What is claimed is:

1. A method of making a population of cells that express a chimeric antigen receptor (CAR), the method comprising:

(i) contacting a population of cells with an agent that stimulates a CD3/TCR complex and/or an agent that stimulates a costimulatory molecule on the surface of the cells;

(ii) contacting the population of cells with a nucleic acid molecule encoding the CAR, thereby providing a population of cells comprising the nucleic acid molecule, and

(iii) harvesting the population of cells for storage or administration;

wherein step (ii) is performed together with step (i) or less than 18 hours after the beginning of step (i), and step (iii) is performed no later than 48 hours after the beginning of step (i);

wherein the population of cells comprises T-cells .

2. The method of claim 1, wherein step (iii) is performed no later than 30 hours after the beginning of step (i).

3. The method of claim 1 or 2, wherein:

(a) the nucleic acid molecule in step (ii) is on a viral vector;

(b) the population of cells comprises a population of T cells;

(c) the population of T cells is isolated from a frozen or fresh leukapheresis product;

(d) the storage of step (iii) comprises reformulating the population of cells in cryopreservation media; and/or

(e) the population of cells contacted in step (i) comprises CD4+ T cells, CD8+ T cells, or both CD4+ T cells and CD8+ T cells selected from an apheresis sample.

4. The method of any one of claims 1-3, wherein:

(a) the agent that stimulates a CD3/TCR complex is an agent that stimulates CD3;

(b) the agent that stimulates a CD3/TCR complex or the agent that stimulates a costimulatory molecule is chosen from an antibody, a small molecule, or a ligand;

(c) the agent that stimulates a CD3/TCR complex or the agent that stimulates a costimulatory molecule does not comprise a bead;

(d) the agent that stimulates a costimulatory molecule is an agent that stimulates CD28, ICOS, CD27, HVEM, LIGHT, CD40, 4-1BB, OX40, DR3, GITR, CD30, TIM1, CD2, CD226, or any combination thereof; and/or

(e) the agent that stimulates a CD3/TCR complex is an anti-CD3 antibody.

5. The method of claim 4, wherein:

(a) the antibody is a single-domain antibody, a heavy chain variable domain antibody, a peptibody, a Fab fragment, or a scFv; and/or

(b) the ligand is a naturally-existing, recombinant, or chimeric ligand.

6. The method of any one of claims 1-5, wherein the agent that stimulates a CD3/TCR complex comprises an anti-CD3 antibody and the agent that stimulates a costimulatory molecule comprises an anti-CD28 antibody.

7. The method of any one of claims 1-6, wherein the agent that stimulates a CD3/TCR complex comprises an anti-CD3 antibody covalently attached to a colloidal polymeric nanomatrix and the agent that stimulates a costimulatory molecule comprises an anti-CD28 antibody covalently attached to a colloidal polymeric nanomatrix.

8. The method of any one of claims 1-7, wherein:

(I) (a) the percentage of naïve cells in the population of cells from step (iii) is the same as or differs by no more than 5 or 10% from the percentage of naïve cells in the population of cells at the beginning of step (i); or

(b) the percentage of naïve cells in the population of cells from step (iii) does not decrease, or decreases by no more than 5 or 10%, as compared to the percentage of naïve cells in the population of cells at the beginning of step (i); and/or

(II) (a) the percentage of central memory cells in the population of cells from step (iii) is the same as or differs by no more than 5 or 10% from the percentage of central memory cells in the population of cells at the beginning of step (i); or

(b) the percentage of central memory cells in the population of cells from step (iii) does not increase, or increases by no more than 5 or 10%, as compared to the percentage of central memory cells in the population of cells at the beginning of step (i).

9. The method of any one of claims 1-8, wherein step (i) increases the percentage of CAR-expressing cells in the population of cells from step (iii), for example, the population of cells from step (iii) shows a higher percentage of CAR-expressing cells, compared with cells made by an otherwise similar method without step (i).

