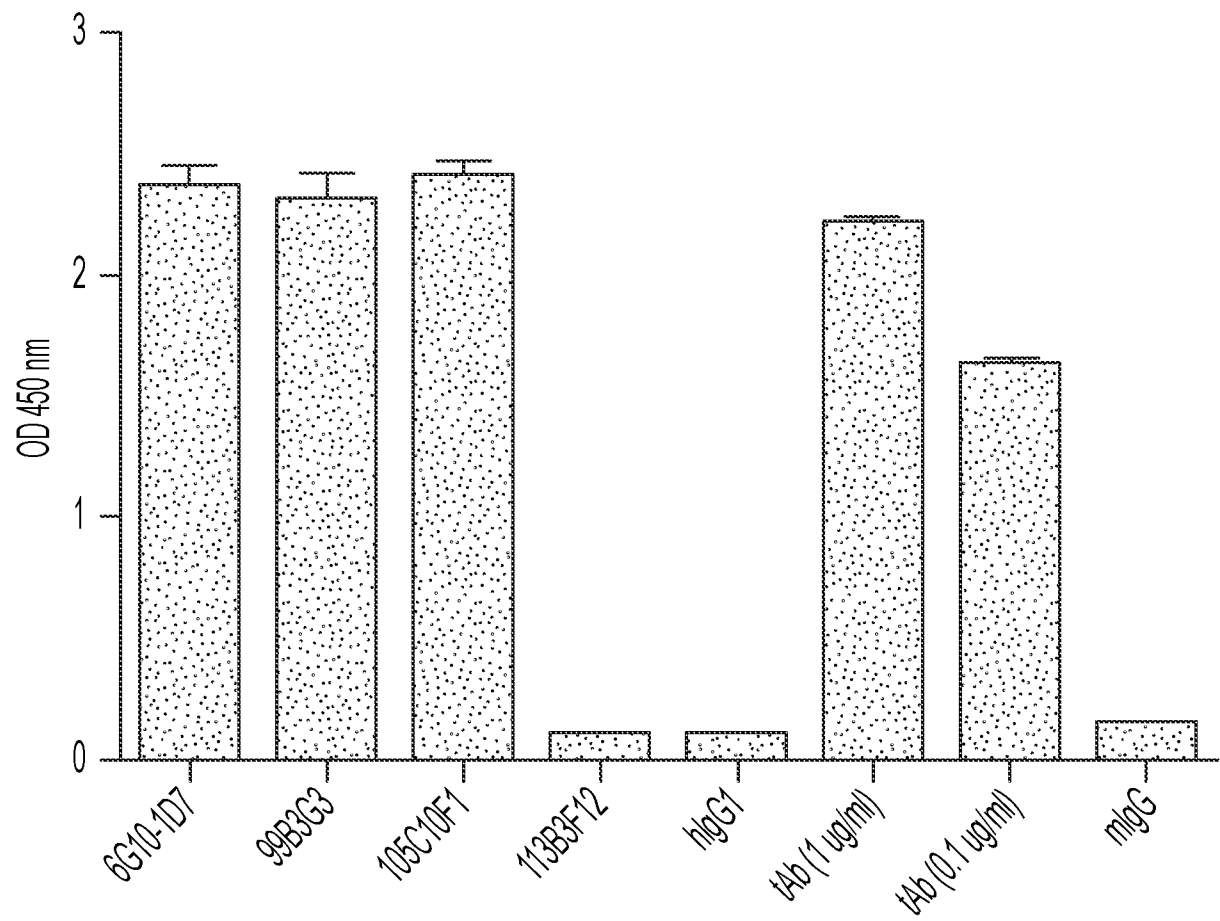


FIG. 15

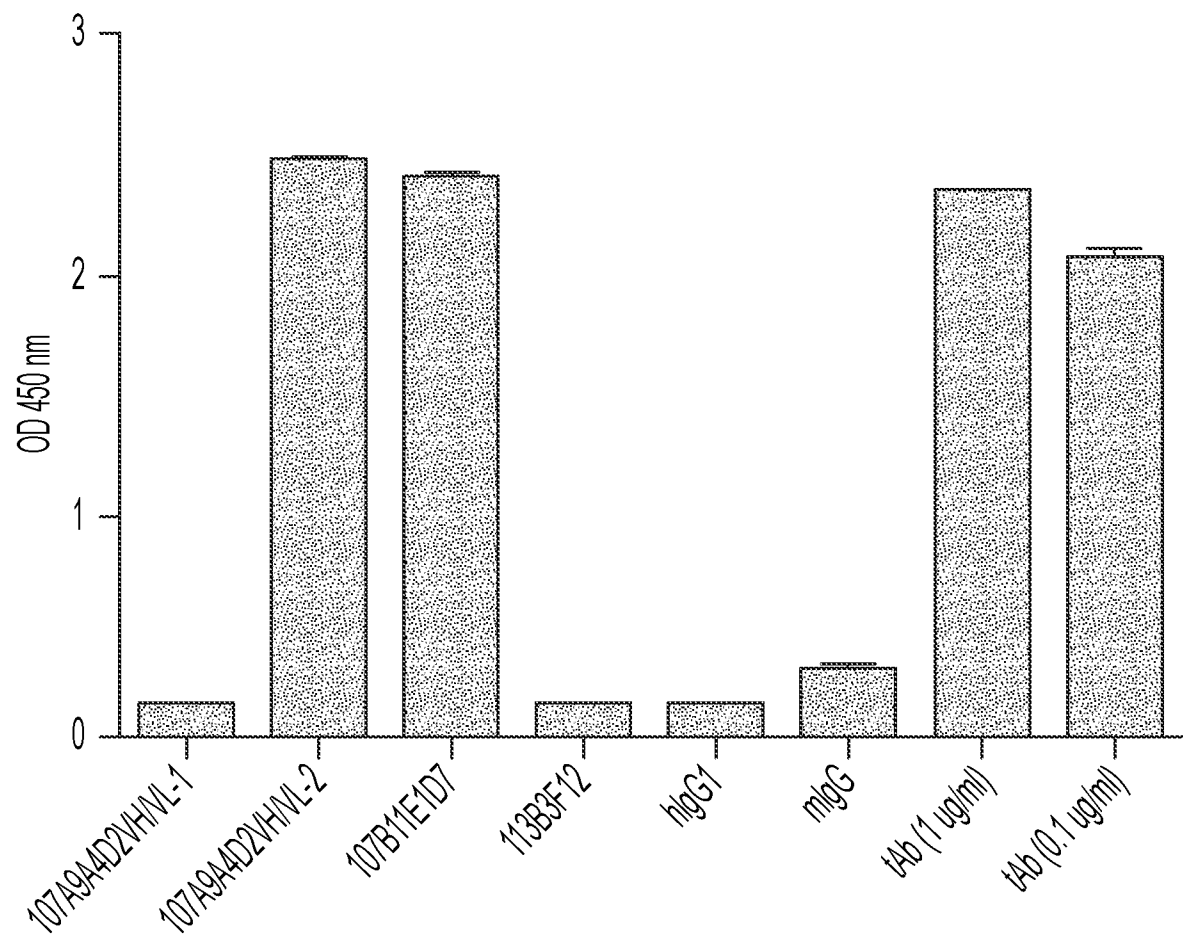


FIG. 15 CONT.