10. The method of any one of claims 1-9, wherein:

(I) (a) the percentage of naïve cells in the population of cells from step (iii) is increased as compared to the percentage of naïve cells, in the population of cells at the beginning of step (i); or

(b) the percentage of CAR-expressing naïve T cells in the population of cells increases during the duration of step (ii), or between 18-24 hours after the beginning of step (ii); and/or

(II) (a) the population of cells from step (iii) shows a higher percentage of naïve cells compared with cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(b) the percentage of naïve cells in the population of cells from step (iii) is higher than the percentage of naïve cells in cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(c) the percentage of CAR-expressing naïve T cells in the population of cells from step (iii) is higher than the percentage of CAR-expressing naïve T cells in cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(d) the population of cells from step (iii) shows a higher percentage of naïve cells, compared with cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days;

(e) the percentage of naïve cells in the population of cells from step (iii) is higher than the percentage of naïve cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days; or

(f) the percentage of CAR-expressing naïve T cells in the population of cells from step (iii) is higher than the percentage of CAR-expressing naïve T cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days.

11. The method of any one of claims 1-10, wherein:

(I) (a) the percentage of central memory cells in the population of cells from step (iii) is reduced by at least 20%, as compared to the percentage of central memory cells in the population of cells at the beginning of step (i); or

(b) the percentage of CAR-expressing central memory T cells decreases during the duration of step (ii) or, between 18-24 hours after the beginning of step (ii); and/or

(II) (a) the population of cells from step (iii) shows a lower percentage of central memory cells compared with cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(b) the percentage of central memory cells in the population of cells from step (iii) is lower than the percentage of central memory cells in cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(c) the percentage of CAR-expressing central memory T cells in the population of cells from step (iii) is lower than the percentage of CAR-expressing central memory T cells in cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(d) the population of cells from step (iii) shows a lower percentage of central memory cells compared with cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days;

(e) the percentage of central memory cells in the population of cells from step (iii) is lower than the percentage of central memory cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days; or

(f) the percentage of CAR-expressing central memory T cells in the population of cells from step (iii) is lower than the percentage of CAR-expressing central memory T cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days.

12. The method of any one of claims 1-11, wherein:

(a) the percentage of stem memory T cells in the population of cells from step (iii) is increased, as compared to the percentage of stem memory T cells in the population of cells at the beginning of step (i);

(b) the percentage of CAR-expressing stem memory T cells in the population of cells from step (iii) is increased, as compared to the percentage of CAR-expressing stem memory T cells in the population of cells at the beginning of step (i);

(c) the percentage of stem memory T cells in the population of cells from step (iii) is higher than the percentage of stem memory T cells in cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(d) the percentage of CAR-expressing stem memory T cells in the population of cells from step (iii) is higher than the percentage of CAR-expressing stem memory T cells in cells

made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i);

(e) the percentage of stem memory T cells in the population of cells from step (iii) is higher than the percentage of stem memory T cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days; or

(f) the percentage of CAR-expressing stem memory T cells in the population of cells from step (iii) is higher than the percentage of CAR-expressing stem memory T cells in cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days.

13. The method of any one of claims 8-12, wherein:

said naïve cells are naïve T cells or CD45RA+ CD45RO- CCR7+ T cells;

said central memory cells are central memory T cells, CD95+ central memory T cells, or CCR7+CD45RO+ cells; and/or

said stem memory T cells are CD45RA+CD95+IL-2 receptor β+CCR7+CD62L+ T cell.

14. The method of any one of claims 1-13, wherein

(a) the population of cells from step (iii), after being incubated with a cell expressing an antigen recognized by the CAR, secretes IL-2 at a higher level than cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i), or cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days;

(b) the population of cells from step (iii), after being administered in vivo, persists longer or expands at a higher level, compared with cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i), or compared with cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days; and/or

(c) the population of cells from step (iii), after being administered in vivo, shows a stronger anti-tumor activity than cells made by an otherwise similar method in which step (iii) is performed more than 5 days after the beginning of step (i), or cells made by an otherwise similar method which further comprises, after step (ii) and prior to step (iii), expanding the population of cells in vitro for more than 3 days.

15. The method of any one of claims 1-14, wherein:

(a) the population of cells from step (iii) are expanded by no more than 5, 10, 15, 20, 25, 30, 35, or 40%, compared to the population of cells at the beginning of step (i);

(b) the population of cells from step (iii) are expanded by no more than 10%, compared to the population of cells at the beginning of step (i);

(c) the population of cells from step (iii) are not expanded, or expanded by no more than 5, 10, 15, 20, 25, 30, 35, or 40%, as assessed by the number of living cells, compared to the population of cells at the beginning of step (i);

(d) the number of living cells in the population of cells from step (iii) decreases from the number of living cells in the population of cells at the beginning of step (i);

(e) step (ii) is performed no later than 12, 13, 14, 15, 16, or 17 hours after the beginning of step (i), and/or step (iii) is performed no later than 22, 23, 24, 25, 26, 27, 28, 29, or 30 hours after the beginning of step (i);

(f) step (ii) is performed less than 18 hours after the beginning of step (i), and step (iii) is performed no later than 24 hours after the beginning of step (i);

(g) step (ii) is performed after the beginning of step (i);

(h) the population of cells from step (iii) are not expanded; and/or

(i) the population of cells from step (iii) are not expanded, as assessed by the number of living cells, compared to the population of cells at the beginning of step (i).

16. The method of any one of claims 1-15, wherein:

(a) steps (i) and/or (ii) are performed in cell media comprising IL-2, IL-15, IL-7, IL-21, IL-6, hetIL-15 (IL15/sIL15Ra), IL-6/IL-6Ra, a LSD1 inhibitor, a MALT1 inhibitor, or a combination thereof;

(b) steps (i) and/or (ii) are performed in serum-free media comprising IL-2, IL-15, IL-7, IL-21, IL-6, hetIL-15 (IL15/sIL15Ra), IL-6/IL-6Ra, a LSD1 inhibitor, a MALT1 inhibitor, or a combination thereof; and/or

(c) steps (i) and/or (ii) are performed in serum-free cell media comprising a serum replacement.

17. The method of any one of claims 1-10, further comprising prior to step (i):

(I) (iv) receiving a fresh leukapheresis product or an alternative source of hematopoietic tissue from an entity, and

(v) isolating the population of cells contacted in step (i) from a fresh leukapheresis product or an alternative source of hematopoietic tissue;

(II) receiving cryopreserved T cells isolated from a leukapheresis product or an alternative source of hematopoietic tissue, from an entity;

(III) (iv) receiving a cryopreserved leukapheresis product or an alternative source of hematopoietic tissue, from an entity, and

(v) isolating the population of cells contacted in step (i) from a cryopreserved leukapheresis product or an alternative source of hematopoietic tissue;

(IV) shipping an apheresis sample obtained from a subject to a cell manufacturing facility either as a frozen sample and then thawing it or as a not frozen sample;

selecting T cells from the apheresis sample; and

seeding the selected population of cells for CAR T cell manufacture; or

(V) selecting T cells from an apheresis sample obtained from a subject;

shipping the selected population of cells to a cell manufacturing facility as a frozen sample; and

thawing the frozen sample and seeding the selected population of cells for CAR T cell manufacture.

18. The method of claim 17, wherein:

(a) step (iii) is performed no later than 35 hours after the beginning of step (v);

(b) the population of cells from step (iii) are not expanded, or expanded by no more than 40%, compared to the population of cells at the end of step (v);

(c) the selected cells undergo one or more rounds of freeze-thaw before the seeing step;

(d) the alternative source of hematopoietic tissue is T cells isolated from:

cryopreserved whole blood, bone marrow, or tumor or organ biopsy or removal, or thymectomy; or

fresh whole blood, bone marrow, or tumor or organ biopsy or removal, or thymectomy;

(e) the T cells are CD4+ T cells and/or CD8+ T cells;

(f) the apheresis sample is a leukapheresis sample;

(g) the apheresis sample is a fresh product; and/or

(h) the entity is a laboratory, hospital, or healthcare provider.

19. The method of any one of claims 1-18, further comprising step (vi):

culturing a portion of the population of cells from step (iii) for at least 2 days, and measuring CAR expression level or the percentage of viable, CAR-expressing cells in the portion.

20. The method of claim 19, wherein step (iii) comprises harvesting and freezing the population of cells and step (vi) comprises thawing a portion of the population of cells from step (iii), culturing the portion for at least 2 days, and measuring CAR expression level or the percentage of viable, CAR-expressing cells in the portion.

21. The method of any one of claims 1-20, wherein:

(a) the population of cells at the beginning of step (i) has been enriched for IL6R-expressing cells and/or cells that are positive for IL6Rα and/or IL6Rβ;

(b) the population of cells at the beginning of step (i) comprises no less than 50% of IL6R-expressing cells and/or cells that are positive for IL6Rα and/or IL6Rβ;

(c) steps (i) and (ii) are performed in cell media comprising IL-15 and/or hetIL-15 (IL15/sIL-15Ra); and/or

(d) IL-15 increases the ability of the population of cells to expand and/or the percentage of IL6Rβ-expressing cells in the population of cells.