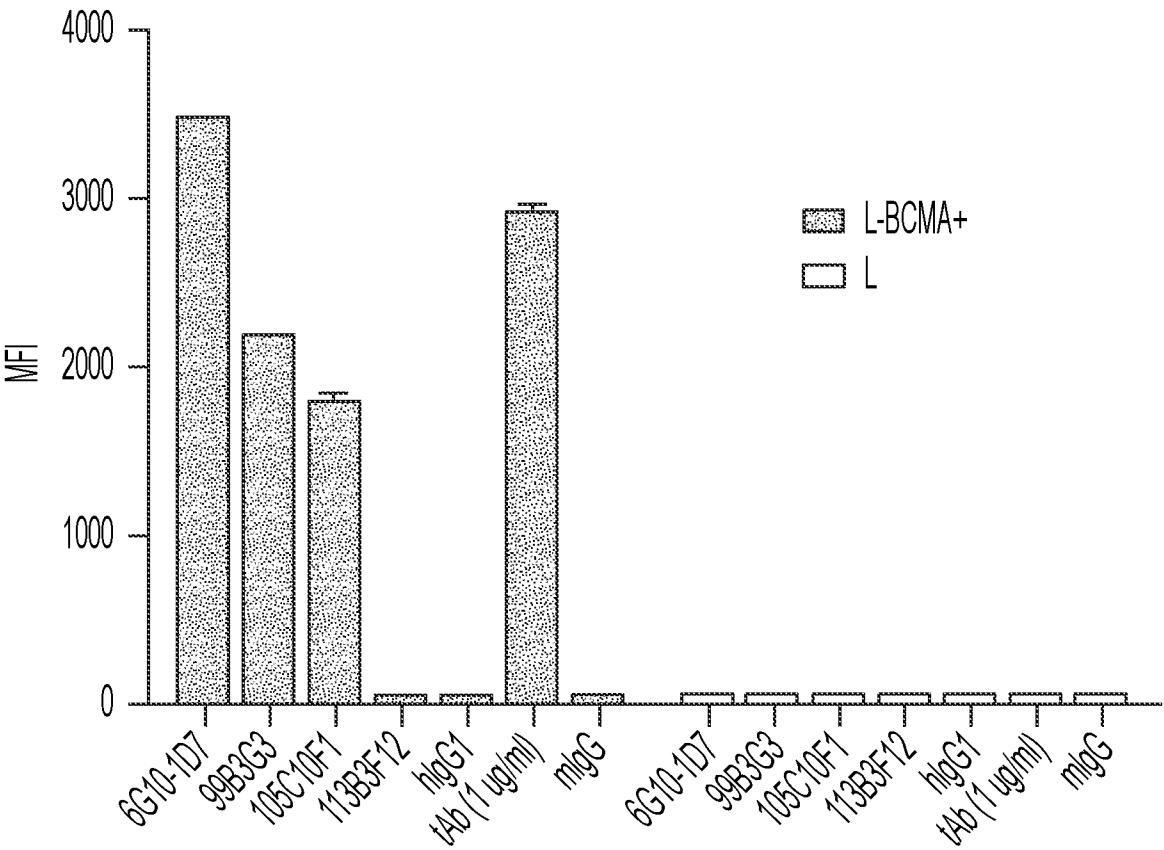


FIG. 16

34/52

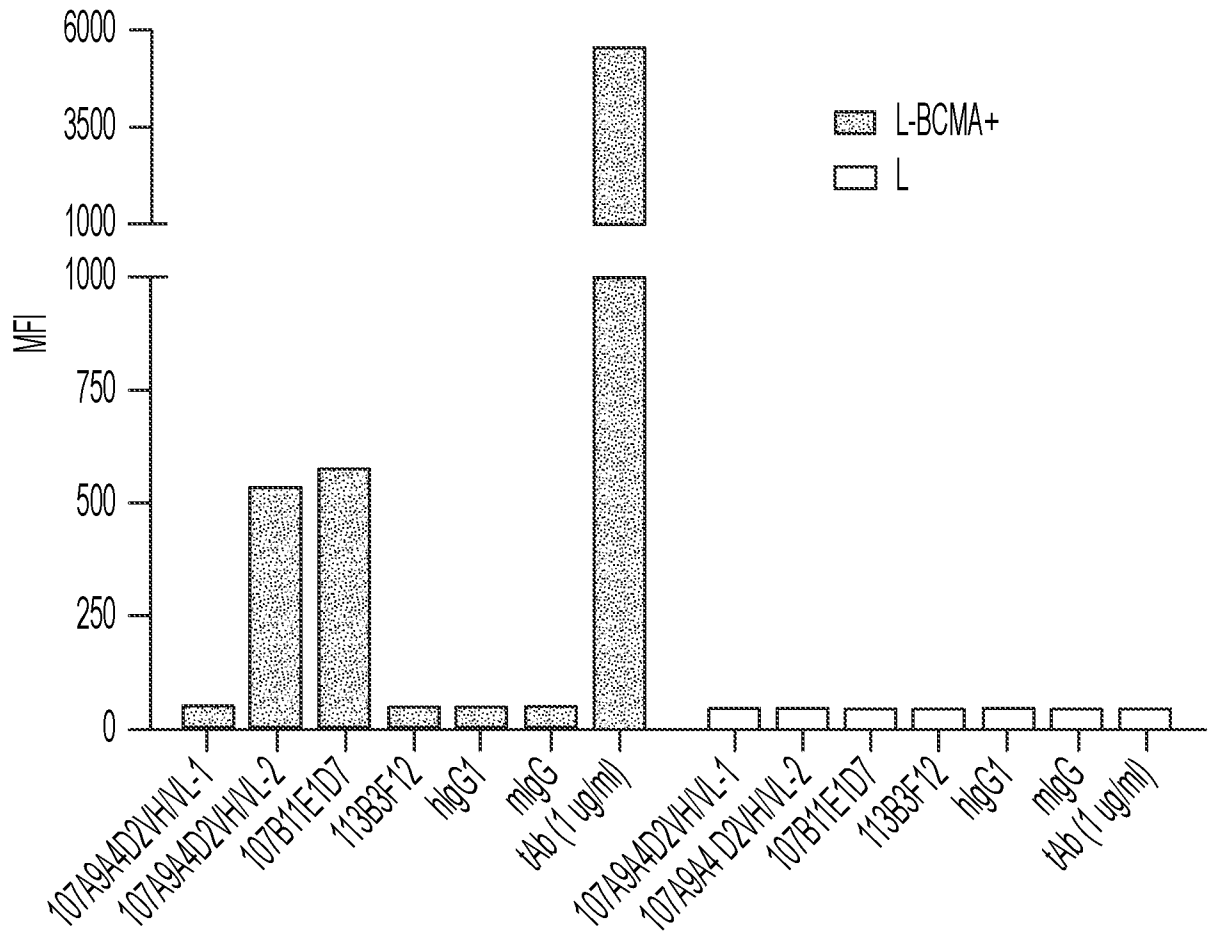


FIG. 16 CONT.

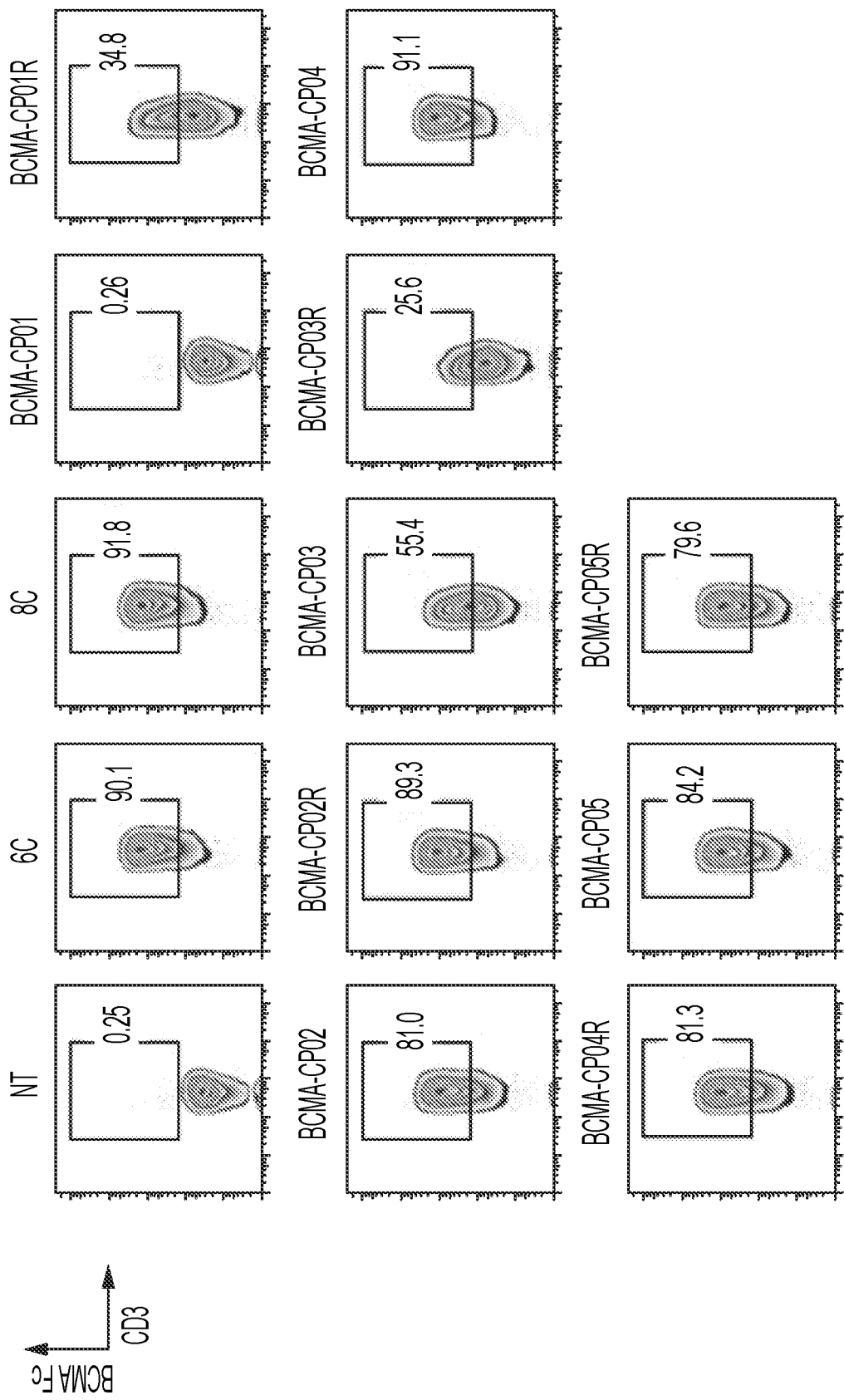


FIG. 17

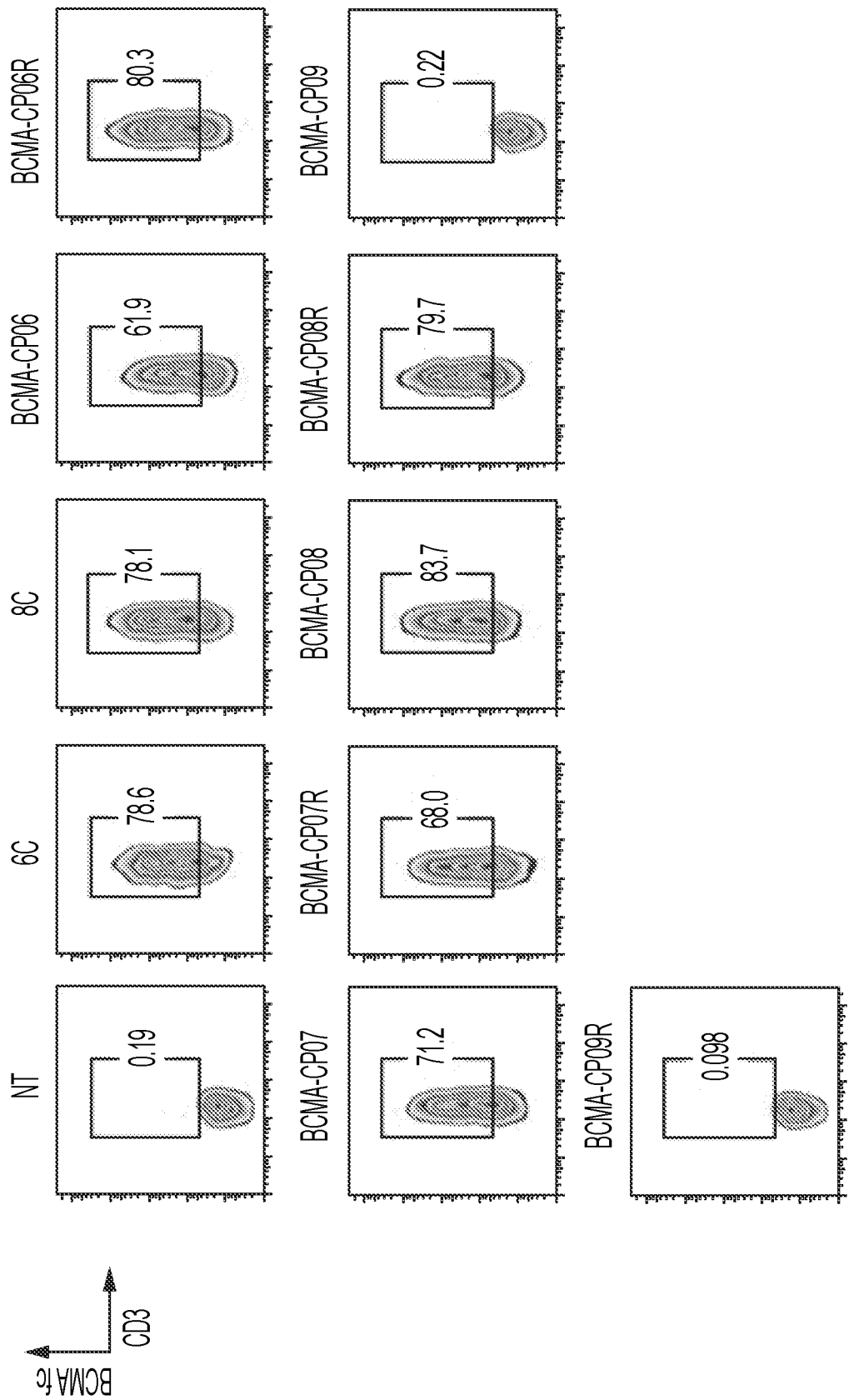


FIG. 17 CONT.