22. The method of any one of claims 1-21, wherein the CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular signaling domain.

23. The method of claim 22, wherein:

(a) the antigen binding domain:

(i) binds to an antigen chosen from: CD19, CD20, CD22, BCMA, mesothelin, EGFRvIII, GD2, Tn antigen, sTn antigen, Tn-O-Glycopeptides, sTn-O-Glycopeptides, PSMA, CD97, TAG72, CD44v6, CEA, EPCAM, KIT, IL-13Ra2, leguman, GD3, CD171, IL-11Ra, PSCA, MAD-CT-1, MAD-CT-2, VEGFR2, LewisY, CD24, PDGFR-beta, SSEA-4, folate receptor alpha, ERBBs (for example, ERBB2), Her2/neu, MUC1, EGFR, NCAM, Ephrin B2, CAIX, LMP2, sLe, HMWMAA, o-acetyl-GD2, folate receptor beta, TEM1/CD248, TEM7R, FAP, Legumain, HPV E6 or E7, ML-IAP, CLDN6, TSHR, GPRC5D, ALK, Polysialic acid, Fos-related antigen, neutrophil elastase, TRP-2, CYP1B1, sperm protein 17, beta human chorionic gonadotropin, AFP, thyroglobulin, PLAC1, globoH, RAGE1, MN-CA IX, human telomerase reverse transcriptase, intestinal carboxyl esterase, mut hsp 70-2, NA-17, NY-BR-1, UPK2, HAVCR1, ADRB3, PANX3, NY-ESO-1, GPR20, Ly6k, OR51E2, TARP, GFRα4, or a peptide of any of these antigens presented on MHC; and/or

(ii) comprises a VH and a VL, wherein the VH and VL are connected by a linker, wherein the linker comprises the amino acid sequence of SEQ ID NO: 63 or 104;

(b) the transmembrane domain comprises a transmembrane domain of a protein chosen from the alpha, beta or zeta chain of T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137 and CD154,

(c) the transmembrane domain comprises a transmembrane domain of CD8,

(d) the transmembrane domain comprises the amino acid sequence of SEQ ID NO: 6, or an amino acid sequence having at least 90% sequence identity thereto, and/or

(e) the nucleic acid molecule comprises a nucleotide sequence encoding the transmembrane domain, wherein the nucleotide sequence comprises the nucleic acid sequence of SEQ ID NO: 17, or a nucleic acid sequence having at least 90% sequence identity thereto.

24. The method of claim 22 or 23, wherein antigen binding domain is connected to the transmembrane domain by a hinge region, wherein:

(a) the hinge region comprises the amino acid sequence of SEQ ID NO: 2, 3, or 4, or an amino acid sequence having at least 90% sequence identity thereto; or

(b) the nucleic acid molecule comprises a nucleotide sequence encoding the hinge region, wherein the nucleotide sequence comprises the nucleic acid sequence of SEQ ID NO: 13, 14, or 15, or a nucleic acid sequence having at least 90% sequence identity thereto.

25. The method of any one of claims 22-24, wherein the intracellular signaling domain comprises a primary signaling domain and/or a costimulatory signaling domain.

26. The method of claim 25, wherein:

(a) the primary signaling domain comprises a functional signaling domain derived from CD3 zeta, TCR zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, CD278 (ICOS), FcεRI, DAP10, DAP12, or CD66d;

(b) the primary signaling domain comprises a functional signaling domain derived from CD3 zeta;

(c) the primary signaling domain comprises the amino acid sequence of SEQ ID NO: 9 or 10, or an amino acid sequence having at least 90% sequence identity thereto;

(d) the nucleic acid molecule comprises a nucleic acid sequence encoding the primary signaling domain, wherein the nucleic acid sequence comprises the nucleic acid sequence of SEQ ID NO: 20 or 21, or a nucleic acid sequence having at least 90% sequence identity thereto;

(e) the costimulatory signaling domain comprises a functional signaling domain derived from a MHC class I molecule, a TNF receptor protein, an Immunoglobulin-like protein, a cytokine receptor, an integrin, a signaling lymphocytic activation molecule (SLAM protein), an activating NK cell receptor, BTLA, a Toll ligand receptor, OX40, CD2, CD7, CD27, CD28, CD30, CD40, CDS, ICAM-1, 4-1BB (CD137), B7-H3, ICOS (CD278), GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, CD28-OX40, CD28-4-1BB, or a ligand that specifically binds with CD83;

(f) the costimulatory signaling domain comprises a functional signaling domain derived from 4-1BB;

(g) the costimulatory signaling domain comprises the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 90% sequence identity thereto; or

(h) the nucleic acid molecule comprises a nucleotide sequence encoding the costimulatory signaling domain, wherein the nucleic acid sequence comprises the nucleic acid

sequence of SEQ ID NO: 18, or a nucleotide sequence having at least 90% sequence identity thereto.

27. The method of any one of claims 22-26, wherein:

(a) the intracellular signaling domain comprises a functional signaling domain derived from 4-1BB and a functional signaling domain derived from CD3 zeta;

(b) the intracellular signaling domain comprises the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 90% sequence identity thereto and the amino acid sequence of SEQ ID NO: 9 or 10, or an amino acid sequence having at least about 90% sequence identity thereto;

(c) the intracellular signaling domain comprises the amino acid sequence of SEQ ID NO: 7 and the amino acid sequence of SEQ ID NO: 9 or 10; and/or

(d) the CAR further comprises a leader sequence comprising the amino acid sequence of SEQ ID NO: 1;

(e) the antigen binding domain binds to BCMA;

(f) the antigen binding domain binds to CD19;

(g) the antigen binding domain binds to CD20; or

(h) the antigen binding domain binds to CD22.

28. The method of any one of claims 1-27, wherein the CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular signaling domain, wherein the antigen binding domain binds to CD19 and comprises a heavy chain complementarity determining region 1 (HC CDR1), an HC CDR2, an HC CDR3, a light chain complementarity determining region 1 (LC CDR 1), an LC CDR2, and an LC CDR3, wherein:

(a) the HC CDR1 comprises the amino acid sequence of SEQ ID NO: 295;

(b) the HC CDR2 comprising the amino acid sequence of SEQ ID NO: 296;

(c) the HC CDR3 comprising the amino acid sequence of SEQ ID NO: 297;

(d) the LC CDR1 comprising the amino acid sequence of SEQ ID NO: 298;

(e) the LC CDR2 comprising the amino acid sequence of SEQ ID NO: 299; and

(f) the LC CDR3 comprising the amino acid sequence of SEQ ID NO: 300.

29. The method of claim 28, wherein:

(i) the CAR comprises an scFv comprising the amino acid sequence of SEQ ID NO: 303, or an amino acid sequence having at least 90% identity thereto;

(ii) the CAR comprises the amino acid sequence of SEQ ID NO: 292 or SEQ ID NO: 301, or an amino acid sequence having at least 90% identity thereto; and/or

(iii) the nucleic acid molecule encoding the CAR comprises the nucleotide sequence of SEQ ID NO: 302, or a nucleotide sequence having at least 90% identity thereto.

30. The method of any one of claims 1-27, wherein the CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular signaling domain, wherein the antigen binding domain binds to CD19 and comprises a heavy chain complementarity determining region 1 (HC CDR1) comprising the amino acid sequence of SEQ ID NO: 295, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 304, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 297, a light chain complementarity determining region 1 (LC CDR1) comprising the amino acid sequence of SEQ ID NO: 298, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 299, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 300.

31. The method of claim 30, wherein:

(i) the CAR comprises an scFv comprising the amino acid sequence of SEQ ID NO: 293, or an amino acid sequence having at least 90% identity thereto;

(ii) the CAR comprises the amino acid sequence of SEQ ID NO: 294 or SEQ ID NO: 306, or an amino acid sequence having at least 90% identity thereto; and/or

(iii) the nucleotide sequence encoding the CAR comprises the nucleotide sequence of SEQ ID NO: 305 or SEQ ID NO: 307, or a nucleotide sequence having at least 90% identity thereto.