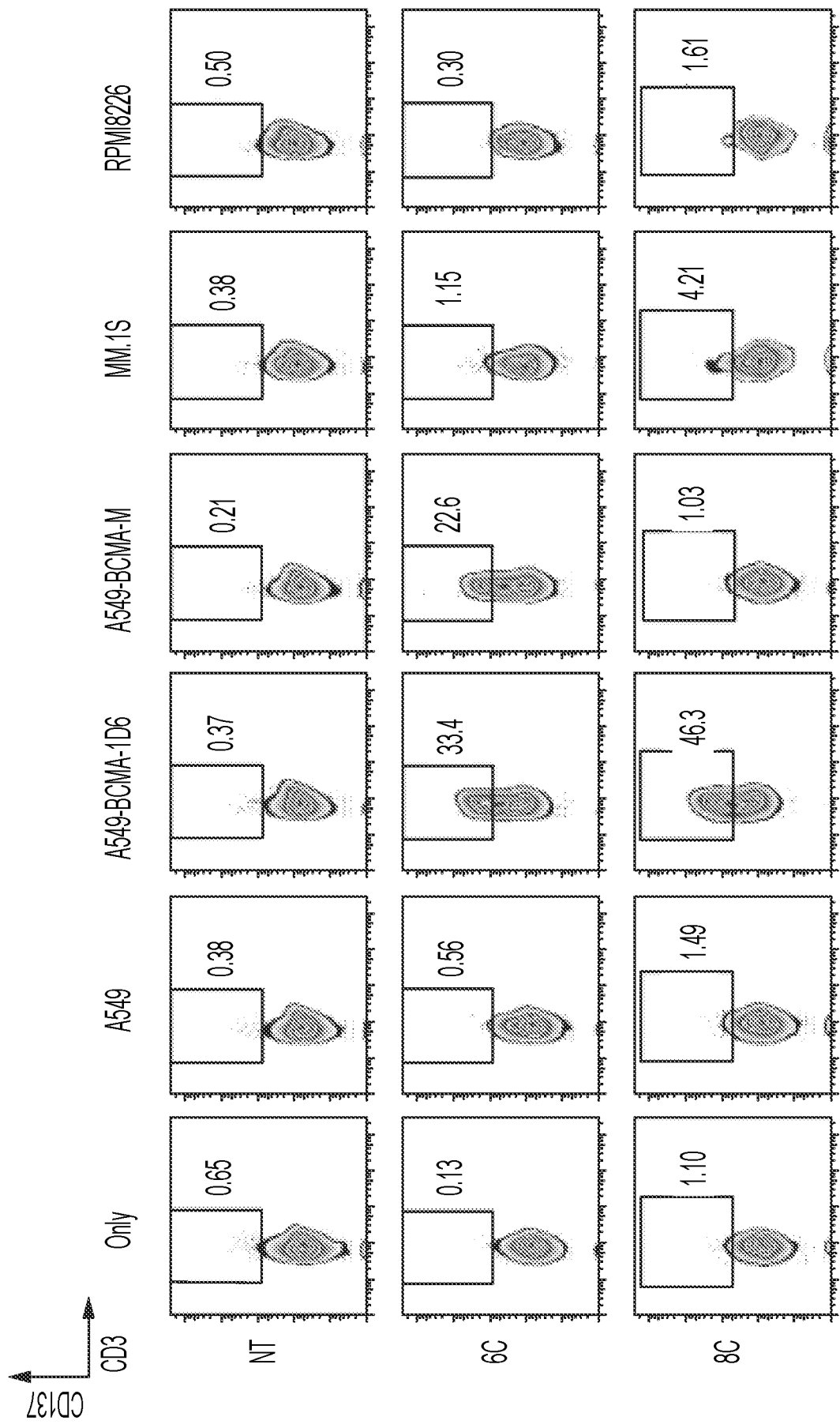


FIG. 18

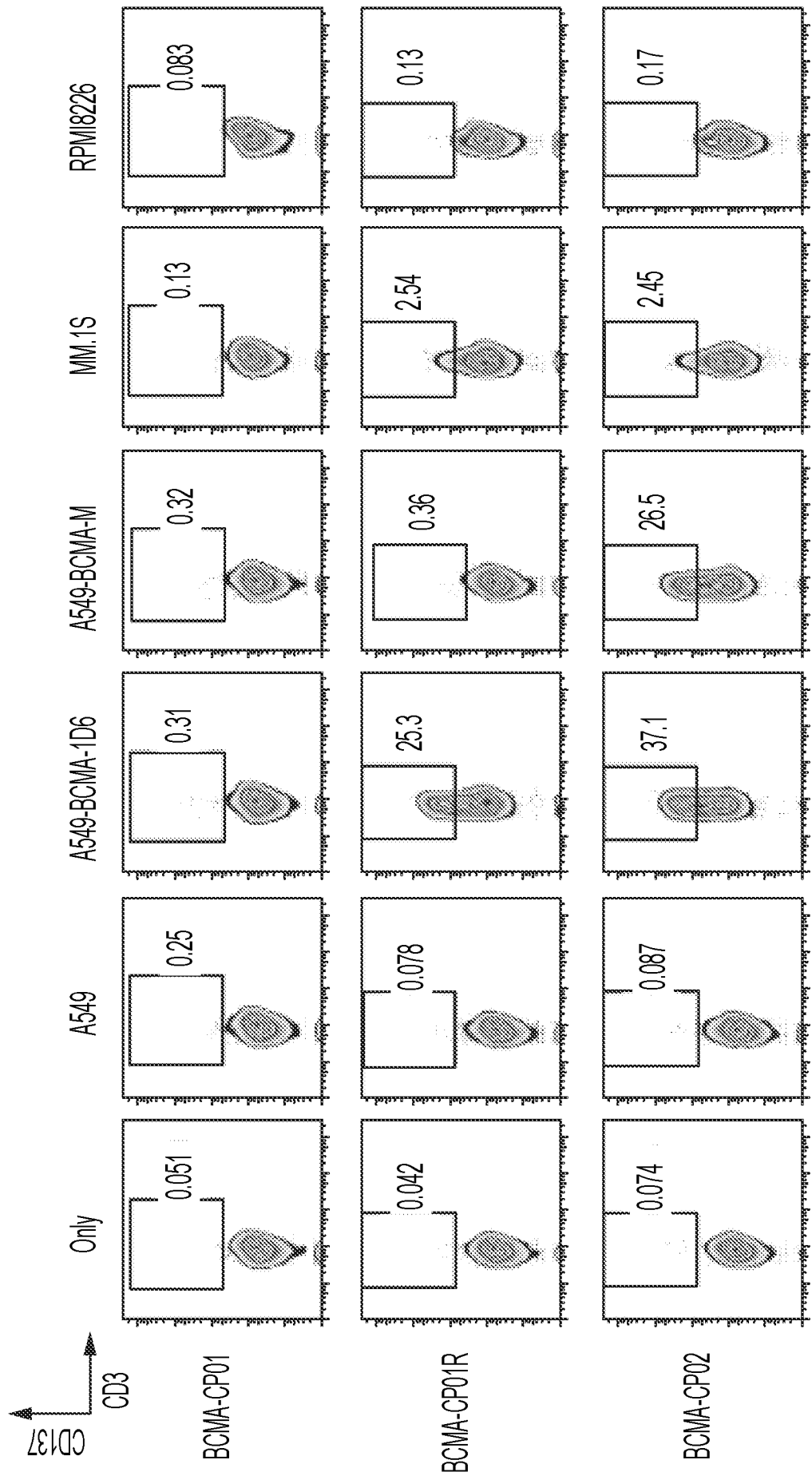


FIG. 18 CONT.

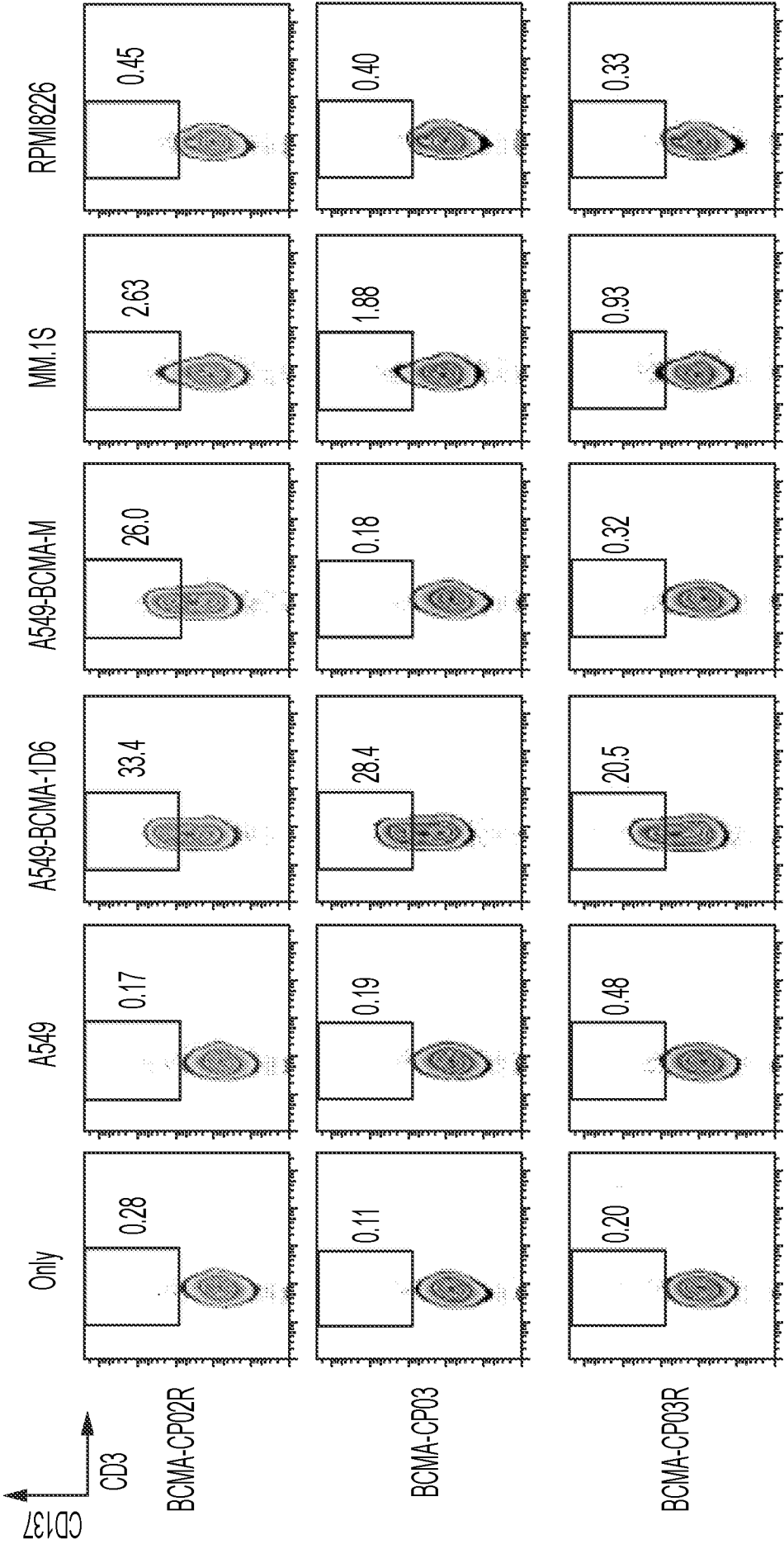


FIG. 18 CONT.

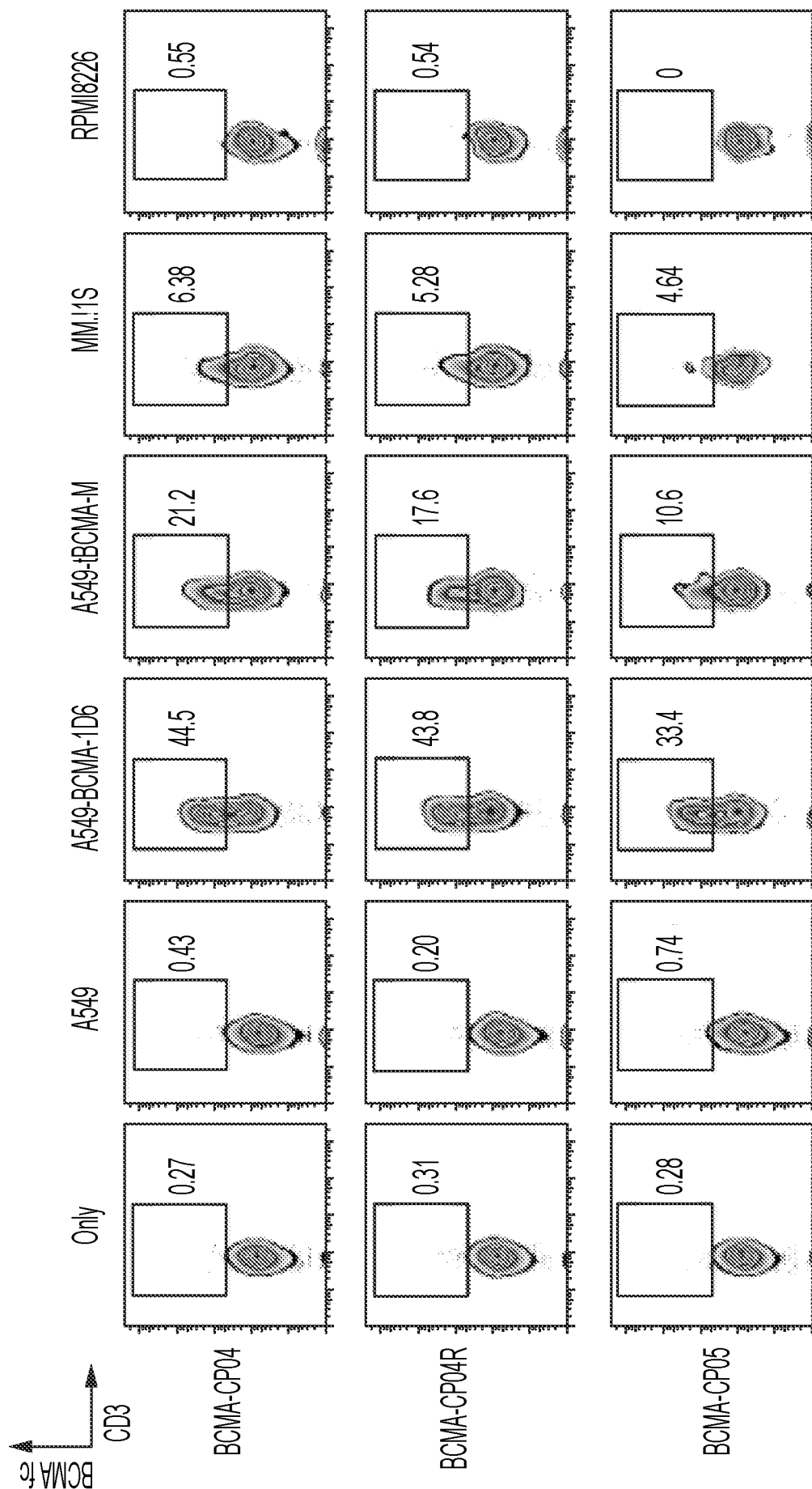
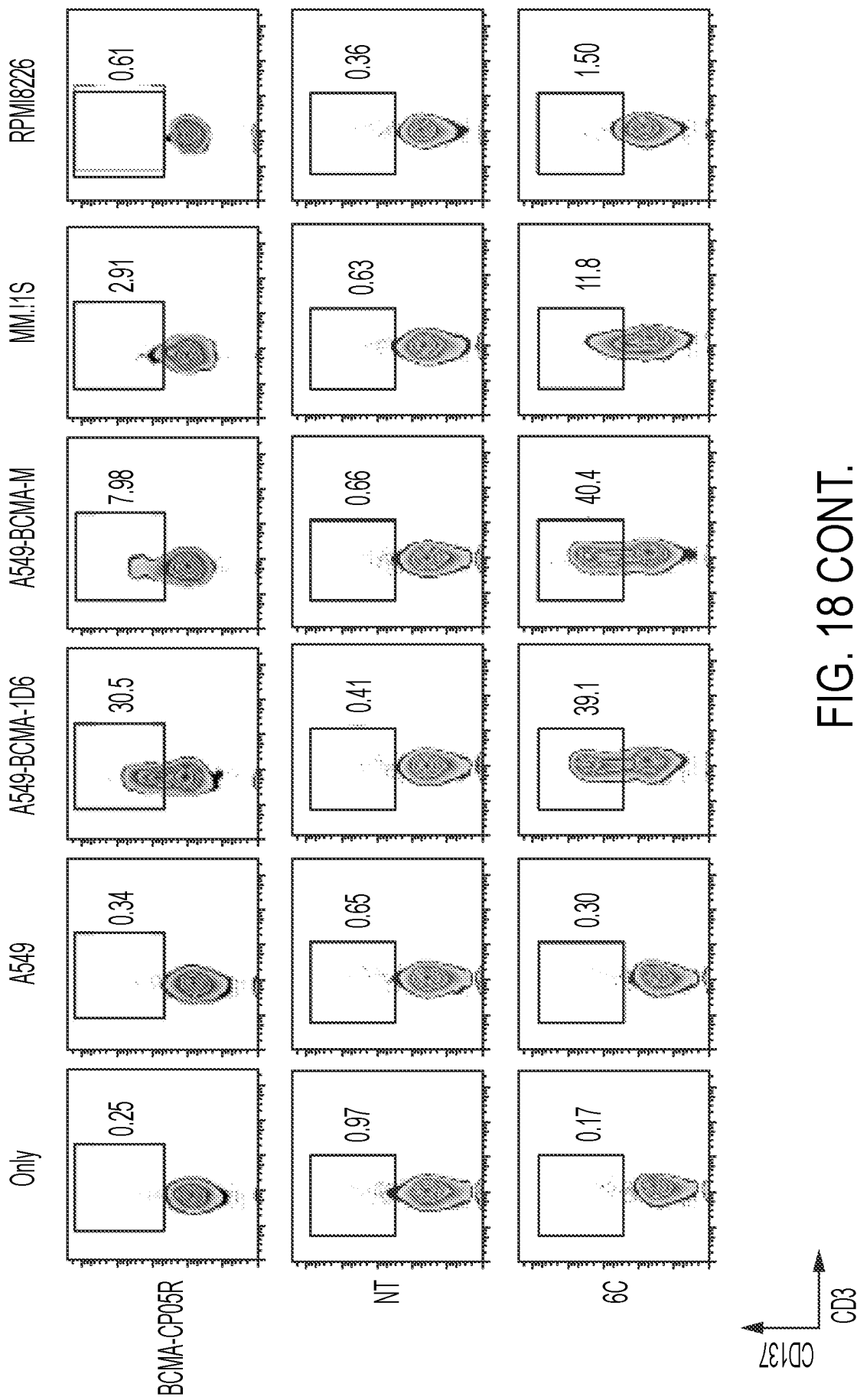
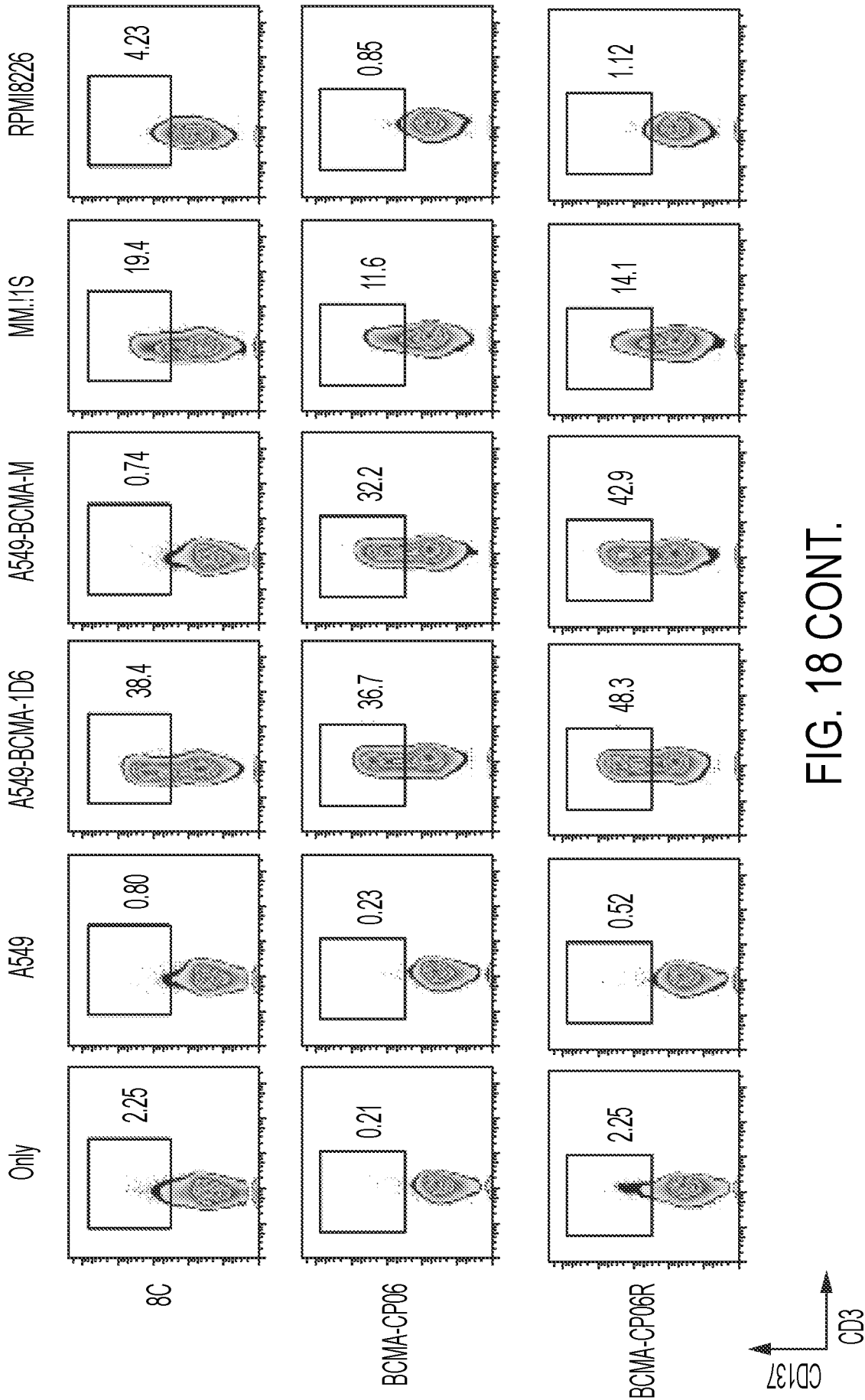


FIG. 18 CONT.





43/52

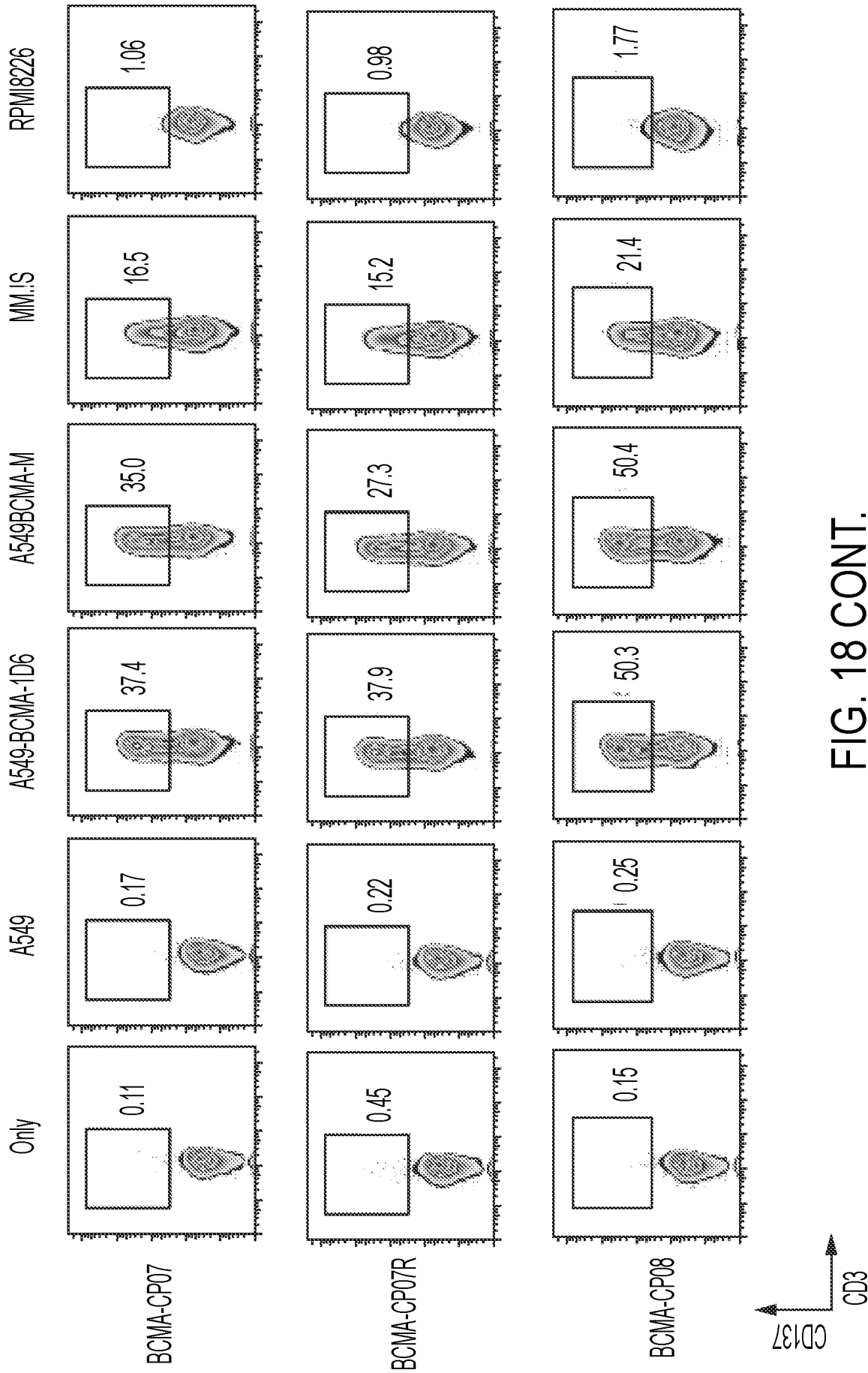


FIG. 18 CONT.

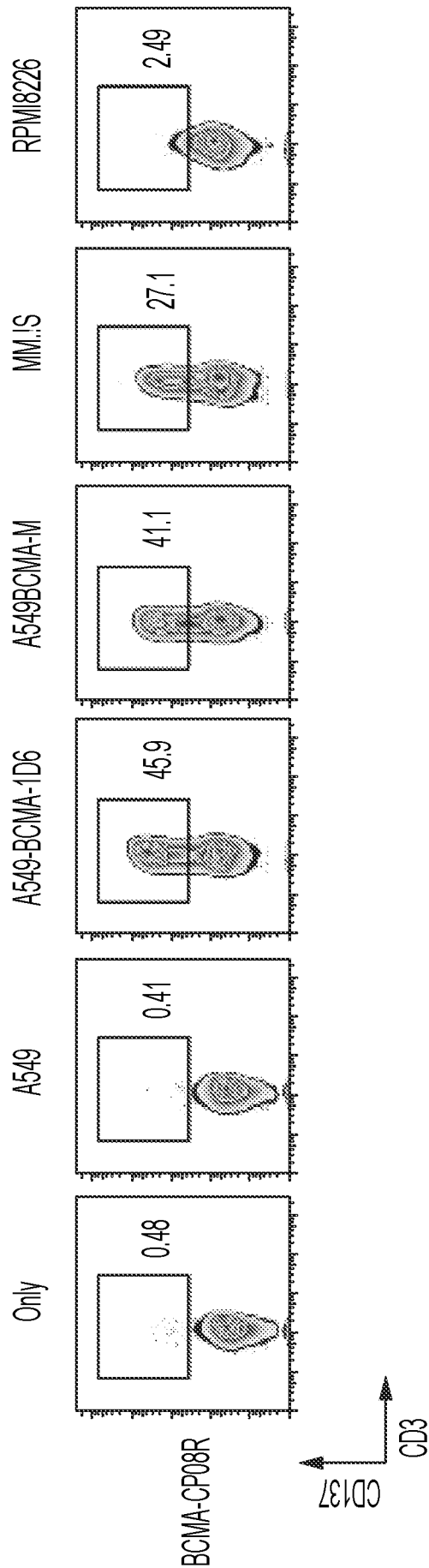


FIG. 18 CONT.

45/52

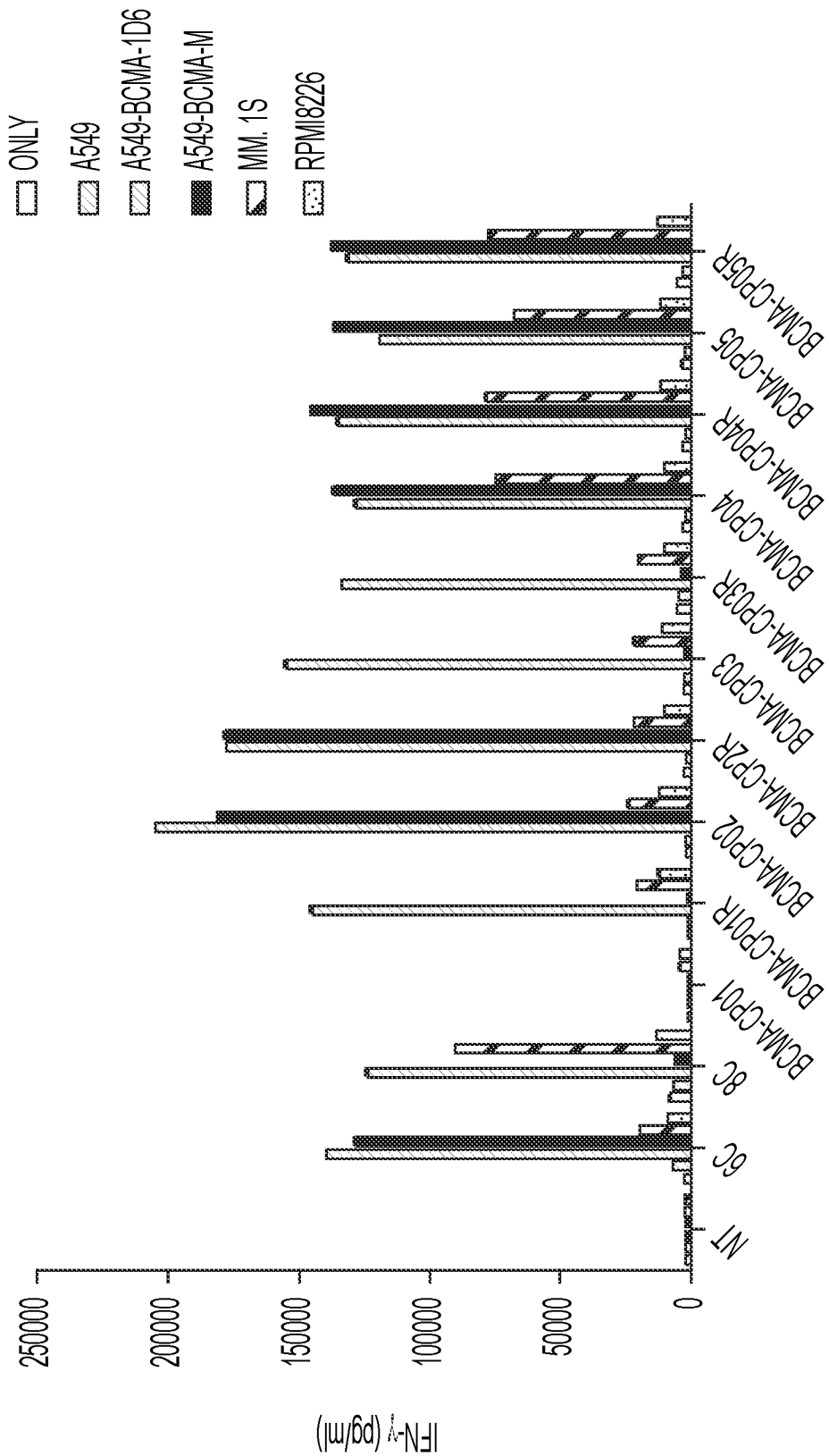


FIG. 19

46/52

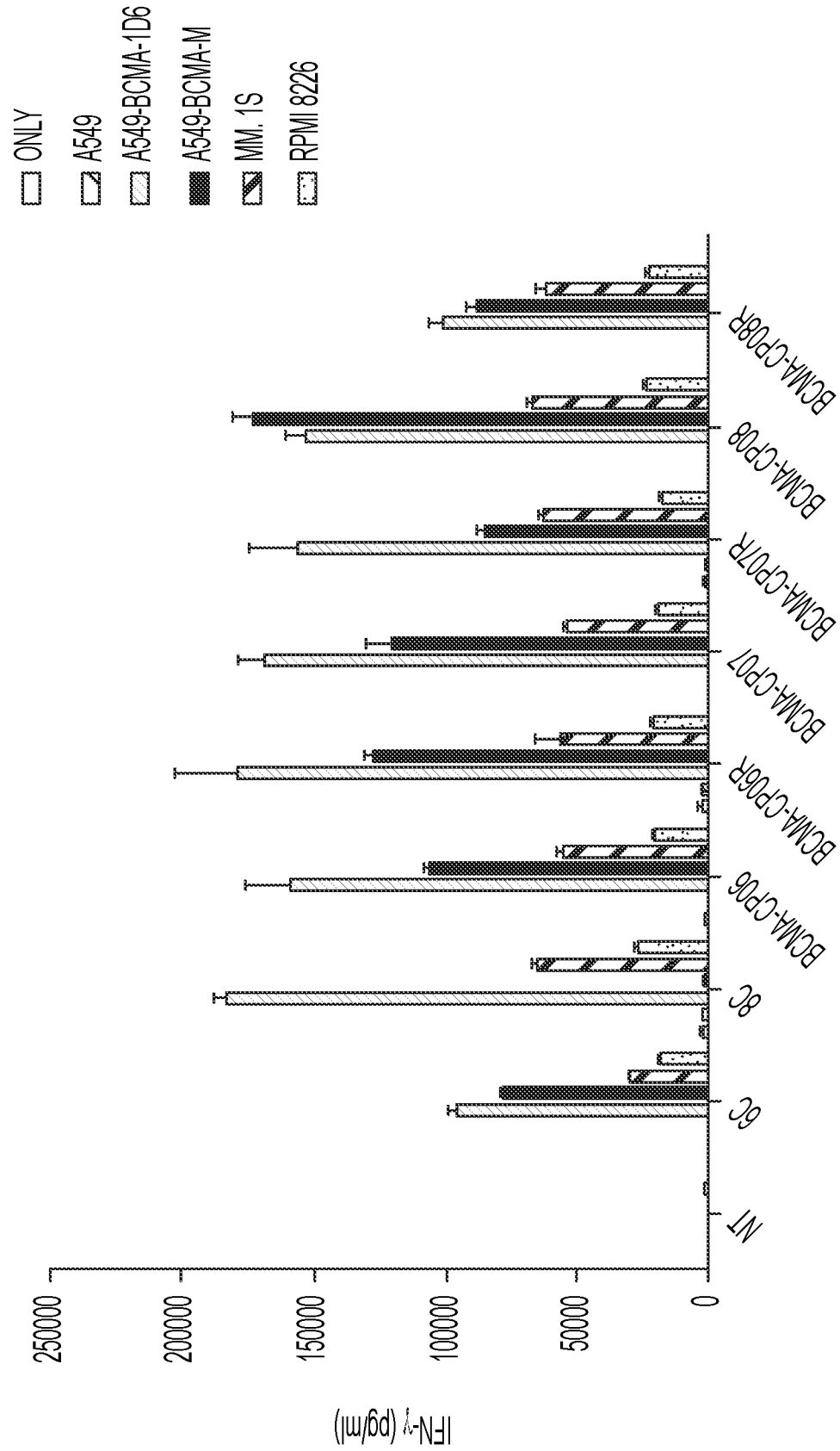


FIG. 19 CONT.

47/52

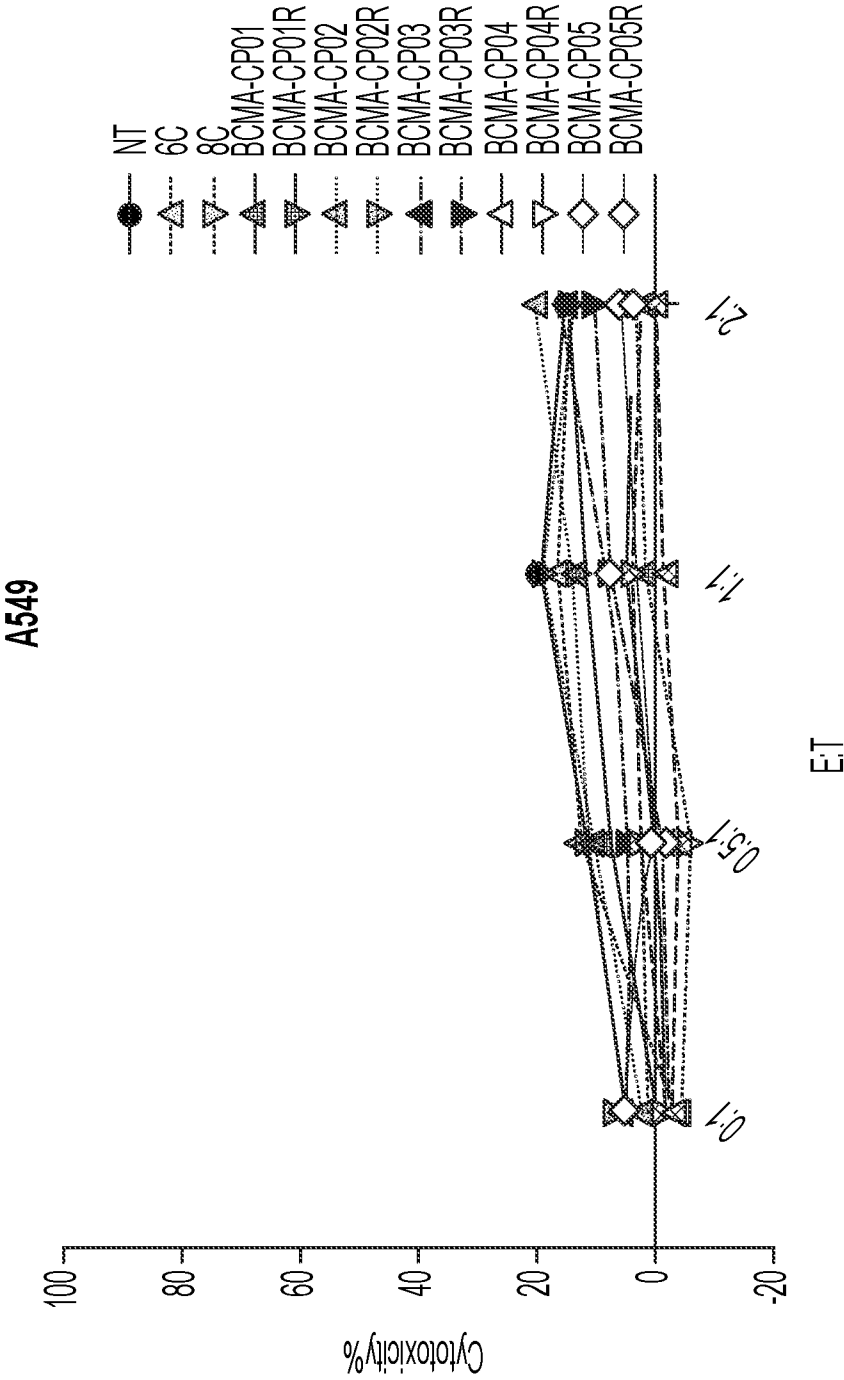


FIG. 20

48/52

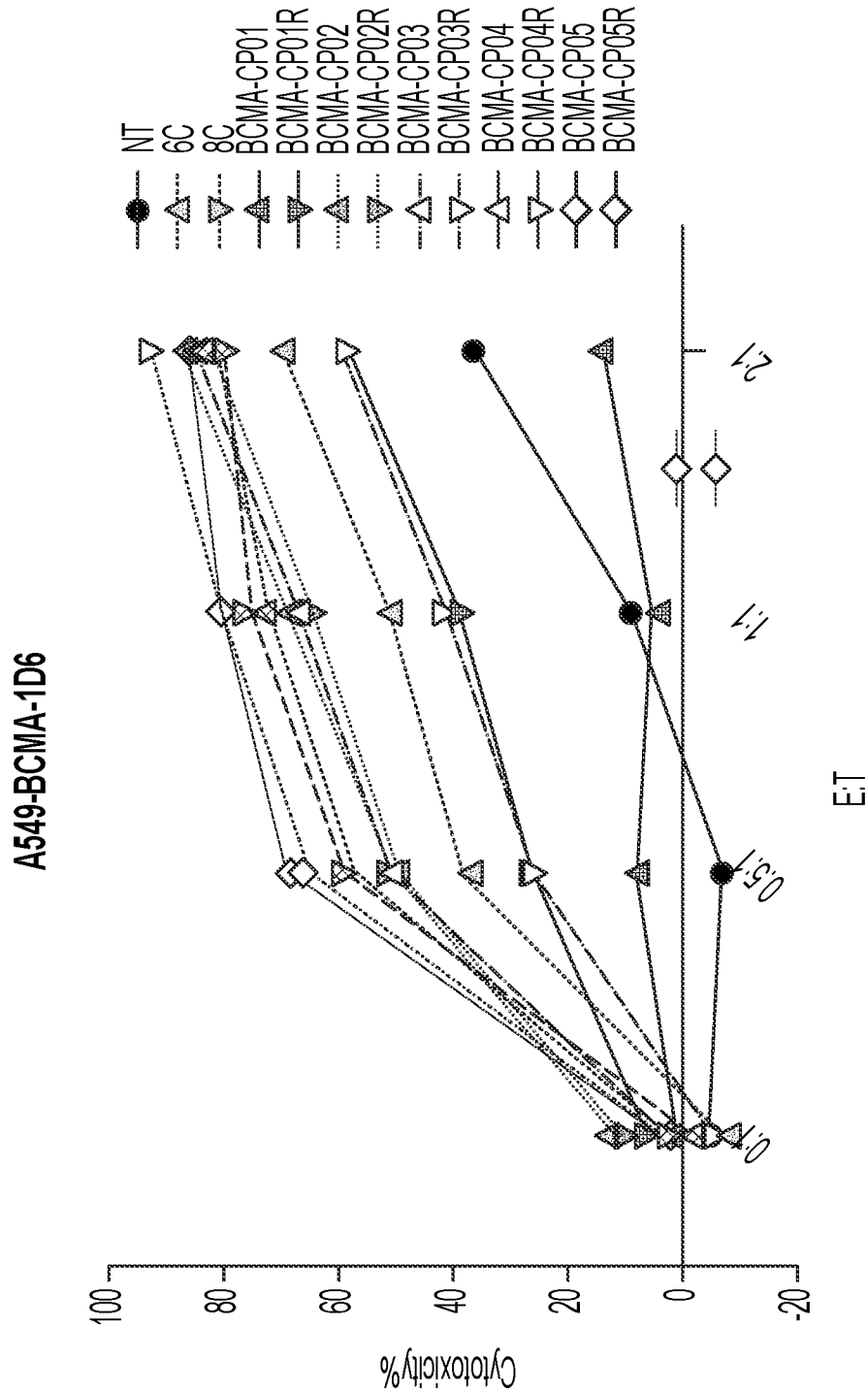


FIG. 20 CONT.

49/52

A549-BCMA-M

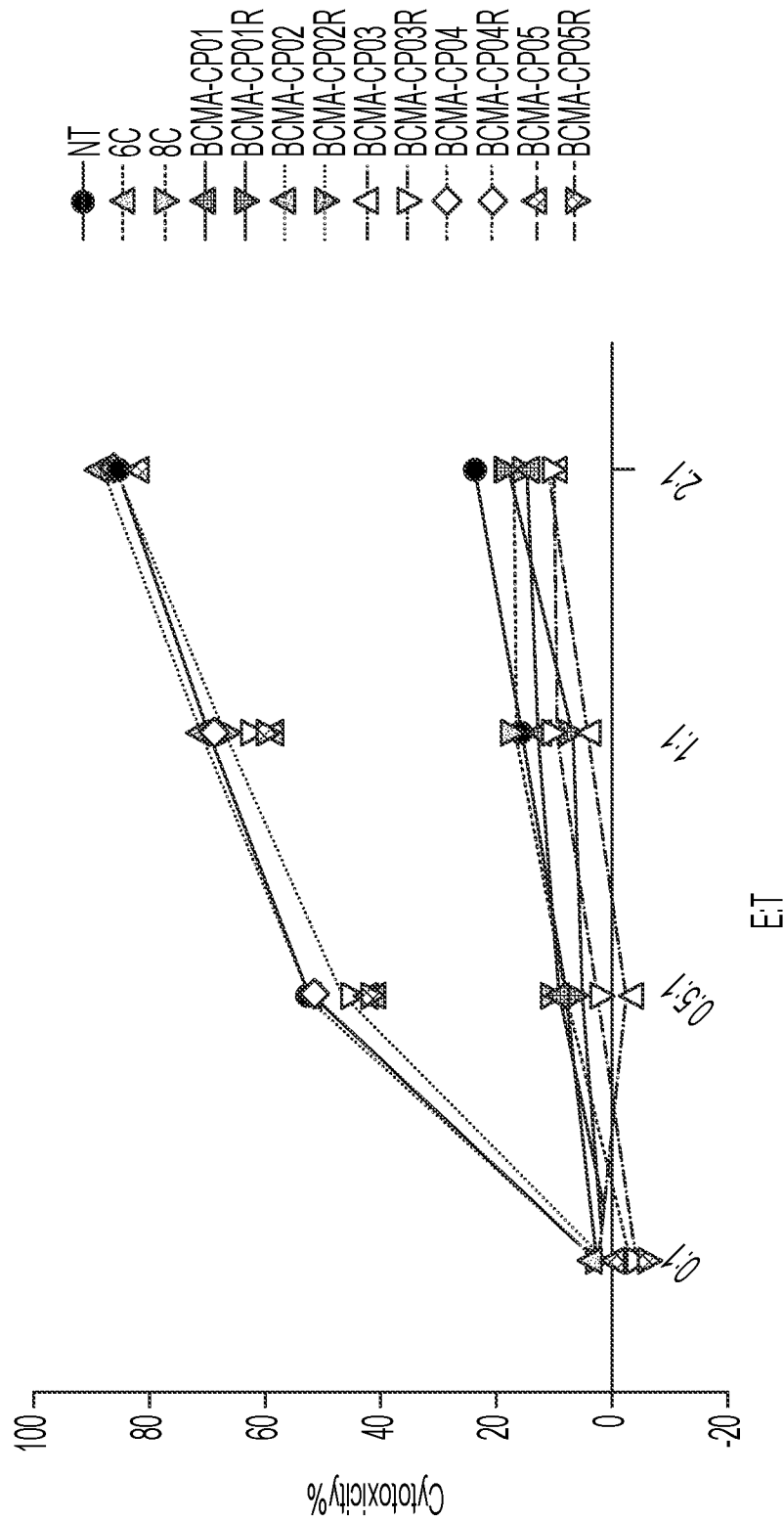


FIG. 20 CONT.

50/52

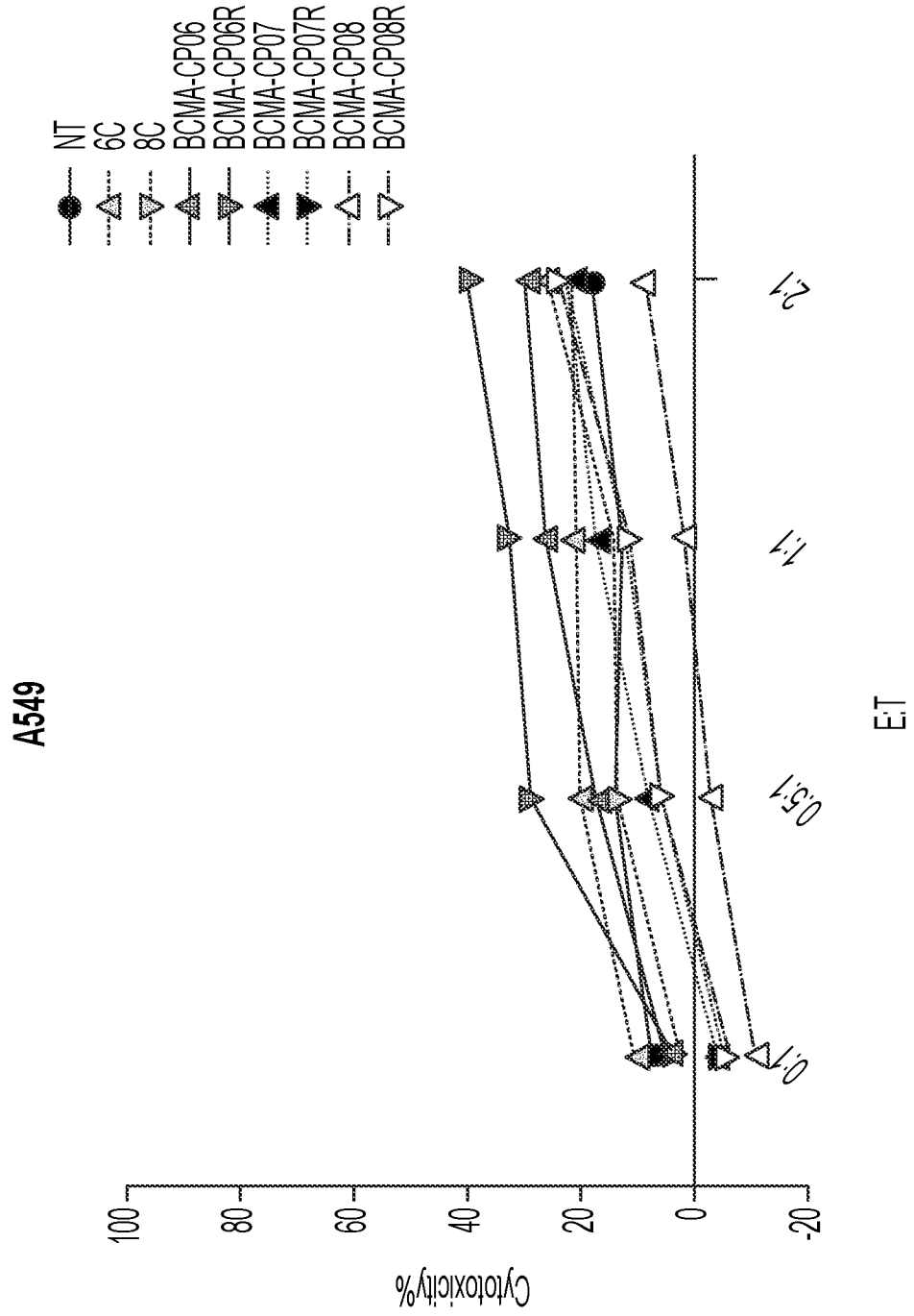


FIG. 20 CONT.

51/52

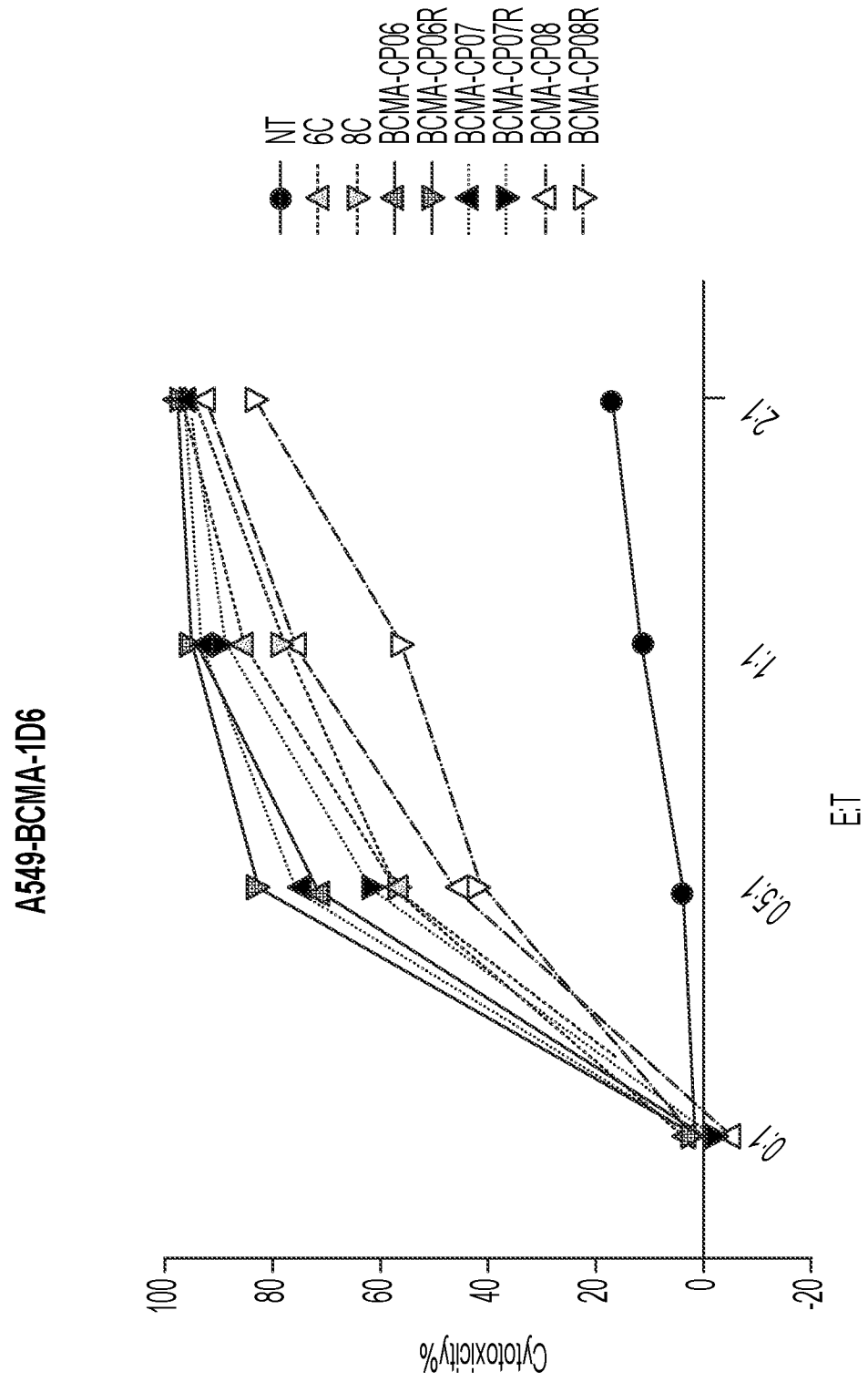


FIG. 20 CONT.

A549-BCMA-M

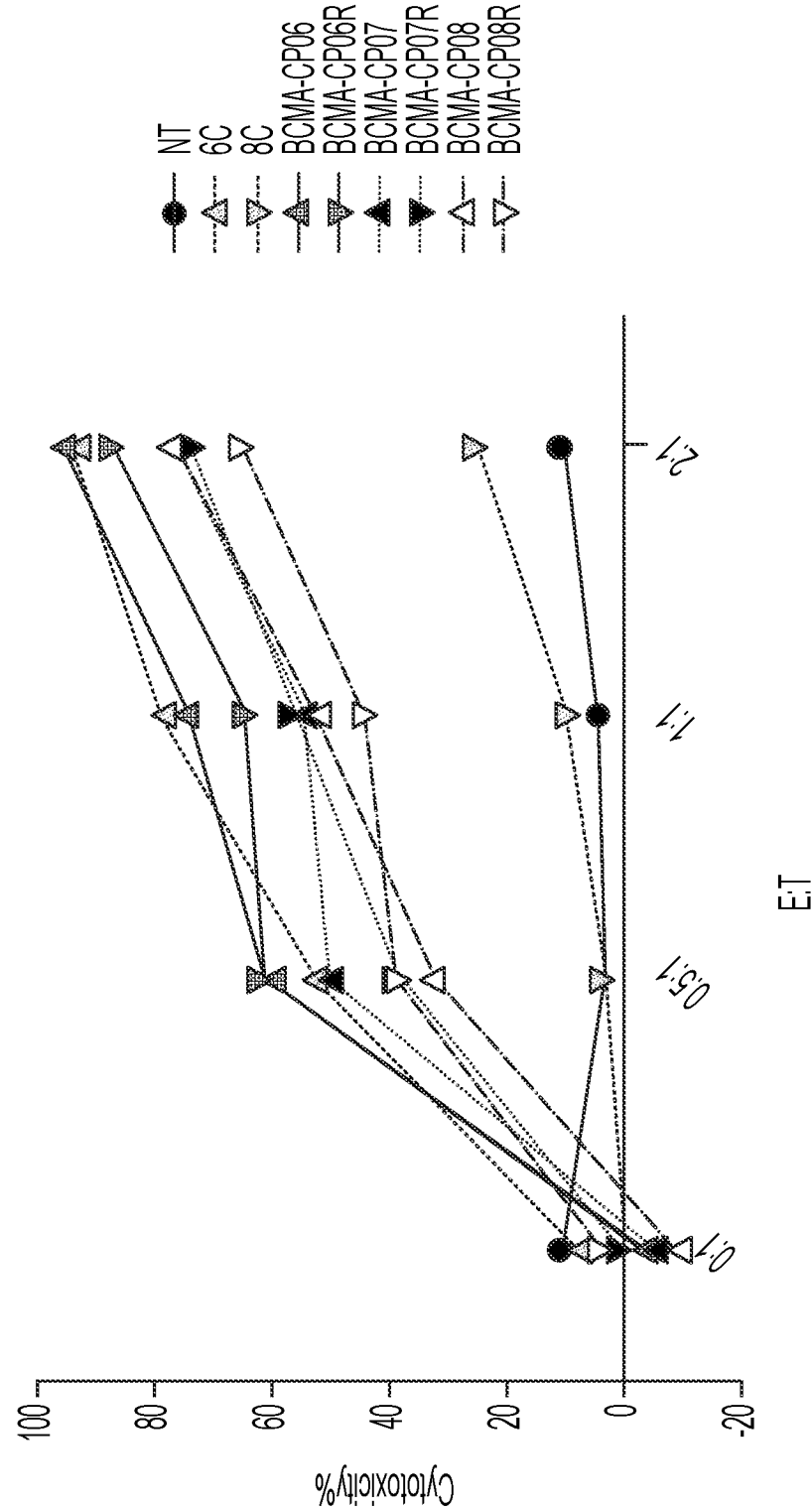


FIG. 20 CONT.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/31299

A. CLASSIFICATION OF SUBJECT MATTER

IPC - A61K 31/454, A61K 35/12, A61K 35/17, C07K 14/535 (2021.01)

CPC - A61P 35/00, A61P 37/06, C07K 14/535, A61K 2039/505

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.
A	US 2019/0112382 A1 (MAX - DELBRUCK - CENTRUM FUR MOLEKULARE MEDIZIN IN DER HELMHOLTZ - GEMEINSCHAFT) 18 April 2019 (18.04.2019) abstract; para [0020], [0037], [0062]; claim 1	1-4
A	US 2017/0298119 A1 (VISTERRA, INC.) 19 October 2017 (19.10.2017) abstract; claim 2	1-4
A	US 2015/0218267 A1 (BOEHRINGER INGELHEIM INTERNATIONAL GMBH) 06 August 2015 (06.08.2015) abstract, claim 1	1-4
A	WO 2010/056898 A2 (UNIVERSITY OF MARYLAND, BALTIMORE) 20 May 2010 (20.05.2010) abstract, claim 9	1-4
A	WO 2016/207304 A2 (MAB DISCOVERY GMBH) 29 December 2016 (29.12.2016) abstract; claim 1	1-4
A	US 8,575,317 B2 (KURAMOCHI et al.) 05 November 2013 (05.11.2013) abstract; col 3, ln 11-12; claim 14	1-4
A	WO 2017/189959 A1 (VOYAGER THERAPEUTICS, INC.) 02 November 2017 (02.11.2017) abstract; claim 1	1-4
A	WO 2016/150899 A2 (BAYER PHARMA AKTIENGESELL-SCHAFT et al.) 29 September 2016 (29.09.2016) abstract; claim 10	1-4

☐ 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

20 August 2021

Date of mailing of the international search report

OCT 14 2021

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 Rodriguez

Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/31299

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. ☒ forming part of the international application as filed:

☒ 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 13ter.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 13ter.1(a)).

☐ on paper or in the form of an image file (Rule 13ter.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 21/31299

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.: 5-11, 15-34
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 Supplemental Box ---

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.:
1-4 limited to SEQ ID NOs: 53-54, 76-81.

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 21/31299

Box No. III Observations where unity of invention is lacking

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 1-4, drawn to an anti-BCMA antibody. The composition will be searched to the extent that the anti-BCMA antibody encompasses LCDR1-3 of SEQ ID NOs: 76, 77 and 78, respectively; HCDR1-3 of SEQ ID NO: 79, 80 and 81, respectively; VL of SEQ ID NO: 53 and VH of SEQ ID NO: 54. It is believed that claims 1-4 encompass this first named invention, and thus these claims will be searched without fee to the extent that they encompass SEQ ID NOs: 53-54, 76-81. Additional anti-BCMA antibody(ies) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected anti-BCMA antibody(ies). 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 an anti-BCMA antibody encompassing LCDR1-3 of SEQ ID NOs: 82, 83 and 84, respectively; HCDR1-3 of SEQ ID NO: 85, 86 and 87, respectively; VL of SEQ ID NO: 55 and VH of SEQ ID NO: 56 (Claims 1-4).

Groups II+: Claims 12-14, drawn to a chimeric antigen receptor (CAR) comprising an anti-BCMA antibody. Group II+ will be searched upon payment of additional fees. The composition may be searched, for example, to the extent that the anti-BCMA antibody encompasses LCDR1-3 of SEQ ID NOs: 76, 77 and 78, respectively; HCDR1-3 of SEQ ID NO: 79, 80 and 81, respectively; VL of SEQ ID NO: 53 and VH of SEQ ID NO: 54; for an additional fee and election as such. It is believed that claims 12-14 read on this exemplary invention. Additional CAR(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected CAR(s). 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. Another exemplary election would be a CAR comprising an anti-BCMA antibody wherein LCDR1-3 comprising SEQ ID NOs: 82, 83 and 84, respectively; HCDR1-3 comprising SEQ ID NO: 85, 86 and 87, respectively; VL of SEQ ID NO: 55 and VH of SEQ ID NO: 56 (Claims 12-14).

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:

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

Additionally, even if Groups I+ and II+ were considered to share the technical features of including: an anti-BCMA antibody, these shared technical features are previously disclosed by US 2019/0112382 A1 to Max-Delbruck-Centrum Fur Molekulare Medizin In Der Helmholtz-Gemeinschaft (hereinafter "MDC") and US 2019/0388528 A1 to Bluebird Bio, Inc. (hereinafter "Bluebird").

MDC discloses (instant claim 1) an anti-BCMA antibody, or an antigen-binding portion thereof (abstract - "the method comprising administering to a subject an isolated antibody or antibody fragment comprising specific VH and VL domain complementary determining region, CDR, sequences, wherein the antibody or fragment thereof specifically binds an epitope of the extracellular domain of CD269, BCMA"), comprising a light chain variable region, VL, and a heavy chain variable region, VH, wherein the light chain variable region comprises three CDRs, CDR1, CDR2 and CDR3 (para [0020] - "The invention further relates to an antibody or antibody fragment, comprising a VL domain that comprises CDR sequences of: L-CDR1...L-CDR2...L-CDR3"; para [0101] - "The antibodies or parts thereof described herein also encompass a sequence with at least 80%, preferably 90%, sequence identity to those humanized sequences"); and wherein the heavy chain variable region comprises three complementarity determining regions, CDRs, CDR1, CDR2 and CDR3 (claim 1 - "an isolated antibody or antibody fragment comprising (a) a VH domain that comprises CDR sequences of: H-CDR...H-CDR2 and H-CDR3"; claim 18 - "wherein the VH domain comprises at least 80% sequence identity to the sequence").

Bluebird discloses (instant claim 12) a chimeric antigen receptor, CAR, comprising an anti-BCMA antigen-binding region (para [0003] - "The present invention relates to improved compositions and methods for treating B cell related conditions. More particularly, the invention relates to improved chimeric antigen receptors (CARs) comprising murine anti-BCMA antibodies or antigen binding fragments thereof, immune effector cells genetically modified to express these CARs, and use of these compositions to effectively treat B cell related conditions").

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.

Item 4 (continued):

Claims 5-11, 15-34 are held unsearchable because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).