32. The method of any one of claims 1-27, wherein the CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular signaling domain, wherein the antigen binding domain binds to BCMA and comprises:

(i) a heavy chain complementarity determining region 1 (HC CDR1) comprising the amino acid sequence of SEQ ID NO: 44, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 45, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 46, 68 or 76, a light chain complementarity determining region 1 (LC CDR1) comprising the amino acid sequence of SEQ ID NO: 54, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 55, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 56;

(ii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 47, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 48, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 46, 68, or 76, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 57, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 58, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 59;

(iii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 49, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 50, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 51, 69 or 77, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 60, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 58, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 56;

(iv) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 86, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 87, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 88, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 95, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 96, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 97;

(v) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 47, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 89, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 88, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 98, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 99, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 100;

(vi) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 90, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 91, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 92, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 101, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 99, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 97;

(vii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 86, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 109, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 88, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 95, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 114, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 97 or 115;

(viii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 47, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 110, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 88, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 98, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 116, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 100 or 117;

(ix) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 90, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 111, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 92, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 101, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 116, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 97 or 115;

(x) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 137, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 138, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 139, an LC CDR1 comprising the amino acid sequence of SEQ ID

NO: 147, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 148, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 149;

(xi) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 140, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 141, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 139, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 150, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 151, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 152;

(xii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 142, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 143, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 144, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 153, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 151, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 149;

(xiii) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 160, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 161, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 162, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 147, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 170, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 171;

(xiv) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 163, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 164, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 162, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 150, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 151, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 172; or

(xv) an HC CDR1 comprising the amino acid sequence of SEQ ID NO: 165, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 166, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 167, an LC CDR1 comprising the amino acid sequence of SEQ ID NO: 153, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 151, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 171.

33. The method of claim 32, wherein:

(a) the CAR comprises a heavy chain variable region (VH) comprising the amino acid sequence of SEQ ID NO: 93, or an amino acid sequence having at least 90% sequence identity thereto; and a light chain variable region (VL) comprising the amino acid sequence of SEQ ID NO: 102, or amino acid sequence having at least 90% sequence identity thereto;

(b) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 52, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 61, or amino acid sequence having at least 90% sequence identity thereto;

(c) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 70, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 61, or amino acid sequence having at least 90% sequence identity thereto;

(d) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 78, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 61, or amino acid sequence having at least 90% sequence identity thereto;

(e) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 112, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 118, or amino acid sequence having at least 90% sequence identity thereto;

(f) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 112, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 124, or amino acid sequence having at least 90% sequence identity thereto;

(g) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 145, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising

the amino acid sequence of SEQ ID NO: 154, or amino acid sequence having at least 90% sequence identity thereto;

(h) the CAR comprises a VH comprising the amino acid sequence of SEQ ID NO: 168, or an amino acid sequence having at least 90% sequence identity thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 173, or amino acid sequence having at least 90% sequence identity thereto;

(i) the CAR comprises an scFv comprising the amino acid sequence of any one of SEQ ID NOs: 64, 72, 80, 105, 120, 126, 156, or 175, or an amino acid sequence having at least 90% identity thereto;

(j) the CAR comprises the amino acid sequence of any one of SEQ ID NOs: 66, 74, 82, 107, 122, 128, 158, 177, or 257, or an amino acid sequence having at least 90% identity thereto; or

(k) the nucleotide sequence encoding the CAR comprises the nucleotide sequence of any one of SEQ ID NOs: 67, 75, 83, 106, 108, 123, 129, 159, 178, 253, or 258, or a nucleotide sequence having at least 90% identity thereto.

34. The method of any one of claims 1-27, wherein the CAR comprises an antigen binding domain, a transmembrane domain, and an intracellular signaling domain, wherein the antigen binding domain binds to CD22 and comprises a heavy chain complementarity determining region 1 (HC CDR1) comprising the amino acid sequence of SEQ ID NO: 288 or 289, an HC CDR2 comprising the amino acid sequence of SEQ ID NO: 290, an HC CDR3 comprising the amino acid sequence of SEQ ID NO: 291, a light chain complementarity determining region 1 (LC CDR1) comprising the amino acid sequence of SEQ ID NO: 95, an LC CDR2 comprising the amino acid sequence of SEQ ID NO: 96, and an LC CDR3 comprising the amino acid sequence of SEQ ID NO: 97.

35. The method of claim 34, wherein the CAR comprises:

(i) a heavy chain variable region (VH) comprising the amino acid sequence of SEQ ID NO: 286, or a sequence having at least 90% identity thereto; and a light chain variable region (VL) comprising the amino acid sequence of SEQ ID NO: 287, or an amino acid sequence having at least 90% identity thereto; and/or

(ii) an scFv comprising the amino acid sequence of SEQ ID NO: 285, or an amino acid sequence having at least 90% identity thereto.

36. The method of any one of claims 1-35, wherein the method further comprises formulating the harvested cells in a pharmaceutical composition in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients.