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(54) Title: CD3 RECONSTITUTION IN ENGINEERED iPSC AND IMMUNE EFFECTOR CELLS

(57) Abstract: Provided are methods and compositions for obtaining functionally enhanced derivative effector cells obtained from directed differentiation of genomically engineered iPSCs. The iPSC-derived cells provided herein have stable and functional genome editing that delivers improved or enhanced therapeutic effects. Also provided are therapeutic compositions and the used thereof comprising the functionally enhanced derivative effector cells alone, or with antibodies or checkpoint inhibitors in combination therapies.

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CD3 RECONSTITUTION IN ENGINEERED iPSC AND IMMUNE EFFECTOR CELLS

RELATED APPLICATION

[0001] This application claims priority to U.S. Provisional Application Serial No. 62/832,622, filed April 11, 2019, which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present disclosure is broadly concerned with the field of off-the-shelf immunocellular products. More particularly, the present disclosure is concerned with the strategies for developing multifunctional effector cells capable of delivering therapeutically relevant properties *in vivo*. The cell products developed under the present disclosure address critical limitations of patient-sourced cell therapies.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0003] This application incorporates by reference a Computer Readable Form (CRF) of a Sequence Listing in ASCII text format submitted with this application, entitled entitled 056932-518001WO_SEQUENCE_LISTING_ST25.TXT, was created on April 2, 2020, and is 76,442 bytes in size.

BACKGROUND OF THE INVENTION

[0004] The field of adoptive cell therapy is currently focused on using patient- and donor-sourced cells, which makes it particularly difficult to achieve consistent manufacturing of cancer immunotherapies and to deliver therapies to all patients who may benefit. There is also the need to improve the efficacy and persistence of adoptively transferred lymphocytes to promote favorable patient outcome. Lymphocytes such as T cells and natural killer (NK) cells are potent anti-tumor effectors that play an important role in innate and adaptive immunity. However, the use of these immune cells for adoptive cell therapies remain to be challenging and have unmet needs for improvement. Therefore, there are significant opportunities remain to harness the full potential of T and NK cells, or other lymphocytes in adoptive immunotherapy.

SUMMARY OF THE INVENTION

[0005] There is a need for functionally improved effector cells that address issues ranging from response rate, cell exhaustion, loss of transfused cells (survival and/or persistence), tumor

escape through target loss or lineage switch, tumor targeting precision, off-target toxicity, off-tumor effect, to efficacy against solid tumors, i.e., tumor microenvironment and related immune suppression, recruiting, trafficking and infiltration.

[0006] It is an object of the present invention to provide methods and compositions to generate derivative non-pluripotent cells differentiated from a single cell derived iPSC (induced pluripotent stem cell) clonal line, which iPSC line comprises one or several genetic modifications in its genome. Said one or several genetic modifications include DNA insertion, deletion, and substitution, and which modifications are retained and remain functional in subsequently derived cells after differentiation, expansion, passaging and/or transplantation.

[0007] The iPSC derived non-pluripotent cells of the present application include, but not limited to, CD34 cells, hemogenic endothelium cells, HSCs (hematopoietic stem and progenitor cells), hematopoietic multipotent progenitor cells, T cell progenitors, NK cell progenitors, T cells, NKT cells, NK cells, and B cells. The iPSC derived non-pluripotent cells of the present application comprise one or several genetic modifications in their genome through differentiation from an iPSC comprising the same genetic modifications. The engineered clonal iPSC differentiation strategy for obtaining genetically engineered iPSC-derived cells requires that the developmental potential of the iPSC in a directed differentiation is not adversely impacted by the engineered modality in the iPSC, and also that the engineered modality functions as intended in the derivative cell. Further, this strategy overcomes the present barrier in engineering primary lymphocytes, such as T cells or NK cells obtained from peripheral blood, umbilical cord blood or any other donor tissues, as such cells are difficult to engineer, with engineering of such cells often lacking reproducibility and uniformity, resulting in cells exhibiting poor cell persistence with high cell death and low cell expansion. Moreover, this strategy avoids production of a heterogenous effector cell population otherwise obtained using primary cell sources which are heterogenous to start with.

[0008] Some aspects of the present invention provide genome-engineered iPSCs obtained using a method comprising (I), (II) or (III), reflecting a strategy of genomic engineering subsequently to, simultaneously with, and prior to the reprogramming process, respectively:

[0009] (I): genetically engineering iPSCs by one or both of (i) and (ii), in any order: (i) introducing into iPSCs one or more construct(s) to allow targeted integration at selected site(s); (ii) (a) introducing into iPSCs one or more double stranded break(s) at selected site(s) using one or more endonuclease capable of selected site recognition; and (b) culturing the iPSCs of step (I)(ii)(a) to allow endogenous DNA repair to generate targeted in/dels at the selected site(s),

simultaneously or sequentially; thereby obtaining genome-engineered iPSCs capable of differentiation into partially or fully differentiated cells.

[00010] (II): genetically engineering reprogramming non-pluripotent cells to obtain the genome-engineered iPSCs comprising: (i) contacting non-pluripotent cells with one or more reprogramming factors, and optionally a small molecule composition comprising a TGFβ receptor/ALK inhibitor, a MEK inhibitor, a GSK3 inhibitor and/or a ROCK inhibitor to initiate reprogramming of the non-pluripotent cells; and (ii) introducing into the reprogramming non-pluripotent cells of step (II)(i) one or both of (a) and (b), in any order: (a) one or more construct(s) to allow targeted integration at selected site(s); (b) one or more double stranded break(s) at a selected site using at least one endonuclease capable of selected site recognition, then the cells of step (II)(ii)(b) are cultured to allow endogenous DNA repair to generate targeted in/dels at the selected site(s); as such the obtained genome-engineered iPSCs comprise at least one functional targeted genomic editing, and said genome-engineered iPSCs are capable of differentiation into partially or fully differentiated cells.

[00011] (III): genetically engineering non-pluripotent cells for reprogramming to obtain genome-engineered iPSCs comprising (i) and (ii): (i) introducing into non-pluripotent cells one or both of (a) and (b), in any order: (a) one or more construct(s) to allow targeted integration at selected site(s); (b) one or more double stranded break(s) at a selected site using at least one endonuclease capable of selected site recognition, wherein the cells of step (III)(i)(b) are cultured to allow endogenous DNA repair to generate targeted in/dels at the selected sites; and (ii) contacting the cells of step (III)(i) with one or more reprogramming factors, and optionally a small molecule composition comprising a TGFβ receptor/ALK inhibitor, a MEK inhibitor, a GSK3 inhibitor and/or a ROCK inhibitor, to obtain genome-engineered iPSCs comprising targeted editing at selected sites; thereby obtaining genome-engineered iPSCs comprising at least one functional targeted genomic editing, and said genome-engineered iPSCs are capable of being differentiated into partially differentiated cells or fully-differentiated cells.

[00012] In one embodiment of the above method, the at least one targeted genomic editing at one or more selected sites comprises insertion of one or more exogenous polynucleotides encoding safety switch proteins, targeting modalities, receptors, signaling molecules, transcription factors, pharmaceutically active proteins and peptides, drug target candidates, or proteins promoting engraftment, trafficking, homing, viability, self-renewal, persistence, and/or survival of the genome-engineered iPSCs or derivative cells therefrom. In some embodiments, the exogenous polynucleotides for insertion are operatively linked to (1) one or more exogenous promoters comprising CMV, EF1α, PGK, CAG, UBC, or other constitutive, inducible, temporal-,

tissue-, or cell type- specific promoters; or (2) one or more endogenous promoters comprised in the selected sites comprising AAVS1, CCR5, ROSA26, collagen, HTRP, H11, beta-2 microglobulin, CD38, GAPDH, TCR or RUNX1, or other locus meeting the criteria of a genome safe harbor. In some embodiments, the genome-engineered iPSCs generated using the above method comprise one or more different exogenous polynucleotides encoding protein comprising caspase, thymidine kinase, cytosine deaminase, modified EGFR, or B-cell CD20, wherein when the genome-engineered iPSCs comprise two or more suicide genes, the suicide genes are integrated in different safe harbor locus comprising AAVS1, CCR5, ROSA26, collagen, HTRP, H11, beta-2 microglobulin, CD38, GAPDH, TCR or RUNX1. In one embodiment, the exogenous polynucleotide encodes a partial or full length peptide of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, IL21, and/or respective receptors thereof. In some embodiments, the partial or full peptide of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, IL21, and/or respective receptors thereof encoded by the exogenous polynucleotide is in a form of fusion protein.

[00013] In some other embodiments, the genome-engineered iPSCs generated using the method provided herein comprise in/del at one or more endogenous genes associated with targeting modality, receptors, signaling molecules, transcription factors, drug target candidates, immune response regulation and modulation, or proteins suppressing engraftment, trafficking, homing, viability, self-renewal, persistence, and/or survival of the iPSCs or derivative cells therefrom. In some embodiments, the endogenous gene for disruption comprises at least one of CD38, B2M, TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region.

[00014] In yet some other embodiments, the genome-engineered iPSCs generated using the method provided herein comprise a caspase encoding exogenous polynucleotide at AAVS1 locus, and a thymidine kinase encoding exogenous polynucleotide at H11 locus.

[00015] In still some other embodiments, approach (I), (II) and/or (III) further comprises: contacting the genome-engineered iPSCs with a small molecule composition comprising a MEK inhibitor, a GSK3 inhibitor and a ROCK inhibitor, to maintain the pluripotency of the genomic-engineered iPSCs. In one embodiments, the obtained genome engineered iPSCs comprising at least one targeted genomic editing are functional, are differentiation potent, and are capable of differentiating into non-pluripotent cells comprising the same functional genomic editing.

[00016] The present invention also provides the followings.

[00017] One aspect of the present application provides a cell or a population thereof, wherein the cell is an induced pluripotent cell (iPSC), a clonal iPSC, or a clonal iPS cell line cell,

or a derivative cell obtained from differentiating any of the above said iPSC; and wherein any of the above said cell comprises at least TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed. In some embodiments of the obtained derivative cell from iPSC differentiation, the derivative cell is a hematopoietic cell, including, but not limited to, CD34 cells, hemogenic endothelium cells, HSCs (hematopoietic stem and progenitor cells), hematopoietic multipotent progenitor cells, T cell progenitors, NK cell progenitors, T cells, NKT cells, NK cells, and B cells; which the derivative hematopoietic cell (i.e., derivative CD34 cell, derivative hemogenic endothelium cells, derivative hematopoietic stem and progenitor cell, derivative hematopoietic multipotent progenitor cell, derivative T cell progenitor, derivative NK cell progenitor, derivative T cell, derivative NKT cell, derivative NK cell, or derivative B cell) comprises longer telomeres in comparison to its native counterpart cell obtained from peripheral blood, umbilical cord blood, or any other donor tissues. In some embodiments of the obtained derivative cell from iPSC differentiation, the derivative cell is a T cell progenitor or a T cell. In some embodiments of the obtained derivative cell from iPSC differentiation, the derivative cell is an NK cell progenitor or an NK cell.

[00018] In some embodiments of said iPSC and its derivative cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, the cell further comprises one or more of the following genomic editing: (i) B2M negative or low; (ii) CIITA negative or low; (iii) introduced expression of HLA-G or non-cleavable HLA-G; (iv) a high affinity non-cleavable CD16 (hnCD16) or a variant thereof; (v) a chimeric antigen receptor (CAR), (vi) a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; (vii) CD38 negative; (viii) at least one of the genotypes listed in Table 1; (ix) deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and (x) introduced or increased expression in at least one of HLA-E, 41BBL, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and a surface triggering receptor for coupling with bi- or multi- specific or universal engager.

[00019] In some embodiments of said iPSC and its derivative cell comprising at least TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and optional additional genomic editing as described above and throughout this application, the cell may comprise (i) one or more exogenous polynucleotides integrated in one

safe harbor locus; or (ii) two or more exogenous polynucleotides integrated in different safe harbor loci. In some embodiments, the safe harbor locus comprises at least one of AAVS1, CCR5, ROSA26, collagen, HTRP, H11, beta-2 microglobulin, CD38, GAPDH, TCR or RUNX1. In one particular embodiment, the safe harbor locus is H11. In one particular embodiment, the safe harbor locus TCR is a constant region of TCR alpha or TCR beta. In some embodiments, the insertion of one or more exogenous polynucleotides at the safe harbor locus resulting in disruption or knock-out of the endogenous gene at the safe harbor, for example, insertion at B2M, CD38 or TCR alpha/beta resulting in knockout of B2M, CD38 or TCR alpha/beta gene.

[00020] In some embodiments of the cell or population thereof, the cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and one or more of the additional genomic editing above is, in some embodiments, a derivative T cell, and in some other embodiments, a derivative NK cell, obtained from an iPSC comprising said genomic editing, and the derivative T or NK cell has at least one of the following characteristics including, but not limited to: (i) improved persistency and/or survival; (ii) increased resistance to native (i.e., recipient) immune cells; (iii) increased cytotoxicity; (iv) improved tumor penetration; (v) enhanced or acquired ADCC; (vi) enhanced ability in migrating, and/or activating or recruiting bystander immune cells, to tumor sites; (vii) enhanced ability to reduce tumor immunosuppression; (viii) improved ability in rescuing tumor antigen escape; and (ix) reduced fratricide, when compared to its native counterpart, primary T or NK cell, obtained from peripheral blood, umbilical cord blood, or any other donor tissues. When compared to TCR^{neg} T or NK cell (primary or derivative), which are cell surface CD3 negative, the derivative T or NK cell comprising both TCR^{neg} and one or more exogenous protein enabling a surface presented CD3 complex or a subunit or a subdomain thereof further has at least one of the following phenotypic and functional characteristics including, but not limited to: cell surface presented a full or partial endogenous or exogenous cell surface CD3 complex, and the capability of responding to molecules that bind to CD3 related cell surface triggering receptor, which molecules include, but are not limited to, CD3 binding antibodies or functional variants thereof, scFV, and/or various CD3 engagers.

[00021] In one embodiment of the cell or population thereof, the cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed further comprises a high affinity non-cleavable CD16 or a variant thereof (hnCD16). Some embodiments of the high affinity non-cleavable CD16 or a variant thereof (hnCD16) comprises

at least any one of the followings: (a) F176V and S197P in ectodomain domain of CD16; (b) a full or partial ectodomain originated from CD64; (c) a non-native (or non-CD16) transmembrane domain; (d) a non-native (or non-CD16) intracellular domain; (e) a non-native (or non-CD16) signaling domain; (f) a non-native stimulatory domain; and (g) transmembrane, signaling, and stimulatory domains that are not originated from CD16, and are originated from a same or different polypeptide. In some embodiments, the non-native transmembrane domain is derived from CD3D, CD3E, CD3G, CD3ζ, CD4, CD8, CD8a, CD8b, CD27, CD28, CD40, CD84, CD166, 4-1BB, OX40, ICOS, ICAM-1, CTLA-4, PD-1, LAG-3, 2B4, BTLA, CD16, IL7, IL12, IL15, KIR2DL4, KIR2DS1, NKp30, NKp44, NKp46, NKG2C, NKG2D, or T cell receptor (TCR) polypeptide. In some embodiments, the non-native stimulatory domain is derived from CD27, CD28, 4-1BB, OX40, ICOS, PD-1, LAG-3, 2B4, BTLA, DAP10, DAP12, CTLA-4, or NKG2D polypeptide. In some other embodiments, the non-native signaling domain is derived from CD3ζ, 2B4, DAP10, DAP12, DNAM1, CD137 (41BB), IL21, IL7, IL12, IL15, NKp30, NKp44, NKp46, NKG2C, or NKG2D polypeptide. In some particular embodiments of a hnCD16 or a variant thereof, the non-native transmembrane domain is derived from NKG2D, the non-native stimulatory domain is derived from 2B4, and the non-native signaling domain is derived from CD3ζ or DAP10.

[00022] In one embodiment of the cell or population thereof, the cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed further comprises at least one chimeric antigen receptor (CAR), and wherein the CAR could be any one or more of the followings: (i) T cell specific or NK cell specific; (ii) bi-specific antigen binding CAR; (iii) a switchable CAR; (iv) a dimerized CAR; (v) a split CAR; (vi) a multi-chain CAR; (vii) an inducible CAR; (viii) co-expressed with another CAR; (ix) co-expressed with a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof, optionally in separate constructs or in a bi- or poly- cistronic construct; (xi) co-expressed with a checkpoint inhibitor, optionally in separate constructs or in a bi- or poly- cistronic construct; (xii) is specific to CD19 or BCMA; and/or (xiii) is specific to any one of ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb-B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor

(AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and a pathogen antigen. In some embodiments, any one of the above CAR may be inserted at a constant region of a TCR locus, such as TCRα or TCRβ. In some embodiments, the CAR inserted at TRAC or TRBC locus may be driven by a respective endogenous promoter of TCR. In some embodiments, the insertion of the CAR at TRAC or TRBC locus leads to TCR negative or knockout. In some embodiments, the TCR negative cell is also CD3 negative.

[00023] In some of the embodiments, in which a checkpoint inhibitor is co-expressed with a CAR, the checkpoint inhibitor is an antagonist to one or more checkpoint molecules comprising PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB, 4-1BBL, A2aR, BATE, BTLA, CD39, CD47, CD73, CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2, Rara (retinoic acid receptor alpha), TLR3, VISTA, NKG2A/HLA-E, or inhibitory KIR. The checkpoint inhibitor co-expressed with the CAR could be an antibody, or humanized or Fc modified variants or fragments and functional equivalents and biosimilars thereof, specific to any of the above checkpoint molecules.

[00024] In one embodiment of the cell or population thereof, the cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed further comprises a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof, and wherein the exogenous cytokine or a receptor thereof may comprise at least one of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, IL21, and respective receptor thereof; or may comprise at least one of: (i) co-expression of IL15 and IL15Rα by using a self-cleaving peptide; (ii) a fusion protein of IL15 and IL15Rα; (iii) an IL15/IL15Rα fusion protein with intracellular domain of IL15Rα truncated (IL15Δ); (iv) a fusion protein of IL15 and membrane bound Sushi domain of IL15Rα; (v) a fusion protein of IL15 and IL15Rβ; (vi) a fusion protein of IL15 and common receptor γC, wherein the common receptor γC is native or

modified; and (vii) a homodimer of IL15Rβ; wherein any one of (i)-(vii) can be co-expressed with a CAR in separate constructs or in a bi- or poly- cistronic construct. In some embodiments, the partial or full peptide of a cell surface exogenous cytokine or a receptor is transiently expressed in the cell provided herein. In one embodiment, the cell or population thereof comprises a polynucleotide encoding an IL15Δ comprising an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NOs: 17, 19 or 21.

[00025] In one embodiment of the cell or population thereof, the cell comprising TCR^{neg}, one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and an IL15 or a variant including those embodiments (i)-(vii) as disclosed above may further comprise one or more of B2M negative or low; CIITA negative or low; introduced expression of HLA-G or non-cleavable HLA-G; a high affinity non-cleavable CD16 or a variant thereof (hnCD16); a chimeric antigen receptor (CAR), a partial or full length peptide of a cell surface expressed an additional exogenous cytokine or a receptor thereof, wherein the cytokine is not IL15; at least one of the genotypes listed in Table 1; deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and introduced or increased expression in at least one of HLA-E, 41BBL, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, A2AR, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi- or multi- specific or universal engagers. In an embodiment of a cell or population thereof comprising both an IL15Δ and a CAR, the IL15Δ can be co-expressed with a CAR in separate constructs or in a bi- or poly-cistronic construct.

[00026] In one embodiment of the cell or population thereof, the cell comprising TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed is a derivative NK or a derivative T cell, wherein the derivative NK or the derivative T cell is capable of reducing tumor immunosuppression in the presence of one or more checkpoint inhibitors. In some embodiments, the presence of the one or more checkpoint inhibitors is through administer the inhibitor(s) to a subject before, during or after receiving said cell. In some other embodiments, the presence of the one or more checkpoint inhibitors is through expressing the inhibitor by said cell by introducing the checkpoint inhibitor expression to said cell using a polynucleotide encoding the selected inhibitor. In some embodiments, the checkpoint inhibitors are antagonists to one or more checkpoint molecules comprising PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB, 4-1BBL, A2aR, BATE, BTLA, CD39,

CD47, CD73, CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2, Rara (retinoic acid receptor alpha), TLR3, VISTA, NKG2A/HLA-E, or inhibitory KIR. In some other embodiments, the checkpoint inhibitors comprise either (a) one or more of atezolizumab, avelumab, durvalumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their derivatives or functional equivalents; or (b) at least one of atezolizumab, nivolumab, and pembrolizumab.

[00027] Another aspect of the present application provides a composition comprising any of the cells or populations thereof as described above, and throughout this application. In some embodiments, the iPSC or iPSC derived cells (also called "derivative cells" herein) may comprise any one of the genotypes listed in Table 1 of this application. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; and a hnCD16. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; hnCD16; and an IL15 or variant thereof. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; a hnCD16; and a CAR. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; a hnCD16; an IL15 or variant thereof; and a CAR. In some embodiments, the TCR^{neg} iPSC or derivative cell therefrom comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; a hnCD16; CD38 negative; a CAR; and a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof as provided above and throughout this application. In some other embodiments, the CAR is specific to any one of ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99,

CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell (e.g., a cell surface antigen), epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and various pathogen antigen known in the art. In yet some embodiments of cells comprising TCR^{neg}, the cell comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; a hnCD16; and a CAR, wherein the CAR is specific to CD19 or CD269 (BCMA). In some embodiments of cells comprising TCR^{neg}, the cell comprises a surface CD3 complex, or a subunit or a subdomain thereof, when expressed in the cell; a hnCD16; an IL15 or variant thereof; and a CAR, wherein the CAR is specific to CD19 or CD269 (BCMA). In some other embodiments of cells comprising TCR^{neg}, the cell comprises a surface CD3 complex, or a subunit or a subdomain thereof, when expressed in the cell; a hnCD16; an IL15 or variant thereof; CD38 negative; and a CAR, wherein the CAR is specific to CD 19 or CD269 (BCMA).

[00028] Accordingly, a further aspect of the present application provides a composition for therapeutic use, which comprises, in addition to any of the derivative cell as provided herein, one or more therapeutic agents. In some embodiments of the composition for therapeutic use, the therapeutic agents comprise a peptide, a cytokine, a checkpoint inhibitor, a mitogen, a growth factor, a small RNA, a dsRNA (double stranded RNA), mononuclear blood cells, feeder cells, feeder cell components or replacement factors thereof, a vector comprising one or more polynucleic acids of interest, an antibody, a chemotherapeutic agent or a radioactive moiety, or an immunomodulatory drug (IMiD). In some embodiments of the composition for therapeutic use, the checkpoint inhibitor used with the provided cells comprises one or more antagonists checkpoint molecules comprising PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB,

4-1BBL, A2aR, BATE, BTLA, CD39, CD47, CD73, CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2, Rara (retinoic acid receptor alpha), TLR3, VISTA, NKG2A/HLA-E, or inhibitory KIR. In some embodiments of the composition for therapeutic use, the checkpoint inhibitor used with the provided cells comprises one or more of atezolizumab, avelumab, durvalumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their derivatives or functional equivalents. In some other embodiments of the composition for therapeutic use, the checkpoint inhibitor used with the provided cells comprises at least one of atezolizumab, nivolumab, and pembrolizumab. In some embodiments of the composition for therapeutic use, the therapeutic agents comprise one or more of venetoclax, azacitidine, and pomalidomide.

[00029] In some embodiments of the composition for therapeutic use, the antibody used with the provided cells comprises any one of the anti-CD20, anti-CD22, anti-HER2, anti-CD52, anti-EGFR, anti-CD123, anti-GD2, anti-PDL1, and/or anti-CD38 antibody. In some embodiments of the composition for therapeutic use, the antibody used with the provided cells comprises one or more of rituximab, veltuzumab, ofatumumab, ublituximab, ocaratuzumab, obinutuzumab, ibritumomab, ocrelizumab, inotuzumab, moxetumomab, epratuzumab, trastuzumab, pertuzumab, alemtuzumab, certuximab, dinutuximab, avelumab, daratumumab, isatuximab, MOR202, 7G3, CSL362, elotuzumab, and their humanized or Fc modified variants or fragments and their functional equivalents and biosimilars. In still some other embodiments of the composition for therapeutic use, the antibody used with the provided cells comprises daratumumab.

[00030] The present application also provides a therapeutic use of the cell or therapeutic composition as described herein by introducing the composition to a subject suitable for adoptive cell therapy. In some embodiments, the subject suitable for and in need of the adoptive cell therapy has an autoimmune disorder; a hematological malignancy; a solid tumor; cancer, or a virus infection.

[00031] A further aspect of the present application provides a method of manufacturing the derivative cell as described herein, and the method comprises differentiating an TCR^{neg} iPSC which comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and optionally one or more of: (i) B2M negative or low; (ii) CIITA negative or low; (iii) introduced expression of HLA-G or non-cleavable HLA-G; (iv) a high affinity non-cleavable CD16 (hnCD16) or a variant thereof; (v) a chimeric antigen receptor (CAR); (vi) a partial or full

length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; (vii) CD38 negative; (viii) at least one of the genotypes listed in Table 1; (ix) deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and (x) introduced or increased expression in at least one of HLA-E, 41BBL, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi- or multi- specific or universal engagers.

[00032] In some embodiments of the manufacturing method, the method further comprises genomically engineering a clonal iPSC (1) to knock out endogenous TCR; and (2) to introduce to the cell one or more polynucleotides encoding at least one exogenous protein comprising tgTRAC, tgTRBC, tgTCRα, tgTCRβ, tgpTCRα, tgCD3(ε-δ)-TRAC, tgCD3(ε-γ)-TRBC, tgCD3(ε-γ)-TRAC, tgCD3(ε-δ)-TRBC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and/or tgCD3(ε- γ/δ)-(28-BB)ζ to provide a surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3), when expressed in the cell, and optionally, to knock out B2M and CIITA, or to introduce expression of HLA-G or non-cleavable HLA-G, a high affinity non-cleavable CD16 or a variant thereof, a CAR, and/or a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; and the CAR and the partial or full peptide of a cell surface expressed exogenous cytokine or a receptor thereof are co-expressed in separate constructs or in a bi- or poly- cistronic construct. In some embodiments of the manufacturing method, the genomic engineering of an iPSC comprises targeted editing. In some embodiments, the targeted editing comprises deletion, insertion, or in/del. In some embodiments, the targeted deletion/knockout and the targeted insertion are carried out simultaneously, wherein the insertion is at the location where the deletion is conducted. In some embodiments, the targeted deletion/knockout and the targeted insertion are carried out consecutively, in any order, wherein the insertion and the deletion may or may not be at the same location. In some embodiments, the targeted editing tool comprises CRISPR, ZFN, TALEN, homing nuclease, homology recombination, or any other functional variation of these methods and composition.

[00033] The present application further provides the targeted editing tool mediated editing of clonal iPSCs, thereby producing edited clonal iPSCs that lack endogenous TCRα or TCRβ and comprise introduced one or more polynucleotides encoding at least one exogenous protein comprising tgTRAC, tgTRBC, tgTCRα, tgTCRβ, tgpTCRα, tgCD3(ε-δ)-TRAC, tgCD3(ε-γ)-TRBC, tgCD3(ε-γ)-TRAC, tgCD3(ε-δ)-TRBC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and/or tgCD3(ε- γ/δ)-(28-BB)ζ to provide a cell surface CD3 complex, or

one or more subunits or subdomains thereof (cs-CD3), when expressed in the cell, or at least one of the genotypes listed in Table 1. In some embodiments of the genome targeting tool mediated editing, the obtained TCR knockout is through targeted disruption of the endogenous TCRα constant region (TRAC). In some embodiments of the genome targeting tool mediated editing, the obtained TCR knockout is through targeted disruption of the endogenous TCRβ constant region (TRBC). In some embodiments of the genome targeting tool mediated editing above, the editing further comprises an insertion of a CAR at the endogenous TRAC or TRBC locus, and/or wherein the CAR is driven by an endogenous promoter of TCRα or TCRβ, and/or wherein the TCR is knocked out by the CAR insertion. In some embodiments of the genome targeting tool mediated editing above, the editing further comprises an insertion at the endogenous TRAC locus a polynucleotide encoding an exogenous protein comprising tgTRAC, tgTCRα, tgpTCRα, tgCD3(ε-δ)-TRAC, tgCD3(ε-γ)-TRAC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, or tgCD3(ε- γ/δ)-(28-BB)ζ to provide a surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3), when expressed in the cell. In some embodiments of the genome targeting tool mediated editing above, the editing further comprises an insertion at the endogenous TRBC locus a polynucleotide encoding an exogenous protein comprising tgTRBC, tgTCRβ, tgCD3(ε-γ)-TRBC, tgCD3(ε-δ)-TRBC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and/or tgCD3(ε- γ/δ)-(28-BB)ζ to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3), when expressed in the cell.

[00034] In one embodiment of the cell or a population thereof as provided, the cell is an induced pluripotent cell (iPSC), a clonal iPSC, or a clonal iPS cell line cell, or a derivative cell obtained from differentiating said iPSC; and the cell is TCR^{neg}, and comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed. In some embodiments, the cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) is associated with a non-binding recombinant TCR (nb-rTCR); a defined recombinant TCR (d-rTCR); a recombinant pre-TCR (p-rTCR); or is anchored to a non-binding recombinant TCR (nb-rTCR-CD3); or is a CD3 chimeric chain (ccCD3). In one embodiment, the nb-rTCR comprises one or both of a tgTRAC and a tgTRBC. In one embodiment, the d-rTCR comprises a tgTCRα, and optionally, a tgTCRβ, wherein each of the tgTCRα and the tgTCRβ comprises a respective defined variable region. In one embodiment, the p-rTCR comprises a tgpTCRα, and optionally a tgTRBC or a tgTCRβ, wherein the tgTCRβ comprises a defined variable region. In one embodiment, the nb-rTCR-CD3 comprises one or more of fusion proteins: (1) a tgCD3(ε-δ)-

TRAC; (2) a tgCD3(ε-γ)-TRBC; (3) a tgCD3(ε-γ)-TRAC; and/or (4) a tgCD3(ε-δ)-TRBC, wherein the fusion protein comprises full or partial length of ectodomains of CD3ε, CD3δ, CD3γ, and/or a full or partial length of TRAC or TRBC. In one embodiment, the ccCD3 comprises at least one of fusion proteins: tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and tgCD3(ε-γ/δ)-(28-BB)ζ, wherein the fusion protein comprising full or partial length of ectodomains of CD3ε, CD3δ and/or CD3γ protein, further comprises a cytoplasmic domain comprising a full or partial length endodomain of CDζ protein, and optionally one or both of a CD28 signaling domain and a 41BB signaling domain. In yet another embodiment, the nb-rTCR-CD3 comprising fusion protein tgCD3(ε-δ)-TRAC further comprises tgTRBC or tgTCRβ. In yet another embodiment, the nb-rTCR-CD3 comprising fusion protein tgCD3(ε-γ)-TRBC further comprises tgTRAC or tgTCRα. Or in yet another embodiment, the d-rTCR comprising a tgTCRα and a tgTCRβ comprises TCRα and TCRβ of an invariant NKT cell.

[00035] In view of the above embodiments, the cell as provided, in some aspects, comprises one of the recombinant TCRs: nb-rTCR, d-rTCR, or the p-rTCR, which recombinant TCR complexes with endogenous CD3 subunits, thereby enabling cell surface presentation of endogenous CD3 subunits and signaling thereof. In some other embodiments, the cell comprises a nb-rTCR-CD3 or a ccCD3, thereby enabling cell surface presentation of exogenous CD3 subunits and signaling thereof.

[00036] One aspect of the present application provides a clonal master cell bank comprising the clonal iPSC cell line cells as described herein. Another aspect of the present application provides a composition comprising the cell or population thereof, including various embodiments of the iPSCs and derivative cells differentiated from said iPSCs as described herein. In some embodiments, the composition comprising said derivative cell is suitable for therapeutic use. In some embodiments of the composition for therapeutic use, the compostion further comprises one or more therapeutic agents in addition to the derivative cell as desired. In some embodiments, said therapeutic agents comprise a peptide, a cytokine, a checkpoint inhibitor, a mitogen, a growth factor, a small RNA, a dsRNA (double stranded RNA), mononuclear blood cells, feeder cells, feeder cell components or replacement factors thereof, a vector comprising one or more polynucleic acids of interest, an antibody, a chemotherapeutic agent or a radioactive moiety, or an immunomodulatory drug (IMiD).

[00037] Additional aspect of the present application provides therapeutic use of said therapeutic composition in various embodiments by introducing the composition to a subject suitable for adoptive cell therapy, wherein the subject has an autoimmune disorder; a hematological malignancy; a solid tumor; cancer, or a virus infection.

[00038] A further aspect of the present application provide a method of manufacturing a derivative effector cell by differentiating a TCR^{neg} iPSC, which iPSC comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and optionally the iPSC further comprises one or more of: (i) B2M negative or low; (ii) CIITA negative or low; (iii) introduced expression of HLA-G or non-cleavable HLA-G; (iv) a high affinity non-cleavable CD16 (hnCD16) or a variant thereof; (v) a chimeric antigen receptor (CAR); (vi) a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; (vii) at least one of the genotypes listed in Table 1; (viii) deletion or reduced expression in at least one of CD38, TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and (ix) introduced or increased expression in at least one of HLA-E, 41BBL, CD3, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, TCR, Fc receptor, an engager, and surface triggering receptor for coupling with bi- or multi- specific or universal engagers. In some embodiments of the method of manufacturing cells of the present application, the method further comprises a step of providing a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) by knocking out TCR of a clonal iPSC to obtain the genomically engineered TCR^{neg} iPSC by, and knocking in, simultaneously or subsequently, one or more polynucleotide encoding one or more exogenous protein; or by reprogramming an invariant NKT cell to iPSC to provide a clonal iPSC comprising iTCRαβ but not T cell-TCR; and an optional step of genomically engineering the TCR negative cell by knocking out B2M and CIITA, or introducing expression of HLA-G or non-cleavable HLA-G, a high affinity non-cleavable CD16 or a variant thereof, a CAR, and/or a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof, and said CAR and the partial or full peptide of a cell surface expressed exogenous cytokine or a receptor thereof are co-expressed in separate constructs or in a bi-cistronic construct.

[00039] In one embodiment of the method of manufacturing the cells, the step of knocking in one or more polynucleotide encoding one or more exogenous protein to provide cs-CD3, further comprises introducing to the iPSC one of: (i) one or both of a tgTRAC and a tgTRBC encoding polynucleotide, to provide a nb-rTCR when expressed; (ii) a tgTCRα, and optionally a tgTCRβ, encoding polynucleotide, to provide a d-rTCR when expressed, wherein each of the tgTCRα and the tgTCRβ comprises a respective defined variable region; (iii) a tgpTCRα, and optionally a tgTRBC or a tgTCRβ, encoding polynucleotide, to provide a p-rTCR, wherein the tgTCRβ comprises a defined variable region; (iv) one or more polynucleotides encoding one or more of fusion proteins: (1) tgCD3(ε-δ)-TRAC, (2) tgCD3(ε-γ)-TRBC, (3) tgCD3(ε-γ)-TRAC,

and/or (4) tgCD3(ε-δ)-TRBC, to provide a nb-rTCR-CD3; wherein the fusion protein comprises full or partial length of ectodomains of CD3ε, CD3δ, CD3γ, and/or a full or partial length of TRAC or TRBC; or (v) one or more polynucleotides encoding one or more of fusion proteins: (1) tgCD3(ε-γ)-ζ, (2) tgCD3(ε-δ)-ζ, (3) tgCD3(ε- γ/δ)-28ζ, (4) tgCD3(ε- γ/δ)-BBζ, and (5) tgCD3(ε-γ/δ)-(28-BB)ζ, to provide ccCD3; wherein the fusion protein comprising full or partial length of ectodomains of CD3ε, CD3δ and/or CD3γ protein, further comprises a cytoplasmic domain comprising a full or partial length endodomain of CDζ protein, and optionally one or both of a CD28 signaling domain and a 41BB signaling domain. In some embodiments of the manufacturing method for the cell as described, the step of introducing to the iPSC one or more polynucleotides encoding fusion protein tgCD3(ε-δ)-TRAC, further comprises introducing a polynucleotide encoding tgTRBC or tgTCRβ, to provide the nb-rTCR-CD3. In some embodiments, the step of introducing to the iPSC one or more polynucleotides encoding fusion protein tgCD3(ε-γ)-TRBC further comprises tgTRAC or tgTCRα, to provide the nb-rTCR-CD3. In some embodiments, the step of introducing to the iPSC one or more polynucleotides encoding fusion protein tgCD3(ε-γ)-TRBC further comprises tgTRAC or tgTCRα, to provide the nb-rTCR-CD3. In some other embodiments, the step of introducing to the iPSC the polynucleotide encoding tgTCRα, and optionally, the polynucleotide encoding tgTCRβ, to provide the d-rTCR, the tgTCRα and the tgTCRβ respectively comprise a TCRα and a TCRβ of an invariant NKT cell.

[00040] In the various embodiments of the manufacturing method of the cell as provided, the genomic engineering is targeted editing, which comprises deletion and/or insertion. Such targeted editing may be carried out by CRISPR, ZFN, TALEN, homing nuclease, homology recombination, or any other functional variation of these tools. One aspect of the present invention provides CRISPR mediated editing of clonal iPSCs of various embodiments as provided herein, thereby obtaining edited iPSCs that are TCR^{neg} and comprise one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, wherein the edited clonal iPSCs comprise at least one of the genotypes listed in Table 1. In some embodiments, the CRISPR mediated editing further comprises an insertion of a CAR at a TRAC or a TRBC locus, and/or wherein the CAR is driven by an endogenous promoter of TCR, and/or wherein the TCR is knocked out by the CAR insertion.

[00041] Still another aspect of the present application provides a method of combinational treatment, and the method comprises providing to a subject under the treatment effector cells comprising TCR^{neg}, and one or more polynucleotide encoding one or more exogenous protein to

provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a selected multi-specific engager, wherein the effector cells comprise the derivative cells as provided. In some embodiments, the selected multi-specific engager in said method is at least one of: (i) a T cell engager; (ii) an NK cell engager; (iii) a bispecific T cell engager (BiTE); (iv) a bispecific killer cell engager (BiKE); (v) a tri-specific killer cell engager (TriKE); (vi) a CD3 engager; or (vii) a CD16 engager. In some embodiments, the selected multispecific engager is a CD3 engager, wherein the CD3 engager comprises a first variable segment that binds to a cs-CD3 and a second variable segment that binds to an antigen comprising at least one of: (i) ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and/or a pathogen antigen; or(ii) BCMA, CD19, CD20, CD33, CD38, CD52, CD123, CEA, EGFR, EpCAM, GD2, GPA33, HER2, MICA/B, PDL1, and/or PSMA; or (iii) CD19, CD33, CD123, CEA, EpCAM, GPA33, HER2, and/or PSMA. In some embodiments, the CD3 engager comprises at least one of: blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05. In some embodiments, the CD3 engager is administered to the subject simultaneously or subsequently with the effector cells. In some embodiments, the effector cells comprise derivative hematopoietic cells comprising derivative NK cells or derivative T cells, wherein the derivative NK cells or derivative T cells comprise a CD38 knockout, a high affinity non-cleavable CD16 or a variant thereof, and optionally

comprise: (i) B2M and CIITA knockout; (ii) introduced expression of HLA-G or non-cleavable HLA-G, a CAR, and/or a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; wherein the CAR and a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof is co-expressed in separate constructs or in a bi-cistronic construct; and/or (iii) at least one of the genotypes listed in Table 1.

[00042] Still another aspect of this application provides a method of reducing or preventing allorejection by recipient T cells against effector cells in an adoptive cell treatment, wherein the method comprises providing to a subject under the treatment (i) an anti-CD3 agent, and (ii) effector cells comprising TCR^{neg}, and a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) preloaded with a CD3 engager, wherein the effector cells comprise the derivative cells provided herein. In some embodiments, said anti-CD3 agent is CD3 antibody or a CD3-CAR, wherein the CD3-CAR is comprised in a NK cell; and wherein the anti-CD3 agent deactivates recipient T cells, thereby reducing or preventing allorejection. In some embodiments, said CD3 engager comprising a first variable segment that binds to a cs-CD3 of the effector cell, comprises a second variable segment that binds to an antigen related to an autoimmune disorder; a hematological malignancy; a solid tumor; cancer, or a virus infection. In some embodiments of the the CD3 engager comprising a second variable segment that binds to an antigen, and the antigen comprises at least one of: (i) ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and/or a pathogen antigen; or (ii) BCMA, CD19, CD20, CD33, CD38, CD52, CD123, CEA,

EGFR, EpCAM, GD2, GPA33, HER2, MICA/B, PDL1, and/or PSMA; or (iii) CD19, CD33, CD123, CEA, EpCAM, GPA33, HER2, and/or PSMA. In yet some other embodiment, the CD3 engager comprises at least one of: blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05.

[00043] Various objects and advantages of the compositions and methods as provided herein will become apparent from the following description taken in conjunction with the accompanying drawings wherein are set forth, by way of illustration and example, certain embodiments of this invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[00044] FIGS. 1A-C show illustrative designs for generating cell surface presented CD3 complex, or a subunit or a subdomain thereof (cs-CD3) associated with recombinant TCR complex, or subunits thereof upon disruption of endogenous TCR in a cell: (1) nb-rTCR (non-binding recombinant TCR); (2) d-rTCR (defined recombinant TCR); (3) p-rTCR (recombinant pre-TCRα, with optional non-binding TCRβ); (4) nb-rTCR-CD3 (non-binding recombinant TCR anchored CD3); and (5) ccCD3 (CD3 chimeric chain).

[00045] FIG. 2 is a graphic representation of several construct designs for cell surface expressed cytokine in iPSC derived cells. IL15 is used as an illustrative example, which can be replaced with other desirable cytokines.

[00046] FIG. 3 shows reprogramming and engineering of αβT Cells into single cell-derived TRAC-targeted CAR TiPSC clones. A: Phase contrast images of cultures at different stages as indicated. B: Flow cytometry profiles of αβT cells before reprogramming (left panel), reprogrammed and engineered cell pool before sorting and a clonal TiPSC clone (right panel).

[00047] FIG. 4 is a graphic representation of flow cytometry of mature TCR^{neg} iPSC-derived NK cells that demonstrates stepwise engineering of hnCD16 expression, B2M knockout (indicated as "B2M"; loss of HLA-A2 expression), HLA-G expression, and IL-15/IL-15ra (LNGFR) construct expression.

[00048] FIG. 5 is a graphic representation of telomere length determined by flow cytometry, and the mature derivative NK cells from iPSC maintain longer telomeres compared to adult peripheral blood NK cells.

[00049] FIG. 6 shows that iNK cells transduced with full-length IL15/IL15Rα fusion construct (filled circles; positive control), or a truncated IL15/IL15Rα fusion construct without cytoplasmic signaling domain (open circles) had a survival advantage compared to non-

transduced or GFP transduced cells in the same cultures independent of exogenous soluble IL2. A: in the presence of exogenous IL2; B: without the presence of exogenous IL2.

[00050] FIG. 7 shows exemplary constructs for transducing invariant NKT TCRα with or without TCRβ.

[00051] FIGS. 8A-B show that CD3 is not expressed by invariant NKT TCR transduced iPSCs or iPSC derived iCD34 progenitor cells.

[00052] FIGS. 9A-C show that invariant NKT TCR supports surface expression of CD3 in TCR deficient iPSC derived T cells. FIG. 9A-B show flow cytometry results at various time points for CD3 and TCR expression. FIG. 9C shows MFI of CD3 on day 25 after iCD34 differentiation.

[00053] FIG. 10 shows that iPSC-derived T cells comprising NKT TCRα with or without NKT TCRβ aggregate upon stimulation with cell surface CD3 binding using tetramers.

[00054] FIG. 11 shows that iPSC-derived T cells comprising NKT TCRα with or without NKT TCRβ have increased CD25 expressing upon CD3 tetramer stimulation.

[00055] FIGS. 12A-B show that iPSC-derived T cells comprising NKT TCRα with or without NKT TCRβ have enhanced cytotoxicity in the presence of CD3 binding BiTEs. FIG. 12A shows representative FACS plots demonstrating the enhanced killing of target cell in the presence of CD19xCD3 and CD20xCD3 BiTEs at 10:1 effector to target ratio. FIG. 12B shows the percentage of specific cytotoxicity for iPSC-derived effector cells comprising NKT TCRα with or without NKT TCRβ.

DETAILED DESCRIPTION OF THE INVENTION

[00056] Genomic modification of iPSCs (induced pluripotent stem cells) includes polynucleotide insertion, deletion and substitution. Exogenous gene expression in genome-engineered iPSCs often encounters problems such as gene silencing or reduced gene expression after prolonged clonal expansion of the original genome-engineered iPSCs, after cell differentiation, and in dedifferentiated cell types from the cells derived from the genome-engineered iPSCs. On the other hand, direct engineering of primary immune cells such as T or NK cells isolated from peripheral blood, umbilical cord blood, or any other donor tissues is challenging, and presents a hurdle to the preparation and delivery of engineered immune cells for adoptive cell therapy. The present invention provides an efficient, reliable, and targeted approach for stably integrating one or more exogenous genes, including suicide genes and other functional modalities, which provide improved therapeutic properties relating to engraftment, trafficking, homing, migration, cytotoxicity, viability, maintenance, expansion, longevity, self-renewal,

persistence, and/or survival, into derivative cells differentiated from iPSC, including but not limited to HSCs (hematopoietic stem and progenitor cell), T cell progenitor cells, NK cell progenitor cells, T cells, NKT cells, NK cells.

[00057] Definitions

[00058] Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[00059] It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims.

[00060] As used herein, the articles "a," "an," and "the" are used herein to refer to one or to more than one (i.e. to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[00061] The use of the alternative (e.g., "or") should be understood to mean either one, both, or any combination thereof of the alternatives.

[00062] The term "and/or" should be understood to mean either one, or both of the alternatives.

[00063] As used herein, the term "about" or "approximately" refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1% compared to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In one embodiment, the term "about" or "approximately" refers a range of quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length ± 15%, ± 10%, ± 9%, ± 8%, ± 7%, ± 6%, ± 5%, ± 4%, ± 3%, ± 2%, or ± 1% about a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[00064] As used herein, the term "substantially" or "essentially" refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that is about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or higher compared to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In one embodiment, the terms "essentially the same" or "substantially the same" refer a range of quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length

that is about the same as a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[00065] As used herein, the terms "substantially free of" and "essentially free of" are used interchangeably, and when used to describe a composition, such as a cell population or culture media, refer to a composition that is free of a specified substance or its source thereof, such as, 95% free, 96% free, 97% free, 98% free, 99% free of the specified substance or its source thereof, or is undetectable as measured by conventional means. The term "free of" or "essentially free of" a certain ingredient or substance in a composition also means that no such ingredient or substance is (1) included in the composition at any concentration, or (2) included in the composition functionally inert, but at a low concentration. Similar meaning can be applied to the term "absence of," where referring to the absence of a particular substance or its source thereof of a composition.

[00066] Throughout this specification, unless the context requires otherwise, the words "comprise," "comprises" and "comprising" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements. In particular embodiments, the terms "include," "has," "contains," and "comprise" are used synonymously.

[00067] By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of." Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present.

[00068] By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that no other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

[00069] Reference throughout this specification to "one embodiment," "an embodiment," "a particular embodiment," "a related embodiment," "a certain embodiment," "an additional embodiment," or "a further embodiment" or combinations thereof means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, the appearances of the foregoing phrases in various places throughout this specification are not necessarily all referring to the same embodiment. Furthermore, the particular features, structures, or characteristics may be combined in any suitable manner in one or more embodiments.

[00070] The term "*ex vivo*" refers generally to activities that take place outside an organism, such as experimentation or measurements done in or on living tissue in an artificial environment outside the organism, preferably with minimum alteration of the natural conditions. In particular embodiments, "*ex vivo*" procedures involve living cells or tissues taken from an organism and cultured in a laboratory apparatus, usually under sterile conditions, and typically for a few hours or up to about 24 hours, but including up to 48 or 72 hours or longer, depending on the circumstances. In certain embodiments, such tissues or cells can be collected and frozen, and later thawed for *ex vivo* treatment. Tissue culture experiments or procedures lasting longer than a few days using living cells or tissue are typically considered to be "*in vitro*," though in certain embodiments, this term can be used interchangeably with *ex vivo*.

[00071] The term "*in vivo*" refers generally to activities that take place inside an organism.

[00072] As used herein, the terms "reprogramming" or "dedifferentiation" or "increasing cell potency" or "increasing developmental potency" refers to a method of increasing the potency of a cell or dedifferentiating the cell to a less differentiated state. For example, a cell that has an increased cell potency has more developmental plasticity (i.e., can differentiate into more cell types) compared to the same cell in the non-reprogrammed state. In other words, a reprogrammed cell is one that is in a less differentiated state than the same cell in a non-reprogrammed state.

[00073] As used herein, the term "differentiation" is the process by which an unspecialized ("uncommitted") or less specialized cell acquires the features of a specialized cell such as, for example, a blood cell or a muscle cell. A differentiated or differentiation- induced cell is one that has taken on a more specialized ("committed") position within the lineage of a cell. The term "committed", when applied to the process of differentiation, refers to a cell that has proceeded in the differentiation pathway to a point where, under normal circumstances, it will continue to differentiate into a specific cell type or subset of cell types, and cannot, under normal circumstances, differentiate into a different cell type or revert to a less differentiated cell type. As used herein, the term "pluripotent" refers to the ability of a cell to form all lineages of the body or soma (i.e., the embryo proper). For example, embryonic stem cells are a type of pluripotent stem cells that are able to form cells from each of the three germs layers, the ectoderm, the mesoderm, and the endoderm. Pluripotency is a continuum of developmental potencies ranging from the incompletely or partially pluripotent cell (e.g., an epiblast stem cell or EpiSC), which is unable to give rise to a complete organism to the more primitive, more pluripotent cell, which is able to give rise to a complete organism (e.g., an embryonic stem cell).

[00074] As used herein, the term "induced pluripotent stem cells" or, iPSCs, means that the stem cells are produced *in vitro*, using reprogramming factor and/or small molecule chemical

driven methods, from differentiated adult, neonatal or fetal cells that have been induced or changed, i.e., reprogrammed into cells capable of differentiating into tissues of all three germ or dermal layers: mesoderm, endoderm, and ectoderm. The iPSCs produced do not refer to cells as they are found in nature.

[00075] As used herein, the term "embryonic stem cell" refers to naturally occurring pluripotent stem cells of the inner cell mass of the embryonic blastocyst. Embryonic stem cells are pluripotent and give rise during development to all derivatives of the three primary germ layers: ectoderm, endoderm and mesoderm. They do not contribute to the extra-embryonic membranes or the placenta, i.e., are not totipotent.

[00076] As used herein, the term "multipotent stem cell" refers to a cell that has the developmental potential to differentiate into cells of one or more germ layers (ectoderm, mesoderm and endoderm), but not all three. Thus, a multipotent cell can also be termed a "partially differentiated cell." Multipotent cells are well known in the art, and examples of multipotent cells include adult stem cells, such as for example, hematopoietic stem cells and neural stem cells. "Multipotent" indicates that a cell may form many types of cells in a given lineage, but not cells of other lineages. For example, a multipotent hematopoietic cell can form the many different types of blood cells (red, white, platelets, etc.), but it cannot form neurons. Accordingly, the term "multipotency" refers to a state of a cell with a degree of developmental potential that is less than totipotent and pluripotent.

[00077] Pluripotency can be determined, in part, by assessing pluripotency characteristics of the cells. Pluripotency characteristics include, but are not limited to: (i) pluripotent stem cell morphology; (ii) the potential for unlimited self-renewal; (iii) expression of pluripotent stem cell markers including, but not limited to SSEA1 (mouse only), SSEA3/4, SSEA5, TRA1-60/81, TRA1-85, TRA2-54, GCTM-2, TG343, TG30, CD9, CD29, CD133/prominin, CD140a, CD56, CD73, CD90, CD105, OCT4, NANOG, SOX2, CD30 and/or CD50; (iv) ability to differentiate to all three somatic lineages (ectoderm, mesoderm and endoderm); (v) teratoma formation consisting of the three somatic lineages; and (vi) formation of embryoid bodies consisting of cells from the three somatic lineages.

[00078] Two types of pluripotency have previously been described: the “primed” or “metastable” state of pluripotency akin to the epiblast stem cells (EpiSC) of the late blastocyst, and the “Naïve” or “Ground” state of pluripotency akin to the inner cell mass of the early/preimplantation blastocyst. While both pluripotent states exhibit the characteristics as described above, the naïve or ground state further exhibits: (i) pre-inactivation or reactivation of the X-chromosome in female cells; (ii) improved clonality and survival during single-cell

culturing; (iii) global reduction in DNA methylation; (iv) reduction of H3K27me3 repressive chromatin mark deposition on developmental regulatory gene promoters; and (v) reduced expression of differentiation markers relative to primed state pluripotent cells. Standard methodologies of cellular reprogramming in which exogenous pluripotency genes are introduced to a somatic cell, expressed, and then either silenced or removed from the resulting pluripotent cells are generally seen to have characteristics of the primed-state of pluripotency. Under standard pluripotent cell culture conditions such cells remain in the primed state unless the exogenous transgene expression is maintained, wherein characteristics of the ground-state are observed.

[00079] As used herein, the term “pluripotent stem cell morphology” refers to the classical morphological features of an embryonic stem cell. Normal embryonic stem cell morphology is characterized by being round and small in shape, with a high nucleus-to-cytoplasm ratio, the notable presence of nucleoli, and typical inter-cell spacing.

[00080] As used herein, the term "subject" refers to any animal, preferably a human patient, livestock, or other domesticated animal.

[00081] A “pluripotency factor,” or “reprogramming factor,” refers to an agent capable of increasing the developmental potency of a cell, either alone or in combination with other agents. Pluripotency factors include, without limitation, polynucleotides, polypeptides, and small molecules capable of increasing the developmental potency of a cell. Exemplary pluripotency factors include, for example, transcription factors and small molecule reprogramming agents.

[00082] "Culture" or "cell culture" refers to the maintenance, growth and/or differentiation of cells in an *in vitro* environment. "Cell culture media," "culture media" (singular "medium" in each case), "supplement" and "media supplement" refer to nutritive compositions that cultivate cell cultures.

[00083] "Cultivate," or “maintain,” refers to the sustaining, propagating (growing) and/or differentiating of cells outside of tissue or the body, for example in a sterile plastic (or coated plastic) cell culture dish or flask. "Cultivation," or “maintaining,” may utilize a culture medium as a source of nutrients, hormones and/or other factors helpful to propagate and/or sustain the cells.

[00084] As used herein, the term “mesoderm” refers to one of the three germinal layers that appears during early embryogenesis and which gives rise to various specialized cell types including blood cells of the circulatory system, muscles, the heart, the dermis, skeleton, and other supportive and connective tissues.

[00085] As used herein, the term "definitive hemogenic endothelium" (HE) or "pluripotent stem cell-derived definitive hemogenic endothelium" (iHE) refers to a subset of endothelial cells that give rise to hematopoietic stem and progenitor cells in a process called endothelial-to-hematopoietic transition. The development of hematopoietic cells in the embryo proceeds sequentially from lateral plate mesoderm through the hemangioblast to the definitive hemogenic endothelium and hematopoietic progenitors.

[00086] The term "hematopoietic stem and progenitor cells," "hematopoietic stem cells," "hematopoietic progenitor cells," or "hematopoietic precursor cells" refers to cells which are committed to a hematopoietic lineage but are capable of further hematopoietic differentiation and include, multipotent hematopoietic stem cells (hematoblasts), myeloid progenitors, megakaryocyte progenitors, erythrocyte progenitors, and lymphoid progenitors. Hematopoietic stem and progenitor cells (HSCs) are multipotent stem cells that give rise to all the blood cell types including myeloid (monocytes and macrophages, neutrophils, basophils, eosinophils, erythrocytes, megakaryocytes/platelets, dendritic cells), and lymphoid lineages (T cells, B cells, NK cells). The term "definitive hematopoietic stem cell" as used herein, refers to CD34+ hematopoietic cells capable of giving rise to both mature myeloid and lymphoid cell types including T cells, NK cells and B cells. Hematopoietic cells also include various subsets of primitive hematopoietic cells that give rise to primitive erythrocytes, megakarocytes and macrophages.

[00087] As used herein, the terms "T lymphocyte" and "T cell" are used interchangeably and refer to a principal type of white blood cell that completes maturation in the thymus and that has various roles in the immune system, including the identification of specific foreign antigens in the body and the activation and deactivation of other immune cells. A T cell can be any T cell, such as a cultured T cell, e.g., a primary T cell, or a T cell from a cultured T cell line, e.g., Jurkat, SupT1, etc., or a T cell obtained from a mammal. The T cell can be CD3+ cells. The T cell can be any type of T cell and can be of any developmental stage, including but not limited to, CD4+/CD8+ double positive T cells, CD4+ helper T cells (e.g., Th1 and Th2 cells), CD8+ T cells (e.g., cytotoxic T cells), peripheral blood mononuclear cells (PBMCs), peripheral blood leukocytes (PBLs), tumor infiltrating lymphocytes (TILs), memory T cells, naïve T cells, regulator T cells, gamma delta T cells ($\gamma\delta$ T cells), and the like. Additional types of helper T cells include cells such as Th3 (Treg), Th17, Th9, or Tfh cells. Additional types of memory T cells include cells such as central memory T cells (Tcm cells), effector memory T cells (Tem cells and TEMRA cells). The T cell can also refer to a genetically engineered T cell, such as a T cell

modified to express a T cell receptor (TCR) or a chimeric antigen receptor (CAR). The T cell can also be differentiated from a stem cell or progenitor cell.

[00088] "CD4+ T cells" refers to a subset of T cells that express CD4 on their surface and are associated with cell-mediated immune response. They are characterized by the secretion profiles following stimulation, which may include secretion of cytokines such as IFN-gamma, TNF-alpha, IL2, IL4 and IL10. "CD4" are 55-kD glycoproteins originally defined as differentiation antigens on T-lymphocytes, but also found on other cells including monocytes/macrophages. CD4 antigens are members of the immunoglobulin supergene family and are implicated as associative recognition elements in MHC (major histocompatibility complex) class II-restricted immune responses. On T-lymphocytes they define the helper/inducer subset.

[00089] "CD8+ T cells" refers to a subset of T cells which express CD8 on their surface, are MHC class I-restricted, and function as cytotoxic T cells. "CD8" molecules are differentiation antigens found on thymocytes and on cytotoxic and suppressor T-lymphocytes. CD8 antigens are members of the immunoglobulin supergene family and are associative recognition elements in major histocompatibility complex class I-restricted interactions.

[00090] As used herein, the term "NK cell" or "Natural Killer cell" refer to a subset of peripheral blood lymphocytes defined by the expression of CD56 or CD16 and the absence of the T cell receptor (CD3). As used herein, the terms "adaptive NK cell" and "memory NK cell" are interchangeable and refer to a subset of NK cells that are phenotypically CD3- and CD56+, expressing at least one of NKG2C and CD57, and optionally, CD16, but lack expression of one or more of the following: PLZF, SYK, FceRγ, and EAT-2. In some embodiments, isolated subpopulations of CD56+ NK cells comprise expression of CD16, NKG2C, CD57, NKG2D, NCR ligands, NKp30, NKp40, NKp46, activating and inhibitory KIRs, NKG2A and/or DNAM-1. CD56+ can be dim or bright expression.

[00091] As used herein, the term "NKT cells" or "natural killer T cells" refers to CD1d-restricted T cells, which express a T cell receptor (TCR). Unlike conventional T cells that detect peptide antigens presented by conventional major histocompatibility (MHC) molecules, NKT cells recognize lipid antigens presented by CD1d, a non-classical MHC molecule. Two types of NKT cells are recognized. Invariant or type I NKT cells express a very limited TCR repertoire - a canonical α-chain (Vα24-Jα18 in humans) associated with a limited spectrum of β chains (Vβ11 in humans). The second population of NKT cells, called non-classical or non-invariant type II NKT cells, display a more heterogeneous TCR αβ usage. Type I NKT cells are considered suitable for immunotherapy. Adaptive or invariant (type I) NKT cells can be identified with the

expression of at least one or more of the following markers, TCR Va24-Ja18, Vb11, CD1d, CD3, CD4, CD8, aGalCer, CD161 and CD56.

[00092] As used herein, the term "isolated" or the like refers to a cell, or a population of cells, which has been separated from its original environment, i.e., the environment of the isolated cells is substantially free of at least one component as found in the environment in which the "un-isolated" reference cells exist. The term includes a cell that is removed from some or all components as it is found in its natural environment, for example, isolated from a tissue or biopsy sample. The term also includes a cell that is removed from at least one, some or all components as the cell is found in non-naturally occurring environments, for example, isolated form a cell culture or cell suspension. Therefore, an isolated cell is partly or completely separated from at least one component, including other substances, cells or cell populations, as it is found in nature or as it is grown, stored or subsisted in non-naturally occurring environments. Specific examples of isolated cells include partially pure cell compositions, substantially pure cell compositions and cells cultured in a medium that is non-naturally occurring. Isolated cells may be obtained from separating the desired cells, or populations thereof, from other substances or cells in the environment, or from removing one or more other cell populations or subpopulations from the environment.

[00093] As used herein, the term "purify" or the like refers to increasing purity. For example, the purity can be increased to at least 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100%.

[00094] As used herein, the term "encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or a mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[00095] A "construct" refers to a macromolecule or complex of molecules comprising a polynucleotide to be delivered to a host cell, either *in vitro* or *in vivo*. A "vector," as used herein refers to any nucleic acid construct capable of directing the delivery or transfer of a foreign genetic material to target cells, where it can be replicated and/or expressed. The term "vector" as used herein comprises the construct to be delivered. A vector can be a linear or a circular

molecule. A vector can be integrating or non-integrating. The major types of vectors include, but are not limited to, plasmids, episomal vector, viral vectors, cosmids, and artificial chromosomes. Viral vectors include, but are not limited to, adenovirus vector, adeno-associated virus vector, retrovirus vector, lentivirus vector, Sendai virus vector, and the like.

[00096] By "integration" it is meant that one or more nucleotides of a construct is stably inserted into the cellular genome, i.e., covalently linked to the nucleic acid sequence within the cell's chromosomal DNA. By "targeted integration" it is meant that the nucleotide(s) of a construct is inserted into the cell's chromosomal or mitochondrial DNA at a pre-selected site or "integration site". The term "integration" as used herein further refers to a process involving insertion of one or more exogenous sequences or nucleotides of the construct, with or without deletion of an endogenous sequence or nucleotide at the integration site. In the case, where there is a deletion at the insertion site, "integration" may further comprise replacement of the endogenous sequence or a nucleotide that is deleted with the one or more inserted nucleotides.

[00097] As used herein, the term "exogenous" is intended to mean that the referenced molecule or the referenced activity is introduced into, or non-native to, the host cell. The molecule can be introduced, for example, by introduction of an encoding nucleic acid into the host genetic material such as by integration into a host chromosome or as non-chromosomal genetic material such as a plasmid. Therefore, the term as it is used in reference to expression of an encoding nucleic acid refers to introduction of the encoding nucleic acid in an expressible form into the cell. The term "endogenous" refers to a referenced molecule or activity that is present in the host cell. Similarly, the term when used in reference to expression of an encoding nucleic acid refers to expression of an encoding nucleic acid contained within the cell and not exogenously introduced.

[00098] As used herein, a "gene of interest" or "a polynucleotide sequence of interest" is a DNA sequence that is transcribed into RNA and in some instances translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. A gene or polynucleotide of interest can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and synthetic DNA sequences. For example, a gene of interest may encode an miRNA, an shRNA, a native polypeptide (i.e. a polypeptide found in nature) or fragment thereof; a variant polypeptide (i.e. a mutant of the native polypeptide having less than 100% sequence identity with the native polypeptide) or fragment thereof; an engineered polypeptide or peptide fragment, a therapeutic peptide or polypeptide, an imaging marker, a selectable marker, and the like.

[00099] As used herein, the term "polynucleotide" refers to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides or analogs thereof. The sequence of a polynucleotide is composed of four nucleotide bases: adenine (A); cytosine (C); guanine (G); thymine (T); and uracil (U) for thymine when the polynucleotide is RNA. A polynucleotide can include a gene or gene fragment (for example, a probe, primer, EST or SAGE tag), exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes and primers. Polynucleotide also refers to both double- and single-stranded molecules.

[000100] As used herein, the term "peptide," "polypeptide," and "protein" are used interchangeably and refer to a molecule having amino acid residues covalently linked by peptide bonds. A polypeptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids of a polypeptide. As used herein, the terms refer to both short chains, which are also commonly referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as polypeptides or proteins. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural polypeptides, recombinant polypeptides, synthetic polypeptides, or a combination thereof.

[000101] As used herein, the term "subunit" as used herein refers to each separate polypeptide chain of a protein complex, where each separate polypeptide chain can form a stable folded structure by itself. Many protein molecules are composed of more than one subunit, where the amino acid sequences can either be identical for each subunit, or similar, or completely different. For example, CD3 complex is composed of CD3α, CD3ε, CD3δ, CD3γ, and CD3ζ subunits, which form the CD3ε/CD3γ, CD3ε/ CD3δ, and CD3ζ/ CD3ζ dimers. Within a single subunit, contiguous portions of the polypeptide chain frequently fold into compact, local, semi-independent units that are called "domains". Many protein domains may further comprise independent "structural subunits", also called subdomains, contributing to a common function of the domain. As such, the term "subdomain" as used herein refers to a protein domain inside of a larger domain, for example, a binding domain within an ectodomain of a cell surface receptor; or a stimulatory domain or a signaling domain of an endodomain of a cell surface receptor.

[000102] "Operably-linked" refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter

is operably-linked with a coding sequence or functional RNA when it is capable of affecting the expression of that coding sequence or functional RNA (i.e., the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

[000103] As used herein, the term "genetic imprint" refers to genetic or epigenetic information that contributes to preferential therapeutic attributes in a source cell or an iPSC, and is retainable in the source cell derived iPSCs, and/or the iPSC-derived hematopoietic lineage cells. As used herein, "a source cell" is a non-pluripotent cell that may be used for generating iPSCs through reprogramming, and the source cell derived iPSCs may be further differentiated to specific cell types including any hematopoietic lineage cells. The source cell derived iPSCs, and differentiated cells therefrom are sometimes collectively called "derived" or "derivative" cells depending on the context. For example, derivative effector cells, or derivative NK cells or derivative T cells, as used throughout this application are cells differentiated from an iPSC, as compared to their primary counterpart obtained from natural/native sources such as peripheral blood, umbilical cord blood, or other donor tissues. As used herein, the genetic imprint(s) conferring a preferential therapeutic attribute is incorporated into the iPSCs either through reprogramming a selected source cell that is donor-, disease-, or treatment response- specific, or through introducing genetically modified modalities to iPSC using genomic editing. In the aspect of a source cell obtained from a specifically selected donor, disease or treatment context, the genetic imprint contributing to preferential therapeutic attributes may include any context specific genetic or epigenetic modifications which manifest a retainable phenotype, i.e. a preferential therapeutic attribute, that is passed on to iPSC-derived cells of the selected source cell, irrespective of the underlying molecular events being identified or not. Donor-, disease-, or treatment response- specific source cells may comprise genetic imprints that are retainable in iPSCs and derived hematopoietic lineage cells, which genetic imprints include but are not limited to, prearranged monospecific TCR, for example, from a viral specific T cell or invariant natural killer T (iNKT) cell; trackable and desirable genetic polymorphisms, for example, homozygous for a point mutation that encodes for the high-affinity CD16 receptor in selected donors; and predetermined HLA requirements, i.e., selected HLA-matched donor cells exhibiting a haplotype with increased population. As used herein, preferential therapeutic attributes include improved engraftment, trafficking, homing, viability, self-renewal, persistence, immune response regulation and modulation, survival, and cytotoxicity of a derived cell. A preferential therapeutic attribute may also relate to antigen targeting receptor expression; HLA presentation or lack thereof; resistance to tumor microenvironment; induction of bystander immune cells and immune

modulations; improved on-target specificity with reduced off-tumor effect; resistance to treatment such as chemotherapy.

[000104] The term "enhanced therapeutic property" as used herein, refers to a therapeutic property of a cell that is enhanced as compared to a typical immune cell of the same general cell type. For example, an NK cell with an "enhanced therapeutic property" will possess an enhanced, improved, and/or augmented therapeutic property as compared to a typical, unmodified, and/or naturally occurring NK cell. Therapeutic properties of an immune cell may include, but are not limited to, cell engraftment, trafficking, homing, viability, self-renewal, persistence, immune response regulation and modulation, survival, and cytotoxicity. Therapeutic properties of an immune cell are also manifested by antigen targeting receptor expression; HLA presentation or lack thereof; resistance to tumor microenvironment; induction of bystander immune cells and immune modulations; improved on-target specificity with reduced off-tumor effect; resistance to treatment such as chemotherapy.

[000105] As used herein, the term "engager" refers to a molecule, e.g. a fusion polypeptide, which is capable of forming a link between an immune cell, e.g. a T cell, a NK cell, a NKT cell, a B cell, a macrophage, a neutrophil, and a tumor cell; and activating the immune cell. Examples of engagers include, but are not limited to, bi-specific T cell engagers (BiTEs), bi-specific killer cell engagers (BiKEs), tri-specific killer cell engagers, or multi- specific killer cell engagers, or universal engagers compatible with multiple immune cell types.

[000106] As used herein, the term "surface triggering receptor" refers to a receptor capable of triggering or initiating an immune response, e.g. a cytotoxic response. Surface triggering receptors may be engineered, and may be expressed on effector cells, e.g. a T cell, a NK cell, a NKT cell, a B cell, a macrophage, a neutrophil. In some embodiments, the surface triggering receptor facilitates bi- or multi- specific antibody engagement between the effector cells and specific target cell e.g. a tumor cell, independent of the effector cell's natural receptors and cell types. Using this approach, one may generate iPSCs comprising a universal surface triggering receptor, and then differentiate such iPSCs into populations of various effector cell types that express the universal surface triggering receptor. By "universal", it is meant that the surface triggering receptor can be expressed in, and activate, any effector cells irrespective of the cell type, and all effector cells expressing the universal receptor can be coupled or linked to the engagers having the same epitope recognizable by the surface triggering receptor, regardless of the engager's tumor binding specificities. In some embodiments, engagers having the same tumor targeting specificity are used to couple with the universal surface triggering receptor. In some embodiments, engagers having different tumor targeting specificity are used to couple with

the universal surface triggering receptor. As such, one or multiple effector cell types can be engaged to kill one specific type of tumor cells in some case, and to kill two or more types of tumors in some other cases. A surface triggering receptor generally comprises a co-stimulatory domain for effector cell activation and an anti-epitope that is specific to the epitope of an engager. A bi-specific engager is specific to the anti-epitope of a surface triggering receptor on one end, and is specific to a tumor antigen on the other end.

[000107] As used herein, the term "safety switch protein" refers to an engineered protein designed to prevent potential toxicity or otherwise adverse effects of a cell therapy. In some instances, the safety switch protein expression is conditionally controlled to address safety concerns for transplanted engineered cells that have permanently incorporated the gene encoding the safety switch protein into its genome. This conditional regulation could be variable and might include control through a small molecule-mediated post-translational activation and tissue-specific and/or temporal transcriptional regulation. The safety switch could mediate induction of apoptosis, inhibition of protein synthesis, DNA replication, growth arrest, transcriptional and post-transcriptional genetic regulation and/or antibody-mediated depletion. In some instance, the safety switch protein is activated by an exogenous molecule, e.g. a prodrug, that when activated, triggers apoptosis and/or cell death of a therapeutic cell. Examples of safety switch proteins, include, but are not limited to suicide genes such as caspase 9 (or caspase 3 or 7), thymidine kinase, cytosine deaminase, B-cell CD20, modified EGFR, and any combination thereof. In this strategy, a prodrug that is administered in the event of an adverse event is activated by the suicide-gene product and kills the transduced cell.

[000108] As used herein, the term "pharmaceutically active proteins or peptides" refer to proteins or peptides that are capable of achieving a biological and/or pharmaceutical effect on an organism. A pharmaceutically active protein has healing curative or palliative properties against a disease and may be administered to ameliorate relieve, alleviate, reverse or lessen the severity of a disease. A pharmaceutically active protein also has prophylactic properties and is used to prevent the onset of a disease or to lessen the severity of such disease or pathological condition when it does emerge. Pharmaceutically active proteins include an entire protein or peptide or pharmaceutically active fragments thereof. It also includes pharmaceutically active analogs of the protein or peptide or analogs of fragments of the protein or peptide. The term pharmaceutically active protein also refers to a plurality of proteins or peptides that act cooperatively or synergistically to provide a therapeutic benefit. Examples of pharmaceutically active proteins or peptides include, but are not limited to, receptors, binding proteins, transcription and translation

factors, tumor growth suppressing proteins, antibodies or fragments thereof, growth factors, and/or cytokines.

[000109] As used herein, the term "signaling molecule" refers to any molecule that modulates, participates in, inhibits, activates, reduces, or increases, the cellular signal transduction. Signal transduction refers to the transmission of a molecular signal in the form of chemical modification by recruitment of protein complexes along a pathway that ultimately triggers a biochemical event in the cell. Signal transduction pathways are well known in the art, and include, but are not limited to, G protein coupled receptor signaling, tyrosine kinase receptor signaling, integrin signaling, toll gate signaling, ligand-gated ion channel signaling, ERK/MAPK signaling pathway, Wnt signaling pathway, cAMP-dependent pathway, and IP3/DAG signaling pathway.

[000110] As used herein, the term "targeting modality" refers to a molecule, e.g., a polypeptide, that is genetically incorporated into a cell to promote antigen and/or epitope specificity that includes but not limited to i) antigen specificity as it related to a unique chimeric antigen receptor (CAR) or T cell receptor (TCR), ii) engager specificity as it related to monoclonal antibodies or bispecific engager, iii) targeting of transformed cell, iv) targeting of cancer stem cell, and v) other targeting strategies in the absence of a specific antigen or surface molecule.

[000111] As used herein, the term "specific" or "specificity" can be used to refer to the ability of a molecule, e.g., a receptor or an engager, to selectively bind to a target molecule, in contrast to non-specific or non-selective binding.

[000112] The term "adoptive cell therapy" as used herein refers to a cell-based immunotherapy that, as used herein, relates to the transfusion of autologous or allogenic lymphocytes, identified as T or B cells, genetically modified or not, that have been expanded *ex vivo* prior to said transfusion.

[000113] A "therapeutically sufficient amount", as used herein, includes within its meaning a non-toxic but sufficient and/or effective amount of the particular therapeutic and/or pharmaceutical composition to which it is referring to provide a desired therapeutic effect. The exact amount required will vary from subject to subject depending on factors such as the patient's general health, the patient's age and the stage and severity of the condition. In particular embodiments, a therapeutically sufficient amount is sufficient and/or effective to ameliorate, reduce, and/or improve at least one symptom associated with a disease or condition of the subject being treated.

[000114] Differentiation of pluripotent stem cells requires a change in the culture system, such as changing the stimuli agents in the culture medium or the physical state of the cells. The most conventional strategy utilizes the formation of embryoid bodies (EBs) as a common and critical intermediate to initiate the lineage-specific differentiation. "Embryoid bodies" are three-dimensional clusters that have been shown to mimic embryo development as they give rise to numerous lineages within their three-dimensional area. Through the differentiation process, typically few hours to days, simple EBs (for example, aggregated pluripotent stem cells elicited to differentiate) continue maturation and develop into a cystic EB at which time, typically days to few weeks, they are further processed to continue differentiation. EB formation is initiated by bringing pluripotent stem cells into close proximity with one another in three-dimensional multilayered clusters of cells, typically this is achieved by one of several methods including allowing pluripotent cells to sediment in liquid droplets, sedimenting cells into "U" bottomed well-plates or by mechanical agitation. To promote EB development, the pluripotent stem cell aggregates require further differentiation cues, as aggregates maintained in pluripotent culture maintenance medium do not form proper EBs. As such, the pluripotent stem cell aggregates need to be transferred to differentiation medium that provides eliciting cues towards the lineage of choice. EB-based culture of pluripotent stem cells typically results in generation of differentiated cell populations (ectoderm, mesoderm and endoderm germ layers) with modest proliferation within the EB cell cluster. Although proven to facilitate cell differentiation, EBs, however, give rise to heterogeneous cells in variable differentiation state because of the inconsistent exposure of the cells in the three-dimensional structure to differentiation cues from the environment. In addition, EBs are laborious to create and maintain. Moreover, cell differentiation through EB is accompanied with modest cell expansion, which also contributes to low differentiation efficiency.

[000115] In comparison, "aggregate formation," as distinct from "EB formation," can be used to expand the populations of pluripotent stem cell derived cells. For example, during aggregate-based pluripotent stem cell expansion, culture media are selected to maintain proliferation and pluripotency. Cells proliferation generally increases the size of the aggregates forming larger aggregates, these aggregates can be routinely mechanically or enzymatically dissociated into smaller aggregates to maintain cell proliferation within the culture and increase numbers of cells. As distinct from EB culture, cells cultured within aggregates in maintenance culture maintain markers of pluripotency. The pluripotent stem cell aggregates require further differentiation cues to induce differentiation.

[000116] As used herein, "monolayer differentiation" is a term referring to a differentiation method distinct from differentiation through three-dimensional multilayered clusters of cells, i.e.,

"EB formation." Monolayer differentiation, among other advantages disclosed herein, avoids the need for EB formation for differentiation initiation. Because monolayer culturing does not mimic embryo development such as EB formation, differentiation towards specific lineages are deemed as minimal as compared to all three germ layer differentiation in EB.

[000117] As used herein, a "dissociated" cell refers to a cell that has been substantially separated or purified away from other cells or from a surface (e.g., a culture plate surface). For example, cells can be dissociated from an animal or tissue by mechanical or enzymatic methods. Alternatively, cells that aggregate *in vitro* can be dissociated from each other, such as by dissociation into a suspension of clusters, single cells or a mixture of single cells and clusters, enzymatically or mechanically. In yet another alternative embodiment, adherent cells are dissociated from a culture plate or other surface. Dissociation thus can involve breaking cell interactions with extracellular matrix (ECM) and substrates (e.g., culture surfaces), or breaking the ECM between cells.

[000118] As used herein, "feeder cells" or "feeders" are terms describing cells of one type that are co-cultured with cells of a second type to provide an environment in which the cells of the second type can grow, expand, or differentiate, as the feeder cells provide stimulation, growth factors and nutrients for the support of the second cell type. The feeder cells are optionally from a different species as the cells they are supporting. For example, certain types of human cells, including stem cells, can be supported by primary cultures of mouse embryonic fibroblasts, or immortalized mouse embryonic fibroblasts. In another example, peripheral blood derived cells or transformed leukemia cells support the expansion and maturation of natural killer cells. The feeder cells may typically be inactivated when being co-cultured with other cells by irradiation or treatment with an anti-mitotic agent such as mitomycin to prevent them from outgrowing the cells they are supporting. Feeder cells may include endothelial cells, stromal cells (for example, epithelial cells or fibroblasts), and leukemic cells. Without limiting the foregoing, one specific feeder cell type may be a human feeder, such as a human skin fibroblast. Another feeder cell type may be mouse embryonic fibroblasts (MEF). In general, various feeder cells can be used in part to maintain pluripotency, direct differentiation towards a certain lineage, enhance proliferation capacity and promote maturation to a specialized cell type, such as an effector cell.

[000119] As used herein, a "feeder-free" (FF) environment refers to an environment such as a culture condition, cell culture or culture media which is essentially free of feeder or stromal cells, and/or which has not been pre-conditioned by the cultivation of feeder cells. "Pre-conditioned" medium refers to a medium harvested after feeder cells have been cultivated within the medium for a period of time, such as for at least one day. Pre-conditioned medium contains many

mediator substances, including growth factors and cytokines secreted by the feeder cells cultivated in the medium. In some embodiments, a feeder-free environment is free of both feeder or stromal cells and is also not pre-conditioned by the cultivation of feeder cells.

[000120] "Functional" as used in the context of genomic editing or modification of iPSC, and derived non-pluripotent cells differentiated therefrom, or genomic editing or modification of non-pluripotent cells and derived iPSCs reprogrammed therefrom, refers to (1) at the gene level--successful knocked-in, knocked-out, knocked-down gene expression, transgenic or controlled gene expression such as inducible or temporal expression at a desired cell development stage, which is achieved through direct genomic editing or modification, or through "passing-on" via differentiation from or reprogramming of a starting cell that is initially genomically engineered; or (2) at the cell level—successful removal, adding, or altering a cell function/characteristics via (i) gene expression modification obtained in said cell through direct genomic editing, (ii) gene expression modification maintained in said cell through "passing-on" via differentiation from or reprogramming of a starting cell that is initially genomically engineered; (iii) down-stream gene regulation in said cell as a result of gene expression modification that only appears in an earlier development stage of said cell, or only appears in the starting cell that gives rise to said cell via differentiation or reprogramming; or (iv) enhanced or newly attained cellular function or attribute displayed within the mature cellular product, initially derived from the genomic editing or modification conducted at the iPSC, progenitor or dedifferentiated cellular origin.

[000121] "HLA deficient", including HLA-class I deficient, or HLA-class II deficient, or both, refers to cells that either lack, or no longer maintain, or have reduced level of surface expression of a complete MHC complex comprising a HLA class I protein heterodimer and/or a HLA class II heterodimer, such that the diminished or reduced level is less than the level naturally detectable by other cells or by synthetic methods.

[000122] "Modified HLA deficient iPSC," as used herein, refers to HLA deficient iPSC that is further modified by introducing genes expressing proteins related but not limited to improved differentiation potential, antigen targeting, antigen presentation, antibody recognition, persistence, immune evasion, resistance to suppression, proliferation, co-stimulation, cytokine stimulation, cytokine production (autocrine or paracrine), chemotaxis, and cellular cytotoxicity, such as non-classical HLA class I proteins (e.g., HLA-E and HLA-G), chimeric antigen receptor (CAR), T cell receptor (TCR), CD16 Fc Receptor, BCL11b, NOTCH, RUNX1, IL15, 41BB, DAP10, DAP12, CD24, CD3z, 41BBL, CD47, CD113, and PDL1. The cells that are "modified HLA deficient" also include cells other than iPSCs.

[000123] "Fc receptors," abbreviated FcR, are classified based on the type of antibody that they recognize. For example, those that bind the most common class of antibody, IgG, are called Fc-gamma receptors (FcγR), those that bind IgA are called Fc-alpha receptors (FcαR) and those that bind IgE are called Fc-epsilon receptors (FcεR). The classes of FcR's are also distinguished by the cells that express them (macrophages, granulocytes, natural killer cells, T and B cells) and the signaling properties of each receptor. Fc-gamma receptors (FcγR) includes several members, FcγRI (CD64), FcγRIIA (CD32), FcγRIIB (CD32), FcγRIIIA (CD16a), FcγRIIIB (CD16b), which differ in their antibody affinities due to their different molecular structure.

[000124] "Chimeric Fc Receptor," abbreviated as CFcR, are terms used to describe engineered Fc receptors having their native transmembrane and/or intracellular signaling domains modified, or replaced, with non-native transmembrane and/or intracellular signaling domains. In some embodiments of the chimeric Fc receptor, in addition to having one of, or both, transmembrane and signaling domains being non-native, one or more stimulatory domains can be introduced to the intracellular portion of the engineered Fc receptor to enhance cell activation, expansion and function upon triggering of the receptor. Unlike chimeric antigen receptor (CAR) which contains antigen binding domain to target antigen, the chimeric Fc receptor binds to an Fc fragment, or the Fc region of an antibody, or the Fc region comprised in an engager or a binding molecule and activating the cell function with or without bringing the targeted cell close in vicinity. For example, a Fcγ receptor can be engineered to comprise selected transmembrane, stimulatory, and/or signaling domains in the intracellular region that respond to the binding of IgG at the extracellular domain, thereby generating a CFcR. In one example, a CFcR is produced by engineering CD16, a Fcγ receptor, by replacing its transmembrane domain and/or intracellular domain. To further improve the binding affinity of the CD16 based CFcR, the extracellular domain of CD64 or the high-affinity variants of CD16 (F176V, for example) can be incorporated. In some embodiments of the CFcR where high affinity CD16 extracellular domain is involved, the proteolytic cleavage site comprising a serine at position 197 is eliminated or is replaced such at the extracellular domain of the receptor is non-cleavable, i.e., not subject to shedding, thereby obtaining a hnCD16 based CFcR.

[000125] CD16, a FcγR receptor, has been identified to have two isoforms, Fc receptors FcγRIIIa (CD16a) and FcγRIIIb (CD16b). CD16a is a transmembrane protein expressed by NK cells, which binds monomeric IgG attached to target cells to activate NK cells and facilitate antibody-dependent cell-mediated cytotoxicity (ADCC). "High affinity CD16," "non-cleavable CD16," or "high affinity non-cleavable CD16 (hnCD16)," as used herein, refers to a natural or non-natural variant of CD16. The wildtype CD16 has low affinity and is subject to ectodomain

shedding, a proteolytic cleavage process that regulates the cells surface density of various cell surface molecules on leukocytes upon NK cell activation. F176V and F158V are exemplary CD16 polymorphic variants having high affinity. A CD16 variant having the cleavage site (position 195-198) in the membrane-proximal region (position 189-212) altered or eliminated is not subject to shedding. The cleavage site and the membrane-proximal region are described in detail in WO2015148926, the complete disclosures of which are incorporated herein by reference. The CD16 S197P variant is an engineered non-cleavable version of CD16. A CD16 variant comprising both F158V and S197P has high affinity and is non-cleavable. Another exemplary high affinity and non-cleavable CD16 (hnCD16) variant is an engineered CD16 comprising an ectodomain originated from one or more of the 3 exons of the CD64 ectodomain.

I. Cells and Compositions Useful for Adoptive Cell Therapies with Enhanced Properties

[000126] Provided herein is a strategy to systematically engineer the regulatory circuitry of a clonal iPSC without impacting the differentiation potency of the iPSC and cell development biology of the iPSC and its derivative cells, while enhancing the therapeutic properties of the derivative cells differentiated from iPSC. The iPSC-derived cells are functionally improved and suitable for adoptive cell therapies following a combination of selective modalities being introduced to the cells at the level of iPSC through genomic engineering. It was unclear, prior to this invention, whether altered iPSCs comprising one or more provided genetic editing still have the capacity to enter cell development, and/or to mature and generate functional differentiated cells while retaining modulated activities. Unanticipated failures during directed cell differentiation from iPSCs have been attributed to aspects including, but not limited to, development stage specific gene expression or lack thereof, requirements for HLA complex presentation, protein shedding of introduced surface expressing modalities, and need for reconfiguration of differentiation protocols enabling phenotypic and/or functional change in the cell. The present application has shown that the one or more selected genomic modifications as provided herein does not negatively impact iPSC differentiation potency, and the functional effector cells derived from the engineered iPSC have enhanced and/or acquired therapeutic properties attributable to the individual or combined genomic modifications retained in the effector cells following the iPSC differentiation.

1. CD3 surface presentation in the absence of endogenous TCR

[000127] Alpha-beta T cell receptors (αβTCR) are antigen specific receptors essential to the immune response and are present on the cell surface of αβ T lymphocytes. Binding of TCRαβ to

peptide-major histocompatibility complex (pMHC) initiates TCR-CD3 intracellular activation, recruitment of numerous signaling molecules, and branching and integrating signaling pathways, leading to mobilization of transcription factors that are critical for gene expression and T cell growth and function acquisition. Although NKT cells are a subset of T cells that also express an αβ TCR, differ from conventional αβ T cells, NKT cells' TCR is composed of a canonical invariant TCR α chain (Vα24-Jα18 in humans) and TCR β chains that use limited Vβ segments (Vβ11 in humans), which is limited in diversity and recognizes a limited number of lipid antigens presented by CD1d.

[000128] Disrupting the constant region of TCR alpha or TCR beta (TRAC or TRBC), either through direct editing of a T cell or through iPSC editing as a source for obtaining modified derivative T cell, is one of the approaches to produce a TCR^{neg} T cell. For example, an insertion of, at a pre-selected position in TRAC or TRBC, a 2A sequence either operatively linked to an endogenous promoter of the TRAC or TRBC or to an exogenous promoter can lead to TRAC or TRBC disruption (or truncation in this example) and a TCR negative cell (TCR^{neg}). In a particular embodiment, the TCR^{neg} cell is an iPSC. In another embodiment, the TCR^{neg} cell is an NK lineage cell. As used herein, the term "TCR negative" or "TCR^{neg}" refers to the lack of ***endogenous*** TCR expression, either due to TCR gene expression disruption (such as in T lineage cells: primary or iPSC-derived T lineage cells) or due to natural absence of TCR gene expression despite the existence of TCR locus in the genome (for example, iPSCs, or NK linage cells: primary or iPSC-derived NK lineage cells). The subsequent directed differentiation of clonally selected engineered iPSC to hematopoietic cells make it possible to generate iPSC derived immune effector cells, and/or a homogenous population thereof, without TCR expression.

[000129] In some embodiments, the targeted truncation or disruption using self-cleaving peptide such as 2A could optionally take place concomitantly with integration of one or more exogenous genes of interest at the location of truncation or disruption, and the expression of the integrated gene(s) could be driven by an operatively linked exogenous promoter or by endogenous promoter of TCR alpha or TCR beta upon integration, which leads to TRAC or TRBC knockout, and thus TCR negative while expressing one or more exogenous genes inserted at the TRAC or TRBC locus.

[000130] iPSC-derived TCR negative T cells (with or without exogenous gene integration) obtained using this approach do not require HLA matching, have reduced alloreactivity and are able to prevent GvHD (Graft versus Host Disease) when used in allogeneic adoptive cell therapies. However, it has been found that TCR disruption also results in the elimination of the CD3 signaling complex from the T-cell surface despite the CD3 subunit gene expression in the

cell. The lack of cell surface CD3 may alter the cells' capacity for expansion and/or survival and reduce the cells' functional potential due to incompatibility with technologies requiring cell surface CD3 recognition and binding, which include, but are not limited to: BiTE, BiKE, or TRiKE (or collectively called, engager) technology; CD3/CD28 T cell activation bead technology; and anti-CD3 antibody or CD3-CAR stimulation technology. Further, when TCR^{neg} iPSCs are used for directed T cell differentiation, there may also be impact on T cell development biology and T cell function maturation. However, overexpressing CD3 in cells that are TCR negative does not seem to restore the cell surface presentation of CD3 complex and/or CD3 signaling. As for cells that do not express TCR despite the existence of TCR genes, for example, NK or NK progenitor cells, the cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) as disclosed herein in a TCR^{neg} NK cell can function as an acquired CD3 related cell surface triggering receptor for binding with molecules including, not limited to, antibodies or functional variants thereof, and/or bi- or multi- specific engagers recognizing CD3 receptor. To address the unresolved issues in the art, among other provided advantages described herein, the following designs, as shown in FIGS. 1A-C, are detailed in this application to reconstitute and/or provide the surface CD3 presentation when without endogenous TCR expression (TCR^{neg} cell), whether due to loss of endogenous TCR gene expression via gene disruption (such as in derivative T lineage cells) or due to natural absence of TCR gene expression (such as in derivative NK linage cells).

[000131] Design 1: Non-binding Recombinant TCR (nb-rTCR)

[000132] As presented in FIG. 1A, in this Design 1, while the endogenous TCRα in a cell is knocked out ($TCR\alpha^{-/-}$) using targeted genomic editing tools, leading to TCR negative (TCR^{neg}), the knockout of TCRβ ($TCR\beta^{-/-}$) is optional; or vice versa, while the endogenous TCRβ in a cell is knocked out ($TCR\beta^{-/-}$) using targeted genomic editing tools, leading to TCR negative (TCR^{neg}), the knockout of TCRα ($TCR\alpha^{-/-}$) is optional. In embodiments which comprises TCRα knockout, a polynucleotide encoding a full or partial length of the constant region of TCRα (transgenic TRAC, or tgTRAC) is introduced to the cell subsequently, or is integrated at TRAC upon targeted TRAC knockout, and the expression of the polynucleotide is driven by the endogenous promoter of TCRα or alternatively by an exogenous promoter that is operatively linked to the polynucleotide. In some embodiments, the polynucleotide encoding a full or partial length of the constant region of TCRα further comprises an appropriate N- terminal signal peptide coupled with the full or partial length of the constant region of TCRα. In the embodiment where the endogenous TCRβ ($TCR\beta^{-/-}$) is knocked out, a polynucleotide encoding a full or partial length of the constant region of TCRβ, (tgTCRβ, or tgTRBC) is introduced to the cell; and the expression

of the tgTCRβ or tgTRBC is driven by the endogenous promoter of TCRβ or alternatively by an exogenous promoter. In some embodiments, the polynucleotide encoding a full or partial length of the constant region of TCRβ further comprises an appropriate N- terminal signal peptide coupled with the full or partial length of the constant region of TCRβ. In some embodiments, the exogenous promoter comprises a constitutive, inducible, temporal-, tissue-, or cell type- specific promoter. In some embodiments, the exogenous promoter comprises one of CMV, EF1α, PGK, CAG, and UBC. In one embodiment, the exogenous promoter comprises at least CAG.

[000133] In some embodiments, the polynucleotide encoding full or partial TCRα constant region (tgTRAC) comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 1. In some embodiments, the polynucleotide encoding TCRβ comprising at least a full or partial constant region (tgTRBC) comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 2 or SEQ ID. 3. In some embodiments of the polynucleotide encoding an N- terminal signal peptide and a full or partial length of TCRα or TCRβ constant region, the polynucleotide further comprises a linker peptide in-between the signal peptide and the sequence related to the TCR constant region. In some embodiments of the polynucleotide encoding an N- terminal signal peptide and a full length of TCRα or TCRβ constant region, the polynucleotide further comprises a poly A tail at the C-terminal. In some embodiments of the polynucleotide encoding an N- terminal signal peptide and a partial length of TCRα or TCRβ constant region, the integration of the polynucleotide is at a site within endogenous constant region (for example, an exon) and is in-frame, i.e., in-frame with the remaining endogenous sequence of TCRα or TCRβ constant region downstream of the integration site, such that a full length transgenic/chimeric TRAC or TRBC is formed with a part of its sequence being exogenous/transgenic and another part being endogenous. In some embodiments of Design 1, at least one of the endogenous TCRα and TCRβ is engineered to essentially remove the respective variable region, while presenting to cell surface the respective transgenic constant region when expressed. In some embodiments, only one of the endogenous TCRα and TCRβ is engineered to essentially remove the related variable region while presenting to cell surface a transgenic constant region and a wildtype TCR subunit (TCRα or TCRβ). In some embodiments, both endogenous TCRα and TCRβ are engineered as provided to remove the respective variable region, while presenting to cell surface both transgenic constant region when expressed. Exemplary N- terminal signal peptide includes MALPVTALLLPLALLLHA (SEQ ID NO. 4; CD8asp) or MDFQVQIFSFLLISASVIMSR (SEQ ID NO. 5; IgKsp), or any signal

peptide sequence or functional variants thereof known in the art. Exemplary linker peptide includes DYKDDDDK (SEQ ID NO. 6; FLAG), or any linker peptide sequence or functional variants thereof known in the art.

SEQ ID NO. 1:

IQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFA
CANAFNNSIIPEDTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS

(TRAC)

SEQ ID NO. 2:

DLNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDS
RYCLSSRLRNHFRCRVSATFWQNPQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSYQQGVL
SATILYEILLGKATLYAVLVSALVLMAMVKRKDF

(TRBC1)

SEQ ID NO. 3

DLKNVFPPKVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDS
RYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVL
SATILYEILLGKATLYAVLVSALVLMAMVKRKDSRG

(TRBC2)

[000134] In this application, it is discovered that the transgenic constant region of either TCR subunits, tgTRAC or tgTRBC, while being capable of forming a recombinant TCR complex (rTCR) by associating with the other TCR subunit (endogenous/wildtype or transgenic; if transgenic, with or without its respective variable region) and endogenous CD3 subunits, does not enable peptide-MHC binding for lack of a TCRα or TCRβ variable region that participates in the antigen recognition. The resulting cell regains the canonical TCR/CD3 signaling through the cell surface presented endogenous CD3 (cs-CD3) complex but does not have alloreactivity due to endogenous TCR knockout and a rTCR without TCRα variable region. As such, in view of Design 1, provided herein is a cell or a population thereof, wherein the cell is an iPSC, a clonal iPSC, a clonal iPS cell line cell, or a derivative cell obtained from differentiating said iPSC; and the cell comprises: a disruption at at least one of endogenous TCRα and TCRβ constant regions such that the endogenous TCR is knocked out (TCR^{neg}), and one or both exogenous polynucleotide encoding the constant region of TCRα (tgTRAC) and/or TCRβ (tgTRBC) that is disrupted; wherein the tgTRAC and/or tgTRAB enables cell surface presentation of endogenous

CD3 (cs-CD3) when expressed. The recombinant TCR complex comprising at least one of tgTRAC and tgTRBC does not bind antigen peptide presented by MHC for not having both variable regions (Vα and Vβ) of the TCR subunits, and is thus termed as non-binding recombinant TCR (nb-rTCR).

[000135] Design 2: Defined recombinant TCR (d-rTCR)

[000136] As presented in FIG. 1A, in this Design 2, both endogenous TCRα and endogenous TCRβ are knocked out ($TCR\alpha^{-/-}$ and $TCR\beta^{-/-}$; or TCR^{neg} $TCR\beta^{neg}$) in a cell using a genomic editing tool, leading to a TCR^{neg} cell. Simultaneously with, or subsequently to, the TCR knockout, a first polynucleotide encoding a TCRα comprising a defined variable region of TCRα and a full or partial constant region (tgTCRα) and a second polynucleotide encoding a TCRβ comprising a defined variable region of TCRβ and a full or partial constant region (tgTCRβ) are introduced to said TCR^{neg} cell. A defined TCRα or TCRβ variable region can be of any given specificity such that its sequence has been, or can be, identified. In some embodiments, one or both of the first and the second polynucleotides is driven by an endogenous promoter of TCRα and TCRβ, respectively. In some other embodiments, one or both of the first and the second polynucleotides is driven by an exogenous promoter. In some embodiments, the second polynucleotide is driven by an endogenous promoter of TCRβ, whereas in some other embodiments, the second polynucleotide is driven by an exogenous promoter. In some embodiments, the exogenous promoter comprises a constitutive, inducible, temporal-, tissue-, or cell type- specific promoter. In some embodiments, the exogenous promoter comprises one of CMV, EF1α, PGK, CAG, and UBC. In one embodiment, the exogenous promoter comprises at least CAG. In some embodiments, the polynucleotide encoding a full or partial length of TCRα constant region and a given defined variable region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 1. In some embodiments, the polynucleotide encoding a full or partial length of TCRβ constant region and a given defined variable region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 2 or SEQ ID NO. 3. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. In some embodiments of the polynucleotide encoding a full length of TCRα or TCRβ constant region, the polynucleotide further comprises a polyA tail at the C' terminal. In some embodiments of the polynucleotide encoding a partial length of TCRα or TCRβ constant region,

the integration of the polynucleotide is at a site within the endogenous constant region and is in frame with the remaining endogenous sequence of TCRα or TCRβ constant region downstream of the integration site, such that a full length transgenic/chimeric TRAC or TRBC is formed with a part of its sequence being exogenous/transgenic and another part being endogenous. Sequences for TCRα or TCRβ variable regions can be found, for example, in the Universal Protein Resource (UniProt) database, and some non-limiting defined TCRα or TCRβ variable regions examples are listed in the following Table A and B, respectively.

TABLE A:

UniProt Sequence Entry No.	Protein Names	Gene Names
A0A0B4J248	TCR alpha variable 1-1	TRAV1-1
A0A0B4J238	TCR alpha variable 1-2	TRAV1-2
A0A0B4J234	TCR alpha variable 2	TRAV2
A0A0B4J244	TCR alpha variable 3	TRAV3
A0A0B4J268	TCR alpha variable 4	TRAV4
A0A0B4J249	TCR alpha variable 5	TRAV5
A0A075B6T7	TCR alpha variable 6	TRAV6
A0A075B6U4	TCR alpha variable 7	TRAV7
A0A0A6YYK1	TCR alpha variable 8-1	TRAV8-1
A0A0B4J237	TCR alpha variable 8-2	TRAV8-2
A0A0A6YYJ7	TCR alpha variable 8-3	TRAV8-3
P01737	TCR alpha variable 8-4	TRAV8-4
A0A0B4J262	TCR alpha variable 8-6	TRAV8-6
A0A075B6U6	TCR alpha variable 8-7	TRAV8-7
A0A075B6T8	TCR alpha variable 9-1	TRAV9-1
A0A087WT02	TCR alpha variable 9-2	TRAV9-2

UniProt Sequence Entry No.	Protein Names	Gene Names
A0A0A6YYK6	TCR alpha variable 16	TRAV16
A0A0B4J275	TCR alpha variable 17	TRAV17
A0A075B6X5	TCR alpha variable 18	TRAV18
A0A0A6YYK7	TCR alpha variable 19	TRAV19
A0A0B4J274	TCR alpha variable 20	TRAV20
A0A0B4J279	TCR alpha variable 21	TRAV21
A0A0B4J277	TCR alpha variable 22	TRAV22
A0A075B6W5	TCR alpha variable 23/delta variable 6	TRAV23DV6
A0A0B4J272	TCR alpha variable 24	TRAV24
A0A0B4J276	TCR alpha variable 25	TRAV25
A0A087WT03	TCR alpha variable 26-1	TRAV26-1
A0A0B4J265	TCR alpha variable 26-2	TRAV26-2
A0A087WT01	TCR alpha variable 27	TRAV27
P04437	TCR alpha variable 29/delta variable 5	TRAV29DV5
A0A087WSZ9	TCR alpha variable 30	TRAV30
A0A0B4J273	TCR alpha variable 34	TRAV34

A0A0B4J240	TCR alpha variable 10	TRAV10
A0A0B4J245	TCR alpha variable 12-1	TRAV12-1
A0A075B6T6	TCR alpha variable 12-2	TRAV12-2
A0A0B4J271	TCR alpha variable 12-3	TRAV12-3
A0A0B4J241	TCR alpha variable 13-1	TRAV13-1
A0A0B4J235	TCR alpha variable 13-2	TRAV13-2
A0A0A6YYC5	TCR alpha variable 14/delta variable 4	TRAV14DV4
P0DPF4	TCR alpha variable 35	TRAV35
A0A075B6V5	TCR alpha variable 36/delta variable 7	TRAV36DV7
A0A0B4J264	TCR alpha variable 38-1	TRAV38-1
A0JD32	TCR alpha variable 38-2/delta variable 8	TRAV38-2DV8
A0A0B4J263	TCR alpha variable 39	TRAV39
A0A0B4J280	TCR alpha variable 40	TRAV40
A0A0B4J266	TCR alpha variable 41	TRAV41

TABLE B:

UniProt Sequence Entry No.	Protein Names	Gene Names
A0A1B0GX68	TCR beta variable 2	TRBV2
A0A576	TCR beta variable 3-1	TRBV3-1
A0A577	TCR beta variable 4-1	TRBV4-1
A0A539	TCR beta variable 4-2	TRBV4-2
A0A589	TCR beta variable 4-3	TRBV4-3
A0A578	TCR beta variable 5-1	TRBV5-1
A0A0C4DH59	TCR beta variable 5-4	TRBV5-4
A0A597	TCR beta variable 5-5	TRBV5-5
A0A599	TCR beta variable 5-6	TRBV5-6
A0A5A2	TCR beta variable 5-8	TRBV5-8
A0A0K0K1D8	TCR beta variable 6-1	TRBV6-1
A0A0J9YXY3	TCR beta variable 6-2	TRBV6-2
P0DPF7	TCR beta variable 6-3	TRBV6-3
A0A1B0GX49	TCR beta variable 6-4	TRBV6-4
A0A1B0GX51	TCR beta variable 7-8	TRBV7-8
P04435	TCR beta variable 7-9	TRBV7-9
A0A0B4J1U6	TCR beta variable 9	TRBV9
A0A0K0K1A3	TCR beta variable 10-1	TRBV10-1
A0A0K0K1G8	TCR beta variable 10-2	TRBV10-2
A0A0K0K1G6	TCR beta variable 10-3	TRBV10-3
A0A0K0K1C0	TCR beta variable 11-1	TRBV11-1
A0A584	TCR beta variable 11-2	TRBV11-2
A0A5A6	TCR beta variable 11-3	TRBV11-3
P01733	TCR beta variable 12-3	TRBV12-3
A0A0B4J2E0	TCR beta variable 12-4	TRBV12-4
A0A1B0GX78	TCR beta variable 12-5	TRBV12-5
A0A0A6YYD4	TCR beta variable 13	TRBV13
A0A5B0	TCR beta variable 14	TRBV14

A0A0K0K1A5	TCR beta variable 6-5	TRBV6-5
A0A0A6YYG2	TCR beta variable 6-6	TRBV6-6
A0A0A6YYG3	TCR beta variable 6-8	TRBV6-8
A0A0J9YX75	TCR beta variable 6-9	TRBV6-9
A0A1B0GXF2	TCR beta variable 7-2	TRBV7-2
A0A1B0GX95	TCR beta variable 7-4	TRBV7-4
A0A1B0GX31	TCR beta variable 7-6	TRBV7-6
A0A0K0K1E9	TCR beta variable 7-7	TRBV7-7

A0A087WV62	TCR beta variable 16	TRBV16
A0A087X0M5	TCR beta variable 18	TRBV18
A0A075B6N1	TCR beta variable 19	TRBV19
A0A075B6N2	TCR beta variable 20-1	TRBV20-1
A0A075B6N3	TCR beta variable 24-1	TRBV24-1
A0A075B6N4	TCR beta variable 25-1	TRBV25-1
A0A0K0K1C4	TCR beta variable 27	TRBV27
A0A5B6	TCR beta variable 28	TRBV28

[000137] Invariant NKT cells are a unique subset of T cells that express a canonical invariant TCRα chain (Vα24-Jα18 in humans; or iTCRα) and TCRβ chains that use limited Vβ segments (Vβ11 in humans; or iTCRβ), resulting in highly conserved TCR and CD1d-dependent antigen presentation. To utilize this property of the TCR of invariant NKT (iTCR or iTCRαβ), in some embodiments of Design 2, a defined TCR comprises either or both of TCRα and TCRβ of invariant NKT cell (iTCRα or iTCRαβ), such that a polynucleotide encoding a full or partial length of TCRα constant region and a given defined variable region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 44; and a polynucleotide encoding a full or partial length of TCRβ constant region and a given defined variable region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 45. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO. 44

MKKHLTTFLVILWLYFYRGNGKNQVEQSPQSLIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIM
TFSENTKSNGRYTATLDADTKQSSLHITASQLSDSASYICVVSDRGSTLGRLYFGRGTQLTVWPDIQNPDP
AVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFN
NSIIPEDTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS

(iNKT TCR α chain of human Vα24Jα18; the underlined portion is the variable region)

SEQ ID NO. 45

MTIRLLCYMGFYFLGAGLMEADIYQTPRYLVIGTGKKITLECSQTMGHDKMYWYQQDPGMELHLIHYSYGV
NSTEKGDLSSESTVSRIRTEHFPLTLESARPSHTSQYLCASEDLNKVFPPEVAVFEPSEAEISHTQKATLV
CLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHFRCQVQFY
GLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLVSALVLMAMV
KRKDF

(iNKT TCR β chain of human Vβ11; the underlined portion is the variable region)

[000138] In this application, it is discovered that a transgenic TCRα (tgTCRα) having a constant region and a defined variable region, optionally with a transgenic TCRβ (tgTCRβ) having a constant region and a defined variable region is capable of forming a recombinant TCR complex (rTCR) by associating with the endogenous CD3 subunits including the CD3ζ chain, while having a defined, or no, peptide-MHC binding due to the specificity of the variable region of tgTCRα and tgTCRβ. In addition to genetic engineering transgenic TCR subunits for defined recombinant TCR, other approaches to take advantage of the TCRα and TCRβ of invariant NKT cells include reprogramming isolated NKT cells to iPSC, and differentiating the iPSC to a T cell, which derived T cell, as a result, comprises the TCRα and TCRβ of invariant NKT cells (iTCRα, iTCRβ; and iTCR, the complex), using the reprogramming and differentiating composition and method disclosed herein. The resulting cell, differentiated from genetically engineered iPSCs or iNKT reprogramed iPSCs, regains the canonical TCR/CD3 signaling through the cell surface presented endogenous CD3 (cs-CD3), while having no, or a known and defined MHC binding specificity. As such, in view of Design 2, provided herein is a cell or a population thereof, wherein the cell is an iPSC, a clonal iPSC, a clonal iPS cell line cell, or a derivative cell obtained from differentiating the iPSC; and the cell comprises: a disruption at each of an endogenous TCRα and an endogenous TCRβ, an exogenous polynucleotide encoding a tgTCRα having a full or partial constant region and a defined variable region, and an exogenous polynucleotide encoding a tgTCRβ having a full or partial constant region and a defined variable region; wherein an endogenous CD3 molecule is present at the cell surface (cs-CD3) when expressed.

[000139] **Design 3: Recombinant pre-TCRα with optional non-binding TCRβ (p-rTCR)**

[000140] Pre-TCRα is a type I transmembrane receptor protein encoded by developmentally controlled gene in immature thymocytes, an early stage in T cell development. The pre-TCRα covalently associates with TCRβ and with the CD3 subunits to form pre-TCR complex. Pre-TCRα, , among other structural and functional difference, has a relatively longer cytoplasmic tail as compared to TCRα chain. As presented in FIG. 1A, in this Design 3, the TCR negative cell has at least the endogenous TCRα knocked out (TCR^{neg}) using a genomic editing tool, with the

knockout of the endogenous TCRβ being optional. Simultaneously with or subsequently to the TCR knockout, a first polynucleotide encoding a full or a partial length of pre-TCRα (tgpTCRα) is introduced to said TCR^{neg} cell. In some embodiments where said TCR^{neg} cell further comprises TCRβ knockout, a second polynucleotide encoding a full or partial TCRβ constant region with or without a given defined variable region (tgTCRβ or tgTRBC) is introduced to the TCR^{neg} cell, wherein the cell is not an early stage, immature thymocytes. In some embodiments of the polynucleotide encoding a full length of TCRα or TCRβ constant region, the polynucleotide further comprises a polyA tail at the C' terminal. In some embodiments of the polynucleotide encoding a partial length of TCRα or TCRβ constant region, the integration of the polynucleotide is at a site within endogenous constant region and is in frame with the remaining endogenous sequence of TCRα or TCRβ constant region downstream of the integration site, such that a full length transgenic/chimeric TRAC or TRBC is formed with a part of its sequence being exogenous/transgenic and another part being endogenous.

[000141] In some embodiments, the first polynucleotide encoding a full or a partial length of pre-TCRα (tgpTCRα) is operatively linked to endogenous promoter of TCRα upon integration. In some embodiments, the first polynucleotide encoding a full or a partial length of pre-TCRα (tgpTCRα) is driven by an exogenous promoter. In some embodiments, the second polynucleotide encoding a full or partial TCRβ constant region with or without a given defined variable region is operatively linked to endogenous promoter of TCRβ upon integration. In some embodiments, the second polynucleotide encoding a full or partial TCRβ constant region with or without a given defined variable region is driven by an exogenous promoter. In some embodiments, the exogenous promoter comprises a constitutive, inducible, temporal-, tissue-, or cell type- specific promoter. In some embodiments, the exogenous promoter comprises one of CMV, EF1α, PGK, CAG, and UBC. In one embodiment, the exogenous promoter comprises at least CAG. In some embodiments, the polynucleotide encoding tgpTCRα comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 23. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. In some embodiments, the polynucleotide encoding tgpTCRα comprises a partial length of SEQ ID NO. 23, which is represented herein as SEQ ID NO. 24. In some embodiments of the polynucleotide encoding tgpTCRα comprising a full or partial length of SEQ ID NO. 23 or any functional variants thereof, the encoded tgpTCRα further comprises a

signal peptide known in the art. One non-limiting exemplary signal peptide comprises a peptide represented by SEQ ID NO. 22.

SEQ ID NO. 22

MAGTWLLLLLALGCPALPTGVGG

SEQ ID NO. 23

TPFPSLAPPIMLLVDGKQQMVVVCLVLDVAPPGLDSPIWFSAGNGSALDAFTYGPSPATDGTWTNLAHLSL
PSEELASWEPLVCHTGPGAEGHSRSTQPMHLSGEASTARTCPQEPLRGGCGLLRAPERFLLAGTPGG**ALWL**
GVLRLLLFKLLLFDLLLTCSCLCDPAGPLPSPATTTRLRALGSHRLHPATETGGREATSSPRPQPRDRRWG
DTPPGRKPGSPVWGEGSYLSSYPTCPAQAWCSRSALRAPSSSLGAFFAGDLPPPLQAGAA

(tgpTCRα with **TM**)

SEQ ID NO. 24

TPFPSLAPPIMLLVDGKQQMVVVCLVLDVAPPGLDSPIWFSAGNGSALDAFTYGPSPATDGTWTNLAHLSL
PSEELASWEPLVCHTGPGAEGHSRSTQPMHLSGEASTARTCPQEPLRGGCGLLRAPERFLLAGTPGG**ALWL**
GVLRLLLFKLLLFDLLLTCSCLCDPAGPLPSPATTTRLRALGSHRLHPATETGGREATSSPRPQPRDRRWG
DTPPGRKPGSPV

(Truncated tgpTCRα with **TM**)

[000142] In some embodiments, the polynucleotide encoding a TCRβ comprising a full or partial constant region and a given defined variable region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 2 or SEQ ID NO. 3. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. A defined TCRβ variable region can be of any given specificity such that its sequence has been or can be identified. Non-limiting defined TCRβ variable region are exemplified in Table B above, and that comprised in SEQ ID NO. 45 (the underlined portion).

[000143] It was unknown previously whether an iPSC having a pre-TCRα expression controlled by a promoter (whether exogenous promoter or endogenous TCRα promoter) different from its native promoter (i.e., pre-TCRα promoter) still has the capacity to differentiate into a functional effector T cell. Here we tried to demonstrate that the cell development biology of iPSC comprising a transgenic pre-TCRα (tgpTCRα) controlled by a non-native promoter could be maintained to an extent that the directed differentiation to iPSC-derived T cell can be carried

out to generate a functional T cell. This is surprising because normally the expression of an endogenous pre-TCR is developmentally regulated. Further, the T cells derived from tgpTCRα TCR^{neg} iPSCs comprise an expressed surface recombinant pre-TCR complex (rpTCR) by associating with the endogenous CD3 subunits including CD3ζ chain, while having no peptide-MHC binding capability. Without being limited by theory, the transgenic pre-TCR/CD3 complex may have nonetheless driven the iPSC-derived T cell maturation through the canonical CD3 signaling via the cell surface presented endogenous CD3 (cs-CD3) complex. In view of the above, the scope of this application also includes various methods of upregulating and/or preventing downregulation of endogenous pre-TCRα. The over-expressed pre-TCRα in a cell that is not an early/immature thymocytes would associate with expressed endogenous TCRβ and CD3 subunits to enable CD3 cell surface presentation while having no peptide-MHC binding capability.

[000144] As such, in view of Design 3, provided herein is a cell or a population thereof, wherein the cell is an iPSC, a clonal iPSC, a clonal iPS cell line cell, or a derivative cell obtained from differentiating said iPSC; and the cell comprises: a disruption at least of an endogenous TCRα or TCRβ such that the endogenous TCR is knocked out (TCR^{neg}), and at least an exogenous polynucleotide encoding a peptide comprising a full or partial length of pre-TCRα; wherein the expression of the pre-TCRα, in the absence of TCRα, results in the reconstitution of cell surface CD3 complex (cs-CD3) in association with the endogenous or transgenic TCRβ in the cells, but also contributes to the directed differentiation of iPSC into functional derivative effector cells including T cells.

[000145] **Design 4: Non-binding recombinant TCR anchored CD3 (nb-rTCR-CD3)**

[000146] As presented in FIG. 1B, in this Design 4, one or both endogenous TCRα and endogenous TCRβ are knocked out (TCR^{neg}; $TCR\alpha^{-/-}$ and $TCR\beta^{-/-}$) in a cell using a genomic editing tool. Simultaneously with, or subsequently to, the TCR knockout, exogenous polynucleotides are introduced to said TCR^{neg} cell, which comprise: a first polynucleotide encoding a recombinant TCRα comprising a TCRα constant region, full or partial length ectodomains of CD3ε and one of CD3δ and CD3γ; and/or a second polynucleotide encoding a recombinant TCRβ comprising a TCRβ constant region, full or partial length of ectodomains of CD3ε and one of CD3δ and CD3γ that is not comprised in the recombinant TCRα; such that one heterodimer between CD3ε and CD3δ encoded by one polynucleotide, and/or another heterodimer between CD3ε and CD3γ encoded by another polynucleotide could form at cell surface.

[000147] In some embodiments, the recombinant TCRα comprises a full or partial TCRα constant region at the C-terminal, fused with full or partial length of CD3ε and CD3δ ectodomains at the N-terminal(tgCD3(ε-δ)-TRAC). In some embodiments, the recombinant TCRα comprises a full or partial TCRα constant region at the C-terminal, fused with full or partial length of ectodomains of CD3ε and CD3γ at the N-terminal (tgCD3(ε-γ)-TRAC). In some embodiments, the recombinant TCRβ comprises a full or partial TCRβ constant region at the C-terminal, fused with full or partial length of ectodomains of CD3ε and CD3γ at the N-terminal (tgCD3(ε-γ)-TRBC). In some embodiments, the recombinant TCRβ comprises a full or partial TCRβ constant region at the C-terminal, fused with full or partial length of ectodomains of CD3ε and CD3δ at the N-terminal (tgCD3(ε-δ)-TRBC). In some embodiments of the polynucleotide encoding a full length of TCRα or TCRβ constant region, the polynucleotide further comprises a polyA tail at the C-terminal. In some embodiments of the polynucleotide encoding a partial length of TCRα or TCRβ constant region, the integration of the polynucleotide is at a site within the respective endogenous constant region and is in-frame with the remaining endogenous sequence of TCRα or TCRβ constant region downstream of the integration site, such that a full length transgenic/chimeric TRAC or TRBC is formed with a part of its sequence being exogenous/transgenic and another part being endogenous.

[000148] In some other embodiments, where both of the first and the second polynucleotide are introduced to a cell, the recombinant TCRα is encoded by the first polynucleotide comprising tgCD3(ε-δ)-TRAC, and the recombinant TCRβ is encoded by the second polynucleotide comprising tgCD3(ε-γ)-TRBC; or the recombinant TCRα is encoded by the first polynucleotide comprising tgCD3(ε-γ)-TRAC, and the recombinant TCRβ is encoded by the second polynucleotide comprising tgCD3(ε-δ)-TRBC. As such, in said embodiments, one heterodimer between CD3ε and CD3δ encoded by one polynucleotide and another heterodimer between CD3ε and CD3γ encoded by another polynucleotide could form at the cell surface.

[000149] In some embodiments, where only one of the first and the second polynucleotides is introduced to a cell, the other TCR subunit is either wildtype/endogenous or is engineered to comprise only a constant region with its endogenous variable region removed with or without being replaced with a defined variable region: for example, tgTRAC or tgTRBC of Design 1 in FIG. 1A (without variable region), or tgTCRα or tgTCRβ of Design 2 in FIG. 1A (with a defined variable region). As such, as shown in Design 4 of FIG. 1B, in one embodiment where a first polynucleotide comprising tgCD3(ε-δ)-TRAC is introduced to a cell to provide a recombinant TCRα subunit, another polynucleotides comprising tgTRBC or tgTCRβ is also introduced to the cell to provide a recombinant TCRβ subunit; such that in this embodiment, one heterodimer

between endogenous CD3ε and endogenous CD3γ, and another heterodimer between CD3ε and CD3δ encoded by the polynucleotide comprising tgCD3(ε-δ)-TRAC could be formed at cell surface. In yet another embodiment of Design 4 of FIG. 1B, where a second polynucleotide comprising tgCD3(ε-γ)-TRBC is introduced to a cell to provide a recombinant TCRβ subunit, another polynucleotide comprising tgTRAC or tgTCRα is also introduced to the cell to provide a recombinant TCRα subunit, such that one heterodimer between endogenous CD3ε and endogenous CD3δ, and another heterodimer between CD3ε and CD3γ encoded by the polynucleotide comprising tgCD3(ε-γ)-TRBC could be formed at cell surface.

[000150] In some embodiments, the first polynucleotide is driven by an endogenous promoter of TCRα, whereas in some other embodiments, the first polynucleotide is driven by an exogenous promoter. In some embodiments, the second polynucleotide is driven by an endogenous promoter of TCRβ, whereas in some other embodiments, the second polynucleotide is driven by an exogenous promoter. In some embodiments, the exogenous promoter for either recombinant TCRα or recombinant TCRβ comprises a constitutive, inducible, temporal-, tissue-, or cell type- specific promoter. In some embodiments, the exogenous promoter comprises one of CMV, EF1α, PGK, CAG, and UBC. In one embodiment, the exogenous promoter comprises at least CAG. In some embodiments, the polynucleotide encoding a TCRα constant region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 1. In some embodiments, the polynucleotide encoding a TCRβ constant region comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 2 or SEQ ID NO. 3. In some embodiments, the polynucleotide encoding a full or partial length of CD3ε ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 25. In some embodiments, the polynucleotide encoding a full or partial length of CD3δ ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 26. In some embodiments, the polynucleotide encoding a full or partial length of CD3γ ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 27. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In

embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. In some embodiments of a polynucleotide encoding a full or partial length of CD3ε, CD3δ, or CD3γ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide. In some embodiments, the signal peptide comprises one of SEQ ID NO. 28, SEQ ID NO. 29, SEQ ID NO. 30, or any other signal peptide known in the art. In some embodiments of a polynucleotide encoding a full or partial length of CD3ε ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 28. In some embodiments of a polynucleotide encoding a full or partial length of CD3δ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 29. In some embodiments of a polynucleotide encoding a full or partial length of CD3γ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 30.

SEQ ID NO. 25

DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQS
GYYVCYPRGSKPEDANFYLYLRARVCENCMEMD

(ecto- CD3ε)

SEQ ID NO. 26

FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRM
CQSCVELDPATVA

(ecto- CD3δ)

SEQ ID NO. 27

QSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWFKDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNK
SKPLQVYYRMCQNCIELNAATIS

(ecto-CD3γ)

SEQ ID NO. 28

MQSGTHWRVLGLCLLSVGVWGQ

SEQ ID NO. 29

MEHSTFLSGLVLATLLSQVSP

SEQ ID NO. 30

MEQGKGLAVLILAIILLQGTLA

[000151] In some embodiments of a polynucleotide encoding tgCD3(ε-δ)-TRAC fusion protein, the polynucleotide comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 31, wherein each of the two linker sequences (SEQ ID NO. 33 and SEQ ID NO. 34) comprised in SEQ ID NO. 31 may be replaced with any that is known in the art. In some embodiments of a polynucleotide encoding tgCD3(ε-γ)-TRBC fusion protein, the polynucleotide comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 32, wherein each of the two linker sequences (SEQ ID NO. 33 and SEQ ID NO. 34) comprised in SEQ ID NO. 32 may be replaced with any that is known in the art. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. In some embodiments of a recombinant TCRα or TCRβ fusion protein, as provided herein, the fusion protein further comprises a signal peptide known in the art. One non-limiting exemplary signal peptide comprises a peptide represented by SEQ ID NO. 28.

SEQ ID NO. 31

DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQS
GYYVCYPRGSKPEDANFYLYLRARVGSADDAKKDAAKKDDAKKDDAKKDGSFKIPIEELEDRVFVNCNTSI
TWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRM**GGGGSGGGGSGGGGS**IQNPD
PAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAF
NNSIIPEDTFFPSPESSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS

(N'-CD3ε-linker-CD3δ-**G4S linker**-TRAC-C')

SEQ ID NO. 32

DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQS
GYYVCYPRGSKPEDANFYLYLRARVGSADDAKKDAAKKDDAKKDDAKKDGSQSIKGNHLVKVYDYQEDGSV
LLTCDAEAKNITWFKDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVYYRM**GGGGSGGGGS**
GGGGSDLNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQP
ALNDSRYCLSSRLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSY
QQGVLSATILYEILLGKATLYAVLVSALVLMAMVKRKDF

(N'-CD3ε-linker-CD3γ-**G4S linker**-TRBC-C')

SEQ ID NO. 33

GSADDAKKDAAKKDDAKKDDAKKDGS

SEQ ID NO. 34

GGGGSGGGGSGGGGS

[000152] In this application, it is discovered that a TCRα or TCRβ constant region fused with ectodomains of CD3ε, and one of CD3δ and CD3γ is capable of associating with a transgenic TCRβ or TCRα constant region with or without fused ectodomains of CD3ε, and one of CD3δ and CD3γ, to form CD3ε/CD3δ and CD3ε/CD3γ heterodimers. The associated transgenic TCRα and TCRβ subunits is capable of further associating with endogenous CD3ζ to support the cell surface expression of CD3 ectodomains (cs-CD3) and signaling transduction through the endogenous CD3ζ, while having no peptide-MHC binding potential. As such, in view of Design 4, provided herein is a cell or a population thereof, wherein the cell is an iPSC, a clonal iPSC, a clonal iPS cell line cell, or a derivative cell obtained from differentiating said iPSC; and the cell comprises: a disruption at each of an endogenous TCRα constant region and an endogenous TCRβ constant region, and at least one of a first exogenous polynucleotide encoding a tgTCRα comprising fused full or partial TCRα constant region, and full or partial ectodomains of CD3ε and one of CD3δ and CD3γ (tgCD3(ε-δ/γ)-TRAC); and a second exogenous polynucleotide encoding a tgTCRβ comprising fused full or partial TCRβ constant region, and full or partial ectodomains of CD3ε and one of CD3δ and CD3γ (tgCD3(ε-γ/δ)-TRBC); wherein the ectodomains of CD3 subunits are present at the cell surface (cs-CD3) when expressed; when only said first exogenous polynucleotide is comprised in the cell, the cell further comprises a tgTRBC or tgTCRβ as provided herein; and when only said second exogenous polynucleotide is comprised in the cell, the cell further comprises a tgTRAC or tgTCRα as provided herein.

[000153] Design 5: CD3 chimeric chain (ccCD3)

[000154] As presented in FIG. 1B, in this Design 5, a cell surface presented CD3 (cs-CD3) is in a form of a CD3 chimeric chain (ccCD3), which is constructed to comprise a full or partial length of CD3ε ectodomain, a full or partial length of ectodomain of either CD3γ or CD3δ, and a full or partial length of endodomain of CD3ζ comprising at least one ITAM (immunoreceptor tyrosine-based activation motif). Cells comprising a polynucleotide encoding said CD3 chimeric chain may further comprise disruption at either or both of endogenous TCRα and TCRβ. When a genomic editing tool is used to generate TCR^{neg} cells by targeted editing of TRAC and/or TRBC, simultaneously with or subsequently to the TCR knockout, at least one polynucleotide encoding

said CD3 chimeric chain is introduced to the cell. In some embodiments, the said polynucleotide is introduced to TRAC or TRBC, and is respectively driven by an endogenous promoter of TCRα or TCRβ; whereas in some other embodiments, the introduced polynucleotide is driven by an exogenous promoter. In some embodiments, the exogenous promoter comprises a constitutive, inducible, temporal-, tissue-, or cell type- specific promoter. In some embodiments, the exogenous promoter comprises one of CMV, EF1α, PGK, CAG, and UBC. In one embodiment, the exogenous promoter comprises at least CAG.

[000155] In some embodiments, the CD3 chimeric chain comprises a full or partial length of CD3ε ectodomain, a full or partial length of ectodomain of CD3γ, and a full or partial length of endodomain of CD3ζ comprising at least one ITAM (tgCD3(ε-γ)-ζ), wherein the CD3 chimeric chain is a fusion protein with either ectodomain at the N-terminal, and wherein the two ectodomains form a heterodimer. In some embodiments, the CD3 chimeric chain comprises a full or partial length of CD3ε ectodomain, a full or partial length of ectodomain of CD3δ, and a full or partial length of endodomain of CD3ζ comprising at least one ITAM (tgCD3(ε-δ)-ζ), wherein the CD3 chimeric chain is a fusion protein with either ectodomain at N-terminal, and wherein the two ectodomains form a heterodimer. In some embodiments of the CD3 chimeric chain, the endodomain of CD3ζ comprises two ITAMs. In some embodiments of the CD3 chimeric chain, the endodomain of CD3ζ comprises all three ITAMs.

[000156] In some embodiments, the polynucleotide encoding a full or partial length of CD3ε ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 25. In some embodiments, the polynucleotide encoding a full or partial length of CD3δ ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 26. In some embodiments, the polynucleotide encoding a full or partial length of CD3γ ectodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 27. In some embodiments of a polynucleotide encoding a full or partial length of CD3ε, CD3δ, or CD3γ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide. In some embodiments, the signal peptide comprises one of SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 30, or any other signal peptide known in the art. In some embodiments of a polynucleotide encoding a full or partial length of CD3ε ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 28. In some embodiments of a

polynucleotide encoding a full or partial length of CD3δ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 29. In some embodiments of a polynucleotide encoding a full or partial length of CD3γ ectodomain, the polynucleotide further comprises nucleic acids encoding a signal peptide of SEQ ID NO. 30. In some embodiments, the polynucleotide encoding a full or partial length of CD3ζ endodomain comprises at least a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 35, which comprises CD3ζ ITAM1, ITAM2, and ITAM3 (SEQ ID NOs. 36-38). In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO. 35

MKWKALFTAAILQAQLPITEAQSFGLLDPKLCYLLDGILFIYGVILTALFLRVKFSRSAD**APAYQQGQNQL**
YNELNLGRREEYDVLDKRRGRDPEMGGK***PRRKNPQEGLYNELQKDKMAEAYSEIGM***KG***ERRRGKGHDGLYQ***
GLSTATKDTYDALHMQALPPR

(…ITAM1…*ITAM2*…*ITAM3*…)

SEQ ID NO. 36

APAYQQGQNQLYNELNLGRREEYDVLDKR

SEQ ID NO. 37

PRRKNPQEGLYNELQKDKMAEAYSEIGM

SEQ ID NO. 38

ERRRGKGHDGLYQGLSTATKDTYDALHMQ

[000157] In some embodiments of the CD3 chimeric chain, the endodomain of CD3ζ comprising at least one, two, or three ITAMs further comprises one or more signaling domains of 2B4, 4-1BB, CD16, CD2, CD28, CD28H, CD3ζ, DAP10, DAP12, DNAM1, FcERIγ IL21R, IL-2Rβ (IL-15Rβ), IL-2Rγ, IL-7R, KIR2DS2, NKG2D, NKp30, NKp44, NKp46, CD3ζ1XX, CS1, or CD8 for signal transduction and/or co-stimulation. In one embodiment of the CD3 chimeric chain, the endodomain of CD3ζ comprising at least one, two, or three ITAMs further comprises at least a signaling domain of CD28 (tgCD3(ε- γ/δ)-28ζ). In some embodiments of the CD3ζ endodomain comprising the signaling domain of CD28, the polynucleotide encoding a full or

partial length of 28ζ endodomain comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 39, from which any one or two CD3ζ ITAMs may be removed. In some embodiments of the CD3 chimeric chain, the endodomain of CD3ζ comprising at least one, two, or three ITAMs further comprises a signaling domain of 41BB (tgCD3(ε- γ/δ)-BBζ). In some embodiments of the CD3ζ endodomain comprising the signaling domain of 41BB, the polynucleotide encoding a full or partial length of BBζ endodomain comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 40, from which any one or two CD3ζ ITAMs may be removed. In some embodiments of the CD3 chimeric chain, the endodomain of CD3ζ comprising at least one, two, or three ITAMs further comprises a signaling domain of CD28 and a signaling domain of 41BB (tgCD3(ε- γ/δ)-(28-BB)ζ). In some embodiments of the CD3ζ endodomain comprising the signaling domain of both 28 and 41BB, the polynucleotide encoding a full or partial length of 28BBζ endodomain comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 41, from which any one or two CD3ζ ITAMs may be removed. In one embodiment of the polynucleotide encoding tgCD3(ε-γ)-(28/BB)ζ, the encoded polypeptide comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 42; from which any one or two CD3ζ ITAMs may be removed, from which the linker sequence may be replaced with any other linker sequence known in the art, or from which the CD28 signaling domain may be replaced with, or enhanced by adding, the 41BB signaling domain in yet some other embodiment. In one embodiment of tgCD3(ε-δ)-(28/BB)ζ, the encoded polypeptide comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to the exemplary sequence, SEQ ID NO. 43; from which any one or two CD3ζ ITAMs may be removed, from which the linker sequence may be replaced with any other linker sequence known in the art, or from which the CD28 signaling domain may be replaced by, or enhanced via further including, the 41BB signaling domain in yet some other embodiment. In some other embodiments of the encoded CD3 chimeric chain tgCD3(ε-γ)-(28/BB)ζ or tgCD3(ε-δ)-(28/BB)ζ, the polypeptide further comprises a signal peptide of SEQ ID NO. 28, or any other signal peptide known in the art. In embodiments, the sequence identity is at

least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO. 39

RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSAD**APAYQQGQNQLYNELNLGRRE**
EYDVLDKRRGRDPEMGGK***PRRKNPQEGLYNELQKDKMAEAYSEIGM***KG***ERRRGKGHDGLYQGLSTATKDTY***
DALHMQALPPR

(…**ITAM1**…***ITAM2***…***ITAM3***…**)**

SEQ ID NO. 40

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSAD**APAYQQGQNQLYNELNLGRR**
EEYDVLDKRRGRDPEMGGK***PRRKNPQEGLYNELQKDKMAEAYSEIGM***KG***ERRRGKGHDGLYQGLSTATKDT***
YDALHMQALPPR

(…**ITAM1**…***ITAM2***…***ITAM3***…**)**

SEQ ID NO. 41

RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC
RFPEEEEGGCELRVKFSRSAD**APAYQQGQNQLYNELNLGRREEYDVLDKR**RGRDPEMGGK***PRRKNPQEGLY***
NELQKDKMAEAYSEIGMKG***ERRRGKGHDGLYQGLSTATKDTYDALHMQ***ALPPR

(…**ITAM1**…***ITAM2***…***ITAM3***…**)**

SEQ ID NO. 42

DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQS
GYYVCYPRGSKPEDANFYLYLRARVGSADDAKKDAAKKDDAKKDDAKKDGS*QSIKGNHLVKVYDYQEDGSV*
*LLTCDAEAKNITWFKDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVYYRM*RAAA***IEVMYP***
PPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSD
YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSAD**APAYQQGQNQLYNELNLGRREEYDVLDKR**RGR
DPEMGGK*PRRKNPQEGLYNELQKDKMAEAYSEIGM*KG***ERRRGKGHDGLYQGLSTATKDTYDALHMQ***ALPPR

(CD3ε-linker-*CD3γ*-***CD28***-CD3ζ **(**…**ITAM1**…*ITAM2*…***ITAM3***…**))**

SEQ ID NO. 43

DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQS
GYYVCYPRGSKPEDANFYLYLRARVGSADDAKKDAAKKDDAKKDDAKKDGS*FKIPIEELEDRVFVNCNTSI*
*TWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRM*RAAA***IEVMYPPPYLDNEKSN***
GTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPG

PTRKHYQPYAPPRDFAAYRSRVKFSRSAD**APAYQQGQNQLYNELNLGRREEYDVLDKR**RGRDPEMGGK*PRR KNPQEGLYNELQKDKMAEAYSEIGMK*G***ERRRGKGHDGLYQGLSTATKDTYDALHMQ***ALPPR

(CD3ε-linker-*CD3δ*-***CD28***-CD3ζ (…**ITAM1**…*ITAM2*…***ITAM3***…))

[000158] In this application, it is discovered that a CD3 chimeric chain as provided herein, wherein the CD3 chimeric chain is a fusion protein comprising a full or partial length of CD3ε ectodomain, at least one of CD3δ and CD3γ full or partial length ectodomain, and a CD3ζ endodomain comprising at least one ITAM and optionally one or more signaling domain, is capable of presenting the chimeric CD3 ectodomain to cell surface when expressed in the cell that is TCR^{neg}. Further the cell surface expression of CD3 ectodomains enables CD3 binding triggered signaling transduction through fused CD3ζ endodomain while having no peptide-MHC binding potential.

[000159] As such, in view of Design 5, provided herein is a cell or a population thereof, wherein the cell is an iPSC, a clonal iPSC, a clonal iPS cell line cell, or a derivative cell obtained from differentiating the iPSC; and the cell comprises: a disruption of at least one of an endogenous TCRα constant region and an endogenous TCRβ constant region, and at least an exogenous polynucleotide encoding a CD3 chimeric chain fusion protein (ccCD3), wherein the fusion protein comprises a full or partial length of ectodomain of CD3ε, and a full or partial length ectodomain of either one of CD3δ and CD3γ, and a full or partial length of endodomain of CD3ζ having at least one ITAM and optionally one or more signaling domain, wherein the ectodomains of the CD3 chimeric chain are present at the cell surface (cs-CD3) when expressed.

[000160] The cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) in a TCR^{neg} cell (TCR^{neg} cs-CD3) as disclosed herein in the various designs of FIGS. 1A-C can function as a CD3 related cell surface triggering receptor for binding with molecules including, not limited to, CD3 specific antibodies or functional variants thereof, CARs, and/or engagers, which are further described below. As provided further, the said TCR^{neg} cs-CD3 cell, or a population thereof may further comprise one or more of: hnCD16 knock-in; a CAR; a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; B2M knockout or knockdown; CIITA knockout or knockdown; an introduced expression of HLA-G or non-cleavable HLA-G; CD38 knockout, and additional engineered modalities described herein. Further provided in this application is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having at least one phenotype as provided herein, including but not limited to, TCR^{neg} cs-CD3, CD16, CAR, CD38 negative, IL15 (fusion protein with receptor or truncated variants), $B2M^{-/-}$ $CIITA^{-/-}$, and $B2M^{-/-}$ $CIITA^{-/-}$ HLA-G, wherein the cell bank provides a platform for additional iPSC engineering and a renewable source for

manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

2. hnCD16 knock-in

[000161] CD16 has been identified as two isoforms, Fc receptors FcγRIIIa (CD16a; NM_000569.6) and FcγRIIIb (CD16b; NM_000570.4). CD16a is a transmembrane protein expressed by NK cells, which binds monomeric IgG attached to target cells to activate NK cells and facilitate antibody-dependent cell-mediated cytotoxicity (ADCC). CD16b is exclusively expressed by human neutrophils. "High affinity CD16," "non-cleavable CD16," or "high affinity non-cleavable CD16," as used herein, refers to various CD16 variants. The wildtype CD16 has low affinity and is subject to down regulation including ectodomain shedding, a proteolytic cleavage process that regulates the cells surface density of various cell surface molecules on leukocytes upon NK cell activation. F176V (also called F158V in some publications) is an exemplary CD16 polymorphic allele/variant having high affinity; whereas S197P variant is an example of genetically engineered non-cleavable version of CD16. An engineered CD16 variant comprising both F176V and S197P has high affinity and is non-cleavable, which was described in greater detail in WO2015/148926, and the complete disclosure of which is incorporated herein by reference. In addition, a chimeric CD16 receptor with the ectodomain of CD16 essentially replaced with at least a portion of CD64 ectodomain can also achieve the desired high affinity and non-cleavable features of a CD16 receptor capable of carrying out ADCC. In some embodiments, the replacement ectodomain of a chimeric CD16 comprises one or more of EC1, EC2, and EC3 exons of CD64 (UniPRotKB_P12314 or its isoform or polymorphic variant).

[000162] As such, a high-affinity non-cleavable CD16 receptor (hnCD16), in some embodiments, comprises both F176V and S197P; and in some embodiments, comprises F176V and with the cleavage region eliminated. In some other embodiments, a hnCD16 comprises a sequence having identity of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 100%, or any percentage in-between, when compared to any of the exemplary sequences, SEQ ID NOs. 7, 8 and 9, each comprises at least a portion of CD64 ectodomain. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%. SEQ ID NOs. 7, 8 and 9 are encoded respectively by exemplifying SEQ ID NOs. 10-12. As used herein and throughout the application, the percent identity between two sequences is a function of the number of identical positions shared by the sequences *(i.e.,* %

identity = # of identical positions/total # of positions x 100), taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm recognized in the art.

SEQ ID NO. 7:

MWFLTTLLLWVPVDGQVDTTKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTATQTSTPSYR
ITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPLALRCHAWKDKLVYNVLYYRNGK
AFKFFHWNSNLTILKTNISHNGTYHCSGMGKHRYTSAGISVTVKELFPAPVLNASVTSPLLEGNLVTLSCE
TKLLLQRPGLQLYFSFYMGSKTLRGRNTSSEYQILTARREDSGLYWCEAATEDGNVLKRSPELELQVLGLQ
LPTPVWFHYQ*VSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDWKDHKFKWRKDPQDK*
(340 a.a. CD64 domain-based construction; *CD16TM*; *CD16ICD*)

SEQ ID NO. 8

MWFLTTLLLWVPVDGQVDTTKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTATQTSTPSYR
ITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPLALRCHAWKDKLVYNVLYYRNGK
AFKFFHWNSNLTILKTNISHNGTYHCSGMGKHRYTSAGISVTVKELFPAPVLNASVTSPLLEGNLVTLSCE
TKLLLQRPGLQLYFSFYMGSKTLRGRNTSSEYQILTARREDSGLYWCEAATEDGNVLKRSPELELQVLGLF
FPPGYQ*VSFCLVMVLLFAVDTGLYFSVKTNIRSSTRDWKDHKFKWRKDPQDK*
(336 a.a. CD64 exon-based construction; *CD16TM*; *CD16ICD*)

SEQ ID NO. 9

MWFLTTLLLWVPVDGQVDTTKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNG
TATQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPL
ALRCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSGMGKHRYTSAG
ISVTVKELFPAPVLNASVTSPLLEGNLVTLSCETKLLLQRPGLQLYFSFYMGSKTLRGRN
TSSEYQILTARREDSGLYWCEAATEDGNVLKRSPELELQVLGFFPPGYQ*VSFCLVMVLLF*
AVDTGLYFSVKTNIRSSTRDWKDHKFKWRKDPQDK

(335 a.a. CD64 exon-based construction; *CD16TM*; *CD16ICD*)

SEQ ID NO. 10

cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa
gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag
gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg
tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt
gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata
cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa
ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt
tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg
aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac
acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca
tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg
ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg
cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg
ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg
gagcttcaag tgcttggcct ccagttacca actcctgtct ggtttcatta ccaagtctct
ttctgcttgg tgatggtact ccttttgca gtggacacag gactatattt ctctgtgaag
acaaacattc gaagctcaac aagagactgg aaggaccata aatttaaatg gagaaaggac
cctcaagaca aa

SEQ ID NO. 11

cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa
gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag
gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg
tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt
gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata
cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa
ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt
tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg
aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac
acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca
tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg
ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg
cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg
ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg
gagcttcaag tgcttggttt gttctttcca cctgggtacc aagtctcttt ctgcttggtg
atggtactcc tttttgcagt ggacacagga ctatatttct ctgtgaagac aaacattcga
agctcaacaa gagactggaa ggaccataaa tttaaatgga gaaaggaccc tcaagacaaa

SEQ ID NO. 12

atgtggttct tgacaactct gctcctttgg gttccagttg atgggcaagt ggacaccaca
aaggcagtga tcactttgca gcctccatgg gtcagcgtgt tccaagagga aaccgtaacc
ttgcactgtg aggtgctcca tctgcctggg agcagctcta cacagtggtt tctcaatggc
acagccactc agacctcgac ccccagctac agaatcacct ctgccagtgt caatgacagt
ggtgaataca ggtgccagag aggtctctca gggcgaagtg accccataca gctggaaatc
cacagaggct ggctactact gcaggtctcc agcagagtct tcacggaagg agaacctctg
gccttgaggt gtcatgcgtg gaaggataag ctggtgtaca atgtgcttta ctatcgaaat
ggcaaagcct ttaagttttt ccactggaac tctaacctca ccattctgaa aaccaacata
agtcacaatg gcacctacca ttgctcaggc atgggaaagc atcgctacac atcagcagga
atatctgtca ctgtgaaaga gctatttcca gctccagtgc tgaatgcatc tgtgacatcc
ccactcctgg aggggaatct ggtcaccctg agctgtgaaa caaagttgct cttgcagagg
cctggtttgc agctttactt ctccttctac atgggcagca agaccctgcg aggcaggaac
acatcctctg aataccaaat actaactgct agaagagaag actctgggtt atactggtgc
gaggctgcca cagaggatgg aaatgtcctt aagcgcagcc ctgagttgga gcttcaagtg
cttggcttct ttccacctgg gtaccaagtc tctttctgct tggtgatggt actccttttt
gcagtggaca caggactata tttctctgtg aagacaaaca ttcgaagctc aacaagagac
tggaaggacc ataaatttaa atggagaaag gaccctcaag acaaa

[000163] Accordingly, provided herein are clonal iPSCs genetically engineered to comprise, among other editing as contemplated and described herein, a high-affinity non-cleavable CD16 receptor (hnCD16), wherein the genetically engineered iPSCs are capable of differentiating into effector cells comprising the hnCD16 introduced to the iPSCs. In some embodiments, the derived effector cells comprising hnCD16 are NK cells. In some embodiments, the derived effector cells comprising hnCD16 are T cells. The exogenous hnCD16 expressed in iPSC or derivative cells therefrom has high affinity in binding to not only ADCC antibodies or fragments thereof, but also to bi-, tri-, or multi- specific engagers or binders that recognize the CD16 or

CD64 extracellular binding domains of said hnCD16 and variants thereof. The bi-, tri-, or multi-specific engagers or binders are further described below in this application (see section I.7). As such, at least one of the aspects of the present application provides a derivative effector cell or a cell population thereof preloaded with one or more pre-selected ADCC antibody through high-affinity binding with the extracellular domain of the hnCD16 expressed on the derivative effector cell, in an amount sufficient for therapeutic use in a treatment of a condition, a disease, or an infection as further detailed in section V. below, wherein said hnCD16 comprises an extracellular binding domain of CD64, or of CD16 having F176V and S197P.

[000164] In some other embodiments, the native CD16 transmembrane- and/or the intracellular- domain of a hnCD16 is further modified or replaced, such that a chimeric Fc receptor (CFcR) is produced to comprise a non-native transmembrane domain, a non-native stimulatory domain and/or a non-native signaling domain. The term "non-native" used herein means that the transmembrane, stimulatory or signaling domain are derived from a different receptor other than the receptor which provides the extracellular domain. In the illustration here, the CFcR based on CD16 or variants thereof does not have a transmembrane, stimulatory or signaling domain that is derived from CD16. In some embodiments, the exogenous hnCD16 based CFcR comprises a non-native transmembrane domain derived from CD3D, CD3E, CD3G, CD3ζ, CD4, CD8, CD8a, CD8b, CD27, CD28, CD40, CD84, CD166, 4-1BB, OX40, ICOS, ICAM-1, CTLA-4, PD-1, LAG-3, 2B4, BTLA, CD16, IL7, IL12, IL15, KIR2DL4, KIR2DS1, NKp30, NKp44, NKp46, NKG2C, NKG2D, T cell receptor polypeptide. In some embodiments, the exogenous hnCD16 based CFcR comprises a non-native stimulatory/inhibitory domain derived from CD27, CD28, 4-1BB, OX40, ICOS, PD-1, LAG-3, 2B4, BTLA, DAP10, DAP12, CTLA-4, or NKG2D polypeptide. In some embodiments, the exogenous hnCD16 based CFcR comprises a non-native signaling domain derived from CD3ζ, 2B4, DAP10, DAP12, DNAM1, CD137 (41BB), IL21, IL7, IL12, IL15, NKp30, NKp44, NKp46, NKG2C, or NKG2D polypeptide. In one embodiment of hnCD16, the provided chimeric receptor comprises a transmembrane domain and a signaling domain both derived from one of IL7, IL12, IL15, NKp30, NKp44, NKp46, NKG2C, and NKG2D polypeptide. One particular embodiment of the hnCD16 based chimeric Fc receptor comprises a transmembrane domain of NKG2D, a stimulatory domain of 2B4, and a signaling domain of CD3ζ; wherein the extracellular domain of the hnCD16 is derived from a full length or partial sequence of the extracellular domain of CD64 or CD16, wherein the extracellular domain of CD16 comprises F176V and S197P. Another embodiment of the hnCD16 based chimeric Fc receptor comprises a transmembrane domain and a signaling domain of CD3ζ; wherein the extracellular domain of the hnCD16 is derived from a

full length or partial sequence of the extracellular domain of CD64 or CD16, wherein the extracellular domain of CD16 comprises F176V and S197P.

[000165] The various embodiments of hnCD16 based chimeric Fc receptor as described above are capable of binding, with high affinity, to the Fc region of an antibody or fragment thereof; or to the Fc region of a bi-, tri-, or multi- specific engager or binder. Upon binding, the stimulatory and/or signaling domains of the chimeric receptor enable the activation and cytokine secretion of the effector cells, and the killing of the tumor cells targeted by the antibody, or said bi-, tri-, or multi- specific engager or binder having a tumor antigen binding component as well as the Fc region. Without being limited by theory, through the non-native transmembrane, stimulatory and/or signaling domains, or through an engager binding to the ectodomain, of the hnCD16 based chimeric Fc receptor, the CFcR could contribute to effector cells' killing ability while increasing the effector cells' proliferation and/or expansion potential,. The antibody and the engager can bring tumor cells expressing the antigen and the effector cells expressing the CFcR into a close proximity, which also contributes to the enhanced killing of the tumor cells. Exemplary tumor antigen for bi-, tri-, multi- specific engager or binders include, but are not limited to, B7H3, BCMA, CD10, CD19, CD20, CD22, CD24, CD30, CD33, CD34, CD38, CD44, CD79a, CD79b, CD123, CD138, CD179b, CEA, CLEC12A, CS-1, DLL3, EGFR, EGFRvIII, EPCAM, FLT-3, FOLR1, FOLR3, GD2, gpA33, HER2, HM1.24, LGR5, MSLN, MCSP, MICA/B, PSMA, PAMA, P-cadherin, and ROR1. Some non-limiting exemplary bi-, tri-, multi- specific engager or binders suitable for engaging effector cells expressing the hnCD16 based CFcR in attacking tumor cells include CD16 (or CD64)-CD30, CD16 (or CD64)-BCMA, CD16 (or CD64)-IL15-EPCAM, and CD16 (or CD64)-IL15-CD33.

[000166] Unlike the endogenous CD16 receptor expressed by primary NK cells which gets cleaved from the cellular surface following NK cell activation, the various non-cleavable versions of CD16 in derivative NK avoids CD16 shedding and maintains constant expression. In derivative NK cell, non-cleavable CD16 increases expression of TNFα and CD107a indicative of improved cell functionality. Non-cleavable CD16 also enhances the antibody-dependent cell-mediated cytotoxicity (ADCC), and the engagement of bi-, tri-, or multi- specific engagers. ADCC is a mechanism of NK cell mediated lysis through the binding of CD16 to antibody-coated target cells. The additional high affinity characteristics of the introduced hnCD16 in derived NK cell also enables *in vitro* loading of ADCC antibody to the NK cell through hnCD16 before administering the cell to a subject in need of a cell therapy. As provided, the hnCD16 may comprise F176V and S197P in some embodiments, or may comprise a full or partial ectodomain originated from CD64 as exemplified by SEQ ID NO: 7, 8 or 9, or may further comprises at least

one of non-native transmembrane domain, stimulatory domain and signaling domain. As disclosed, the present application also provides a derivative NK cell or a cell population thereof, preloaded with one or more pre-selected ADCC antibody in an amount sufficient for therapeutic use in a treatment of a condition, a disease, or an infection as further detailed in section V. below.

[000167] Unlike primary NK cells, mature T cells from a primary source (i.e., natural/native sources such as peripheral blood, umbilical cord blood, or other donor tissues) do not express CD16. It was unexpected that iPSC comprising an expressed exogenous non-cleavable CD16 did not impair the T cell developmental biology and was able to differentiate into functional derivative T cells that not only express the exogenous CD16, but also are capable of carrying out function through an acquired ADCC mechanism. This acquired ADCC in the derivative T cell can additionally be used as an approach for dual targeting and/or to rescue antigen escape often occurred with CAR-T cell therapy, where the tumor relapses with reduced or lost CAR-T targeted antigen expression or expression of a mutated antigen to avoid recognition by the CAR (chimerical antigen receptor). When said derivative T cell comprises acquired ADCC through exogenous CD16 expression, and when an antibody targets a different tumor antigen from the one targeted by the CAR, the antibody can be used to rescue CAR-T antigen escape and reduce or prevent relapse or recurrence of the targeted tumor often seen in CAR-T treatment. Such a strategy to reduce and/or prevent antigen escape while achieving dual targeting is equally applicable to NK cells expressing one or more CARs. The various CARs that can be used in this antigen escape reduction and prevention strategy is further delineated below.

[000168] As such, the present invention provides a derivative T cell comprising an exogenous CD16. In some embodiments, the hnCD16 comprised in the derivative T cell comprises F176V and S197P. In some other embodiments, the hnCD16 comprised in the derivative T cell comprises a full or partial ectodomain originated from CD64 as exemplified by SEQ ID NO: 7, 8 or 9; or may further comprises at least one of non-native transmembrane domain, stimulatory domain and signaling domain. As explained, such derivative T cells have an acquired mechanism to target tumors with a monoclonal antibody meditated by ADCC to enhance the therapeutic effect of the antibody. As disclosed, the present application also provides a derivative T cell, or a cell population thereof, preloaded with one or more pre-selected ADCC antibody in an amount sufficient for therapeutic use in a treatment of a condition, a disease, or an infection as further detailed in section V. below.

[000169] Additionally provided in this application is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having at least one phenotype as provided herein, including but not limited to, CD16, wherein the cell bank provides a platform for

additional iPSC engineering and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, including but not limited to derivative NK and T cells, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

3. CAR expression

[000170] Applicable to the genetically engineered iPSC and derivative effector cell thereof may be any CAR design known in the art. CAR, a chimerical antigen receptor, is a fusion protein generally including an ectodomain that comprises an antigen recognition region, a transmembrane domain, and an endo-domain. In some embodiments, the ectodomain can further include a signal peptide or leader sequence and/or a spacer. In some embodiments, the endo-domain can further comprise a signaling peptide that activates the effector cell expressing the CAR. In some embodiments, the antigen recognition domain can specifically bind an antigen. In some embodiments, the antigen recognition domain can specifically bind an antigen associated with a disease or pathogen. In some embodiments, the disease-associated antigen is a tumor antigen, wherein the tumor may be a liquid or a solid tumor. In some embodiments, the CAR is suitable to activate either T or NK cells expressing said CAR. In some embodiments, the CAR is NK cell specific for comprising NK-specific signaling components. In certain embodiments, said T cells are derived from a CAR expressing iPSCs, and the derivative T cells may comprise T helper cells, cytotoxic T cells, memory T cells, regulatory T cells, natural killer T cells, αβ T cells, γδ T cells, or a combination thereof. In certain embodiments, said NK cells are derived from a CAR expressing iPSCs.

[000171] In certain embodiments, said antigen recognition region comprises a murine antibody, a human antibody, a humanized antibody, a camel Ig, a shark heavy-chain-only antibody (VNAR), Ig NAR, a chimeric antibody, a recombinant antibody, or antibody fragment thereof. Non-limiting examples of antibody fragment include Fab, Fab′, F(ab)′2, F(ab)′3, Fv, single chain antigen binding fragment (scFv), $(scFv)_2$, disulfide stabilized Fv (dsFv), minibody, diabody, triabody, tetrabody, single-domain antigen binding fragments (sdAb, Nanobody), recombinant heavy-chain-only antibody (VHH), and other antibody fragments that maintain the binding specificity of the whole antibody. Non-limiting examples of antigen that may be targeted by a CAR include ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CD269 (BCMA), CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell (e.g., a cell surface antigen), epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40),

epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb-B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and various pathogen antigen known in the art. Non-limiting examples of pathogen includes virus, bacteria, fungi, parasite and protozoa capable of causing diseases.

[000172] In some embodiments, the transmembrane domain of a CAR comprises a full length or at least a portion of the native or modified transmembrane region of CD3D, CD3E, CD3G, CD3ζ, CD4, CD8, CD8a, CD8b, CD27, CD28, CD40, CD84, CD166, 4-1BB, OX40, ICOS, ICAM-1, CTLA-4, PD-1, LAG-3, 2B4, BTLA, CD16, IL7, IL12, IL15, KIR2DL4, KIR2DS1, NKp30, NKp44, NKp46, NKG2C, NKG2D, T cell receptor polypeptide.

[000173] In some embodiments, the signaling peptide of the endo-domain (or intracellular domain) comprises a full length or at least a portion of a polypeptide of CD3ζ, 2B4, DAP10, DAP12, DNAM1, CD137 (41BB), IL21, IL7, IL12, IL15, NKp30, NKp44, NKp46, NKG2C, or NKG2D. In one embodiment, the signaling peptide of a CAR comprises an amino acid sequence that is at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% identity to at least one ITAM (immunoreceptor tyrosine-based activation motif) of CD3ζ.

[000174] In certain embodiments, said endo-domain further comprises at least one costimulatory signaling region. Said costimulatory signaling region can comprise a full length or at least a portion of a polypeptide of CD27, CD28, 4-1BB, OX40, ICOS, PD-1, LAG-3, 2B4, BTLA, DAP10, DAP12, CTLA-4, or NKG2D, or any combination thereof.

[000175] In one embodiment, the CAR applicable to the cells provided in this application comprises a co-stimulatory domain derived from CD28, and a signaling domain comprising the native or modified ITAM1 of CD3ζ, represented by an amino acid sequence of at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% identity to SEQ ID NO: 13. In a further embodiment, the CAR comprising a co-stimulatory domain derived from CD28, and a native or modified ITAM1 of CD3ζ also comprises a hinge domain and trans-

membrane domain derived from CD28, wherein an scFv may be connected to the trans-membrane domain through the hinge, and the CAR comprises an amino acid sequence of at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% identity to SEQ ID NO: 14. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO: 13

RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQ
LYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSEIGMKGE
RRRGKGHDGLFQGLSTATKDTFDALHMQALPPR

(153 a.a. CD28 co-stim + CD3ζITAM)

SEQ ID NO: 14

*IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP*FWVLVVVGGVLACYSLLVTVA
FIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAY
QQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLFNELQKDKMAEAFSE
IGMKGERRRGKGHDGLFQGLSTATKDTFDALHMQALPPR

(219 a.a. CD28 *hinge* + CD28 TM + CD28 co-stim + CD3ζITAM)

[000176] In another embodiment, the CAR applicable to the cells provided in this application comprises a transmembrane domain derived from NKG2D, a co-stimulatory domain derived from 2B4, and a signaling domain comprising the native or modified CD3ζ, represented by an amino acid sequence of at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% identity to SEQ ID NO: 15. Said CAR comprising a transmembrane domain derived from NKG2D, a co-stimulatory domain derived from 2B4, and a signaling domain comprising the native or modified CD3ζ may further comprise a CD8 hinge, wherein the amino acid sequence of such a structure is of at least about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, or about 99% identity to SEQ ID NO: 16. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO: 15

SNLFVASWIAVMIIFRIGMAVAIFCCFFFPSWRRKRKEKQSETSPKEFLTIYEDVKDLKT
RRNHEQEQTFPGGGSTIYSMIQSQSSAPTSQEPAYTLYSLIQPSRKSGSRKRNHSPSFNS
TIYEVIGKSQPKAQNPARLSRKELENFDVYSRVKFSRSADAPAYKQGQNQLYNELNLGRR
EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL
YQGLSTATKDTYDALHMQALPPR

(263 a.a NKG2D TM + 2B4 + CD3ζ)

SEQ ID NO: 16

*TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD*SNLFVASWIAVMIIF
RIGMAVAIFCCFFFPSWRRKRKEKQSETSPKEFLTIYEDVKDLKTRRNHEQEQTFPGGGS

TIYSMIQSQSSAPTSQEPAYTLYSLIQPSRKSGSRKRNHSPSFNSTIYEVIGKSQPKAQN
PARLSRKELENFDVYSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE
MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL
HMQALPPR

(308 a.a CD8 *hinge* + NKG2D TM + 2B4 + CD3ζ)

[000177] Non-limiting CAR strategies further include heterodimeric, conditionally activated CAR through dimerization of a pair of intracellular domain (see for example, U.S. Pat. No. 9587020); split CAR, where homologous recombination of antigen binding, hinge, and endo-domains to generate a CAR (see for example, U.S. Pub. No. 20170183407); multi-chain CAR that allows non-covalent link between two transmembrane domains connected to an antigen binding domain and a signaling domain, respectively (see for example, U.S. Pub. No. 20140134142); CARs having bispecific antigen binding domain (see for example, U.S. Pat. No. 9447194), or having a pair of antigen binding domains recognizing same or different antigens or epitopes (see for example, U.S. Pat No. 8409577), or a tandem CAR (see for example, Hegde et al., *J Clin Invest.* 2016;126(8):3036-3052); inducible CAR (see for example, U.S. Pub. Nos. 20160046700, 20160058857, 20170166877); switchable CAR (see for example, U.S. Pub. No: 20140219975); and any other designs known in the art.

[000178] Provided herein therefore include derivative cells obtained from differentiating genomically engineered iPSCs, wherein both the iPSCs and the derivative cells comprise one or more CARs along with additional modified modalities, including, but not limited to, TCR^{neg} cs-CD3, and/or hnCD16. Additionally provided in this application is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having at least one phenotype as provided herein, including but not limited to, CAR and one or both of TCR^{neg} cs-CD3 and hnCD16, wherein the cell bank provides a platform for additional iPSC engineering and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner. In one particular embodiment, the iPSC and its derivative cells comprises TCR^{neg} cs-CD3, hnCD16, and a CAR targeting a selected tumor or viral antigen, wherein the derivative cells are NK or T cells, and wherein the derivative cells may be used with, through hnCD16 binding, one or more ADCC antibodies or a bi-, tri- or multi-specific engager that target a tumor antigen different from the one targeted by CAR to avoid or to reduce tumor antigen escape while achieving dual targeting of the same tumor.

[000179] In a further embodiment, the iPSC and its derivative T cells comprising a CAR have the CAR inserted in a TCR constant region, leading to TCR knockout, and placing CAR expression under the control of the endogenous TCR promoter. Additional insertion sites include but are not limited to AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M,

TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT. In some embodiments, derivative TCR negative CAR-T cell derived from engineered iPSCs further comprise hnCD16 having an ectodomain native to CD16 (F176V and/or S197P) or derived from CD64, and native or non-native transmembrane, stimulatory and signaling domains. In another embodiment, the iPSC and its derivative NK cells comprising a CAR have the CAR inserted in the NKG2A locus or NKG2D locus, leading to NKG2A or NKG2D knock out, and placing CAR expression under the control of the endogenous NKG2A or NKG2D promoter. Additionally provided is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having at least one phenotype as provided herein, including but not limited to, CAR, wherein the cell bank provides a platform for additional iPSC engineering and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

4. Exogenously introduced cytokine and/or cytokine signaling

[000180] By avoiding systemic high-dose administration of clinically relevant cytokines, the risk of dose-limiting toxicities due to such a practice is reduced while cytokine mediated cell autonomy being established. To achieve lymphocyte autonomy without the need to additionally administer soluble cytokines, a partial or full length peptide of one or more of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, IL21, and/or their respective receptor is introduced to the cell to enable cytokine signaling with or without the expression of the cytokine itself, thereby maintaining or improving cell growth, proliferation, expansion, and/or effector function with reduced risk of cytokine toxicities. In some embodiments, the introduced cytokine and/or its respective native or modified receptor for cytokine signaling are expressed on the cell surface. In some embodiments, the cytokine signaling is constitutively activated. In some embodiments, the activation of the cytokine signaling is inducible. In some embodiments, the activation of the cytokine signaling is transient and/or temporal.

[000181] FIG. 2 presents several construct designs using IL15 as an illustrative example. The transmembrane (TM) domain of any of the designs in FIG. 2 can be native to the IL15 receptor or may be modified or replaced with transmembrane domain of any other membrane bound proteins.

[000182] FIG. 2 Design 1: IL15 and IL15Rα are co-expressed by using a self-cleaving peptide, mimicking trans-presentation of IL15, without eliminating cis-presentation of IL15.

[000183] FIG. 2 Design 2: IL15Rα is fused to IL15 at the C-terminus through a linker, mimicking trans-presentation without eliminating cis-presentation of IL15 as well as ensuring IL15 membrane-bound.

[000184] FIG. 2 Design 3: IL15Rα with truncated intracellular domain is fused to IL15 at the C-terminus through a linker, mimicking trans-presentation of IL15, maintaining IL15 membrane-bound, and additionally eliminating cis-presentation and/or any other potential signal transduction pathways mediated by a normal IL15R through its intracellular domain. The intracellular domain of IL15Rα has been deemed as critical for the receptor to express in the IL15 responding cells, and for the responding cells to expand and function. Such a truncated construct comprises an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NO: 17, which may be encoded by an exemplary nucleic acid sequence represented by SEQ ID NO:18. In one embodiment of the truncated IL15/IL15Rα, the construct does not comprise the last 4 amino acid "KSRQ" of SEQ ID NO:17, and comprises an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NO: 21. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO: 17

MDWTWILFLVAAATRVHSGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDA
TLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITC
PPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKC
IRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGSQLM
PSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTV
LLCGLSAVSLLACYLKSRQ

(379 a.a.; signal and linker peptides are underlined)

SEQ ID NO:18

ATGGACTGGACCTGGATTCTGTTCCTGGTCGCGGCTGCAACGCGAGTCCATAGCGGTATC
CATGTTTTTATTCTTGGGTGTTTTTCTGCTGGGCTGCCTAAGACCGAGGCCAACTGGGTA
AATGTCATCAGTGACCTCAAGAAAATAGAAGACCTTATACAAAGCATGCACATTGATGCT
ACTCTCTACACTGAGTCAGATGTACATCCCTCATGCAAAGTGACGGCCATGAAATGTTTC
CTCCTCGAACTTCAAGTCATATCTCTGGAAAGTGGCGACGCGTCCATCCACGACACGGTC
GAAAACCTGATAATACTCGCTAATAATAGTCTCTCTTCAAATGGTAACGTAACCGAGTCA
GGTTGCAAAGAGTGCGAAGAGTTGGAAGAAAAAAACATAAAGGAGTTCCTGCAAAGTTTC
GTGCACATTGTGCAGATGTTCATTAATACCTCTAGCGGCGGAGGATCAGGTGGCGGTGGA
AGCGGAGGTGGAGGCTCCGGTGGAGGAGGTAGTGGCGGAGGTTCTCTTCAAATAACTTGT
CCTCCACCGATGTCCGTAGAACATGCGGATATTTGGGTAAAATCCTATAGCTTGTACAGC
CGAGAGCGGTATATCTGCAACAGCGGCTTCAAGCGGAAGGCCGGCACAAGCAGCCTGACC
GAGTGCGTGCTGAACAAGGCCACCAACGTGGCCCACTGGACCACCCCTAGCCTGAAGTGC
ATCAGAGATCCCGCCCTGGTGCATCAGCGGCCTGCCCCTCCAAGCACAGTGACAACAGCT
GGCGTGACCCCCCAGCCTGAGAGCCTGAGCCCTTCTGGAAAAGAGCCTGCCGCCAGCAGC

CCCAGCAGCAACAATACTGCCGCCACCACAGCCGCCATCGTGCCTGGATCTCAGCTGATG
CCCAGCAAGAGCCCTAGCACCGGCACCACCGAGATCAGCAGCCACGAGTCTAGCCACGGC
ACCCCATCTCAGACCACCGCCAAGAACTGGGAGCTGACAGCCAGCGCCTCTCACCAGCCT
CCAGGCGTGTACCCTCAGGGCCACAGCGATACCACAGTGGCCATCAGCACCTCCACCGTG
CTGCTGTGTGGACTGAGCGCCGTGTCACTGCTGGCCTGCTACCTGAAGTCCAGACAGTGA

(1140 n.a.)

SEQ ID NO: 21

MDWTWILFLVAAATRVHSGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDA
TLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITC
PPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKC
IRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGSQLM
PSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTV
LLCGLSAVSLLACYL

(375 a.a.; signal and linker peptides are underlined)

[000185] One having ordinary skill in the art would appreciate that the signal peptide and the linker sequences above are illustrative and in no way limit their variations suitable for use as a signal peptide or linker. There are many suitable signal peptide or linker sequences known and available to those in the art. The ordinary skilled in the art understands that the signal peptide and/or linker sequences may be substituted for another sequence without altering the activity of the functional peptide led by the signal peptide or linked by the linker.

[000186] FIG. 2 Design 4: Since Design 3 construct was shown to be functional in promoting effector cell survival and expansion, demonstrating that the cytoplasmic domain of IL15Rα can be omitted without negatively impacting the autonomous feature of the effector cell equipped with IL15 in such a design, Design 4 is a construct providing another working alternative of Design 3, from which essentially the entire IL15Rα is removed except for the Sushi domain fused with IL15 at one end and a transmembrane domain on the other (mb-Sushi), optionally with a linker between the Sushi domain and the trans-membrane domain. The fused IL15/mb-Sushi is expressed at cell surface through the transmembrane domain of any membrane bound protein. With a construct such as Design 4, unnecessary signaling through IL15Rα, including cis-presentation, is eliminated when only the desirable trans-presentation of IL15 is retained. In some embodiments, the component comprising IL15 fused with Sushi domain comprises an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NO: 19, which may be encoded by an exemplary nucleic acid sequence represented by SEQ ID NO: 20. In embodiments, the sequence identity is at least 80%. In embodiments, the sequence identity is at least 90%. In embodiments, the sequence identity is at least 95%. In embodiments, the sequence identity is 100%.

SEQ ID NO: 19

MDWTWILFLVAAATRVHSGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDA
TLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITC
PPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKC
IR

(242 a.a.; signal and linker peptides are underlined)

SEQ ID NO: 20

ATGGACTGGACCTGGATTCTGTTCCTGGTCGCGGCTGCAACGCGAGTCCATAGCGGTATC
CATGTTTTTATTCTTGGGTGTTTTTCTGCTGGGCTGCCTAAGACCGAGGCCAACTGGGTA
AATGTCATCAGTGACCTCAAGAAAATAGAAGACCTTATACAAAGCATGCACATTGATGCT
ACTCTCTACACTGAGTCAGATGTACATCCCTCATGCAAAGTGACGGCCATGAAATGTTTC
CTCCTCGAACTTCAAGTCATATCTCTGGAAAGTGGCGACGCGTCCATCCACGACACGGTC
GAAAACCTGATAATACTCGCTAATAATAGTCTCTCTTCAAATGGTAACGTAACCGAGTCA
GGTTGCAAAGAGTGCGAAGAGTTGGAAGAAAAAAACATAAAGGAGTTCCTGCAAAGTTTC
GTGCACATTGTGCAGATGTTCATTAATACCTCTAGCGGCGGAGGATCAGGTGGCGGTGGA
AGCGGAGGTGGAGGCTCCGGTGGAGGAGGTAGTGGCGGAGGTTCTCTTCAAATAACTTGT
CCTCCACCGATGTCCGTAGAACATGCGGATATTTGGGTAAAATCCTATAGCTTGTACAGC
CGAGAGCGGTATATCTGCAACAGCGGCTTCAAGCGGAAGGCCGGCACAAGCAGCCTGACC
GAGTGCGTGCTGAACAAGGCCACCAACGTGGCCCACTGGACCACCCCTAGCCTGAAGTGC
ATCAGA

(726 n.a.)

[000187] One having ordinary skill in the art would appreciate that the signal peptide and the linker sequences above are illustrative and in no way limit their variations suitable for use as a signal peptide or linker. There are many suitable signal peptide or linker sequences known and available to those in the art. The ordinary skilled in the art understands that the signal peptide and/or linker sequences may be substituted for another sequence without altering the activity of the functional peptide led by the signal peptide or linked by the linker.

[000188] FIG. 2 Design 5: A native or modified IL15Rβ is fused to IL15 at the C-terminus through a linker, enabling constitutive signaling and maintaining IL15 membrane-bound and trans-representation.

[000189] FIG. 2 Design 6: A native or modified common receptor γC is fused to IL15 at the C-terminus through a linker for constitutive signaling and membrane bound trans-presentation of the cytokine. The common receptor γC is also called the common gamma chain or CD132, also known as IL2 receptor subunit gamma or IL2RG. γC is a cytokine receptor sub-unit that is common to the receptor complexes for many interleukin receptors, including, but not limited to, IL2, IL4, IL7, IL9, IL15 and IL21 receptor.

[000190] FIG. 2 Design 7: Engineered IL15Rβ that forms homodimer in absence of IL15 is useful for producing constitutive signaling of the cytokine.

[000191] In some embodiments, one or more of cytokine IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18 and IL21, and/or receptors thereof, may be introduced to iPSC using one or more of the designs in FIG. 2, and to its derivative cells upon iPSC differentiation. In some embodiments, IL2 or IL15 cell surface expression and signaling is through the construct illustrated in any one of Designs 1-7. In some embodiments, IL4, IL7, IL9, or IL21 cell surface expression and signaling is through the construct illustrated in Design 5, 6, or 7, by using either a common receptor or a cytokine specific receptor. In some embodiments, IL7 surface expression and signaling is through the construct illustrated in Design 5, 6, or 7, by using either a common receptor or a cytokine specific receptor, such as an IL4 receptor. The transmembrane (TM) domain of any of the designs in FIG. 2 can be native to respective cytokine receptor or may be modified or replaced with transmembrane domain of any other membrane bound proteins.

[000192] In addition to an induced pluripotent cell (iPSC), a clonal iPSC, a clonal iPS cell line cell, or iPSC derived cells, comprising at least one engineered modality as disclosed herein, also provided is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having at least an exogenously introduced cytokine and/or cytokine receptor signaling as described in this section, wherein the cell bank provides a platform for additional iPSC engineering and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner. In iPSCs and derivative cells therefrom comprising both CAR and exogenous cytokine and/or cytokine receptor signaling, the CAR and IL may be expressed in separate construct, or may be co-expressed in a bi-cistronic construct comprising both CAR and IL. In some further embodiments, IL15 in a form represented by any of the construct designs in FIG. 2 can be linked to either the 5' or the 3' end of a CAR expression construct through a self-cleaving 2A coding sequence, illustrated as, for example, CAR-2A-IL15 or IL15-2A-CAR. As such, the IL15 and CAR are in a single open reading frame (ORF). In one embodiment, the CAR-2A-IL15 or IL15-2A-CAR construct comprises IL15 in Design 3 of FIG. 2. In another embodiment, the CAR-2A-IL15 or IL15-2A-CAR construct comprises IL15 in Design 3 of FIG. 2. In yet another embodiment, the CAR-2A-IL15 or IL15-2A-CAR construct comprises IL15 in Design 7 of FIG. 2. When CAR-2A-IL15 or IL15-2A-CAR is expressed, the self-cleaving 2A peptide allows the expressed CAR and IL15 dissociate, and the dissociated IL15 can then be presented at cell surface. The CAR-2A-IL15 or IL15-2A-CAR bi-cistronic design allows a coordinated CAR and IL15 expression both in timing and quantity, and under the same control mechanism that may be chosen to incorporate, for example, an inducible promoter for the expression of the single ORF. Self-cleaving peptides are found in members of the Picornaviridae

virus family, including aphthoviruses such as foot-and-mouth disease virus (FMDV), equine rhinitis A virus (ERAV), Thosea asigna virus (TaV) and porcine tescho virus- 1 (PTV-I) (Donnelly, ML, et al, J. Gen. Virol, 82, 1027-101 (2001); Ryan, MD, et al., J. Gen. Virol., 72, 2727-2732 (2001)), and cardioviruses such as Theilovirus (e.g., Theiler's murine encephalomyelitis) and encephalomyocarditis viruses. The 2 A peptides derived from FMDV, ERAV, PTV-I, and TaV are sometimes also referred to as "F2A", "E2A", "P2A", and "T2A", respectively.

[000193] The bi-cistronic CAR-2A-IL15 or IL15-2A-CAR embodiment as disclosed herein for IL15 is also contemplated for expression of any other cytokine provided herein, for example, IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL18, and IL21. In some embodiments, IL2 cell surface expression and signaling is through the construct illustrated in any of the Designs 1-7. In some other embodiments, IL4, IL7, IL9, or IL21 cell surface expression and signaling is through the construct illustrated in Design 5, 6, or 7, either using a common receptor and/or a cytokine specific receptor.

[000194] In iPSCs and derivative cells therefrom comprising both CAR and exogenous cytokine and/or cytokine receptor signaling, including but not limited to IL15, the iPSCs and derivative cells may further comprise TCR^{neg} cs-CD3, and/or CD16.

5. HLA-I- and HLA-II- deficiency

[000195] Multiple HLA class I and class II proteins must be matched for histocompatibility in allogeneic recipients to avoid allogeneic rejection problems. Provided herein is an iPSC cell line and its derivative cells differentiated therefrom with eliminated or substantially reduced expression of both HLA class I and HLA class II proteins. HLA class I deficiency can be achieved by functional deletion of any region of the HLA class I locus (chromosome 6p21), or deletion or reducing the expression level of HLA class-I associated genes including, but not limited to, beta-2 microglobulin (B2M) gene, TAP 1 gene, TAP 2 gene and Tapasin. For example, the B2M gene encodes a common subunit essential for cell surface expression of all HLA class I heterodimers. B2M negative cells are HLA-I deficient. HLA class II deficiency can be achieved by functional deletion or reduction of HLA-II associated genes including, but not limited to, RFXANK, CIITA, RFX5 and RFXAP. CIITA is a transcriptional coactivator, functioning through activation of the transcription factor RFX5 required for class II protein expression. CIITA negative cells are HLA-II deficient. Provided herein is an iPSC line and its derivative cells with both HLA-I and HLA-II deficiency, for example for lacking both B2M and CIITA expression, wherein the obtained derivative effector cells enable allogeneic cell therapies

by eliminating the need for MHC (major histocompatibility complex) matching, and avoid recognition and killing by host (allogeneic) T cells.

[000196] For some cell types, a lack of class I expression leads to lysis by NK cells. To overcome this "missing self" response, HLA-G may be optionally knocked in to avoid NK cell recognition and killing of the HLA-I deficient effector cells derived from an engineered iPSC. In one embodiment, the HLA-I deficient iPSC and its derivative cells further comprise HLA-G knock-in. In some embodiments, the provided HLA-I deficient iPSC and its derivative cells further comprise one or both of CD58 knockout and CD54 knockout. CD58 (or LFA-3) and CD54 (or ICAM-1) are adhesion proteins initiating signal-dependent cell interactions, and facilitating cell, including immune cell, migration. It was shown that CD58 knockout has a higher efficiency in reducing allogeneic NK cell activation than CD54 knockout; while double knockout of both CD58 and CD54 has the most enhanced reduction of NK cell activation. In some observation, the CD58 and CD54 double knockout is even more effective than HLA-G overexpression for HLA-I deficient cells in overcoming "missing-self" effect. As provided herein is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having TCR^{neg} cs-CD3, HLA-I and HLA-II deficiency, and one or more of hnCD16, CAR and IL, without adversely impacting the differentiation potential of the iPSC and function of the derived effector cells including derivative T and NK cells. As provided above, in some embodiments, the HLA-I and HLA-II deficient iPSC and its derivative cells have an exogenous polynucleotide encoding HLA-G. In some embodiments, the HLA-I and HLA-II deficient iPSC and its derivative cells are CD58 null. In some other embodiments, the HLA-I and HLA-II deficient iPSC and its derivative cells are CD54 null. In yet some other embodiments, the HLA-I and HLA-II deficient iPSC and its derivative cells are CD58 null and CD54 null. Said cell bank provides a platform for additional iPSC engineering, and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

6. CD38 knockout

[000197] Cell surface molecule CD38 is highly upregulated in multiple hematologic malignancies derived from both lymphoid and myeloid lineages, including multiple myeloma and a CD20 negative B-cell malignancy, which makes it an attractive target for antibody therapeutics to deplete cancer cell. Antibody mediated cancer cell depletion is usually attributable to a combination of direct cell apoptosis induction and activation of immune effector mechanisms such as ADCC (antibody-dependent cell-mediated cytotoxicity). In addition to ADCC, the

immune effector mechanisms in concert with the therapeutic antibody may also include phagocytosis (ADCP) and/or complement-dependent cytotoxicity (CDC).

[000198] Other than being highly expressed on malignant cells, CD38 is also expressed on plasma cells as well as on NK cells, and activated T and B cells. During hematopoiesis, CD38 is expressed on $CD34^+$ stem cells and lineage-committed progenitors of lymphoid, erythroid, and myeloid, and during the final stages of maturation which continues through the plasma cell stage. As a type II transmembrane glycoprotein, CD38 carries out cell functions as both a receptor and a multifunctional enzyme involved in the production of nucleotide-metabolites. As an enzyme, CD38 catalyzes the synthesis and hydrolysis of the reaction from NAD^+ to ADP-ribose, thereby producing secondary messengers CADPR and NAADP which stimulate release of calcium from the endoplasmic reticulum and lysosomes, critical for the process of cell adhesion which process is calcium dependent. As a receptor, CD38 recognizes CD31 and regulates cytokine release and cytotoxicity in activated NK cells. CD38 is also reported to associate with cell surface proteins in lipid rafts, to regulate cytoplasmic Ca^{2+} flux, and to mediate signal transduction in lymphoid and myeloid cells.

[000199] In malignancy treatment, systemic use of CD38 antigen binding receptor transduced T cells have been shown to lyse the CD38+ fractions of CD34+ hematopoietic progenitor cells, monocytes, NK cells, T cells and B cells, leading to incomplete treatment responses and reduced or eliminated efficacy because of the impaired recipient immune effector cell function. In addition, in multiple myeloma patients treated with daratumumab, a CD38 specific antibody, NK cell reduction in both bone marrow and peripheral blood was observed, although other immune cell types, such as T cells and B cells, were unaffected despite their CD38 expression (Casneuf et al., Blood Advances. 2017; 1(23):2105-2114). Without being limited by theories, the present application provides a strategy to leverage the full potential of CD38 targeted cancer treatment by overcoming CD38 specific antibody and/or CD38 antigen binding domain induced effector cell depletion or reduction through fratricide. In addition, since CD38 is upregulated on activated lymphocytes such as T or B cells, by suppressing activation of these recipient lymphocytes using CD38 specific antibody such as daratumumab in the recipient of allogeneic effector cells, the allorejection against these effector cells would be reduced and/or prevented and thereby increasing effector cell survival and persistency. As such, the present application also provides a strategy to enhance effector cell persistency and/or survival through reducing or preventing allorejection by using CD38 specific antibody, a secreted CD38 specific engager or a CD38 CAR (chimeric antigen receptor) against activation of recipient T and B cells, i.e., lymphodepletion of activated T and B cells, often prior to adoptive cell transferring. Specifically, the strategies as

provided include generating a CD38 knockout iPSC line, a master cell bank comprising single cell sorted and expanded clonal CD38 negative iPSCs, and obtaining CD38 negative ($CD38^{neg}$) derivative effector cells through directed differentiation of the engineered iPSC line, wherein the derivative effector cells are protected against fratricide and allorejection among other advantages when CD38 targeted therapeutic moieties are employed with the effector cells. In addition, anti-CD38 monoclonal antibody therapy significantly depletes a patient's activated immune system without adversely affecting the patient's hematopoietic stem cell compartment. CD38 negative derivative cell has the ability to resist CD38 antibody mediated depletion, and may be effectively administered in combination with anti-CD38 or CD38-CAR without the use of toxic conditioning agents and thus reduce and/or replace chemotherapy based lymphodepletion. The master cell bank comprising single cell sorted and expanded clonal $CD38^{neg}$ iPSCs provides a platform for additional iPSC engineering, including but not limited to one or more of TCR^{neg} cs-CD3, hnCD16, CAR, IL and HLA I and II deficiency, and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

[000200] In one embodiment as provided herein, the CD38 knockout in an iPSC line is a bi-allelic knockout. As disclosed herein, the provided CD38 negative iPSC line further comprises at least TCR^{neg} and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; and said iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells including, but not limited to, mesodermal cells with definitive hemogenic endothelium (HE) potential, definitive HE, CD34 hematopoietic cells, hematopoietic stem and progenitor cells, hematopoietic multipotent progenitors (MPP), T cell progenitors, NK cell progenitors, myeloid cells, neutrophil progenitors, T cells, NKT cells, NK cells, B cells, neutrophils, dendritic cells, and macrophages. In some embodiments, when an anti-CD38 antibody is used to induce ADCC or an anti-CD38 CAR is used for targeted cell killing, the $CD38^{neg}$ iPSC and/or its derivative effector cells thereof are not eliminated by the anti-CD38 antibody, the anti-CD38 CAR, or recipient activated T or B cells, thereby increasing the iPSC and its effector cell persistence and/or survival in the presence of, and/or after exposure to, such therapeutic moieties. In some embodiments, the effector cell has increased persistence and/or survival *in vivo* in the presence of, and/or after exposure to, such therapeutic moieties.

7. Additional modifications

[000201] In some embodiments, the iPSC, and its derivative effector cells comprising TCR^{neg} cs-CD3 and one or more of CD16, CAR, IL, HLA I and II deficiency and $CD38^{-/-}$ may

additionally comprise deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; or introduced or increased expression in at least one of HLA-E, 41BBL, CD4, CD8, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, TCR, Fc receptor, an engager, and surface triggering receptor for coupling with bi-, multi- specific or universal engagers.

[000202] Bi- or multi- specific engagers are fusion proteins consisting of two or more single-chain variable fragments (scFvs), or other functional variants, of different antibodies, with at least one scFv binds to an effector cell surface molecule or "surface triggering receptor", and at least another to a tumor cell via a tumor specific surface molecule. As used herein the term "surface triggering receptor" refers to a receptor capable of triggering or initiating an immune response, e.g. a cytotoxic response, of the effector cell. Surface triggering receptors may be engineered, and may be an endogenous surface protein expressed on effector cells, e.g. a T cell, a NK cell, a NKT cell, a B cell, a macrophage, a neutrophil. In some embodiments, the surface triggering receptor facilitates bi- or multi- specific antibody engagement between the effector cells and specific target cell e.g. a tumor cell, independent of the effector cell's natural receptors and cell types. In some other embodiments, one or more exogenous surface triggering receptors could be introduced to the effector cells using the methods and compositions provided herein, i.e., through engineering of an iPSC, optionally generating a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs, and then directing the differentiation of the iPSC to T, NK or any other effector cells comprising the same genotype as the source iPSC.

[000203] Using this approach, one may also generate iPSCs comprising a universal surface triggering receptor, and then differentiate such iPSCs into populations of various effector cell types that express the universal surface triggering receptor. By "universal", it is meant that the surface triggering receptor can be expressed in, and activate, any effector cells irrespective of the cell type, and all effector cells expressing the universal receptor can be coupled or linked to the engagers having the same epitope recognizable by the surface triggering receptor, regardless of the engager's tumor binding specificities. In some embodiments, engagers having the same tumor targeting specificity are used to couple with different universal surface triggering receptor. In some embodiments, engagers having different tumor targeting specificity are used to couple with the same universal surface triggering receptor. As such, one or multiple effector cell types can be engaged to kill one specific type of tumor cells in some case, and to kill two or more types of tumors in some other cases. A surface triggering receptor generally comprises a co-stimulatory domain for effector cell activation and an anti-epitope that is specific to the epitope

of an engager, or vice versa, the surface triggering receptor comprises an epitope that is recognizable or specific to the anti-epitope of the engager. For example, a bi-specific engager is specific to the anti-epitope/epitope of a surface triggering receptor on one end and is specific to a tumor antigen on the other end.

[000204] As provided herein, the various forms of cell surface presented CD3 molecule as disclosed are applicable, among other function, as a CD3 related cell surface triggering receptor for engager recognition, which is particular useful in a cell that is TCR negative such that expressed CD3 molecule does not present on cell surface despite its expression. In some embodiments, the CD3 related surface triggering receptor for engager recognition is comprised in a complete or partial CD3 molecule (i.e., subunits or subdomains of a CD3 complex) presented at the cell surface of an effector cell when expressed. In some embodiments, the complete or partial CD3 molecule presented at the effector cell surface comprises (1) at least a complete or partial length of at least one ectodomain from one or more CD3 subunits comprising CD3ε, CD3δ, and/or CD3ε; and optionally (2) a complete or partial length of an endodomain of CD3ζ. In some embodiments, all subunits or subdomains of the complete or partial CD3 molecule comprising the CD3 related surface triggering receptor are endogenous. In some embodiments, at least one subunit or subdomain of the complete or partial CD3 molecule comprising the CD3 related surface triggering receptor is exogenous. In some embodiments, the bispecific antibody engaging CD3 related cell surface triggering receptor as disclosed herein is CD3-CD19. In still another embodiment, the bispecific antibody is CD3-CD33. In yet another embodiment, the bispecific antibody further comprises a linker between the effector cell and tumor cell antigen binding domains, for example, a modified IL15 as a linker for effector NK cells to facilitate effector cell expansion (called TriKE, or Tri-specific Killer Engager, in some publications).

[000205] Other than CD3, additional effector cell surface molecules, or surface triggering receptor, that can be used for bi- or multi- specific engager recognition, or coupling, include, but are not limited to, CD28, CD5, CD16, NKG2D, CD64, CD32, CD89, NKG2C, and a chimeric Fc receptor as disclosed herein. In some embodiments, the CD16 expressed on the surface of effector cells for engager recognition is a hnCD16, comprising CD16 (containing F176V and optionally S197P) or CD64 extracellular domain, and native or non-native transmembrane, stimulatory and/or signaling domains as described in section I.2. In some embodiments, the CD16 expressed on the surface of effector cells for engager recognition is a hnCD16 based chimeric Fc receptor (CFcR). In some embodiments, the hnCD16 based CFcR comprises a transmembrane domain of NKG2D, a stimulatory domain of 2B4, and a signaling domain of CD3ζ; wherein the extracellular domain of the hnCD16 is derived from a full length or partial

sequence of the extracellular domain of CD64 or CD16; and wherein the extracellular domain of CD16 comprises F176V and optionally S197P.

[000206] The exemplary tumor cell surface molecules for bi- or multi- specific engager recognition include, but are not limited to, B7H3, BCMA, CD10, CD19, CD20, CD22, CD24, CD30, CD33, CD34, CD38, CD44, CD79a, CD79b, CD123, CD138, CD179b, CEA, CLEC12A, CS-1, DLL3, EGFR, EGFRvIII, EPCAM, FLT-3, FOLR1, FOLR3, GD2, gpA33, HER2, HM1.24, LGR5, MSLN, MCSP, MICA/B, PSMA, PAMA, P-cadherin, ROR1.

[000207] In view of the above, for engaging CD3 on the effector cells, in one embodiment, the bispecific antibody is CD3-CD19; and in another embodiment, the bispecific antibody is CD3-CD33. For engaging CD16 on the effector cells the bispecific antibody is CD16-CD30 or CD64-CD30. In another embodiment, the bispecific antibody is CD16-BCMA or CD64-BCMA. In yet another embodiment, the bispecific antibody further comprises a linker between the effector cell and tumor cell antigen binding domains, for example, a modified IL15 as a linker for effector NK cells to facilitate effector cell expansion (called TriKE, or Tri-specific Killer Engager, in some publications). In one embodiment, the TriKE is CD16-IL15-EPCAM or CD64-IL15-EPCAM. In another embodiment, the TriKE is CD16-IL15-CD33 or CD64-IL15-CD33. In yet another embodiment, the TriKE is NKG2C-IL15-CD33. The linker may also originate from other cytokines including, but not limited to, IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL18, and IL21.

8. Genetically engineered iPSC line and iPSC-derived cells provided herein

[000208] In light of the above, the present application provides a TCR^{neg} cell, or a population thereof, comprising a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed (TCR^{neg} cs-CD3), wherein the cell is an induced pluripotent cell (iPSC), a clonal iPSC, a clonal iPS cell line cell, or iPSC derived cells obtained from directed differentiation of TCR^{neg} cs-CD3 iPSC. Also provided is a master cell bank comprising single cell sorted and expanded clonal engineered iPSCs having a phenotype as described herein, wherein the cell bank provides a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

[000209] In some embodiments, the iPSC derived cells are hematopoietic cells including, but not limited to, mesodermal cells with definitive hemogenic endothelium (HE) potential, definitive HE, CD34 hematopoietic cells, hematopoietic stem and progenitor cells, hematopoietic multipotent progenitors (MPP), T cell progenitors, NK cell progenitors, myeloid cells, neutrophil progenitors, T cells, NKT cells, NK cells, B cells, neutrophils, dendritic cells, and macrophages.

In some embodiments, the iPSC derived hematopoietic cells comprise effector cells such as T, NK, and regulatory cells, which are TCR^{neg} and comprise a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed. In a further embodiment, the present application provides an iPSC derived TCR^{neg} T cell, or a population thereof, comprising a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) (TCR^{neg} cs-CD3), wherein the T cell is obtained from directed differentiation of TCR^{neg} cs-CD3 iPSC.

[000210] As used herein, TCR^{neg} is also referred to as TCR negative, $TCR^{-/-}$, "TCR null", or TCR knockout, which comprises cells without endogenous TCR expression either by nature (for example, NK cell or iPSC derived NK cell), by gene expression regulation, or by genomic editing of an iPSC cell (for example, iPSC, iPSC reprogrammed from T cell (TiPSC)) or a T cell to knock out an endogenous TCR or one or more subunits thereof, or by obtaining TCR negative derivative cells differentiated from iPSC having TCR knocked out. As such, the TCR that is knocked out in a cell as disclosed is an endogenous TCR complex. Disrupting the expression of the constant region of either TCRα or TCRβ of TCR in a cell is one of many methods of knocking out the endogenous TCR complex of the cell. TCR^{neg} cells are discovered as not being able to present CD3 complex to the cell surface despite of the expression of all CD3 subunits in the TCR^{neg} cells, which adversely affect cell functions that requires cell surface CD3 recognition, binding and/or signaling. The cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) as disclosed herein in a TCR^{neg} cell can function as a CD3 related cell surface triggering receptor for binding with molecules including, not limited to, antibodies or functional variants thereof, and/or engagers as described herein.

[000211] Provided herein also is an iPSC or iPSC-derived cell comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, wherein the cell is optionally TCR negative. When the cs-CD3 is expressed, it functions as a CD3 related cell surface triggering receptor. In some embodiments of the CD3 related surface triggering receptor as provided in a TCR^{neg} cell, the receptor is comprised in a complete or partial endogenous CD3 molecule presented at effector cell surface when expressed, wherein the endogenous CD3 molecule presentation, otherwise does not take place in a TCR^{neg} cell even when expressed, is enabled by its association with a recombinant TCR comprising one or more of a full or partial length of an exogenous TCRα, an exogenous TCRβ, and any variants thereof as provided in this application. In some embodiments, the cell surface presentation of a complete or partial endogenous CD3 molecule in a TCR^{neg} cell is enabled by additionally expressing in said cell at

least a recombinant TCR comprising a non-binding recombinant TCR (nb-rTCR), a defined recombinant TCR (d-rTCR), and/or a recombinant pre-TCR.

[000212] In some embodiments, the TCR^{neg} cell comprising a CD3 related surface triggering receptor comprises a non-binding recombinant TCR (nb-rTCR), wherein the nb-rTCR comprises one or both of a tgTRAC (transgenic TCRα constant region) and a tgTRBC (transgenic TCRβ constant region); as such the TCR^{neg} iPSC or iPSC-derived cell comprises one or more polynucleotides encoding tgTRAC and/or tgTRBC. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgTRAC, said polynucleotide is inserted in a TRAC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRAC thereby leading to endogenous TCR knockout, and optionally wherein the inserted polynucleotide is driven by an endogenous promoter of TRAC or a heterologous promoter. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgTRBC, said polynucleotide is inserted in a TRBC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRBC thereby leading to endogenous TCR knockout, and optionally wherein the inserted polynucleotide is driven by an endogenous promoter of TRBC or a heterologous promoter.

[000213] In some embodiments, the TCR^{neg} cell comprising a CD3 related surface triggering receptor comprises a defined recombinant TCR (d-rTCR), wherein the d-rTCR comprises a tgTCRα (transgenic TCRα) and a tgTCRβ (transgenic TCRβ), wherein each of the tgTCRα and the tgTCRβ comprises a respective defined variable region in addition to a respective constant region (i.e., TRAC and TRBC); as such the TCR^{neg} iPSC or iPSC-derived cell comprises one or more polynucleotides encoding tgTCRα and/or tgTCRβ. In some embodiments, the defined variable region is originated from TCR alpha and beta of T cell having known TCR specificity. In some embodiments, the defined variable region is originated from TCR alpha and beta of invariant NKT cells. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgTCRα, said polynucleotide is inserted in a TRAC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRAC thereby leading to endogenous TCR knockout, and optionally wherein the inserted polynucleotide is driven by an endogenous promoter of TRAC or a heterologous promoter. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgTCRβ, said polynucleotide is inserted in a TRBC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRBC thereby leading to endogenous TCR knockout, and optionally wherein the inserted polynucleotide is driven by an endogenous promoter of TRBC or a heterologous promoter.

[000214] In some embodiments, the TCR^{neg} cell comprising a CD3 related surface triggering receptor comprises a recombinant pre-TCR (p-rTCR), wherein the p-rTCR comprises a tgpTCRα

(transgenic pre-TCRα), and optionally a tgTRBC or a tgTCRβ, wherein the tgTCRβ comprises a defined variable region; as such the TCR^{neg} iPSC or iPSC-derived cell comprises at least a polynucleotide encoding tgpTCRα. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgpTCRα, said polynucleotide is inserted in a TRAC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRAC thereby leading to endogenous TCR knockout, and optionally wherein the inserted polynucleotide is driven by an endogenous promoter of TRAC or a heterologous promoter. In some embodiments of the TCR^{neg} cell comprising a polynucleotide encoding tgTRBC or tgTCRβ in addition to tgpTCRα, said tgTRBC or tgTCRβ encoding polynucleotide is inserted in a TRBC locus, wherein the inserted polynucleotide disrupts expression of endogenous TRBC thereby leading to endogenous TCR knockout, and optionally wherein the inserted tgTRBC or tgTCRβ encoding polynucleotide is driven by an endogenous promoter of TRBC or a heterologous promoter. respective defined variable region.

[000215] In some embodiments of the CD3 related surface triggering receptor in a TCR^{neg} cell, the receptor is comprised in a complete or partial CD3 molecule comprising at least one exogenous subunit or subdomain from one or more of CD3ε, CD3δ, and CD3γ. In one embodiment, the CD3 related surface triggering receptor for engager recognition in a TCR^{neg} cell is comprised in a partial CD3 molecule comprising at least a full or partial length ectodomain of CD3ε. In one embodiment, the CD3 related surface triggering receptor for engager recognition in a TCR^{neg} cell is comprised in a partial CD3 molecule comprising at least a full or partial length ectodomain of CD3ε, and additionally a full or partial length ectodomain of CD3γ or CD3δ. In one embodiment, said CD3 molecule comprises at least a full or partial length of an ectodomain of CD3ε, CD3γ and/or CD3δ, wherein the full or partial length of ectodomain(s) is fused with a constant region of TCRα or TCRβ, and wherein the partial fusion proteins each comprising TRAC or TRBC are capable of forming heterodimer with endogenous CD3ζ. As such, in one embodiment of the TCR^{neg} iPSC or iPSC-derived cell having a CD3 related surface triggering receptor, the cell comprises at least one of: (i) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a TCRα constant region (tgCD3(ε-δ)-TRAC); (ii) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a TCRβ constant region (tgCD3(ε-γ)-TRBC); (iii) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a TCRα constant region (tgCD3(ε-γ)-TRAC); and/or (iv) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a TCRβ constant region (tgCD3(ε-δ)-TRBC). In some embodiments of the TCR^{neg} cell having a CD3 related surface triggering receptor, the cell

comprises a heterodimer comprising a transgenic fusion protein comprising a TCRα constant region fused with a full or partial length of ectodomain of at least CD3ε and a transgenic fusion protein comprising a TCRβ constant region fused with a full or partial length of ectodomain of at least CD3ε.

[000216] In some embodiments of the CD3 related surface triggering receptor in a TCR^{neg} cell, the receptor is comprised in a complete or partial CD3 molecule comprising at least one exogenous subunit or subdomain from one or more of CD3ε, CD3δ, CD3γ, and/or CD3ζ, and optionally one or more signaling domains of 2B4, 4-1BB, CD16, CD2, CD28, CD28H, CD3ζ, DAP10, DAP12, DNAM1, FcERIγ IL21R, IL-2Rβ (IL-15Rβ), IL-2Rγ, IL-7R, KIR2DS2, NKG2D, NKp30, NKp44, NKp46, CD3ζ1XX, CS1, or CD8 for signal transduction and/or co-stimulation, wherein all subunits or subdomains, including the signaling domains are fused to form a chimeric chain. In one embodiment, the CD3 related surface triggering receptor for engager recognition in a TCR^{neg} cell is comprised in a CD3 chimeric chain comprising at least a full or partial length ectodomain of CD3ε; a full or partial length ectodomain of one or both of CD3δ and CD3γ; and a full or partial length of endodomain of CDζ. In one embodiment, the CD3 related surface triggering receptor for engager recognition in a TCR^{neg} cell is comprised in a CD3 chimeric chain comprising a full or partial length ectodomain of CD3ε; a full or partial length ectodomain of one or both of CD3δ and CD3γ; a full or partial length of endodomain of CDζ, further comprises a cytoplasmic signaling domain of one or both of CD28 and 41BBL. As such, in one embodiment of the TCR^{neg} iPSC or iPSC-derived cell having a CD3 related surface triggering receptor, the cell comprises at least one of: (i) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a full or partial length of endodomain of CD3ζ [tgCD3(ε-γ)-ζ]; (ii) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a full or partial length of endodomain of CD3ζ [tgCD3(ε-δ)-ζ]; (iii) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3ε, a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, and a signaling domain of CD28 [tgCD3(ε- γ/δ)-28ζ]; (iv) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3ε, a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, and a signaling domain of 41BB [tgCD3(ε- γ/δ)-BBζ]; and/or (v) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, a signaling domain of CD28, and a signaling domain of 41BB [tgCD3(ε- γ/δ)-(28-BB)ζ].

[000217] Further provided herein is an iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a polynucleotide encoding a high affinity non-cleavable CD16 (hnCD16), wherein the iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells. In some embodiments, the effector cells comprise T cells. In some embodiments, the effector cells comprise NK cells.

[000218] An iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a polynucleotide encoding a target specific chimeric antigen receptor (CAR) is provided herein, wherein the iPSC is capable of directed differentiation to produce functional derivative effector cells.

[000219] Additionally provided is an iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a polynucleotide encoding at least one exogenous cytokine and/or its receptor (IL) to enable cytokine signaling contributing to cell survival, persistence and/or expansion, wherein the iPSC line is capable of directed differentiation to produce functional derivative hematopoietic cells having improved survival, persistency, expansion, and effector cell function. In some embodiments, the iPSC comprising cs-CD3 is TCR negative (TCR^{neg} cs-CD3). The exogenously introduced cytokine signaling(s) comprise the signaling of any one, or two, or more of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, and IL21. In some embodiments, the introduced partial or full peptide of cytokine and/or its respective receptor for cytokine signaling are expressed on the cell surface. In some embodiments, the cytokine signaling is constitutively activated. In some embodiments, the activation of the cytokine signaling is inducible. In some embodiments, the activation of the cytokine signaling is transient and/or temporal. In some embodiments, the transient/temporal expression of a cell surface cytokine/cytokine receptor is through a retrovirus, Sendai virus, an adenovirus, an episome, mini-circle, or RNAs including mRNA. In some embodiments, the exogenous cell surface cytokine and/or receptor comprised in the TCR^{neg} cs-CD3 iPSC or derivative cells therefrom enables IL7 signaling. In some embodiments, the exogenous cell surface cytokine and/or receptor comprised in the TCR^{neg} cs-CD3 iPSC or derivative cells therefrom enables IL10 signaling. In some embodiments, the exogenous cell surface cytokine and/or receptor comprised in the TCR^{neg} cs-CD3 iPSC or derivative cells therefrom enables IL15 signaling. In some embodiments of said TCR^{neg} cs-CD3 IL iPSC, the IL15 expression is through construct 3 of FIG. 2. In some embodiments of said TCR^{neg} cs-CD3 IL iPSC, the IL15

expression is through construct 4 of FIG. 2. Said TCR^{neg} cs-CD3 IL iPSC and its derivative cells of the above embodiments are capable of maintaining or improving cell growth, proliferation, expansion, and/or effector function autonomously without contacting additionally supplied soluble cytokines *in vitro* or *in vivo*. In some embodiments, TCR^{neg} cs-CD3 IL iPSC and its derivative effector cells can be used with an anti-CD38 antibody to induce ADCC without causing effector cell elimination, thereby synergistically increasing the iPSC and its effector cell persistence and/or survival.

[000220] Further provided is an iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a CD38 knockout, wherein the iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells having improved survival, persistency, expansion, and effector cell function. In some embodiments, the iPSC comprising cs-CD3 is TCR negative (TCR^{neg} cs-CD3). Cell surface molecule CD38 is highly upregulated in multiple hematologic malignancies derived from both lymphoid and myeloid lineages, including multiple myeloma and a CD20 negative B-cell malignancy, which makes it an attractive target for antibody therapeutics to deplete cancer cell. Other than being highly expressed on malignant cells, CD38 is also expressed on plasma cells as well as on NK cells, and activated T and B cells. In some embodiments, when an anti-CD38 antibody, a CD38 binding CAR, or an CD3 engager comprising anti-CD38 scFV is used to induce the ADCC and/or tumor cell targeting, the TCR^{neg} cs-CD3 $CD38^{-/-}$ iPSC and/or its derivative effector cells can target the CD38 expressing (tumor) cells without causing effector cell elimination, i.e., reduction or depletion of CD38 expressing effector cells, thereby increasing the iPSC and its effector cell persistence and/or survival.

[000221] Also provided is an iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, a B2M knockout and a CIITA knockout, and optionally, a polynucleotide encoding HLA-G, wherein the iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells. In some embodiments, the iPSC comprising cs-CD3 is TCR negative (TCR^{neg} cs-CD3). In some embodiments, said TCR^{neg} cs-CD3 $B2M^{-/-}$ $CIITA^{-/-}$ iPSC and its derivative effector cells are both HLA-I and HLA-II deficient.

[000222] In view of the above, provided herein include an iPSC comprising one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and optionally one,

two, three or all four of: hnCD16, CAR, an exogenous cytokine/receptor, and B2M/CIITA knockout; wherein when B2M is knocked out, a polynucleotide encoding HLA-G, or alternatively, one or both of CD58 and CD54 knockout, is optionally introduced, and wherein the iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells. In some embodiments, the iPSC comprising cs-CD3 is TCR negative (TCR^{neg} cs-CD3). Also included in this application are functional iPSC derivative hematopoietic cells comprising a TCR^{neg}, cs-CD3, and optionally one, two, three or all four of: hnCD16, B2M/CIITA knockout, CAR, and an exogenous cytokine/receptor; wherein when B2M is knocked out, a polynucleotide encoding HLA-G, or alternatively, one or both of CD58 and CD54 knockout, is optionally introduced, and wherein the derivative hematopoietic cells include, but are not limited to, mesodermal cells with definitive hemogenic endothelium (HE) potential, definitive HE, CD34 hematopoietic cells, hematopoietic stem and progenitor cells, hematopoietic multipotent progenitors (MPP), T cell progenitors, NK cell progenitors, myeloid cells, neutrophil progenitors, T cells, NKT cells, NK cells, B cells, neutrophils, dendritic cells, and macrophages.

[000223] Another aspect provided herein includes an iPSC or iPSC derived cells comprising TCR^{neg}, cs-CD3, and a truncated fusion protein of IL15 and IL15Rα, wherein the fusion protein does not comprise an intracellular domain. Shown as "IL15Rα(ΔICD) fusion" and "IL5/mb-Sushi" in FIG. 2, these embodiments are further collectively abbreviated as IL15Δ throughout this application. In some embodiments, the truncated IL15/IL15Rα fusion protein lacking intracellular domain comprises an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NOs: 17, 19 or 21. In some embodiments, the truncated IL15/IL15Rα fusion protein lacking intracellular domain comprises an amino acid sequence of SEQ ID NO: 17. In some embodiments, the truncated IL15/IL15Rα fusion protein lacking intracellular domain comprises an amino acid sequence of SEQ ID NO: 19 . In some embodiments, the truncated IL15/IL15Rα fusion protein lacking intracellular domain comprises an amino acid sequence of SEQ ID NO: 21. In yet some other embodiments, the iPSC or iPSC derived cells comprising TCR^{neg}, cs-CD3, a truncated IL15/IL15Rα fusion protein lacking intracellular domain (IL15Δ) further comprise one or more of: CD38 knockout, hnCD16, CAR, an exogenous cytokine/receptor, and B2M/CIITA knockout; wherein when B2M is knocked out, a polynucleotide encoding HLA-G is optionally introduced, and wherein the iPSC is capable of directed differentiation to produce functional derivative hematopoietic cells, and wherein the derivative hematopoietic cells include, but are not limited to, mesodermal cells with definitive hemogenic endothelium (HE) potential, definitive HE, CD34 hematopoietic cells, hematopoietic stem and progenitor cells, hematopoietic multipotent progenitors (MPP), T cell progenitors, NK

cell progenitors, myeloid cells, neutrophil progenitors, T cells, NKT cells, NK cells, B cells, neutrophils, dendritic cells, and macrophages.

[000224] As such, the present application provides iPSCs and its functional derivative hematopoietic cells, which comprise any one of the following genotypes in Table 1. "IL", as provided in Table 1 stands for one of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, and IL21, depending on which specific cytokine/receptor expression is selected; and when IL stands for IL15, it also comprises IL15Δ, which is detailed above as a truncated fusion protein of IL15 and IL15Rα but without an intracellular domain. Further, when iPSCs and its functional derivative hematopoietic cells have a genotype comprising both CAR and IL, the CAR and IL are optionally comprised in a bi-cistronic expression cassette comprising a 2A sequence. As comparison, in some other embodiments, CAR and IL are in separate expression cassettes comprised in iPSCs and its functional derivative hematopoietic cells. In one particular embodiment, comprised in the iPSCs and its functional derivative effector cells expressing both CAR and IL, IL is IL15 in a construct 3 or 4 of FIG. 2, wherein the IL15 construct is comprised in an expression cassette with, or separate from, the CAR.

Table 1: Applicable Genotypes of the Cells Provided:

cs-CD3	TCR^{neg}	hnCD16	CAR	IL	CD38-/-	$B2M^{-/-}CIITA^{-/-}$	HLA-G or ($CD58^{-/-}$ w/or w/o $CD54^{-/-}$)	Genotype
√								1. cs-CD3
√	√							2. cs-CD3 TCR^{neg}
√		√						3. cs-CD3 hnCD16
√			√					4. cs-CD3 CAR
√				√				5. cs-CD3 IL
√					√			6. cs-CD3 CD38-/-
√						√		7. cs-CD3 $B2M^{-/-}CIITA^{-/-}$
√						√	√	8. cs-CD3 $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ 9. cs-CD3 $B2M^{-/-}CIITA^{-/-}$ $CD54^{-/-}$ 10. cs-CD3 $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ $CD54^{-/-}$ 11. cs-CD3 $B2M^{-/-}CIITA^{-/-}$ HLA-G
√	√	√						12. cs-CD3 TCR^{neg} hnCD16
√	√		√					13. cs-CD3 TCR^{neg} CAR
√	√			√				14. cs-CD3 TCR^{neg} IL
√	√				√			15. cs-CD3 TCR^{neg} CD38-/-
√	√					√		16. cs-CD3 TCR^{neg} $B2M^{-/-}CIITA^{-/-}$
√	√					√	√	17. cs-CD3 TCR^{neg} $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ 18. cs-CD3 TCR^{neg} $B2M^{-/-}CIITA^{-/-}$ $CD54^{-/-}$ 19. cs-CD3 TCR^{neg} $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ $CD54^{-/-}$ 20. cs-CD3 TCR^{neg} $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√					21. cs-CD3 hnCD16 CAR
√		√		√				22. cs-CD3 hnCD16 IL
√		√			√			23. cs-CD3 hnCD16 CD38-/-
√		√				√		24. cs-CD3 hnCD16 $B2M^{-/-}CIITA^{-/-}$
√		√				√	√	25. cs-CD3 hnCD16 $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ 26. cs-CD3 hnCD16 $B2M^{-/-}CIITA^{-/-}$ $CD54^{-/-}$ 27. cs-CD3 hnCD16 $B2M^{-/-}CIITA^{-/-}$ $CD58^{-/-}$ $CD54^{-/-}$ 28. cs-CD3 hnCD16 $B2M^{-/-}CIITA^{-/-}$ HLA-G
√			√	√				29. cs-CD3 CAR IL

√		√	√			30.	cs-CD3 CAR CD38-/-
√		√		√		31.	cs-CD3 CAR B2M$^{-/-}$CIITA$^{-/-}$
√		√		√	√	32.	cs-CD3 CAR B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
						33.	cs-CD3 CAR B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
						34.	cs-CD3 CAR B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
						35.	cs-CD3 CAR B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√			√	√		36.	cs-CD3 IL CD38-/-
√			√		√	37.	cs-CD3 IL B2M$^{-/-}$CIITA$^{-/-}$
√			√		√	38.	cs-CD3 IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
						39.	cs-CD3 IL B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
						40.	cs-CD3 IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
						41.	cs-CD3 IL B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√				√	√	42.	cs-CD3 CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√				√	√	43.	cs-CD3 CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
						44.	cs-CD3 CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
						45.	cs-CD3 CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
						46.	cs-CD3 CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√			47.	cs-CD3 TCR^{neg} hnCD16 CAR
√	√	√		√		48.	cs-CD3 TCR^{neg} hnCD16 IL
√	√	√			√	49.	cs-CD3 TCR^{neg} hnCD16 CD38-/-
√	√	√				50.	cs-CD3 TCR^{neg} hnCD16 B2M$^{-/-}$CIITA$^{-/-}$
√	√	√			√	51.	cs-CD3 TCR^{neg} B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
						52.	cs-CD3 TCR^{neg} B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
						53.	cs-CD3 TCR^{neg} B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
						54.	cs-CD3 TCR^{neg} B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√			55.	cs-CD3 TCR^{neg} CAR IL
√	√	√		√		56.	cs-CD3 TCR^{neg} CAR CD38-/-
√	√	√		√		57.	cs-CD3 TCR^{neg} CAR B2M$^{-/-}$CIITA$^{-/-}$
√	√	√	√		√	58.	cs-CD3 TCR^{neg} CAR B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
						59.	cs-CD3 TCR^{neg} CAR B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
						60.	cs-CD3 TCR^{neg} CAR B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
						61.	cs-CD3 TCR^{neg} CAR B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√			√	√	62.	cs-CD3 TCR^{neg} IL CD38-/-
√	√		√		√	63.	cs-CD3 TCR^{neg} IL B2M$^{-/-}$CIITA$^{-/-}$

√			√	√	√	64.	cs-CD3 TCR^{neg} IL $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						65.	cs-CD3 TCR^{neg} IL $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						66.	cs-CD3 TCR^{neg} IL $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						67.	cs-CD3 TCR^{neg} IL $B2M^{-/-}CIITA^{-/-}$ HLA-G
√	√		√	√		68.	cs-CD3 TCR^{neg} CD38-/- $B2M^{-/-}CIITA^{-/-}$
√	√		√	√	√	69.	cs-CD3 TCR^{neg} CD38-/- $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						70.	cs-CD3 TCR^{neg} CD38-/- $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						71.	cs-CD3 TCR^{neg} CD38-/- $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						72.	cs-CD3 TCR^{neg} CD38-/- $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√			73.	cs-CD3 hnCD16 CAR IL
√		√	√	√		74.	cs-CD3 hnCD16 CAR CD38-/-
√		√	√	√		75.	cs-CD3 hnCD16 CAR $B2M^{-/-}CIITA^{-/-}$
√		√	√	√	√	76.	cs-CD3 hnCD16 CAR $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						77.	cs-CD3 hnCD16 CAR $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						78.	cs-CD3 hnCD16 CAR $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						79.	cs-CD3 hnCD16 CAR $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√			80.	cs-CD3 hnCD16 IL CD38-/-
√		√	√	√		81.	cs-CD3 hnCD16 IL $B2M^{-/-}CIITA^{-/-}$
√		√	√	√	√	82.	cs-CD3 $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						83.	cs-CD3 $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						84.	cs-CD3 $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						85.	cs-CD3 $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√	√		86.	cs-CD3 hnCD16 CD38-/- $B2M^{-/-}CIITA^{-/-}$
√		√	√	√	√	87.	cs-CD3 hnCD16 CD38-/- $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						88.	cs-CD3 hnCD16 CD38-/- $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						89.	cs-CD3 hnCD16 CD38-/- $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						90.	cs-CD3 hnCD16 CD38-/- $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√	√		91.	cs-CD3 CAR IL CD38-/-
√		√	√	√		92.	cs-CD3 CAR IL $B2M^{-/-}CIITA^{-/-}$
√		√	√	√	√	93.	cs-CD3 CAR IL $B2M^{-/-}CIITA^{-/-}CD58^{-/-}$
						94.	cs-CD3 CAR IL $B2M^{-/-}CIITA^{-/-}CD54^{-/-}$
						95.	cs-CD3 CAR IL $B2M^{-/-}CIITA^{-/-}CD58^{-/-}CD54^{-/-}$
						96.	cs-CD3 CAR IL $B2M^{-/-}CIITA^{-/-}$ HLA-G
√		√	√	√		97.	cs-CD3 CAR CD38-/- $B2M^{-/-}CIITA^{-/-}$

√		√		√	√	√	98.	cs-CD3 CAR CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							99.	cs-CD3 CAR CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							100.	cs-CD3 CAR CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							101.	cs-CD3 CAR CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√			√	√	√		102.	cs-CD3 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√			√	√	√	√	103.	cs-CD3 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							104.	cs-CD3 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							105.	cs-CD3 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							106.	cs-CD3 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√				107.	cs-CD3 TCR^{neg} hnCD16 CAR IL
√	√	√		√			108.	cs-CD3 TCR^{neg} hnCD16 CAR CD38-/-
√	√	√			√		109.	cs-CD3 TCR^{neg} hnCD16 CAR B2M$^{-/-}$CIITA$^{-/-}$
√	√	√			√	√	110.	cs-CD3 TCR^{neg} hnCD16 B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							111.	cs-CD3 TCR^{neg} hnCD16 B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							112.	cs-CD3 TCR^{neg} hnCD16 B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							113.	cs-CD3 TCR^{neg} hnCD16 B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√	√			114.	cs-CD3 hnCD16 CAR IL CD38-/-
√	√	√	√		√		115.	cs-CD3 hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$
√	√	√	√	√	√	√	116.	cs-CD3 hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							117.	cs-CD3 hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							118.	cs-CD3 hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							119.	cs-CD3 hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√		√		√	√		120.	cs-CD3 hnCD16 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√		√		√	√	√	121.	cs-CD3 hnCD16 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							122.	cs-CD3 hnCD16 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							123.	cs-CD3 hnCD16 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							124.	cs-CD3 hnCD16 IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√			√	√	√		125.	cs-CD3 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√			√	√	√	√	126.	cs-CD3 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							127.	cs-CD3 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							128.	cs-CD3 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							129.	cs-CD3 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√	√			130.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/-
√	√	√	√	√	√		131.	cs-CD3 TCR^{neg} hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$

√	√	√	√	√	√	√	132.	cs-CD3 TCR^{neg} hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							133.	cs-CD3 TCR^{neg} hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							134.	cs-CD3 TCR^{neg} hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							135.	cs-CD3 TCR^{neg} hnCD16 CAR IL B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√	√	√		136.	cs-CD3 hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√	√	√	√	√	√	√	137.	cs-CD3 hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							138.	cs-CD3 hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							139.	cs-CD3 hnCD16 CAR IL CD38-/-B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							140.	cs-CD3 hnCD16 CAR IL CD38-/-B2M$^{-/-}$CIITA$^{-/-}$ HLA-G
√	√	√	√	√	√		141.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$
√	√	√	√	√	√	√	142.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$
							143.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD54$^{-/-}$
							144.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ CD58$^{-/-}$ CD54$^{-/-}$
							145.	cs-CD3 TCR^{neg} hnCD16 CAR IL CD38-/- B2M$^{-/-}$CIITA$^{-/-}$ HLA-G

9. Antibodies for immunotherapy

[000225] In some embodiments, in addition to the genomically engineered effector cells as provided herein, additional therapeutic agent comprising an antibody, or an antibody fragment that targets an antigen associated with a condition, a disease, or an indication may be used with these effector cells in a combinational therapy. In some embodiments, the antibody is a monoclonal antibody. In some embodiments, the antibody is a humanized antibody, a humanized monoclonal antibody, or a chimeric antibody. In some embodiments, the antibody, or antibody fragment, specifically binds to a viral antigen. In other embodiments, the antibody, or antibody fragment, specifically binds to a tumor antigen. In some embodiments, the tumor or viral specific antigen activates the administered iPSC derived effector cells to enhance their killing ability. In some embodiments, the antibodies suitable for combinational treatment as an additional therapeutic agent to the administered iPSC derived effector cells include, but are not limited to, anti-CD20 (rituximab, veltuzumab, ofatumumab, ublituximab, ocaratuzumab, obinutuzumab, ibritumomab, ocrelizumab), anti-CD22 (inotuzumab, moxetumomab, epratuzumab), anti-HER2 (trastuzumab, pertuzumab), anti-CD52 (alemtuzumab), anti-EGFR (certuximab), anti-GD2 (dinutuximab), anti-PDL1 (avelumab), anti-CD38 (daratumumab, isatuximab, MOR202), anti-CD123 (7G3, CSL362), anti-SLAMF7 (elotuzumab), and their humanized or Fc modified variants or fragments or their functional equivalents and biosimilars. In some embodiments, the antibodies suitable for combinational treatment as an additional therapeutic agent to the administered iPSC derived effector cells further include bispecific or multi-specific antibodies that target more than one antigen or epitope on a target cell or recruit effector cells (T cell, NK cell, or macrophage cell) toward target cells while targeting the target cells. Such bispecific or multi-specific antibodies function as an engager capable of directing an effector cell, e.g. a T cell, a NK cell, an NKT cell, a B cell, a macrophage, and/or a neutrophil to a tumor cell and activating the immune effector cell, and have shown great potential to maximize the benefits of antibody therapy. An engager is specific to at least one tumor antigen and is specific to at least one surface triggering receptor of an immune effector cell. Examples of engagers include, but are not limited to, bi-specific T cell engagers (BiTEs), bi-specific killer cell engagers (BiKEs), tri-specific killer cell engagers (TriKEs), or multi- specific killer cell engagers, or universal engagers compatible with multiple immune cell types.

[000226] In some embodiments, the iPSC derived effector cells comprise hematopoietic lineage cells comprising a genotype listed in Table 1. In some embodiments, the iPSC derived effector cells comprise NK cells comprising a genotype listed in Table 1. In some embodiments, the iPSC derived effector cells comprise T cells comprising a genotype listed in Table 1. In some

embodiments of a combination useful for treating liquid or solid tumors, the combination comprises iPSC derived NK or T cells comprising at least TCR^{neg} cs-CD3, and a bi-specific or multi-specific antibody that engages cells having cell surface CD3. The CD3 engager comprises at least a first variable segment that binds to a cs-CD3 and a second variable segment that binds to an antigen comprising at least one of ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and/or a pathogen antigen.

[000227] In some embodiments of the CD3 engager, the engager comprises at least a first variable segment that binds to a cs-CD3 and a second variable segment that binds to an antigen comprising at least one of BCMA, CD19, CD20, CD33, CD38, CD52, CD123, CEA, EGFR, EpCAM, GD2, GPA33, HER2, MICA/B, PDL1, and/or PSMA. In yet some other embodiments of the CD3 engager, the engager comprises a second variable segment that binds to an antigen comprising at least one of CD19, CD33, CD123, CEA, EpCAM, GPA33, HER2, and/or PSMA. In still some other embodiments of the CD3 engager, the engager is at least one of: blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05. In one embodiment, the combination comprises a CD3 engager and iPSC derived NK cells comprising TCR^{neg} cs-CD3 and hnCD16. In one embodiment, the combination comprises a CD3 engager and iPSC derived NK cells comprising TCR^{neg} cs-CD3 and hnCD16. In some further embodiments, the iPSC derived NK cells

comprised in the combination with a CD3 engager comprise TCR^{neg} cs-CD3, hnCD16, IL15, and a CAR targeting one of CD19, BCMA, CD20, CD22, CD38, CD123, HER2, CD52, EGFR, GD2, and PDL1; wherein the IL15 is co- or separately expressed with the CAR; and IL15 is in any one of the forms presented in constructs 1 to 7 of FIG. 2. In some particular embodiments, IL15 is in a form of construct 3, 4, or 7 when it is co- or separately expressed with the CAR.

10. ***Checkpoint inhibitors***

[000228] Checkpoints are cell molecules, often cell surface molecules, capable of suppressing or downregulating immune responses when not inhibited. It is now clear that tumors co-opt certain immune-checkpoint pathways as a major mechanism of immune resistance, particularly against T cells that are specific for tumor antigens. Checkpoint inhibitors (CI) are antagonists capable of reducing checkpoint gene expression or gene products, or deceasing activity of checkpoint molecules, thereby block inhibitory checkpoints, restoring immune system function. The development of checkpoint inhibitors targeting PD1/PDL1 or CTLA4 has transformed the oncology landscape, with these agents providing long term remissions in multiple indications. However, many tumor subtypes are resistant to checkpoint blockade therapy, and relapse remains a significant concern. One aspect of the present application provides a therapeutic approach to overcome CI resistance by including genomically engineered functional iPSC-derived cells as provided in a combination therapy with CI. In one embodiment of the combination therapy, the iPSC-derived cells are NK cells. In another embodiment of the combination therapy, the iPSC-derived cells are T cells. In addition to exhibiting direct antitumor capacity, the derivative NK cells provided herein have been shown to resist PDL1-PD1 mediated inhibition, and to have the ability to enhance T cell migration, to recruit T cells to the tumor microenvironment, and to augment T cell activation at the tumor site. Therefore, the tumor infiltration of T cell facilitated by the functionally potent genomically engineered derivative NK cells indicate that said NK cells are capable of synergizing with T cell targeted immunotherapies, including the checkpoint inhibitors, to relieve local immunosuppression and to reduce tumor burden.

[000229] In one embodiment, the derived TCR^{neg} NK cell for checkpoint inhibitor combination therapy comprises cs-CD3, and optionally one, two, three or all four of: hnCD16 expression, B2M/CIITA knockout, CAR expression, CD38 knockout, and an exogenous cell surface cytokine and/or receptor expression; wherein when B2M is knocked out, a polynucleotide encoding HLA-G or knockout of one or both of CD58 and CD54 is optionally included. In some embodiments, the derivative NK cell comprises any one of the genotypes listed in Table 1. In some embodiments, the above derivative NK cell additionally comprises

deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; or introduced or increased expression in at least one of HLA-E, 41BBL, CD3, CD4, CD8, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi-, multi- specific or universal engagers.

[000230] In another embodiment, the derived TCR^{neg} T cell for checkpoint inhibitor combination therapy comprises cs-CD3, and optionally one, two, three or all four of: hnCD16 expression, B2M/CIITA knockout, CAR expression, a CD38 knockout, and an exogenous cell surface cytokine and/or receptor expression; wherein when B2M is knocked out, a polynucleotide encoding HLA-G or knockout of one or both of CD58 and CD54 is optionally included. In some embodiments, the derivative T cell comprises any one of the genotypes listed in Table 1. In some embodiments, the above derivative T cell additionally comprises deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; or introduced or increased expression in at least one of HLA-E, 41BBL, CD3, CD4, CD8, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi-, multi- specific or universal engagers.

[000231] Above said derivative NK or T cell is obtained from differentiating an iPSC clonal line comprising TCR^{neg} cs-CD3, and optionally one, two, three or all four of: hnCD16 expression, B2M/CIITA knockout, CAR expression, CD38 knockout, and an exogenous cell surface cytokine expression; wherein when B2M is knocked out, a polynucleotide encoding HLA-G or knockout of one or both of CD58 and CD54 is optionally introduced. In some embodiments, above said iPSC clonal line further comprises deletion or reduced expression in at least one of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; or introduced or increased expression in at least one of HLA-E, 41BBL, CD3, CD4, CD8, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi-, multi- specific or universal engagers.

[000232] Suitable checkpoint inhibitors for combination therapy with the derivative NK or T cells as provided herein include, but are not limited to, antagonists of PD-1 (Pdcdl, CD279), PDL-1 (CD274), TIM-3 (Havcr2), TIGIT (WUCAM and Vstm3), LAG-3 (Lag3, CD223), CTLA-4 (Ctla4, CD152), 2B4 (CD244), 4-1BB (CD137), 4-1BBL (CD137L), A2aR, BATE, BTLA, CD39 (Entpdl), CD47, CD73 (NT5E), CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2,

MAFB, OCT-2 (Pou2f2), retinoic acid receptor alpha (Rara), TLR3, VISTA, NKG2A/HLA-E, and inhibitory KIR (for example, 2DL1, 2DL2, 2DL3, 3DL1, and 3DL2).

[000233] In some embodiments, the antagonist inhibiting any of the above checkpoint molecules is an antibody. In some embodiments, the checkpoint inhibitory antibodies may be murine antibodies, human antibodies, humanized antibodies, a camel Ig, a shark heavy-chain-only antibody (VNAR), Ig NAR, chimeric antibodies, recombinant antibodies, or antibody fragments thereof. Non-limiting examples of antibody fragments include Fab, Fab', F(ab)'2, F(ab)'3, Fv, single chain antigen binding fragments (scFv), (scFv)2, disulfide stabilized Fv (dsFv), minibody, diabody, triabody, tetrabody, single-domain antigen binding fragments (sdAb, Nanobody), recombinant heavy-chain-only antibody (VHH), and other antibody fragments that maintain the binding specificity of the whole antibody, which may be more cost-effective to produce, more easily used, or more sensitive than the whole antibody. In some embodiments, the one, or two, or three, or more checkpoint inhibitors comprise at least one of atezolizumab (anti-PDL1 mAb), avelumab (anti-PDL1 mAb), durvalumab (anti-PDL1 mAb), tremelimumab (anti-CTLA4 mAb), ipilimumab (anti-CTLA4 mAb), IPH4102 (anti-KIR), IPH43 (anti-MICA), IPH33 (anti-TLR3), lirimumab (anti-KIR), monalizumab (anti-NKG2A), nivolumab (anti-PD1 mAb), pembrolizumab (anti-PD1 mAb), and any derivatives, functional equivalents, or biosimilars thereof.

[000234] In some embodiments, the antagonist inhibiting any of the above checkpoint molecules is microRNA-based, as many miRNAs are found as regulators that control the expression of immune checkpoints (Dragomir et al., Cancer Biol Med. 2018, 15(2):103-115). In some embodiments, the checkpoint antagonistic miRNAs include, but are not limited to, miR-28, miR-15/16, miR-138, miR-342, miR-20b, miR-21, miR-130b, miR-34a, miR-197, miR-200c, miR-200, miR-17-5p, miR-570, miR-424, miR-155, miR-574-3p, miR-513, and miR-29c.

[000235] Some embodiments of the combination therapy with the provided iPSC-derived NK or T cells comprise at least one checkpoint inhibitor to target at least one checkpoint molecule; wherein the iPSC-derived cells have a genotype listed in Table 1. Some other embodiments of the combination therapy with the provided derivative NK or T cells comprise two, three or more checkpoint inhibitors such that two, three, or more checkpoint molecules are targeted. In some embodiments of the combination therapy comprising at least one checkpoint inhibitor and the iPSC-derived cells having a genotype listed in Table 1, said checkpoint inhibitor is an antibody, or a humanized or Fc modified variant or fragment, or a functional equivalent or biosimilar thereof, and said checkpoint inhibitor is produced by the iPSC-derived cells by expressing an exogenous polynucleotide sequence encoding said antibody, or a fragment or

variant thereof. In some embodiments, the exogenous polynucleotide sequence encoding the antibody, or a fragment or a variant thereof that inhibits a checkpoint is co-expressed with a CAR, either in separate constructs or in a bi-cistronic construct comprising both CAR and the sequence encoding the antibody, or the fragment thereof. In some further embodiments, the sequence encoding the antibody or the fragment thereof can be linked to either the 5' or the 3' end of a CAR expression construct through a self-cleaving 2A coding sequence, illustrated as, for example, CAR-2A-CI or CI-2A-CAR. As such, the coding sequences of the checkpoint inhibitor and the CAR are in a single open reading frame (ORF). When the checkpoint inhibitor is delivered, expressed and secreted as a payload by the derivative effector cells capable of infiltrating the tumor microenvironment (TME), it counteracts the inhibitory checkpoint molecule upon engaging the TME, allowing activation of the effector cells by activating modalities such as CAR or activating receptors. In some embodiments, the checkpoint inhibitor co-expressed with CAR inhibits at least one of the checkpoint molecules: PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB, 4-1BBL, A2aR, BATE, BTLA, CD39 (Entpdl), CD47, CD73 (NT5E), CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2 (Pou2f2), retinoic acid receptor alpha (Rara), TLR3, VISTA, NKG2A/HLA-E, and inhibitory KIR. In some embodiments, the checkpoint inhibitor co-expressed with CAR in a derivative cell having a genotype listed in Table 1 is selected from a group comprising atezolizumab, avelumab, durvalumab, tremelimumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their humanized, or Fc modified variants, fragments and their functional equivalents or biosimilars. In some embodiments, the checkpoint inhibitor co-expressed with CAR is atezolizumab, or its humanized, or Fc modified variants, fragments or their functional equivalents or biosimilars. In some other embodiments, the checkpoint inhibitor co-expressed with CAR is nivolumab, or its humanized, or Fc modified variants, fragments or their functional equivalents or biosimilars. In some other embodiments, the checkpoint inhibitor co-expressed with CAR is pembrolizumab, or its humanized, or Fc modified variants, fragments or their functional equivalents or biosimilars.

[000236] In some other embodiments of the combination therapy comprising the iPSC-derived cells provided herein and at least one antibody inhibiting a checkpoint molecule, said antibody is not produced by, or in, the iPSC-derived cells and is additionally administered before, with, or after the administering of the iPSC-derived cells having a genotype listed in Table 1. In some embodiments, the administering of one, two, three or more checkpoint inhibitors in a combination therapy with the provided derivative NK or T cells are simultaneous or sequential.

In one embodiment of the combination treatment comprising derived NK cells or T cells having a genotype listed in Table 1, the checkpoint inhibitor included in the treatment is one or more of atezolizumab, avelumab, durvalumab, tremelimumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their humanized or Fc modified variants, fragments and their functional equivalents or biosimilars. In some embodiments of the combination treatment comprising derived NK cells or T cells having a genotype listed in Table 1, the checkpoint inhibitor included in the treatment is atezolizumab, or its humanized or Fc modified variant, fragment and its functional equivalent or biosimilar. In some embodiments of the combination treatment comprising derived NK cells or T cells having a genotype listed in Table 1, the checkpoint inhibitor included in the treatment is nivolumab, or its humanized or Fc modified variant, fragment or its functional equivalent or biosimilar. In some embodiments of the combination treatment comprising derived NK cells or T cells having a genotype listed in Table 1, the checkpoint inhibitor included in the treatment is pembrolizumab, or its humanized or Fc modified variant, fragment or its functional equivalent or biosimilar.

II. Methods for Targeted Genome Editing at Selected Locus in iPSCs

[000237] Genome editing, or genomic editing, or genetic editing, as used interchangeably herein, is a type of genetic engineering in which DNA is inserted, deleted, and/or replaced in the genome of a targeted cell. Targeted genome editing (interchangeable with "targeted genomic editing" or "targeted genetic editing") enables insertion, deletion, and/or substitution at pre-selected sites in the genome. When an endogenous sequence is deleted at the insertion site during targeted editing, an endogenous gene comprising the affected sequence may be knocked-out or knocked-down due to the sequence deletion. Therefore, targeted editing may also be used to disrupt endogenous gene expression with precision. Similarly used herein is the term "targeted integration," referring to a process involving insertion of one or more exogenous sequences, with or without deletion of an endogenous sequence at the insertion site. In comparison, randomly integrated genes are subject to position effects and silencing, making their expression unreliable and unpredictable. For example, centromeres and sub-telomeric regions are particularly prone to transgene silencing. Reciprocally, newly integrated genes may affect the surrounding endogenous genes and chromatin, potentially altering cell behavior or favoring cellular transformation. Therefore, inserting exogenous DNA in a pre-selected locus such as a safe harbor locus, or genomic safe harbor (GSH) is important for safety, efficiency, copy number control, and for reliable gene response control.

[000238] Targeted editing can be achieved either through a nuclease-independent approach, or through a nuclease-dependent approach. In the nuclease-independent targeted editing approach, homologous recombination is guided by homologous sequences flanking an exogenous polynucleotide to be inserted, through the enzymatic machinery of the host cell.

[000239] Alternatively, targeted editing could be achieved with higher frequency through specific introduction of double strand breaks (DSBs) by specific rare-cutting endonucleases. Such nuclease-dependent targeted editing utilizes DNA repair mechanisms including non-homologous end joining (NHEJ), which occurs in response to DSBs. Without a donor vector containing exogenous genetic material, the NHEJ often leads to random insertions or deletions (in/dels) of a small number of endogenous nucleotides. In comparison, when a donor vector containing exogenous genetic material flanked by a pair of homology arms is present, the exogenous genetic material can be introduced into the genome during homology directed repair (HDR) by homologous recombination, resulting in a "targeted integration." In some situations, the targeted integration site is intended to be within a coding region of a selected gene, and thus the targeted integration could disrupt the gene expression, resulting in simultaneous knock-in and knockout (KI/KO) in one single editing step.

[000240] Inserting one or more transgenes at a selected position in a gene locus of interest (GOI) to knock out the gene at the same time can be achieved. Gene loci suitable for simultaneous knock-in and knockout (KI/KO) include, but are not limited to, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, and TIGIT. With respective site-specific targeting homology arms for position-selective insertion, it allows the transgene(s) to express either under an endogenous promoter at the site or under an exogenous promoter comprised in the construct. When two or more transgenes are to be inserted at a selected location (e.g., in a CD38 locus), a linker sequence, for example, a 2A linker or IRES, is placed between any two transgenes. The 2A linker encodes a self-cleaving peptide derived from FMDV, ERAV, PTV-I, or TaV (referred to as "F2A", "E2A", "P2A", and "T2A", respectively), allowing for separate proteins to be produced from a single translation. In some embodiments, insulators are included in the construct to reduce the risk of transgene and/or exogenous promoter silencing. The exogenous promoter may be CAG, or other constitutive, inducible, temporal-, tissue-, or cell type- specific promoters including, but not limited to CMV, EF1α, PGK, and UBC.

[000241] Available endonucleases capable of introducing specific and targeted DSBs include, but not limited to, zinc-finger nucleases (ZFN), transcription activator-like effector nucleases

(TALEN), RNA-guided CRISPR (Clustered Regular Interspaced Short Palindromic Repeats) systems. Additionally, DICE (dual integrase cassette exchange) system utilizing phiC31 and Bxb1 integrases is also a promising tool for targeted integration.

[000242] ZFNs are targeted nucleases comprising a nuclease fused to a zinc finger DNA binding domain. By a "zinc finger DNA binding domain" or "ZFBD" it is meant a polypeptide domain that binds DNA in a sequence-specific manner through one or more zinc fingers. A zinc finger is a domain of about 30 amino acids within the zinc finger binding domain whose structure is stabilized through coordination of a zinc ion. Examples of zinc fingers include, but not limited to, C_2H_2 zinc fingers, C_3H zinc fingers, and C_4 zinc fingers. A "designed" zinc finger domain is a domain not occurring in nature whose design/composition results principally from rational criteria, e.g., application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP designs and binding data. See, for example, U.S. Pat. Nos. 6,140,081; 6,453,242; and 6,534,261; see also WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536 and WO 03/016496. A "selected" zinc finger domain is a domain not found in nature whose production results primarily from an empirical process such as phage display, interaction trap or hybrid selection. ZFNs are described in greater detail in U.S. Pat. No. 7,888,121 and U.S. Pat. No. 7,972,854, the complete disclosures of which are incorporated herein by reference. The most recognized example of a ZFN in the art is a fusion of the FokI nuclease with a zinc finger DNA binding domain.

[000243] A TALEN is a targeted nuclease comprising a nuclease fused to a TAL effector DNA binding domain. By "transcription activator-like effector DNA binding domain", "TAL effector DNA binding domain", or "TALE DNA binding domain" it is meant the polypeptide domain of TAL effector proteins that is responsible for binding of the TAL effector protein to DNA. TAL effector proteins are secreted by plant pathogens of the genus *Xanthomonas* during infection. These proteins enter the nucleus of the plant cell, bind effector-specific DNA sequences via their DNA binding domain, and activate gene transcription at these sequences via their transactivation domains. TAL effector DNA binding domain specificity depends on an effector-variable number of imperfect 34 amino acid repeats, which comprise polymorphisms at select repeat positions called repeat variable-diresidues (RVD). TALENs are described in greater detail in US Patent Application No. 2011/0145940, which is herein incorporated by reference. The most recognized example of a TALEN in the art is a fusion polypeptide of the FokI nuclease to a TAL effector DNA binding domain.

[000244] Another example of a targeted nuclease that finds use in the subject methods is a targeted Spo11 nuclease, a polypeptide comprising a Spo11 polypeptide having nuclease activity

fused to a DNA binding domain, e.g. a zinc finger DNA binding domain, a TAL effector DNA binding domain, etc. that has specificity for a DNA sequence of interest. See, for example, U.S. Application No. 61/555,857, the disclosure of which is incorporated herein by reference.

[000245] Additional examples of targeted nucleases suitable for the present invention include, but not limited to Bxb1, phiC31, R4, PhiBT1, and Wβ/SPBc/TP901-1, whether used individually or in combination.

[000246] Other non-limiting examples of targeted nucleases include naturally occurring and recombinant nucleases; CRISPR related nucleases from families including cas, cpf, cse, csy, csn, csd, cst, csh, csa, csm, and cmr; restriction endonucleases; meganucleases; homing endonucleases, and the like.

[000247] As an exemplary example, CRISPR/Cas9 requires two major components: (1) a Cas9 endonuclease and (2) the crRNA-tracrRNA complex. When co-expressed, the two components form a complex that is recruited to a target DNA sequence comprising PAM and a seeding region near PAM. The crRNA and tracrRNA can be combined to form a chimeric guide RNA (gRNA) to guide Cas9 to target selected sequences. These two components can then be delivered to mammalian cells via transfection or transduction. When use the CRISPR/Cpf system, it requires a Cpf endonuclease (Cpf1, MAD7 and many more known in the art) and (2) the gNA, which often does not need tracrRNA, to guide Cpf endonuclease to target selected sequences.

[000248] DICE mediated insertion uses a pair of recombinases, for example, phiC31 and Bxb1, to provide unidirectional integration of an exogenous DNA that is tightly restricted to each enzymes' own small attB and attP recognition sites. Because these target att sites are not naturally present in mammalian genomes, they must be first introduced into the genome, at the desired integration site. See, for example, U.S. Application Publication No. 2015/0140665, the disclosure of which is incorporated herein by reference.

[000249] One aspect of the present invention provides a construct comprising one or more exogenous polynucleotides for targeted genome integration. In one embodiment, the construct further comprises a pair of homologous arm specific to a desired integration site, and the method of targeted integration comprises introducing the construct to cells to enable site specific homologous recombination by the cell host enzymatic machinery. In another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more exogenous polynucleotides to the cell and introducing a ZFN expression cassette comprising a DNA-binding domain specific to a desired integration site to the cell to enable a ZFN-mediated insertion. In yet another embodiment, the method of targeted integration in a cell

comprises introducing a construct comprising one or more exogenous polynucleotides to the cell and introducing a TALEN expression cassette comprising a DNA-binding domain specific to a desired integration site to the cell to enable a TALEN-mediated insertion. In another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more exogenous polynucleotides to the cell, introducing a Cas9 expression cassette, and a gRNA comprising a guide sequence specific to a desired integration site to the cell to enable a Cas9-mediated insertion. In still another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more att sites of a pair of DICE recombinases to a desired integration site in the cell, introducing a construct comprising one or more exogenous polynucleotides to the cell, and introducing an expression cassette for DICE recombinases, to enable DICE-mediated targeted integration.

[000250] Promising sites for targeted integration include, but are not limited to, safe harbor loci, or genomic safe harbor (GSH), which are intragenic or extragenic regions of the human genome that, theoretically, are able to accommodate predictable expression of newly integrated DNA without adverse effects on the host cell or organism. A useful safe harbor must permit sufficient transgene expression to yield desired levels of the vector-encoded protein or non-coding RNA. A safe harbor also must not predispose cells to malignant transformation nor alter cellular functions. For an integration site to be a potential safe harbor locus, it ideally needs to meet criteria including, but not limited to: absence of disruption of regulatory elements or genes, as judged by sequence annotation; is an intergenic region in a gene dense area, or a location at the convergence between two genes transcribed in opposite directions; keep distance to minimize the possibility of long-range interactions between vector-encoded transcriptional activators and the promoters of adjacent genes, particularly cancer-related and microRNA genes; and has apparently ubiquitous transcriptional activity, as reflected by broad spatial and temporal expressed sequence tag (EST) expression patterns, indicating ubiquitous transcriptional activity. This latter feature is especially important in stem cells, where during differentiation, chromatin remodeling typically leads to silencing of some loci and potential activation of others. Within the region suitable for exogenous insertion, a precise locus chosen for insertion should be devoid of repetitive elements and conserved sequences and to which primers for amplification of homology arms could easily be designed.

[000251] Suitable sites for human genome editing, or specifically, targeted integration, include, but are not limited to the adeno-associated virus site 1 (AAVS1), the chemokine (CC motif) receptor 5 (*CCR5*) gene locus and the human orthologue of the mouse ROSA26 locus. Additionally, the human orthologue of the mouse H11 locus may also be a suitable site for

insertion using the composition and method of targeted integration disclosed herein. Further, collagen and HTRP gene loci may also be used as safe harbor for targeted integration. However, validation of each selected site has been shown to be necessary especially in stem cells for specific integration events, and optimization of insertion strategy including promoter election, exogenous gene sequence and arrangement, and construct design is often needed.

[000252] For targeted in/dels, the editing site is often comprised in an endogenous gene whose expression and/or function is intended to be disrupted. In one embodiments, the endogenous gene comprising a targeted in/del is associated with immune response regulation and modulation. In some other embodiments, the endogenous gene comprising a targeted in/del is associated with targeting modality, receptors, signaling molecules, transcription factors, drug target candidates, immune response regulation and modulation, or proteins suppressing engraftment, trafficking, homing, viability, self-renewal, persistence, and/or survival of stem cells and/or progenitor cells, and the derived cells therefrom.

[000253] As such, one aspect of the present invention provides a method of targeted integration in a selected locus including genome safe harbor or a preselected locus known or proven to be safe and well-regulated for continuous or temporal gene expression such as the B2M, TAP1, TAP2, Tapasin, TRAC, or CD38 locus as provided herein. In one embodiment, the genome safe harbor for the method of targeted integration comprises one or more desired integration site comprising AAVS1, CCR5, ROSA26, collagen, HTRP, H11, beta-2 microglobulin, CD38, GAPDH, TCR or RUNX1, or other loci meeting the criteria of a genome safe harbor. In some embodiments, the targeted integration is in one or more gene loci where the knock-down or knockout of the gene as a result of the integration is desired, wherein such gene loci include, but are not limited to, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, and TIGIT.

[000254] In one embodiment, the method of targeted integration in a cell comprising introducing a construct comprising one or more exogenous polynucleotides to the cell, and introducing a construct comprising a pair of homologous arm specific to a desired integration site and one or more exogenous sequence, to enable site specific homologous recombination by the cell host enzymatic machinery, wherein the desired integration site comprises AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT.

[000255] In another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more exogenous polynucleotides to the cell, and introducing a ZFN expression cassette comprising a DNA-binding domain specific to a desired integration site to the cell to enable a ZFN-mediated insertion, wherein the desired integration site comprises AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT. In yet another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more exogenous polynucleotides to the cell, and introducing a TALEN expression cassette comprising a DNA-binding domain specific to a desired integration site to the cell to enable a TALEN-mediated insertion, wherein the desired integration site comprises AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT. In another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more exogenous polynucleotides to the cell, introducing a Cas9 expression cassette, and a gRNA comprising a guide sequence specific to a desired integration site to the cell to enable a Cas9-mediated insertion, wherein the desired integration site comprises AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT. In still another embodiment, the method of targeted integration in a cell comprises introducing a construct comprising one or more att sites of a pair of DICE recombinases to a desired integration site in the cell, introducing a construct comprising one or more exogenous polynucleotides to the cell, and introducing an expression cassette for DICE recombinases, to enable DICE-mediated targeted integration, wherein the desired integration site comprises AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT.

[000256] Further, as provided herein, the above method for targeted integration in a safe harbor is used to insert any polynucleotide of interest, for example, polynucleotides encoding safety switch proteins, targeting modality, receptors, signaling molecules, transcription factors, pharmaceutically active proteins and peptides, drug target candidates, and proteins promoting

engraftment, trafficking, homing, viability, self-renewal, persistence, and/or survival of stem cells and/or progenitor cells. In some other embodiments, the construct comprising one or more exogenous polynucleotides further comprises one or more marker genes. In one embodiment, the exogenous polynucleotide in a construct of the invention is a suicide gene encoding safety switch protein. Suitable suicide gene systems for induced cell death include, but not limited to Caspase 9 (or caspase 3 or 7) and AP1903; thymidine kinase (TK) and ganciclovir (GCV); cytosine deaminase (CD) and 5-fluorocytosine (5-FC). Additionally, some suicide gene systems are cell type specific, for example, the genetic modification of T lymphocytes with the B-cell molecule CD20 allows their elimination upon administration of mAb Rituximab. Further, modified EGFR containing epitope recognized by cetuximab can be used to deplete genetically engineered cells when the cells are exposed to cetuximab. As such, one aspect of the invention provides a method of targeted integration of one or more suicide genes encoding safety switch proteins selected from caspase 9 (caspase 3 or 7), thymidine kinase, cytosine deaminase, modified EGFR, and B-cell CD20.

[000257] In some embodiments, one or more exogenous polynucleotides integrated by the method herein are driven by operatively linked exogenous promoters comprised in the construct for targeted integration. The promoters may be inducible, or constructive, and may be temporal-, tissue- or cell type- specific. Suitable constructive promoters for methods of the invention include, but not limited to, cytomegalovirus (CMV), elongation factor 1α (EF1α), phosphoglycerate kinase (PGK), hybrid CMV enhancer/chicken β-actin (CAG) and ubiquitin C (UBC) promoters. In one embodiment, the exogenous promoter is CAG.

[000258] The exogenous polynucleotides integrated by the method herein may be driven by endogenous promoters in the host genome, at the integration site. In one embodiment, the method of the invention is used for targeted integration of one or more exogenous polynucleotides at AAVS1 locus in the genome of a cell. In one embodiment, at least one integrated polynucleotide is driven by the endogenous AAVS1 promoter. In another embodiment, the method of the invention is used for targeted integration at ROSA26 locus in the genome of a cell. In one embodiment, at least one integrated polynucleotide is driven by the endogenous ROSA26 promoter. In still another embodiment, the method of the invention is used for targeted integration at H11 locus in the genome of a cell. In one embodiment, at least one integrated polynucleotide is driven by the endogenous H11 promoter. In another embodiment, the method of the invention is used for targeted integration at collagen locus in the genome of a cell. In one embodiment, at least one integrated polynucleotide is driven by the endogenous collagen promoter. In still another embodiment, the method of the invention is used for targeted

integration at HTRP locus in the genome of a cell. In one embodiment, at least one integrated polynucleotide is driven by the endogenous HTRP promoter. Theoretically, only correct insertions at the desired location would enable gene expression of an exogenous gene driven by an endogenous promoter.

[000259] In some embodiments, the one or more exogenous polynucleotides comprised in the construct for the methods of targeted integration are driven by one promoter. In some embodiments, the construct comprises one or more linker sequences between two adjacent polynucleotides driven by the same promoter to provide greater physical separation between the moieties and maximize the accessibility to enzymatic machinery. The linker peptide of the linker sequences may consist of amino acids selected to make the physical separation between the moieties (exogenous polynucleotides, and/or the protein or peptide encoded therefrom) more flexible or more rigid depending on the relevant function. The linker sequence may be cleavable by a protease or cleavable chemically to yield separate moieties. Examples of enzymatic cleavage sites in the linker include sites for cleavage by a proteolytic enzyme, such as enterokinase, Factor Xa, trypsin, collagenase, and thrombin. In some embodiments, the protease is one which is produced naturally by the host or it is exogenously introduced. Alternatively, the cleavage site in the linker may be a site capable of being cleaved upon exposure to a selected chemical, e.g., cyanogen bromide, hydroxylamine, or low pH. The optional linker sequence may serve a purpose other than the provision of a cleavage site. The linker sequence should allow effective positioning of the moiety with respect to another adjacent moiety for the moieties to function properly. The linker may also be a simple amino acid sequence of a sufficient length to prevent any steric hindrance between the moieties. In addition, the linker sequence may provide for post-translational modification including, but not limited to, e.g., phosphorylation sites, biotinylation sites, sulfation sites, γ-carboxylation sites, and the like. In some embodiments, the linker sequence is flexible so as not hold the biologically active peptide in a single undesired conformation. The linker may be predominantly comprised of amino acids with small side chains, such as glycine, alanine, and serine, to provide for flexibility. In some embodiments about 80 or 90 percent or greater of the linker sequence comprises glycine, alanine, or serine residues, particularly glycine and serine residues. In several embodiments, a G4S linker peptide separates the end-processing and endonuclease domains of the fusion protein. In other embodiments, a 2A linker sequence allows for two separate proteins to be produced from a single translation. Suitable linker sequences can be readily identified empirically. Additionally, suitable size and sequences of linker sequences also can be determined by conventional computer modeling techniques. In one embodiment, the linker sequence encodes a self-cleaving peptide. In one

embodiment, the self-cleaving peptide is 2A. In some other embodiments, the linker sequence provides an Internal Ribosome Entry Sequence (IRES). In some embodiments, any two consecutive linker sequences are different.

[000260] The method of introducing into cells a construct comprising exogenous polynucleotides for targeted integration can be achieved using a method of gene transfer to cells known per se. In one embodiment, the construct comprises backbones of viral vectors such as adenovirus vector, adeno-associated virus vector, retrovirus vector, lentivirus vector, Sendai virus vector. In some embodiments, the plasmid vectors are used for delivering and/or expressing the exogenous polynucleotides to target cells (e.g., pAl- 11, pXTl, pRc/CMV, pRc/RSV, pcDNAI/Neo) and the like. In some other embodiments, the episomal vector is used to deliver the exogenous polynucleotide to target cells. In some embodiments, recombinant adeno-associated viruses (rAAV) can be used for genetic engineering to introduce insertions, deletions or substitutions through homologous recombinations. Unlike lentiviruses, rAAVs do not integrate into the host genome. In addition, episomal rAAV vectors mediate homology-directed gene targeting at much higher rates compared to transfection of conventional targeting plasmids. In some embodiments, an AAV6 or AAV2 vector is used to introduce insertions, deletions or substitutions in a target site in the genome of iPSCs. In some embodiments, the genomically modified iPSCs and its derivative cells obtained using the methods and composition herein comprise at least one genotype listed in Table 1.

III. Method of Obtaining and Maintaining Genome-engineered iPSCs

[000261] The present invention provides a method of obtaining and maintaining genome-engineered iPSCs comprising one or more targeted editing at one or more desired sites, wherein the targeted editing remains intact and functional in expanded genome-engineered iPSCs or the iPSCs derived non-pluripotent cells at the respective selected editing site. The targeted editing introduces into the genome iPSC, and derivative cells therefrom, insertions, deletions, and/or substitutions, i.e., targeted integration and/or in/dels at selected sites. In comparison to direct engineering patient-sourced, peripheral blood originated primary effector cells, the many benefits of obtaining genomically engineered iPSC-derived through editing and differentiating iPSC as provided herein include, but are not limited to: unlimited source for engineered effector cells; no need for repeated manipulation of the effector cells especially when multiple engineered modalities are involved; the obtained effector cells are rejuvenated for having elongated telomere and experiencing less exhaustion; the effector cell population is homogeneous in terms of editing site, copy number, and void of allelic variation, random mutations and expression variegation, largely due to the enabled clonal selection in engineered iPSCs as provided herein.

[000262] In particular embodiments, the genome-engineered iPSCs comprising one or more targeted editing at one or more selected sites are maintained, passaged and expanded as single cells for an extended period in the cell culture medium shown in Table 2 as Fate Maintenance Medium (FMM), wherein the iPSCs retain the targeted editing and functional modification at the selected site(s). The components of the medium may be present in the medium in amounts within an optimal range shown in Table 2. The iPSCs cultured in FMM have been shown to continue to maintain their undifferentiated, and ground or naïve, profile; genomic stability without the need for culture cleaning or selection; and are readily to give rise to all three somatic lineages, *in vitro* differentiation via embryoid bodies or monolayer (without formation of embryoid bodies); and *in vivo* differentiation by teratoma formation. See, for example, U.S. Application No. 61/947,979, the disclosure of which is incorporated herein by reference.

Table 2: Exemplary media for iPSC reprogramming and maintenance

Conventional hESC Medium (Conv.)	**Fate Reprogramming Medium (FRM)**	**Fate Maintenance Medium (FMM)**
DMEM/F12	DMEM/F12	DMEM/F12
Knockout Serum Replacement (20%)	Knockout Serum Replacement (20%)	Knockout Serum Replacement (20%)
	N2	
	B27	
Glutamine	Glutamine	Glutamine (1x)
Non-Essential Amino Acids (1x)	Non-Essential Amino Acids (1x)	Non-Essential Amino Acids (1x)
β-mercaptoethanol (100μM)	β-mercaptoethanol (100μM)	β-mercaptoethanol (100μM)
bFGF (0.2-50 ng/mL)	bFGF (2-500 ng/mL)	bFGF (2-500 ng/mL)
	LIF (0.2-50 ng/mL)	LIF (0.2-50 ng/mL)
	Thiazovivin (0.1-25 μM)	Thiazovivin (0.1-25 μM)
	PD0325901 (0.005-2 μM)	PD0325901 (0.005-2 μM)
	CHIR99021 (0.02-5 μM)	CHIR99021 (0.02-5 μM)
	SB431542 (0.04-10 μM)	
In combination with MEF feeder cells	Feeder-free, in combination with Matrigel™ or Vitronectin	

[000263] In some embodiments, the genome-engineered iPSCs comprising one or more targeted integration and/or in/dels are maintained, passaged and expanded in a medium comprising a MEK inhibitor, a GSK3 inhibitor, and a ROCK inhibitor, and free of, or essentially free of, TGFβ receptor/ALK5 inhibitors, wherein the iPSCs retain the intact and functional targeted editing at the selected sites.

[000264] Another aspect of the invention provides a method of generating genome-engineered iPSCs through targeted editing of iPSCs; or through first generating genome-engineered non-pluripotent cells by targeted editing, and then reprogramming the selected/isolated genome-engineered non-pluripotent cells to obtain iPSCs comprising the same targeted editing as the non-pluripotent cells. A further aspect of the invention provides genome-engineering non-pluripotent cells which are concurrently undergoing reprogramming by introducing targeted integration and/or targeted in/dels to the cells, wherein the contacted non-pluripotent cells are under sufficient conditions for reprogramming, and wherein the conditions for reprogramming comprise contacting non-pluripotent cells with one or more reprogramming factors and small molecules. In various embodiments of the method for concurrent genome-engineering and reprogramming, the targeted integration and/or targeted in/dels may be introduced to the non-pluripotent cells prior to, or essentially concomitantly with, initiating reprogramming by contacting the non-pluripotent cells with one or more reprogramming factors and optionally small molecules.

[000265] In some embodiments, to concurrently genome-engineer and reprogram non-pluripotent cells, the targeted integration and/or in/dels may also be introduced to the non-pluripotent cells after the multi-day process of reprogramming is initiated by contacting the non-pluripotent cells with one or more reprogramming factors and small molecules, and wherein the vectors carrying the constructs are introduced before the reprogramming cells present stable expression of one or more endogenous pluripotent genes including but not limited to SSEA4, Tra181 and CD30.

[000266] In some embodiments, the reprogramming is initiated by contacting the non-pluripotent cells with at least one reprogramming factor, and optionally a combination of a TGFβ receptor/ALK inhibitor, a MEK inhibitor, a GSK3 inhibitor and a ROCK inhibitor (FRM; Table 2). In some embodiments, the genome-engineered iPSCs through any methods above are further maintained and expanded using a mixture of comprising a combination of a MEK inhibitor, a GSK3 inhibitor and a ROCK inhibitor (FMM; Table 2).

[000267] In some embodiments of the method of generating genome-engineered iPSCs, the method comprises: genomic engineering an iPSC by introducing one or more targeted integration

and/or in/dels into iPSCs to obtain genome-engineered iPSCs having at least one genotype listed in Table 1. Alternatively, the method of generating genome-engineered iPSCs comprises: (a) introducing one or more targeted editing into non-pluripotent cells to obtain genome-engineered non-pluripotent cells comprising targeted integration and/or in/dels at selected sites, and (b) contacting the genome-engineered non-pluripotent cells with one or more reprogramming factors, and optionally a small molecule composition comprising a TGFβ receptor/ALK inhibitor, a MEK inhibitor, a GSK3 inhibitor and/or a ROCK inhibitor, to obtain genome-engineered iPSCs comprising targeted integration and/or in/dels at selected sites. Alternatively, the method of generating genome-engineered iPSCs comprises: (a) contacting non-pluripotent cells with one or more reprogramming factors, and optionally a small molecule composition comprising a TGFβ receptor/ALK inhibitor, a MEK inhibitor, a GSK3 inhibitor and/or a ROCK inhibitor to initiate the reprogramming of the non-pluripotent cells; (b) introducing one or more targeted integration and/or in/dels into the reprogramming non-pluripotent cells for genome-engineering; and (c) obtaining genome-engineered iPSCs comprising targeted integration and/or in/dels at selected sites. Any of the above methods may further comprise single cell sorting genome-engineered iPSCs to obtain a clonal iPSC. Through clonal expansion of this genome-engineered iPSC, a master cell bank is generated to comprise single cell sorted and expanded clonal engineered iPSCs having at least one phenotype as provided herein in Table 1. The master cell bank is subsequently cryopreserved, providing a platform for additional iPSC engineering and a renewable source for manufacturing off-the-shelf, engineered, homogeneous cell therapy products, which are well-defined and uniform in composition, and can be mass produced at significant scale in a cost-effective manner.

[000268] The reprogramming factors are selected from the group consisting of OCT4, SOX2, NANOG, KLF4, LIN28, C-MYC, ECAT1, UTF1, ESRRB, SV40LT, HESRG, CDH1, TDGF1, DPPA4, DNMT3B, ZIC3, L1TD1, and any combinations thereof as disclosed in PCT/US2015/018801 and PCT/US16/57136, the disclosure of which are incorporated herein by reference. The one or more reprogramming factors may be in a form of polypeptide. The reprogramming factors may also be in a form of polynucleotides, and thus are introduced to the non-pluripotent cells by vectors such as, a retrovirus, a Sendai virus, an adenovirus, an episome, a plasmid, and a mini-circle. In particular embodiments, the one or more polynucleotides encoding at least one reprogramming factor are introduced by a lentiviral vector. In some embodiments, the one or more polynucleotides introduced by an episomal vector. In various other embodiments, the one or more polynucleotides are introduced by a Sendai viral vector. In some embodiments, the one or more polynucleotides introduced by a combination of plasmids.

See, for example, U.S. Application No. 62/571,105, the disclosure of which is incorporated herein by reference.

[000269] In some embodiments, the non-pluripotent cells are transferred with multiple constructs comprising different exogenous polynucleotides and/or different promoters by multiple vectors for targeted integration at the same or different selected sites. These exogenous polynucleotides may comprise a suicide gene, or a gene encoding targeting modality, receptors, signaling molecules, transcription factors, pharmaceutically active proteins and peptides, drug target candidates, or a gene encoding a protein promoting engraftment, trafficking, homing, viability, self-renewal, persistence, and/or survival of the iPSCs or derivative cells therefrom. In some embodiments, the exogenous polynucleotides encode RNA, including but not limited to siRNA, shRNA, miRNA and antisense nucleic acids. These exogenous polynucleotides may be driven by one or more promoters selected form the group consisting of constitutive promoters, inducible promoters, temporal-specific promoters, and tissue or cell type specific promoters. Accordingly, the polynucleotides are expressible when under conditions that activate the promoter, for example, in the presence of an inducing agent or in a particular differentiated cell type. In some embodiments, the polynucleotides are expressed in iPSCs and/or in cells differentiated from the iPSCs. In one embodiment, one or more suicide gene is driven by a constitutive promoter, for example Capase-9 driven by CAG. These constructs comprising different exogenous polynucleotides and/or different promoters can be transferred to non-pluripotent cells either simultaneously or consecutively. The non-pluripotent cells subjecting to targeted integration of multiple constructs can simultaneously contact the one or more reprogramming factors to initiate the reprogramming concurrently with the genomic engineering, thereby obtaining genome-engineered iPSCs comprising multiple targeted integration in the same pool of cells. As such, this robust method enables a concurrent reprogramming and engineering strategy to derive a clonal genomically engineered hiPSC with multiple modalities integrated to one or more selected target sites. In some embodiments, the genomically modified iPSCs and its derivative cells obtained using the methods and composition herein comprise at least one genotype listed in Table 1.

IV. A method of Obtaining Genetically-Engineered Effector Cells by Differentiating Genome-engineered iPSC

[000270] A further aspect of the present invention provides a method of *in vivo* differentiation of genome-engineered iPSC by teratoma formation, wherein the differentiated cells derived *in vivo* from the genome-engineered iPSCs retain the intact and functional targeted

editing including targeted integration and/or in/dels at the desired site(s). In some embodiments, the differentiated cells derived *in vivo* from the genome-engineered iPSCs via teratoma comprise one or more inducible suicide genes integrated at one or more desired site comprising AAVS1, CCR5, ROSA26, collagen, HTRP H11, beta-2 microglobulin, CD38, GAPDH, TCR or RUNX1, or other loci meeting the criteria of a genome safe harbor. In some other embodiments, the differentiated cells derived *in vivo* from the genome-engineered iPSCs via teratoma comprise polynucleotides encoding targeting modality, or encoding proteins promoting trafficking, homing, viability, self-renewal, persistence, and/or survival of stem cells and/or progenitor cells. In some embodiments, the differentiated cells derived *in vivo* from the genome-engineered iPSCs via teratoma comprising one or more inducible suicide genes further comprises one or more in/dels in endogenous genes associated with immune response regulation and mediation. In some embodiments, the in/del is comprised in one or more endogenous check point genes. In some embodiments, the in/del is comprised in one or more endogenous T cell receptor genes. In some embodiments, the in/del is comprised in one or more endogenous MHC class I suppressor genes. In some embodiments, the in/del is comprised in one or more endogenous genes associated with the major histocompatibility complex. In some embodiments, the in/del is comprised in one or more endogenous genes including, but not limited to, AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT. In one embodiment, the genome-engineered iPSC comprising one or more exogenous polynucleotides at selected site(s) further comprises a targeted editing in B2M (beta-2-microglobulin) encoding gene.

[000271] In particular embodiments, the genome-engineered iPSCs comprising one or more genetic modifications as provided herein are used to derive hematopoietic cell lineages or any other specific cell types *in vitro*, wherein the derived non-pluripotent cells retain the functional genetic modifications including targeted editing at the selected site(s). In some embodiments, the genome-engineered iPSCs used to derive hematopoietic cell lineages or any other specific cell types *in vitro* are master cell bank cells that are cryopreserved and thawed right before their usage. In one embodiment, the genome-engineered iPSC-derived cells include, but are not limited to, mesodermal cells with definitive hemogenic endothelium (HE) potential, definitive HE, CD34 hematopoietic cells, hematopoietic stem and progenitor cells, hematopoietic multipotent progenitors (MPP), T cell progenitors, NK cell progenitors, myeloid cells, neutrophil progenitors, T cells, NKT cells, NK cells, B cells, neutrophils, dendritic cells, and macrophages,

wherein these cells derived from the genome-engineered iPSCs retain the functional genetic modifications including targeted editing at the desired site(s).

[000272] Applicable differentiation methods and compositions for obtaining iPSC-derived hematopoietic cell lineages include those depicted in, for example, International Application No. PCT/US2016/044122, the disclosure of which is incorporated herein by reference. As provided, the methods and compositions for generating hematopoietic cell lineages are through definitive hemogenic endothelium (HE) derived from pluripotent stem cells, including hiPSCs, under serum-free, feeder-free, and/or stromal-free conditions and in a scalable and monolayer culturing platform without the need of EB formation. Cells that may be differentiated according to the provided methods range from pluripotent stem cells, to progenitor cells that are committed to particular terminally differentiated cells and transdifferentiated cells, and to cells of various lineages directly transitioned to hematopoietic fate without going through a pluripotent intermediate. Similarly, the cells that are produced by differentiating stem cells range from multipotent stem or progenitor cells, to terminally differentiated cells, and to all intervening hematopoietic cell lineages.

[000273] The methods for differentiating and expanding cells of the hematopoietic lineage from pluripotent stem cells in monolayer culturing comprise contacting the pluripotent stem cells with a BMP pathway activator, and optionally, bFGF. As provided, the pluripotent stem cell-derived mesodermal cells are obtained and expanded without forming embryoid bodies from pluripotent stem cells. The mesodermal cells are then subjected to contact with a BMP pathway activator, bFGF, and a WNT pathway activator to obtain expanded mesodermal cells having definitive hemogenic endothelium (HE) potential without forming embryoid bodies from the pluripotent stem cells. By subsequent contact with bFGF, and optionally, a ROCK inhibitor, and/or a WNT pathway activator, the mesodermal cells having definitive HE potential are differentiated to definitive HE cells, which are also expanded during differentiation.

[000274] The methods provided herein for obtaining cells of the hematopoietic lineage are superior to EB-mediated pluripotent stem cell differentiation, because EB formation leads to modest to minimal cell expansion, does not allow monolayer culturing which is important for many applications requiring homogeneous expansion, and homogeneous differentiation of the cells in a population, and is laborious and low efficiency.

[000275] The provided monolayer differentiation platform facilitates differentiation towards definitive hemogenic endothelium resulting in the derivation of hematopoietic stem cells and differentiated progeny such as T, B, NKT and NK cells. The monolayer differentiation strategy combines enhanced differentiation efficiency with large-scale expansion enables the delivery of

therapeutically relevant number of pluripotent stem cell-derived hematopoietic cells for various therapeutic applications. Further, the monolayer culturing using the methods provided herein leads to functional hematopoietic lineage cells that enable full range of *in vitro* differentiation, *ex vivo* modulation, and *in vivo* long term hematopoietic self-renewal, reconstitution and engraftment. As provided, the iPSC derived hematopoietic lineage cells include, but not limited to, definitive hemogenic endothelium, hematopoietic multipotent progenitor cells, hematopoietic stem and progenitor cells, T cell progenitors, NK cell progenitors, T cells, NK cells, NKT cells, B cells, macrophages, and neutrophils.

[000276] The method for directing differentiation of pluripotent stem cells into cells of a definitive hematopoietic lineage, wherein the method comprises: (i) contacting pluripotent stem cells with a composition comprising a BMP activator, and optionally bFGF, to initiate differentiation and expansion of mesodermal cells from the pluripotent stem cells; (ii) contacting the mesodermal cells with a composition comprising a BMP activator, bFGF, and a GSK3 inhibitor, wherein the composition is optionally free of TGFβ receptor/ALK inhibitor, to initiate differentiation and expansion of mesodermal cells having definitive HE potential from the mesodermal cells; (iii) contacting the mesodermal cells having definitive HE potential with a composition comprising a ROCK inhibitor; one or more growth factors and cytokines selected from the group consisting of bFGF, VEGF, SCF, IGF, EPO, IL6, and IL11; and optionally, a Wnt pathway activator, wherein the composition is optionally free of TGFβ receptor/ALK inhibitor, to initiate differentiation and expansion of definitive hemogenic endothelium from pluripotent stem cell-derived mesodermal cells having definitive hemogenic endothelium potential.

[000277] In some embodiments, the method further comprises contacting pluripotent stem cells with a composition comprising a MEK inhibitor, a GSK3 inhibitor, and a ROCK inhibitor, wherein the composition is free of TGFβ receptor/ALK inhibitors, to seed and expand the pluripotent stem cells. In some embodiments, the pluripotent stem cells are iPSCs, or naïve iPSCs, or iPSCs comprising one or more genetic imprints; and the one or more genetic imprints comprised in the iPSC are retained in the hematopoietic cells differentiated therefrom. In some embodiments of the method for directing differentiation of pluripotent stem cells into cells of a hematopoietic lineage, the differentiation of the pluripotent stem cells into cells of hematopoietic lineage is void of generation of embryoid bodies and is in a monolayer culturing form.

[000278] In some embodiments of the above method, the obtained pluripotent stem cell-derived definitive hemogenic endothelium cells are CD34+. In some embodiments, the obtained definitive hemogenic endothelium cells are CD34+CD43-. In some embodiments, the definitive hemogenic endothelium cells are CD34+CD43-CXCR4-CD73-. In some embodiments, the

definitive hemogenic endothelium cells are CD34+ CXCR4-CD73-. In some embodiments, the definitive hemogenic endothelium cells are CD34+CD43-CD93-. In some embodiments, the definitive hemogenic endothelium cells are CD34+ CD93-.

[000279] In some embodiments of the above method, the method further comprises (i) contacting pluripotent stem cell-derived definitive hemogenic endothelium with a composition comprising a ROCK inhibitor; one or more growth factors and cytokines selected from the group consisting of VEGF, bFGF, SCF, Flt3L, TPO, and IL7; and optionally a BMP activator; to initiate the differentiation of the definitive hemogenic endothelium to pre-T cell progenitors; and optionally, (ii) contacting the pre-T cell progenitors with a composition comprising one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, and IL7, but free of one or more of VEGF, bFGF, TPO, BMP activators and ROCK inhibitors, to initiate the differentiation of the pre-T cell progenitors to T cell progenitors or T cells. In some embodiments of the method, the pluripotent stem cell-derived T cell progenitors are CD34+CD45+CD7+. In some embodiments of the method, the pluripotent stem cell-derived T cell progenitors are CD45+CD7+.

[000280] In yet some embodiments of the above method for directing differentiation of pluripotent stem cells into cells of a hematopoietic lineage, the method further comprises: (i) contacting pluripotent stem cell-derived definitive hemogenic endothelium with a composition comprising a ROCK inhibitor; one or more growth factors and cytokines selected from the group consisting of VEGF, bFGF, SCF, Flt3L, TPO, IL3, IL7, and IL15; and optionally, a BMP activator, to initiate differentiation of the definitive hemogenic endothelium to pre-NK cell progenitor; and optionally, (ii) contacting pluripotent stem cells-derived pre-NK cell progenitors with a composition comprising one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, IL3, IL7, and IL15, wherein the medium is free of one or more of VEGF, bFGF, TPO, BMP activators and ROCK inhibitors, to initiate differentiation of the pre-NK cell progenitors to NK cell progenitors or NK cells. In some embodiments, the pluripotent stem cell-derived NK progenitors are CD3-CD45+CD56+CD7+. In some embodiments, the pluripotent stem cell-derived NK cells are CD3-CD45+CD56+, and optionally further defined by NKp46+, CD57+ and CD16+.

[000281] Therefore, using the above differentiation methods, one may obtain one or more population of iPSC derived hematopoietic cells (i) CD34+ HE cells (iCD34), using one or more culture medium selected from iMPP-A, iTC-A2, iTC-B2, iNK-A2, and iNK-B2; (ii) definitive hemogenic endothelium (iHE), using one or more culture medium selected from iMPP-A, iTC-A2, iTC-B2, iNK-A2, and iNK-B2; (iii) definitive HSCs, using one or more culture medium

selected from iMPP-A, iTC-A2, iTC-B2, iNK-A2, and iNK-B2; (iv) multipotent progenitor cells (iMPP), using iMPP-A; (v) T cell progenitors (ipro-T), using one or more culture medium selected from iTC-A2, and iTC-B2; (vi) T cells (iTC), using iTC-B2; (vii) NK cell progenitors (ipro-NK), using one or more culture medium selected from iNK-A2, and iNK-B2; and/or (viii) NK cells (iNK), and iNK-B2. In some embodiments, the medium:

a. iCD34-C comprises a ROCK inhibitor, one or more growth factors and cytokines selected from the group consisting of bFGF, VEGF, SCF, IL6, IL11, IGF, and EPO, and optionally, a Wnt pathway activator; and is free of TGFβ receptor/ALK inhibitor;
b. iMPP-A comprises a BMP activator, a ROCK inhibitor, and one or more growth factors and cytokines selected from the group consisting of TPO, IL3, GMCSF, EPO, bFGF, VEGF, SCF, IL6, Flt3L and IL11;
c. iTC-A2 comprises a ROCK inhibitor; one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, TPO, and IL7; and optionally, a BMP activator;
d. iTC-B2 comprises one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, and IL7;
e. iNK-A2 comprises a ROCK inhibitor, and one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, TPO, IL3, IL7, and IL15; and optionally, a BMP activator, and
f. iNK-B2 comprises one or more growth factors and cytokines selected from the group consisting of SCF, Flt3L, IL7 and IL15.

[000282] In some embodiments, the genome-engineered iPSC-derived cells obtained from the above methods comprise one or more inducible suicide gene integrated at one or more desired integration sites comprising AAVS1, CCR5, ROSA26, collagen, HTRP, H11, GAPDH, RUNX1, B2M, TAP1, TAP2, tapasin, NLRC5, CIITA, RFXANK, CIITA, RFX5, RFXAP, TCR α or β constant region, NKG2A, NKG2D, CD38, CD58, CD54, CD56, CIS, CBL-B, SOCS2, PD1, CTLA4, LAG3, TIM3, or TIGIT, or other loci meeting the criteria of a genome safe harbor. In some other embodiments, the genome-engineered iPSC-derived cells comprise polynucleotides encoding safety switch proteins, targeting modality, receptors, signaling molecules, transcription factors, pharmaceutically active proteins and peptides, drug target candidates, or proteins promoting trafficking, homing, viability, self-renewal, persistence, and/or survival of stem cells and/or progenitor cells. In some embodiments, the genome-engineered iPSC-derived cells comprising one or more suicide genes further comprise one or more in/del comprised in one or more endogenous genes associated with immune response regulation and mediation, including,

but not limited to, check point genes, endogenous T cell receptor genes, and MHC class I suppressor genes. In one embodiment, the genome-engineered iPSC-derived cells comprising one or more suicide genes further comprise an in/del in B2M gene, wherein the B2M is knocked out.

[000283] Additionally, applicable dedifferentiation methods and compositions for obtaining genomic-engineered hematopoietic cells of a first fate to genomic-engineered hematopoietic cells of a second fate include those depicted in, for example, International Publication No. WO2011/159726, the disclosure of which is incorporated herein by reference. The method and composition provided therein allows partially reprogramming a starting non-pluripotent cell to a non-pluripotent intermediate cell by limiting the expression of endogenous Nanog gene during reprogramming; and subjecting the non-pluripotent intermediate cell to conditions for differentiating the intermediate cell into a desired cell type. In some embodiments, the genomically modified iPSCs and its derivative cells obtained using the methods and composition herein comprise at least one genotype listed in Table 1.

V. Therapeutic Use of Derivative Immune Cells with Functional Modalities Differentiated from Genetically Engineered iPSCs

[000284] The present invention provides, in some embodiments, a composition comprising an isolated population or subpopulation functionally enhanced derivative immune cells that have been differentiated from genomically engineered iPSCs using the methods and compositions as disclosed. In some embodiments, the iPSCs comprise one or more targeted genetic editing which are retainable in the iPSC-derived immune cells, wherein the genetically engineered iPSCs and derivative cells therefrom are suitable for cell based adoptive therapies. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell comprises iPSC derived CD34 cells. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell comprises iPSC derived HSC cells. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell comprises iPSC derived proT or T cells. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell comprises iPSC derived proNK or NK cells. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell comprises iPSC derived immune regulatory cells or myeloid derived suppressor cells (MDSCs). In some embodiments, the iPSC derived genetically engineered immune cells are further modulated *ex vivo* for improved therapeutic potential. In one embodiment, an isolated population or subpopulation of genetically engineered immune cells that have been derived from iPSC comprises an increased number or ratio of naïve T cells, stem cell memory T cells, and/or central memory T cells. In one embodiment, the isolated population or subpopulation of genetically engineered immune cell that

have been derived from iPSC comprises an increased number or ratio of type I NKT cells. In another embodiment, the isolated population or subpopulation of genetically engineered immune cell that have been derived from iPSC comprises an increased number or ratio of adaptive NK cells. In some embodiments, the isolated population or subpopulation of genetically engineered CD34 cells, HSC cells, T cells, NK cells, or myeloid derived suppressor cells derived from iPSC are allogeneic. In some other embodiments, the isolated population or subpopulation of genetically engineered CD34 cells, HSC cells, T cells, NK cells, or MDSC derived from iPSC are autogenic.

[000285] In some embodiments, the iPSC for differentiation comprises genetic imprints selected to convey desirable therapeutic attributes in effector cells, provided that cell development biology during differentiation is not disrupted, and provided that the genetic imprints are retained and functional in the differentiated hematopoietic cells derived from said iPSC.

[000286] In some embodiments, the genetic imprints of the pluripotent stem cells comprise (i) one or more genetically modified modalities obtained through genomic insertion, deletion or substitution in the genome of the pluripotent cells during or after reprogramming a non-pluripotent cell to iPSC; or (ii) one or more retainable therapeutic attributes of a source specific immune cell that is donor-, disease-, or treatment response- specific, and wherein the pluripotent cells are reprogrammed from the source specific immune cell, wherein the iPSC retain the source therapeutic attributes, which are also comprised in the iPSC derived hematopoietic lineage cells.

[000287] In some embodiments, the genetically modified modalities comprise one or more of: safety switch proteins, targeting modalities, receptors, signaling molecules, transcription factors, pharmaceutically active proteins and peptides, drug target candidates; or proteins promoting engraftment, trafficking, homing, viability, self-renewal, persistence, immune response regulation and modulation, and/or survival of the iPSCs or derivative cells therefrom. In some embodiments, the genetically modified iPSC and the derivative cells therefrom comprise a genotype listed in Table 1. In some other embodiments, the genetically modified iPSC and the derivative cells therefrom comprising a genotype listed in Table 1 further comprise additional genetically modified modalities comprising (1) one or more of deletion or reduced expression of TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, or RFXAP, RAG1, and any gene in the chromosome 6p21 region; and (2) introduced or increased expression of HLA-E, 41BBL, CD3, CD4, CD8, CD47, CD113, CD131, CD137, CD80, PDL1, A2AR, CAR, Fc receptor, or surface triggering receptors for coupling with bi- or multi- specific or universal engagers.

[000288] In still some other embodiments, the hematopoietic lineage cells comprise the therapeutic attributes of the source specific immune cell relating to a combination of at least two of the followings: (i) one or more antigen targeting receptor expression; (ii) modified HLA; (iii) resistance to tumor microenvironment; (iv) recruitment of bystander immune cells and immune modulations; (iv) improved on-target specificity with reduced off-tumor effect; and (v) improved homing, persistence, cytotoxicity, or antigen escape rescue.

[000289] In some embodiments, the iPSC derivative hematopoietic cells comprising a genotype listed in Table 1, and said cells express at least one cytokine and/or its receptor comprising IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, or IL21, or any modified protein thereof, and express at least a CAR. In some embodiments, the engineered expression of the cytokine(s) and the CAR(s) is NK cell specific. In some other embodiments, the engineered expression of the cytokine(s) and the CAR(s) is T cell specific. In one embodiment, the CAR comprises a CD38 binding domain. In some embodiments, the iPSC derivative hematopoietic effector cells are antigen specific. In some embodiments, the antigen specific derivative effector cells target a liquid tumor. In some embodiments, the antigen specific derivative effector cells target a solid tumor. In some embodiments, the antigen specific iPSC derivative hematopoietic effector cells are capable of rescuing tumor antigen escape.

[000290] A variety of diseases may be ameliorated by introducing the immune cells of the invention to a subject suitable for adoptive cell therapy. In some embodiments, the iPSC derivative hematopoietic cells as provided is for allogeneic adoptive cell therapies. Additionally, the present invention provides, in some embodiments, therapeutic use of the above therapeutic compositions by introducing the composition to a subject suitable for adoptive cell therapy, wherein the subject has an autoimmune disorder; a hematological malignancy; a solid tumor; or an infection associated with HIV, RSV, EBV, CMV, adenovirus, or BK polyomavirus. Examples of hematological malignancies include, but are not limited to, acute and chronic leukemias (acute myelogenous leukemia (AML), acute lymphoblastic leukemia (ALL), chronic myelogenous leukemia (CML), lymphomas, non-Hodgkin lymphoma (NHL), Hodgkin's disease, multiple myeloma, and myelodysplastic syndromes. Examples of solid cancers include, but are not limited to, cancer of the brain, prostate, breast, lung, colon, uterus, skin, liver, bone, pancreas, ovary, testes, bladder, kidney, head, neck, stomach, cervix, rectum, larynx, and esophagus. Examples of various autoimmune disorders include, but are not limited to, alopecia areata, autoimmune hemolytic anemia, autoimmune hepatitis, dermatomyositis, diabetes (type 1), some forms of juvenile idiopathic arthritis, glomerulonephritis, Graves' disease, Guillain-Barré syndrome, idiopathic thrombocytopenic purpura, myasthenia gravis, some forms of myocarditis,

multiple sclerosis, pemphigus/pemphigoid, pernicious anemia, polyarteritis nodosa, polymyositis, primary biliary cirrhosis, psoriasis, rheumatoid arthritis, scleroderma/systemic sclerosis, Sjögren's syndrome, systemic lupus, erythematosus, some forms of thyroiditis, some forms of uveitis, vitiligo, granulomatosis with polyangiitis (Wegener's). Examples of viral infections include, but are not limited to, HIV- (human immunodeficiency virus), HSV- (herpes simplex virus), KSHV- (Kaposi's sarcoma-associated herpesvirus), RSV- (Respiratory Syncytial Virus), EBV- (Epstein-Barr virus), CMV- (cytomegalovirus), VZV (Varicella zoster virus), adenovirus-, a lentivirus-, a BK polyomavirus- associated disorders.

[000291] The treatment using the derived hematopoietic lineage cells of embodiments disclosed herein could be carried out upon symptom, or for relapse prevention. The terms "treating," "treatment," and the like are used herein to generally mean obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any intervention of a disease in a subject and includes: preventing the disease from occurring in a subject which may be predisposed to the disease but has not yet been diagnosed as having it; inhibiting the disease, *i.e.*, arresting its development; or relieving the disease, *i.e.*, causing regression of the disease. The therapeutic agent or composition may be administered before, during or after the onset of a disease or an injury. The treatment of ongoing disease, where the treatment stabilizes or reduces the undesirable clinical symptoms of the patient, is also of particular interest. In particular embodiments, the subject in need of a treatment has a disease, a condition, and/or an injury that can be contained, ameliorated, and/or improved in at least one associated symptom by a cell therapy. Certain embodiments contemplate that a subject in need of cell therapy, includes, but is not limited to, a candidate for bone marrow or stem cell transplantation, a subject who has received chemotherapy or irradiation therapy, a subject who has or is at risk of having a hyperproliferative disorder or a cancer, e.g. a hyperproliferative disorder or a cancer of hematopoietic system, a subject having or at risk of developing a tumor, e.g., a solid tumor, a subject who has or is at risk of having a viral infection or a disease associated with a viral infection.

[000292] When evaluating responsiveness to the treatment comprising the derived hematopoietic lineage cells of embodiments disclosed herein, the response can be measured by criteria comprising at least one of: clinical benefit rate, survival until mortality, pathological complete response, semi-quantitative measures of pathologic response, clinical complete remission, clinical partial remission, clinical stable disease, recurrence-free survival, metastasis

free survival, disease free survival, circulating tumor cell decrease, circulating marker response, and RECIST (Response Evaluation Criteria In Solid Tumors) criteria.

[000293] The therapeutic composition comprising derived hematopoietic lineage cells as disclosed can be administered in a subject before, during, and/or after other treatments. As such the method of a combinational therapy can involve the administration or preparation of iPSC derived immune cells before, during, and/or after the use of an additional therapeutic agent. As provided above, the one or more additional therapeutic agents comprise a peptide, a cytokine, a checkpoint inhibitor, a mitogen, a growth factor, a small RNA, a dsRNA (double stranded RNA), mononuclear blood cells, feeder cells, feeder cell components or replacement factors thereof, a vector comprising one or more polynucleic acids of interest, an antibody, a chemotherapeutic agent or a radioactive moiety, or an immunomodulatory drug (IMiD). The administration of the iPSC derived immune cells can be separated in time from the administration of an additional therapeutic agent by hours, days, or even weeks. Additionally, or alternatively, the administration can be combined with other biologically active agents or modalities such as, but not limited to, an antineoplastic agent, a non-drug therapy, such as, surgery.

[000294] In some embodiments of a combinational cell therapy, the therapeutic combination comprises the iPSC derived hematopoietic lineage cells provided herein and an additional therapeutic agent that is an antibody, or an antibody fragment. In some embodiments, the antibody is a monoclonal antibody. In some embodiments, the antibody may be a humanized antibody, a humanized monoclonal antibody, or a chimeric antibody. In some embodiments, the antibody, or antibody fragment, specifically binds to a viral antigen. In other embodiments, the antibody, or antibody fragment, specifically binds to a tumor antigen. In some embodiments, the tumor or viral specific antigen activates the administered iPSC derived hematopoietic lineage cells to enhance their killing ability. In some embodiments, the antibodies suitable for combinational treatment as an additional therapeutic agent to the administered iPSC derived hematopoietic lineage cells include, but are not limited to, anti-CD20 (e.g., rituximab, veltuzumab, ofatumumab, ublituximab, ocaratuzumab, obinutuzumab, ibritumomab, ocrelizumab), anti-CD22 (inotuzumab, moxetumomab, epratuzumab), anti-HER2 (e.g., trastuzumab, pertuzumab), anti-CD52 (e.g., alemtuzumab), anti-EGFR (e.g., certuximab), anti-GD2 (e.g., dinutuximab), anti-PDL1 (e.g., avelumab), anti-CD38 (e.g., daratumumab, isatuximab, MOR202), anti-CD123 (e.g., 7G3, CSL362), anti-SLAMF7 (elotuzumab), and their humanized or Fc modified variants or fragments or their functional equivalents or biosimilars.

[000295] In some embodiments, the additional therapeutic agent comprises one or more checkpoint inhibitors. Checkpoints are referred to cell molecules, often cell surface molecules,

capable of suppressing or downregulating immune responses when not inhibited. Checkpoint inhibitors are antagonists capable of reducing checkpoint gene expression or gene products, or deceasing activity of checkpoint molecules. Suitable checkpoint inhibitors for combination therapy with the derivative effector cells, including NK or T cells, as provided herein include, but are not limited to, antagonists of PD-1 (Pdcdl, CD279), PDL-1 (CD274), TIM-3 (Havcr2), TIGIT (WUCAM and Vstm3), LAG-3 (Lag3, CD223), CTLA-4 (Ctla4, CD152), 2B4 (CD244), 4-1BB (CD137), 4-1BBL (CD137L), A2aR, BATE, BTLA, CD39 (Entpdl), CD47, CD73 (NT5E), CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2 (Pou2f2), retinoic acid receptor alpha (Rara), TLR3, VISTA, NKG2A/HLA-E, and inhibitory KIR (for example, 2DL1, 2DL2, 2DL3, 3DL1, and 3DL2).

[000296] Some embodiments of the combination therapy comprising the provided derivative effector cells further comprise at least one inhibitor targeting a checkpoint molecule. Some other embodiments of the combination therapy with the provided derivative effector cells comprise two, three or more inhibitors such that two, three, or more checkpoint molecules are targeted. In some embodiments, the effector cells for combination therapy as described herein are derivative NK cells as provided. In some embodiments, the effector cells for combination therapy as described herein are derivative T cells. In some embodiments, the derivative NK or T cells for combination therapies are functionally enhanced as provided herein. In some embodiments, the two, three or more checkpoint inhibitors may be administered in a combination therapy with, before, or after the administering of the derivative effector cells. In some embodiments, the two or more checkpoint inhibitors are administered at the same time, or one at a time (sequential).

[000297] In some embodiments, the antagonist inhibiting any of the above checkpoint molecules is an antibody. In some embodiments, the checkpoint inhibitory antibodies may be murine antibodies, human antibodies, humanized antibodies, a camel Ig, a shark heavy-chain-only antibody (VNAR), Ig NAR, chimeric antibodies, recombinant antibodies, or antibody fragments thereof. Non-limiting examples of antibody fragments include Fab, Fab′, F(ab)′2, F(ab)′3, Fv, single chain antigen binding fragments (scFv), (scFv)2, disulfide stabilized Fv (dsFv), minibody, diabody, triabody, tetrabody, single-domain antigen binding fragments (sdAb, Nanobody), recombinant heavy-chain-only antibody (VHH), and other antibody fragments that maintain the binding specificity of the whole antibody, which may be more cost-effective to produce, more easily used, or more sensitive than the whole antibody. In some embodiments, the one, or two, or three, or more checkpoint inhibitors comprise at least one of atezolizumab,

avelumab, durvalumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their derivatives or functional equivalents.

[000298] The combination therapies comprising the derivative effector cells and one or more check inhibitors are applicable to treatment of liquid and solid cancers, including but not limited to cutaneous T-cell lymphoma, non-Hodgkin lymphoma (NHL), Mycosis fungoides, Pagetoid reticulosis, Sezary syndrome, Granulomatous slack skin, Lymphomatoid papulosis, Pityriasis lichenoides chronica, Pityriasis lichenoides et varioliformis acuta, CD30+ cutaneous T-cell lymphoma, Secondary cutaneous CD30+ large cell lymphoma, non- mycosis fungoides CD30 cutaneous large T-cell lymphoma, Pleomorphic T-cell lymphoma, Lennert lymphoma, subcutaneous T-cell lymphoma, angiocentric lymphoma, blastic NK-cell lymphoma, B-cell Lymphomas, hodgkins lymphoma (HL), Head and neck tumor; Squamous cell carcinoma, rhabdomyocarcoma, Lewis lung carcinoma (LLC), non-small cell lung cancer, esophageal squamous cell carcinoma, esophageal adenocarcinoma, renal cell carcinoma (RCC), colorectal cancer (CRC), acute myeloid leukemia (AML), breast cancer, gastric cancer, prostatic small cell neuroendocrine carcinoma (SCNC), liver cancer, glioblastoma, liver cancer, oral squamous cell carcinoma, pancreatic cancer, thyroid papillary cancer, intrahepatic cholangiocellular carcinoma, hepatocellular carcinoma, bone cancer, metastasis, and nasopharyngeal carcinoma.

[000299] In some embodiments, other than the derivative effector cells as provided herein, a combination for therapeutic use comprises one or more additional therapeutic agents comprising a chemotherapeutic agent or a radioactive moiety. Chemotherapeutic agent refers to cytotoxic antineoplastic agents, that is, chemical agents which preferentially kill neoplastic cells or disrupt the cell cycle of rapidly-proliferating cells, or which are found to eradicate stem cancer cells, and which are used therapeutically to prevent or reduce the growth of neoplastic cells. Chemotherapeutic agents are also sometimes referred to as antineoplastic or cytotoxic drugs or agents, and are well known in the art.

[000300] In some embodiments, the chemotherapeutic agent comprises an anthracycline, an alkylating agent, an alkyl sulfonate, an aziridine, an ethylenimine, a methylmelamine, a nitrogen mustard, a nitrosourea, an antibiotic, an antimetabolite, a folic acid analog, a purine analog, a pyrimidine analog, an enzyme, a podophyllotoxin, a platinum-containing agent, an interferon, and an interleukin. Exemplary chemotherapeutic agents include, but are not limited to, alkylating agents (cyclophosphamide, mechlorethamine, mephalin, chlorambucil, heamethylmelamine, thiotepa, busulfan, carmustine, lomustine, semustine), animetabolites (methotrexate, fluorouracil, floxuridine, cytarabine, 6-mercaptopurine, thioguanine, pentostatin), vinca alkaloids (vincristine, vinblastine, vindesine), epipodophyllotoxins (etoposide, etoposide orthoquinone, and teniposide),

antibiotics (daunorubicin, doxorubicin, mitoxantrone, bisanthrene, actinomycin D, plicamycin, puromycin, and gramicidine D), paclitaxel, colchicine, cytochalasin B, emetine, maytansine, and amsacrine. Additional agents include aminglutethimide, cisplatin, carboplatin, mitomycin, altretamine, cyclophosphamide, lomustine (CCNU), carmustine (BCNU), irinotecan (CPT-11), alemtuzamab, altretamine, anastrozole, L-asparaginase, azacitidine, bevacizumab, bexarotene, bleomycin, bortezomib, busulfan, calusterone, capecitabine, celecoxib, cetuximab, cladribine, clofurabine, cytarabine, dacarbazine, denileukin diftitox, diethlstilbestrol, docetaxel, dromostanolone, epirubicin, erlotinib, estramustine, etoposide, ethinyl estradiol, exemestane, floxuridine, 5-flourouracil, fludarabine, flutamide, fulvestrant, gefitinib, gemcitabine, goserelin, hydroxyurea, ibritumomab, idarubicin, ifosfamide, imatinib, interferon alpha (2a, 2b), irinotecan, letrozole, leucovorin, leuprolide, levamisole, meclorethamine, megestrol, melphalin, mercaptopurine, methotrexate, methoxsalen, mitomycin C, mitotane, mitoxantrone, nandrolone, nofetumomab, oxaliplatin, paclitaxel, pamidronate, pemetrexed, pegademase, pegasparagase, pentostatin, pipobroman, plicamycin, polifeprosan, porfimer, procarbazine, quinacrine, rituximab, sargramostim, streptozocin, tamoxifen, temozolomide, teniposide, testolactone, thioguanine, thiotepa, topetecan, toremifene, tositumomab, trastuzumab, tretinoin, uracil mustard, valrubicin, vinorelbine, and zoledronate. Other suitable agents are those that are approved for human use, including those that will be approved, as chemotherapeutics or radiotherapeutics, and known in the art. Such agents can be referenced through any of a number of standard physicians' and oncologists' references (e.g. Goodman & Gilman's The Pharmacological Basis of Therapeutics, Ninth Edition, McGraw-Hill, N.Y., 1995) or through the National Cancer Institute website (fda.gov/cder/cancer/druglistfrarne.htm), both as updated from time to time.

[000301] Immunomodulatory drugs (IMiDs) such as thalidomide, lenalidomide, and pomalidomide stimulate both NK cells and T cells. As provided herein, IMiDs may be used with the iPSC derived therapeutic immune cells for cancer treatments.

[000302] Other than an isolated population of iPSC derived hematopoietic lineage cells included in the therapeutic compositions, the compositions suitable for administration to a patient can further include one or more pharmaceutically acceptable carriers (additives) and/or diluents (*e.g.*, pharmaceutically acceptable medium, for example, cell culture medium), or other pharmaceutically acceptable components. Pharmaceutically acceptable carriers and/or diluents are determined in part by the particular composition being administered, as well as by the particular method used to administer the therapeutic composition. Accordingly, there is a wide variety of suitable formulations of therapeutic compositions of the present invention (see, *e.g.*,

Remington's Pharmaceutical Sciences, 17th ed. 1985, the disclosure of which is hereby incorporated by reference in its entirety).

[000303] In one embodiment, the therapeutic composition comprises the pluripotent cell derived T cells made by the methods and composition disclosed herein. In one embodiment, the therapeutic composition comprises the pluripotent cell derived NK cells made by the methods and composition disclosed herein. In one embodiment, the therapeutic composition comprises the pluripotent cell derived CD34+ HE cells made by the methods and composition disclosed herein. In one embodiment, the therapeutic composition comprises the pluripotent cell derived HSCs made by the methods and composition disclosed herein. In one embodiment, the therapeutic composition comprises the pluripotent cell derived MDSC made by the methods and composition disclosed herein. A therapeutic composition comprising a population of iPSC derived hematopoietic lineage cells as disclosed herein can be administered separately by intravenous, intraperitoneal, enteral, or tracheal administration methods or in combination with other suitable compounds to affect the desired treatment goals.

[000304] These pharmaceutically acceptable carriers and/or diluents can be present in amounts sufficient to maintain a pH of the therapeutic composition of between about 3 and about 10. As such, the buffering agent can be as much as about 5% on a weight to weight basis of the total composition. Electrolytes such as, but not limited to, sodium chloride and potassium chloride can also be included in the therapeutic composition. In one aspect, the pH of the therapeutic composition is in the range from about 4 to about 10. Alternatively, the pH of the therapeutic composition is in the range from about 5 to about 9, from about 6 to about 9, or from about 6.5 to about 8. In another embodiment, the therapeutic composition includes a buffer having a pH in one of said pH ranges. In another embodiment, the therapeutic composition has a pH of about 7. Alternatively, the therapeutic composition has a pH in a range from about 6.8 to about 7.4. In still another embodiment, the therapeutic composition has a pH of about 7.4.

[000305] The invention also provides, in part, the use of a pharmaceutically acceptable cell culture medium in particular compositions and/or cultures of the present invention. Such compositions are suitable for administration to human subjects. Generally speaking, any medium that supports the maintenance, growth, and/or health of the iPSC derived immune cells in accordance with embodiments of the invention are suitable for use as a pharmaceutical cell culture medium. In particular embodiments, the pharmaceutically acceptable cell culture medium is a serum free, and/or feeder-free medium. In various embodiments, the serum-free medium is animal-free, and can optionally be protein-free. Optionally, the medium can contain biopharmaceutically acceptable recombinant proteins. Animal-free medium refers to medium

wherein the components are derived from non-animal sources. Recombinant proteins replace native animal proteins in animal-free medium and the nutrients are obtained from synthetic, plant or microbial sources. Protein-free medium, in contrast, is defined as substantially free of protein. One having ordinary skill in the art would appreciate that the above examples of media are illustrative and in no way limit the formulation of media suitable for use in the present invention and that there are many suitable media known and available to those in the art.

[000306] The isolated pluripotent stem cell derived hematopoietic lineage cells can have at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% T cells, NK cells, NKT cells, proT cells, proNK cells, CD34+ HE cells, HSCs, B cells, myeloid-derived suppressor cells (MDSCs), regulatory macrophages, regulatory dendritic cells, or mesenchymal stromal cells. In some embodiments, the isolated pluripotent stem cell derived hematopoietic lineage cells has about 95% to about 100% T cells, NK cells, proT cells, proNK cells, CD34+ HE cells, or myeloid-derived suppressor cells (MDSCs). In some embodiments, the present invention provides therapeutic compositions having purified T cells or NK cells, such as a composition having an isolated population of about 95% T cells, NK cells, proT cells, proNK cells, CD34+ HE cells, or myeloid-derived suppressor cells (MDSCs) to treat a subject in need of the cell therapy.

[000307] In one embodiment, the combinational cell therapy comprises a therapeutic protein or peptide that is a CD3 engager and a population of NK cells derived from genomically engineered iPSCs comprising a genotype listed in Table 1, wherein the derived NK cells comprise TCR^{neg} cs-CD3. In another embodiment, the combinational cell therapy comprises a therapeutic protein or peptide that is a CD3 engager and a population of T cells derived from genomically engineered iPSCs comprising a genotype listed in Table 1, wherein the derived T cells comprise TCR^{neg} cs-CD3. In some embodiments, the combinational cell therapy comprises one of blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05, and a population of NK or T cells derived from genomically engineered iPSCs comprising a genotype listed in Table 1, wherein the derived NK or T cells comprise TCR^{neg} cs-CD3, and optionally, hnCD16. In yet some other embodiments, the combinational cell therapy comprises one of blinatumomab, catumaxomab, and ertumaxomab, and a population of NK or T cells derived from genomically engineered iPSCs comprising a genotype listed in Table 1, wherein the derived NK or T cells comprise TCR^{neg} cs-CD3, hnCD16, and a CAR targeting CD19, BCMA, CD38, CD20, CD22, or CD123. In still some additional embodiments, the combinational cell therapy comprises one of blinatumomab, catumaxomab, and ertumaxomab, and a population of NK or T cells derived from genomically

engineered iPSCs comprising a genotype listed in Table 1, wherein the derived NK or T cells comprise TCR^{neg} cs-CD3, hnCD16, a CAR and one or more exogenous cytokine.

[000308] As a person of ordinary skill in the art would understand, both autologous and allogeneic hematopoietic lineage cells derived from iPSC based on the methods and composition herein can be used in cell therapies as described above. For autologous transplantation, the isolated population of derived hematopoietic lineage cells are either complete or partial HLA-match with the patient. In another embodiment, the derived hematopoietic lineage cells are not HLA-matched to the subject, wherein the derived hematopoietic lineage cells are NK cells or T cell with HLA I and HLA II null.

[000309] In some embodiments, the number of derived hematopoietic lineage cells in the therapeutic composition is at least 0.1 x 10^5 cells, at least 1 x 10^5 cells, at least 5 x 10^5 cells, at least 1 x 10^6 cells, at least 5 x 10^6 cells, at least 1 x 10^7 cells, at least 5 x 10^7 cells, at least 1 x 10^8 cells, at least 5 x 10^8 cells, at least 1 x 10^9 cells, or at least 5 x 10^9 cells, per dose. In some embodiments, the number of derived hematopoietic lineage cells in the therapeutic composition is about 0.1 x 10^5 cells to about 1 x 10^6 cells, per dose; about 0.5 x 10^6 cells to about 1x 10^7 cells, per dose; about 0.5 x 10^7 cells to about 1 x 10^8 cells, per dose; about 0.5 x 10^8 cells to about 1 x 10^9 cells, per dose; about 1 x 10^9 cells to about 5 x 10^9 cells, per dose; about 0.5 x 10^9 cells to about 8 x 10^9 cells, per dose; about 3 x 10^9 cells to about 3 x 10^{10} cells, per dose, or any range in-between. Generally, 1 x 10^8 cells/dose translates to 1.67 x 10^6 cells/kg for a 60 kg patient.

[000310] In one embodiment, the number of derived hematopoietic lineage cells in the therapeutic composition is the number of immune cells in a partial or single cord of blood, or is at least 0.1 x 10^5 cells/kg of bodyweight, at least 0.5 x 10^5 cells/kg of bodyweight, at least 1 x 10^5 cells/kg of bodyweight, at least 5 x 10^5 cells/kg of bodyweight, at least 10 x 10^5 cells/kg of bodyweight, at least 0.75 x 10^6 cells/kg of bodyweight, at least 1.25 x 10^6 cells/kg of bodyweight, at least 1.5 x 10^6 cells/kg of bodyweight, at least 1.75 x 10^6 cells/kg of bodyweight, at least 2 x 10^6 cells/kg of bodyweight, at least 2.5 x 10^6 cells/kg of bodyweight, at least 3 x 10^6 cells/kg of bodyweight, at least 4 x 10^6 cells/kg of bodyweight, at least 5 x 10^6 cells/kg of bodyweight, at least 10 x 10^6 cells/kg of bodyweight, at least 15 x 10^6 cells/kg of bodyweight, at least 20 x 10^6 cells/kg of bodyweight, at least 25 x 10^6 cells/kg of bodyweight, at least 30 x 10^6 cells/kg of bodyweight, 1 x 10^8 cells/kg of bodyweight, 5 x 10^8 cells/kg of bodyweight, or 1 x 10^9 cells/kg of bodyweight.

[000311] In one embodiment, a dose of derived hematopoietic lineage cells is delivered to a subject. In one illustrative embodiment, the effective amount of cells provided to a subject is at least 2 x 10^6 cells/kg, at least 3 x 10^6 cells/kg, at least 4 x 10^6cells/kg, at least 5 x 10^6 cells/kg, at

least 6 x 10^6 cells/kg, at least 7 x 10^6 cells/kg, at least 8 x 10^6 cells/kg, at least 9 x 10^6 cells/kg, or at least 10 x 10^6 cells/kg, or more cells/kg, including all intervening doses of cells.

[000312] In another illustrative embodiment, the effective amount of cells provided to a subject is about 2 x 10^6 cells/kg, about 3 x 10^6 cells/kg, about 4 x 10^6 cells/kg, about 5 x 10^6 cells/kg, about 6 x 10^6 cells/kg, about 7 x 10^6 cells/kg, about 8 x 10^6 cells/kg, about 9 x 10^6 cells/kg, or about 10 x 10^6 cells/kg, or more cells/kg, including all intervening doses of cells.

[000313] In another illustrative embodiment, the effective amount of cells provided to a subject is from about 2 x 10^6 cells/kg to about 10 x 10^6 cells/kg, about 3 x 10^6 cells/kg to about 10 x 10^6 cells/kg, about 4 x 10^6 cells/kg to about 10 x 10^6 cells/kg, about 5 x 10^6 cells/kg to about 10 x 10^6 cells/kg, 2 x 10^6 cells/kg to about 6 x 10^6 cells/kg, 2 x 10^6 cells/kg to about 7 x 10^6 cells/kg, 2 x 10^6 cells/kg to about 8 x 10^6 cells/kg, 3 x 10^6 cells/kg to about 6 x 10^6 cells/kg, 3 x 10^6 cells/kg to about 7 x 10^6 cells/kg, 3 x 10^6 cells/kg to about 8 x 10^6 cells/kg, 4 x 10^6 cells/kg to about 6 x 10^6 cells/kg, 4 x 10^6 cells/kg to about 7 x 10^6 cells/kg, 4 x 10^6 cells/kg to about 8 x 10^6 cells/kg, 5 x 10^6 cells/kg to about 6 x 10^6 cells/kg, 5 x 10^6 cells/kg to about 7 x 10^6 cells/kg, 5 x 10^6 cells/kg to about 8 x 10^6 cells/kg, or 6 x 10^6 cells/kg to about 8 x 10^6 cells/kg, including all intervening doses of cells.

[000314] In some embodiments, the therapeutic use of derived hematopoietic lineage cells is a single-dose treatment. In some embodiments, the therapeutic use of derived hematopoietic lineage cells is a multi-dose treatment. In some embodiments, the multi-dose treatment is one dose every day, every 3 days, every 7 days, every 10 days, every 15 days, every 20 days, every 25 days, every 30 days, every 35 days, every 40 days, every 45 days, or every 50 days, or any number of days in-between. In some embodiments, the multi-dose treatment comprises three, or four, or five, once weekly doses. In some embodiments of the multi-dose treatment comprising three, or four, or five, once weekly doses further comprise an observation period for determining whether additional single or multi doses are needed.

[000315] The compositions comprising a population of derived hematopoietic lineage cells of the invention can be sterile, and can be suitable and ready for administration (i.e., can be administered without any further processing) to human patients. A cell based composition that is ready for administration means that the composition does not require any further processing or manipulation prior to transplant or administration to a subject. In other embodiments, the invention provides an isolated population of derived hematopoietic lineage cells that are expanded and/or modulated prior to administration with one or more agents. For derived hematopoietic lineage cells that genetically engineered to express recombinant TCR or CAR, the

cells can be activated and expanded using methods as described, for example, in U.S. Patents 6,352,694.

[000316] In certain embodiments, the primary stimulatory signal and the co- stimulatory signal for the derived hematopoietic lineage cells can be provided by different protocols. For example, the agents providing each signal can be in solution or coupled to a surface. When coupled to a surface, the agents can be coupled to the same surface (i.e., in "cis" formation) or to separate surfaces (i.e., in "trans" formation). Alternatively, one agent can be coupled to a surface and the other agent in solution. In one embodiment, the agent providing the co-stimulatory signal can be bound to a cell surface and the agent providing the primary activation signal is in solution or coupled to a surface. In certain embodiments, both agents can be in solution. In another embodiment, the agents can be in soluble form, and then cross-linked to a surface, such as a cell expressing Fc receptors or an antibody or other binding agent which will bind to the agents such as disclosed in U.S. Patent Application Publication Nos. 20040101519 and 20060034810 for artificial antigen presenting cells (aAPCs) that are contemplated for use in activating and expanding T lymphocytes in embodiments of the present invention.

[000317] Some variation in dosage, frequency, and protocol will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose, frequency and protocol for the individual subject.

EXAMPLES

[000318] The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1 – Materials and Methods

[000319] To effectively select and test suicide systems under the control of various promoters in combination with different safe harbor loci integration strategies, a proprietary hiPSC platform of the applicant was used, which enables single cell passaging and high-throughput, 96-well plate-based flow cytometry sorting, to allow for the derivation of clonal hiPSCs with single or multiple genetic modulations.

[000320] ***hiPSC Maintenance in Small Molecule Culture*:** hiPSCs were routinely passaged as single cells once confluency of the culture reached 75%–90%. For single-cell dissociation, hiPSCs were washed once with PBS (Mediatech) and treated with Accutase (Millipore) for 3–5 min at 37°C followed with pipetting to ensure single-cell dissociation. The single-cell suspension

was then mixed in equal volume with conventional medium, centrifuged at 225 × g for 4 min, resuspended in FMM, and plated on Matrigel-coated surface. Passages were typically 1:6–1:8, transferred tissue culture plates previously coated with Matrigel for 2–4 hr in 37°C and fed every 2–3 days with FMM. Cell cultures were maintained in a humidified incubator set at 37°C and 5% CO2.

[000321] ***Human iPSC engineering with ZFN, CRISPR for targeted editing of modalities of interest*:** Using ROSA26 targeted insertion as an example, for ZFN mediated genome editing, 2 million iPSCs were transfected with mixture of 2.5ug ZFN-L (FTV893), 2.5ug ZFN-R (FTV894) and 5ug donor construct, for AAVS1 targeted insertion. For CRISPR mediated genome editing, 2 million iPSCs were transfected with mixture of 5ug ROSA26-gRNA/Cas9 (FTV922) and 5ug donor construct, for ROSA26 targeted insertion. Transfection was done using Neon transfection system (Life Technologies) using parameters 1500V, 10ms, 3 pulses. On day 2 or 3 after transfection, transfection efficiency was measured using flow cytometry if the plasmids contain artificial promoter-driver GFP and/or RFP expression cassette. On day 4 after transfection, puromycin was added to the medium at concentration of 0.1ug/ml for the first 7 days and 0.2ug/ml after 7 days to select the targeted cells. During the puromycin selection, the cells were passaged onto fresh matrigel-coated wells on day 10. On day 16 or later of puromycin selection, the surviving cells were analyzed by flow cytometry for GFP+ iPS cell percentage.

[000322] ***Bulk sort and clonal sort of genome-edited iPSCs*:** iPSCs with genomic targeted editing using ZFN or CRISPR-Cas9 were bulk sorted and clonal sorted of GFP+SSEA4+TRA181+ iPSCs after 20 days of puromycin selection. Single cell dissociated targeted iPSC pools were resuspended in chilled staining buffer containing Hanks' Balanced Salt Solution (MediaTech), 4% fetal bovine serum (Invitrogen), 1x penicillin/streptomycin (Mediatech) and 10 mM Hepes (Mediatech); made fresh for optimal performance. Conjugated primary antibodies, including SSEA4-PE, TRA181-Alexa Fluor-647 (BD Biosciences), were added to the cell solution and incubated on ice for 15 minutes. All antibodies were used at 7 μL in 100 μL staining buffer per million cells. The solution was washed once in staining buffer, spun down at 225 g for 4 minutes and resuspended in staining buffer containing 10 μM Thiazovivn and maintained on ice for flow cytometry sorting. Flow cytometry sorting was performed on FACS Aria II (BD Biosciences). For bulk sort, GFP+SSEA4+TRA181+ cells were gated and sorted into 15 ml canonical tubes filled with 7 ml FMM. For clonal sort, the sorted cells were directly ejected into 96-well plates using the 100 μM nozzle, at concentrations of 3 events per well. Each well was prefilled with 200 μL FMM supplemented with 5 μg/mL fibronectin and 1x penicillin/streptomycin (Mediatech) and previously coated overnight with 5x Matrigel. 5x

Matrigel precoating includes adding one aliquot of Matrigel into 5 mL of DMEM/F12, then incubated overnight at 4°C to allow for proper resuspension and finally added to 96-well plates at 50 μL per well followed by overnight incubation at 37°C. The 5x Matrigel is aspirated immediately before the addition of media to each well. Upon completion of the sort, 96-well plates were centrifuged for 1-2 min at 225 g prior to incubation. The plates were left undisturbed for seven days. On the seventh day, 150 μL of medium was removed from each well and replaced with 100 μL FMM. Wells were refed with an additional 100 μL FMM on day 10 post sort. Colony formation was detected as early as day 2 and most colonies were expanded between days 7-10 post sort. In the first passage, wells were washed with PBS and dissociated with 30 μL Accutase for approximately 10 min at 37°C. The need for extended Accutase treatment reflects the compactness of colonies that have sat idle in culture for prolonged duration. After cells are seen to be dissociating, 200 μL of FMM is added to each well and pipetted several times to break up the colony. The dissociated colony is transferred to another well of a 96-well plate previously coated with 5x Matrigel and then centrifuged for 2 min at 225 g prior to incubation. This 1:1 passage is conducted to spread out the early colony prior to expansion. Subsequent passages were done routinely with Accutase treatment for 3-5 min and expansion of 1:4-1:8 upon 75-90% confluency into larger wells previously coated with 1x Matrigel in FMM. Each clonal cell line was analyzed for GFP fluorescence level and TRA1-81 expression level. Clonal lines with near 100% GFP+ and TRA1-81+ were selected for further PCR screening and analysis, and cryopreserved as a master cell bank. Flow cytometry analysis was performed on Guava EasyCyte 8 HT (Millipore) and analyzed using Flowjo (FlowJo, LLC).

EXAMPLE 2 – Application of the iPSC Platform for the Generation of Master Clonal iPSC Lines Engineered with Multiple Modalities for Enhanced Functions

[000323] Genetic engineering of αβT Cells was initiated 2-3 weeks after reprogramming using the methods provided in this application. It was then followed by single cell sorting into 96-well plates and screening clones for specific engineering. In this particular example, the engineering was for TRAC locus targeted transgene integration, using CD3ζ1XX CD19 CAR as illustration. The homologous recombination leading to the specific integration of the CD3ζ 1XX CD19 CAR into the TRAC locus. Par A of FIG. 3 demonstrates phase contrast images of cultures at different stages. Part B of FIG. 3 shows flow cytometry profiles of αβT cells before reprogramming (left panel), reprogrammed and engineered cell pool before sorting and a clonal TiPSC clone (right panel).

[000324] The specific bi-allelic integration of a transgene, such as a CAR, into the TRAC locus was further confirmed by methods including PCR assays, SNP phasing assays, and further

by the digital droplet PCR to analyze the copy numbers of integrated transgene. The off-target editing in TRAC-targeted CAR TiPSC clones was also analyzed using SITE-Seq to ensure the selected clonal TiPSC having biallelic TRAC-targeted transgene integration does not have any off-target editing and maintains genomic integrity. After confirmation and verification, a few selected clonal TiPSC lines were each expanded and cryopreserved as individual master cell bank.

[000325] Next, the constructs for enabling cs-CD3 designs in FIGS. 1A-C were made and introduced to T cells using similar methods and procedures.

EXAMPLE 3 -- Stepwise Genomic Engineering of iPSC and iPSC-derived Effector Cells

[000326] Other than TCR negative, induced pluripotent stem cells were also serially engineered to obtain high affinity non-cleavable CD16 expression, loss of HLA-I by knocking out B2M gene, loss of HLA-II by knocking out CIITA, overexpression of the non-classical HLA molecule HLA-G, and expression of a linked IL15/IL15 receptor alpha construct. After each engineering step, iPSCs were sorted for the desired phenotype prior to the next engineering step. The engineered iPSCs can then be maintained *in vitro* or for derivative cell generation. FIG. 4 showed the hnCD16 expression, B2M knockout, HLA-G expression and IL15/IL15Rα expression in the iPSC-derived NK cells. These data demonstrate that these genetically engineered modalities are maintained during hematopoietic differentiation without perturbing the *in vitro* directed development of the cell into a desired cell fate.

[000327] T cell-derived iPSCs in which CD19-CAR had been targeted to the TRAC locus, resulting in TCR knock-out (TCRα KO), were transduced with lentivirus to constitutively express the invariant NKT (iTCRα) or both the invariant NKT TCRα and invariant NKT TCRβ (iTCRβ), as shown in FIG. 7, resulting in recombinant TCR complex with defined TCR (see FIGS. 1A and 1C, accompanying text with regard to Design 2 in Section I. 1, and SEQ ID Nos: 44 and 45 for further references). The transduced constructs included Thy1.1 as an exemplary reporter for the purpose of assaying for transduction efficiency and enrichment through cell sorting. The resulting iPSC lines were then differentiated, along with wild-type (WT) and TRAC-targeted CD19-CAR control lines, to an iPSC-derived CD34+ hematopoietic progenitor cells (iCD34) and subsequently to derivative T cells (iT).

[000328] iPSCs from the control and transduced lines were then assayed by extracellular flow cytometry for (i) the pluripotency markers SSEA4 and TRA181, (ii) the T cell co-receptor CD3 trafficked to the cell surface with expressed TCRα and/or TCRβ using a pan-TCRαβ probe (detecting endogenous and exogenous TCRs), and (iii) the construct reporter Thy1.1. As seen in

FIG. 8A, transduction with iTCRα or iTCRαβ did not affect iPSC identity as shown by pluripotency markers. While Thy1.1 expression in both transduced iPSC lines was observed, same as the observation in WT iPSC, CD3 was not detected on the cell surface of the transduced iPSCs, which is consistent with the fact that TCRs do not express at the iPSC stage.

[000329] The control and transduced iPSCs were then differentiated to iCD34 hematopoietic progenitor cells using the composition and methods described herein and assayed by flow cytometry for CD3, Thy1.1, and TCRαβ using a pan-TCRαβ probe, respectively. As seen in FIG. 8B, lines transduced with iTCRα or iTCRαβ maintained Thy1.1 expression, yet without detectable cell surface CD3. CD3 and TCRab were not observed in WT iPSC derived iCD34 either, suggesting that iTCRα or iTCRαβ transduction does not express or lead to CD3 expression on the cell surface at the iCD34 cell stage.

[000330] iCD34s were further differentiated into derivative T cells (iT) using the compositions and methods described herein and assayed by flow cytometry at various timepoints (cell development stages), during the differentiation process for CD3 and TCRαβ expression (endogenous TCR for control cells, exogenous for transduced cells). As shown in FIGS. 9A-B, CD3 and TCRαβ expression was upregulated over the course of iT cell differentiation in the WT, iTCRα and iTCRαβ lines. CD3 and TCRαβ expression was absent in the TCR KO line, as expected. Additionally, CD3 mean fluorescence intensity (MFI) was similar between the WT and iTCRα and iTCRαβ transduced lines. This data suggests that iTCRα alone or together with iTCRβ expression is sufficient to induce or traffick CD3 expression on the cell surface during the course of iT cell differentiation, and beyond the iCD34 cell stage. FIG. 9C, further demonstrated CD3 and TCRαβ expression in indicated cell lines on day 25 after iCD34 stage.

[000331] Telomere shortening occurs with cellular aging and is associated with stem cell dysfunction and cellular senescence. It is shown here that the mature iNK cells maintain longer telomeres compared to adult peripheral bold NK cells. Telomere length was determined by flow cytometry for iPSC, adult peripheral blood NK cells, and iPSC-derived NK cells using the 1301 T cell leukemia line as a control (100%) with correction for the DNA index of $G_{0/1}$ cells. As shown in FIG. 5, iPSC-derived NK cells maintain significantly longer telomere length when compared to adult peripheral blood NK cells (p=.105, ANOVA), representing greater proliferation, survival and persistence potential in the iPSC derived NK cells. Similar observation was made in iPSC derived T cells in comparison to primary T cells obtained from peripheral blood.

EXAMPLE 4 – CD3 Stimulation of Derivative T cells and Cell Response

[000332] To assess whether iTCR-induced CD3 cell surface expressing iTs respond to CD3/CD2/CD28-tetramer stimulation, iT cells derived from each iPSC cell line as described above were cryopreserved, thawed, and then cultured with or without CD3/CD2/CD28 tetramers in the presence of cytokines and assayed for markers of activation. 72hrs post tetramer stimulation, iT cell aggregation is readily apparent by brightfield microscopy in derivative T cells differentiated from WT, iTCRα and iTCRαβ transduced iPSC lines but is largely absent in TCR KO iT cells (FIG. 10). T cell aggregation is a hallmark of activation and the data suggests that derivative T cells differentiated from iPSC transduced with iTCRα alone or together with iTCRβ are capable of stimulation and activation through iTCR-induced cell surface CD3 expression.

[000333] Tetramer-stimulated iT cells were assayed by flow cytometry after 72hrs for the T cell activation marker CD25. WT, iTCRα and iTCRαβ transduced lines stimulated with tetramer upregulated CD25 expression compared to untreated control cultures. This response is absent absent in TCR KO iT cells. The CD25 flow cytometry data demonstrates that iTCR transduced lines are capable of stimulation and activation through iTCR-induced cell surface CD3 expression.

[000334] It was known that, upon activation, T cells would switch from expressing CD45RA to CD45RO. For further function verification, the tetramer-stimulated iT cells were assayed by flow cytometry after 72hrs for this hallmark phenotype change. As shown in FIG. 11, after being stimulated with tetramer, iT cells derived from WT, iTCRα and iTCRαβ transduced iPSC lines demonstrated upregulated expression of CD45RO and downregulated expression of CD45RA as compared to the respective untreated iT cell control cultures. This response is absent in iT derived from TCR KO iPSCs. This data demonstrates that iT cells derived from iPSC transduced with iTCRα alone or together with iTCRβ are capable of stimulation and activation through expressed CD3 trafficked to cell surface by a defined recombinant TCR (d-rTCR) exemplified by the one, as exemplified herein, comprising a defined transgenic TCRα (tgTCRα) with or without a defined transgenic TCRβ (tgTCRα) originated from invariant NKT cells.

EXAMPLE 5 – BiTE Mediated Cellular Cytotoxicity Through Reconstituted Cell Surface CD3

[000335] Effector cell cytotoxicity was assessed by co-cultivating iT effector cells derived from iTCRα and iTCRαβ transduced iPSC lines with a 50:50 target cell mixture consisting of Nalm6 CD19WT cells labeled with cell proliferation dye eFluor™ 450 and Nalm6-CD19KO cells labeled with cell proliferation dye eFluor™ 670. Mixed target cells were plated in 96 well U

bottom plates, and effector cells of various concentrations were added to each well for desired effector to target (E:T) range from 0:1, 1:1, 3.16:1, and 10:1 with or without CD19xCD3 BiTE (Invivogen, San Diego, CA) or CD20xCD3 BiTE (G&P Biosciences, Santa Clara, CA) for about 4hrs and analyzed subsequently by flow cytometry. The percentage of apoptotic target cells was determined based on the percentage of caspase 3/7+ cells among eFluor™ 450+ Nalm6 CD19WT cells, or the percentage of caspase 3/7+ cells among eFluor™ 670+ Nalm6-CD19KO cells.

[000336] As shown in FIG. 12A, iTCRα and iTCRαβ expressing iT cells exhibited enhanced specific cytotoxicity in the presence of BiTEs. It was observed that the BiTE itself (either CD19xCD3 or CD20xCD3) did not trigger enhanced cell apoptosis, whereas the addition of effector iT cells expressing cell surface CD3 increased tumor cell apoptosis. Thus, the cytotoxicity of the iPSC derived effector cells is further enhanced with the BiTE binding to the reconstituted CD3. The improved effector cell functionality was further demonstrated through the decreased EC50 of effector iT cells in the presence of BiTE compared to that of effector iT cells alone in both lines (FIG. 12B).

EXAMPLE 6 – Function Profiling of Derivative NK cells With Improved Persistency

[000337] In addition, the expression of exogenous truncated IL15/IL15Rα fusion protein lacking the intracellular domain of IL15Rα was shown to support the survival of iPSC derived NK cells *in vitro* independent of addition of soluble, exogenous IL2. The IL15Rα without its intracellular domain was fused to IL15 at the C-terminus through a linker to generate a truncated IL15/IL15Ra fusion construct having no signaling domain (or called "IL15Δ" in this application). Exemplary IL15Δ as provide herein includes those having a structure such as the Design 3 or 4 of FIG. 2. As shown in FIG. 5, iNK cells were transduced with lentiviral overexpression vectors expressing either GFP (squares; negative control), full-length IL15/IL15Ra fusion construct (filled circles; positive control; Design 2 of FIG. 2), or a truncated IL15/IL15Ra fusion construct (open circles; Design 3 of FIG. 2). Neither of the IL15 constructs nor GFP showed enrichment in the presence of exogenous IL2 (FIG. 6, left), indicating that transduced cells survived at comparable rates with non-transduced cells. In the absence of exogenous IL2, cells transduced with either IL15/IL15Ra fusion construct were enriched over time while GFP transduced cells were not, indicating that without IL2, cells transduced with either IL15/IL15Ra construct had a survival advantage compared to non-transduced cells in the same cultures (FIG. 6, right). Moreover, since the intracellular domain of IL15Rα has been deemed as critical for the receptor to express in the IL15 responding cells and for the cells to expand and function in response, it is surprising that the intracellular domain truncated IL15/IL15Ra fusion construct not only is stably

expressed in the transduced iNK cell, but also supports iNK cell at a higher expansion rate than the full-length IL15/IL15Ra fusion construct, as shown in right plot of FIG. 6. As such, the IL15Δ as provided herein is capable of expressing and maintaining IL15 in a membrane-bound form, and can replace a full-length IL15/IL15Ra fusion protein to provide the trans-presentation of IL15 in a cell. Without fully understand the underlying mechanism, removing the intracellular domain of IL15R seems to have given the responding cells additional vigor, fitness, or certain advantage, in survival, expansion and persistence, possibly by entirely eliminating cis-presentation and/or any other potential signal transduction pathways mediated by a normal IL15R through its intracellular domain.

[000338] One skilled in the art would readily appreciate that the methods, compositions, and products described herein are representative of exemplary embodiments, and not intended as limitations on the scope of the invention. It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the present disclosure disclosed herein without departing from the scope and spirit of the invention.

[000339] All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the present disclosure pertains. All patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated as incorporated by reference.

[000340] The present disclosure illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising," "consisting essentially of," and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the present disclosure claimed. Thus, it should be understood that although the present disclosure has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

CLAIMS

What is claimed is:

1. A cell or a population thereof, wherein

(i) the cell is an induced pluripotent cell (iPSC), a clonal iPSC, or a clonal iPS cell line cell, or a derivative cell obtained from differentiating said iPSC; and

(ii) the cell is TCR^{neg}, and comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed.

2. The cell or population thereof of claim 1, wherein the cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3):

(i) is associated with a non-binding recombinant TCR (nb-rTCR);

(ii) is associated with a defined recombinant TCR (d-rTCR);

(iii) is associated with a recombinant pre-TCR (p-rTCR);

(iv) is anchored to a non-binding recombinant TCR (nb-rTCR-CD3); or

(v) is a CD3 chimeric chain (ccCD3).

3. The cell or population thereof of claim 1, wherein the one or more polynucleotide encodes exogenous protein comprising one or more of:

(i) a transgenic TCRα constant region (tgTRAC);

(ii) a transgenic TCRβ constant region (tgTRBC);

(iii) a transgenic TCRα (tgTCRα);

(iv) a transgenic TCRβ (tgTCRβ);

(v) a transgenic pre-TCRα (tgpTCRα);

(vi) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a full or partial TCRα constant region (tgCD3(ε-δ)-TRAC);

(vii) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a full or partial TCRβ constant region (tgCD3(ε-γ)-TRBC);

(viii) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a full or partial TCRα constant region (tgCD3(ε-γ)-TRAC);

(ix) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a full or partial TCRβ constant region (tgCD3(ε-δ)-TRBC);

(x) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3γ, and a full or partial length of endodomain of CD3ζ (tgCD3(ε-γ)-ζ);

(xi) a transgenic fusion protein comprising full or partial length of ectodomains of CD3ε and CD3δ, and a full or partial length of endodomain of CD3ζ (tgCD3(ε-δ)-ζ);

(xii) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3ε, a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, and a signaling domain of CD28 (tgCD3(ε- γ/δ)-28ζ);

(xiii) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3ε, a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, and a signaling domain of 41BB (tgCD3(ε- γ/δ)-BBζ); and/or

(xiv) a transgenic fusion protein comprising a full or partial length of ectodomain of CD3γ or CD3δ, a full or partial length of endodomain of CD3ζ, a signaling domain of CD28, and a signaling domain of 41BB (tgCD3(ε- γ/δ)-(28-BB)ζ).

4. The cell or population thereof of claim 3,

wherein the one or more polynucleotide encoding tgTRAC, tgTCRα, tgpTCRα, tgCD3(ε-δ)-TRAC, tgCD3(ε-γ)-TRAC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, or tgCD3(ε- γ/δ)-(28-BB)ζ is inserted in a TRAC locus, and optionally upon insertion, is operatively linked to endogenous promoter of TRAC; or

wherein the one or more polynucleotide encoding tgTRBC, tgTCRβ, tgCD3(ε-γ)-TRBC, tgCD3(ε-δ)-TRBC, tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and/or tgCD3(ε- γ/δ)-(28-BB)ζ is inserted in a TRBC locus, and optionally upon insertion, is operatively linked to endogenous promoter of TRBC.

5. The cell or population thereof of claim 4,

wherein the polynucleotide encoding tgTRAC comprises a sequence encoding a full or partial length of the constant region of TCRα, and optionally an N-terminal signal peptide; or

wherein the polynucleotide encoding tgTRAC comprises a sequence encoding a full length of the constant region of TCRα and a poly A tail at C-terminal, and optionally an N-terminal signal peptide; or

wherein the polynucleotide encoding tgTRAC comprises a sequence encoding a partial length of the constant region of TCRα, and optionally an N-terminal signal peptide; and wherein the insertion of the polynucleotide is in an exon of the constant region and is in frame; or

wherein the polynucleotide encoding tgTRBC comprises a sequence encoding a full or partial length of the constant region of TCRβ, and optionally an N-terminal signal peptide; or

wherein the polynucleotide encoding tgTRBC comprises a sequence encoding a full length of the constant region of TCRβ and a poly A tail at C-terminal, and optionally an N-terminal signal peptide; or

wherein the polynucleotide encoding tgTRBC comprises a sequence encoding a partial length of the constant region of TCRβ, and optionally an N-terminal signal peptide; and wherein the insertion of the polynucleotide is in an exon of the constant region and is in frame.

6. The cell or population thereof of claim 4, wherein the one or more polynucleotide inserted in TRAC and/or TRBC locus disrupts expression of TRAC and TRBC, respectively, leading to TCR^{neg} cell.

7. The cell or population thereof of claim 6, wherein the one or more polynucleotide inserted in TRAC and/or TRBC locus is driven by (i) an endogenous promoter of TRAC and TRBC respectively, or (ii) a heterologous promoter.

8. The cell or population thereof of claim 7, wherein the heterologous promoter comprises: (i) at least one of constitutive, inducible, temporal-, tissue-, or cell type- specific promoters; or (ii) one of CMV, EF1α, PGK, CAG, and UBC; or (iii) CAG.

9. The cell or population thereof of claim 2, wherein

(i) the nb-rTCR comprises one or both of a tgTRAC and a tgTRBC;

(ii) the d-rTCR comprises a tgTCRα, and optionally, a tgTCRβ, wherein each of the tgTCRα and the tgTCRβ comprises a respective defined variable region;

(iii) the p-rTCR comprises a tgpTCRα, and optionally a tgTRBC or a tgTCRβ, wherein the tgTCRβ comprises a defined variable region;

(iv) the nb-rTCR-CD3 comprises one or more of fusion proteins: (1) a tgCD3(ε-δ)-TRAC; (2) a tgCD3(ε-γ)-TRBC; (3) a tgCD3(ε-γ)-TRAC; and/or (4) a tgCD3(ε-δ)-TRBC, wherein the fusion protein comprises full or partial length of ectodomains of CD3ε, CD3δ, CD3γ, and/or a full or partial length of TRAC or TRBC; or

(v) the ccCD3 comprises at least one of fusion proteins: tgCD3(ε-γ)-ζ, tgCD3(ε-δ)-ζ, tgCD3(ε- γ/δ)-28ζ, tgCD3(ε- γ/δ)-BBζ, and tgCD3(ε-γ/δ)-(28-BB)ζ, wherein the fusion protein comprising full or partial length of ectodomains of CD3ε, CD3δ and/or CD3γ protein, further comprises a cytoplasmic domain comprising a full or partial length endodomain of CDζ protein, and optionally one or both of a CD28 signaling domain and a 41BB signaling domain.

10. The cell or population thereof of claim 9, wherein the nb-rTCR-CD3 comprising fusion protein tgCD3(ε-δ)-TRAC further comprises tgTRBC or tgTCRβ; or wherein the nb-rTCR-CD3 comprising fusion protein tgCD3(ε-γ)-TRBC further comprises tgTRAC or tgTCRα; or wherein the d-rTCR comprising a tgTCRα and a tgTCRβ comprises TCRα and TCRβ of an invariant NKT cell.

11. The cell or population thereof of claim 9, wherein

(i) the cell comprises one of the recombinant TCRs: nb-rTCR, d-rTCR, or the p-rTCR, wherein the recombinant TCR complexes with endogenous CD3 subunits, thereby enabling cell surface presentation of endogenous CD3 subunits and signaling thereof; or wherein

(ii) the cell comprises a nb-rTCR-CD3 or a ccCD3, thereby enabling cell surface presentation of exogenous CD3 subunits and signaling thereof.

12. The cell or population thereof of claim 1, wherein the derivative cell is a hematopoietic cell and comprises longer telomeres in comparison to its native counterpart cell obtained from peripheral blood, umbilical cord blood, or any other donor tissues.

13. The cell or population thereof of claim 1, wherein the cell further comprises one or more of:

(i) B2M negative or low;

(ii) CIITA negative or low;

(iii) introduced expression of HLA-G or non-cleavable HLA-G;

(iv) a high affinity non-cleavable CD16 (hnCD16) or a variant thereof;

(v) a chimeric antigen receptor (CAR),

(vi) a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof;

(vii) at least one of the genotypes listed in Table 1;

(viii) deletion or reduced expression in at least one of CD38, TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and

(ix) introduced or increased expression in at least one of HLA-E, 41BBL, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, Fc receptor, an engager, and surface triggering receptor for coupling with bi- or multi- specific or universal engagers.

14. The cell or population thereof of claim 1 or 13, wherein the cell is a derivative NK or a derivative T cell, and has at least one of the following characteristics comprising:

(i) improved persistency and/or survival;

(ii) increased resistance to native immune cells;

(iii) increased cytotoxicity;

(iv) improved tumor penetration;

(v) enhanced or acquired ADCC;

(vi) enhanced ability in migrating, and/or activating or recruiting bystander immune cells, to tumor sites;

(vii) enhanced ability to reduce tumor immunosuppression;

(viii) improved ability in rescuing tumor antigen escape; and

(ix) reduced fratricide,

in comparison to its native counterpart cell obtained from peripheral blood, umbilical cord blood, or any other donor tissues.

15. The cell or population thereof of claim 13, wherein the cell further comprises a high affinity non-cleavable CD16 (hnCD16) or a variant thereof.

16. The cell or population thereof of claim 15, wherein the high affinity non-cleavable CD16 (hnCD16) or a variant thereof comprises at least one of:

(a) F176V and S197P in ectodomain domain of CD16;

(b) a full or partial ectodomain originated from CD64;

(c) a non-native (or non-CD16) transmembrane domain;

(d) a non-native (or non-CD16) intracellular domain;

(e) a non-native (or non-CD16) signaling domain;

(f) a non-native stimulatory domain; and

(g) transmembrane, signaling, and stimulatory domains that are not originated from CD16, and are originated from a same or different polypeptide.

17. The cell or population thereof of claim 16, wherein

(a) the non-native transmembrane domain is derived from CD3D, CD3E, CD3G, CD3ζ, CD4, CD8, CD8a, CD8b, CD27, CD28, CD40, CD84, CD166, 4-1BB, OX40, ICOS, ICAM-1, CTLA-4, PD-1, LAG-3, 2B4, BTLA, CD16, IL7, IL12, IL15, KIR2DL4, KIR2DS1, NKp30, NKp44, NKp46, NKG2C, NKG2D, or T cell receptor (TCR) polypeptide;

(b) the non-native stimulatory domain is derived from CD27, CD28, 4-1BB, OX40, ICOS, PD-1, LAG-3, 2B4, BTLA, DAP10, DAP12, CTLA-4, or NKG2D polypeptide;

(c) the non-native signaling domain is derived from CD3ζ, 2B4, DAP10, DAP12, DNAM1, CD137 (41BB), IL21, IL7, IL12, IL15, NKp30, NKp44, NKp46, NKG2C, or NKG2D polypeptide; or

(d) the non-native transmembrane domain is derived from NKG2D, the non-native stimulatory domain is derived from 2B4, and the non-native signaling domain is derived from CD3ζ.

18. The cell or population thereof of claim 13, wherein the cell further comprises a chimeric antigen receptor (CAR), and wherein the CAR is:

(i) T cell specific or NK cell specific;

(ii) bi-specific antigen binding CAR;

(iii) a switchable CAR;

(iv) a dimerized CAR;

(v) a split CAR;

(vi) a multi-chain CAR;

(vii) an inducible CAR;

(viii) co-expressed with another CAR;

(ix) co-expressed with a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof, optionally in separate constructs or in a bi-cistronic construct;

(xi) co-expressed with a checkpoint inhibitor, optionally in separate constructs or in a bi-cistronic construct;

(xii) specific to CD19 or BCMA; and/or

(xiii) specific to any one of ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion

molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBC1, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and a pathogen antigen;

wherein the CAR of any one of (i) to (xiii) is optionally inserted at TRAC locus, and/or is driven by an endogenous promoter of TCR, and/or the TCR is knocked out by the CAR insertion.

19. The cell or population thereof of claim 13, wherein the cell comprising a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof, the exogenous cytokine or a receptor thereof

(a) comprises at least one of IL2, IL4, IL6, IL7, IL9, IL10, IL11, IL12, IL15, IL18, IL21, and its respective receptor; or

(b) comprises at least one of:

(i) co-expression of IL15 and IL15Rα by using a self-cleaving peptide;

(ii) a fusion protein of IL15 and IL15Rα;

(iii) an IL15/IL15Rα fusion protein with intracellular domain of IL15Rα truncated;

(iv) a fusion protein of IL15 and membrane bound Sushi domain of IL15Rα;

(v) a fusion protein of IL15 and IL15Rβ;

(vi) a fusion protein of IL15 and common receptor γC, wherein the common receptor γC is native or modified; and

(vii) a homodimer of IL15Rβ;

wherein any one of (i)-(vii) can be co-expressed with a CAR in separate constructs or in a bi-cistronic construct;

and optionally,

(c) is transiently expressed.

20. The cell or population thereof of claim 13, wherein the cell is a derivative NK or a derivative T cell, wherein the derivative NK cell is capable of recruiting, and/or migrating T cells to tumor sites, and wherein the derivative NK or the derivative T cell is capable of reducing tumor immunosuppression in the presence of one or more checkpoint inhibitors.

21. The cell or population thereof of claim 18 or 20, wherein the checkpoint inhibitors are antagonists to one or more checkpoint molecules comprising PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB, 4-1BBL, A2aR, BATE, BTLA, CD39, CD47, CD73, CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2, Rara (retinoic acid receptor alpha), TLR3, VISTA, NKG2A/HLA-E, or inhibitory KIR.

22. The cell or population thereof of claim 21, wherein the checkpoint inhibitors comprise:

(a) one or more of atezolizumab, avelumab, durvalumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their derivatives or functional equivalents; or

(b) at least one of atezolizumab, nivolumab, and pembrolizumab.

23. The cell or population thereof of claim 1, wherein the derivative cell comprises derivative CD34 cell, derivative hematopoietic stem and progenitor cell, derivative hematopoietic multipotent progenitor cell, derivative T cell progenitor, derivative NK cell progenitor, derivative T cell, derivative NKT cell, derivative NK cell, or derivative B cell.

24. The cell or population thereof of claim 1, wherein the cell comprises:

(i) one or more exogenous polynucleotides integrated in one safe harbor locus; or

(ii) more than two exogenous polynucleotides integrated in different safe harbor loci; or

(iii) a polynucleotide encoding an IL15Δ comprising an amino acid sequence of at least 75%, 80%, 85%, 90%, 95% or 99% identity to SEQ ID NOs: 17, 19 or 21.

25. The cell or population thereof of claim 24, wherein the safe harbor locus comprises at least one of AAVS1, CCR5, ROSA26, collagen, HTRP, H11, beta-2 microglobulin, CD38, GAPDH, TCR, CD38, RUNX1, or TCR.

26. The cell or population thereof of claim 25, wherein the safe harbor locus TCR is a constant region of TCR alpha or TCR beta.

27. A clonal master cell bank comprising the clonal iPSC cell line cells of any one of the claims 1-26.

28. A composition comprising the cell or population thereof of any one of the claims 1-26.

29. A composition for therapeutic use comprising the derivative cell of any one of the claims 1-26, and one or more therapeutic agents.

30. The composition of claim 29, wherein the therapeutic agents comprise a peptide, a cytokine, a checkpoint inhibitor, a mitogen, a growth factor, a small RNA, a dsRNA (double stranded RNA), mononuclear blood cells, feeder cells, feeder cell components or replacement factors thereof, a vector comprising one or more polynucleic acids of interest, an antibody, a chemotherapeutic agent or a radioactive moiety, or an immunomodulatory drug (IMiD).

31. The composition of claim 30, wherein

(a) the checkpoint inhibitor comprises:

(i) one or more antagonists checkpoint molecules comprising PD-1, PDL-1, TIM-3, TIGIT, LAG-3, CTLA-4, 2B4, 4-1BB, 4-1BBL, A2aR, BATE, BTLA, CD39, CD47, CD73, CD94, CD96, CD160, CD200, CD200R, CD274, CEACAM1, CSF-1R, Foxpl, GARP, HVEM, IDO, EDO, TDO, LAIR-1, MICA/B, NR4A2, MAFB, OCT-2, Rara (retinoic acid receptor alpha), TLR3, VISTA, NKG2A/HLA-E, or inhibitory KIR;

(ii) one or more of atezolizumab, avelumab, durvalumab, ipilimumab, IPH4102, IPH43, IPH33, lirimumab, monalizumab, nivolumab, pembrolizumab, and their derivatives or functional equivalents;

(iii) at least one of atezolizumab, nivolumab, and pembrolizumab; or

(b) the therapeutic agents comprise one or more of venetoclax, azacitidine, and pomalidomide.

32. The composition of claim 30, wherein the antibody comprises:

(a) anti-CD20, anti-CD22, anti-HER2, anti-CD52, anti-EGFR, anti-CD123, anti-GD2, anti-PDL1, and/or anti-CD38 antibody;

(b) one or more of rituximab, veltuzumab, ofatumumab, ublituximab, ocaratuzumab, obinutuzumab, ibritumomab, ocrelizumab, inotuzumab, moxetumomab, epratuzumab, trastuzumab, pertuzumab, alemtuzumab, certuximab, dinutuximab, avelumab, daratumumab, isatuximab, MOR202, 7G3, CSL362, elotuzumab, and their humanized or Fc modified variants or fragments and their functional equivalents and biosimilars; or

(c) daratumumab, and wherein the derivative hematopoietic cells comprise derivative NK cells or derivative T cells comprising a CD38 knockout, and optionally an expression of hnCD16 or a variant thereof.

33. Therapeutic use of the composition of any one of the claims 28-31 by introducing the composition to a subject suitable for adoptive cell therapy, wherein the subject has an autoimmune disorder; a hematological malignancy; a solid tumor; cancer, or a virus infection.

34. A method of manufacturing the cell of any one of the claims 1-26 comprising differentiating a TCR^{neg} iPSC, wherein the iPSC comprises one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and optionally the iPSC further comprises one or more of:

(i) B2M negative or low;

(ii) CIITA negative or low;

(iii) introduced expression of HLA-G or non-cleavable HLA-G;

(iv) a high affinity non-cleavable CD16 (hnCD16) or a variant thereof;

(v) a chimeric antigen receptor (CAR);

(vi) a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof;

(vii) at least one of the genotypes listed in Table 1;

(viii) deletion or reduced expression in at least one of CD38, TAP1, TAP2, Tapasin, NLRC5, PD1, LAG3, TIM3, RFXANK, CIITA, RFX5, RFXAP, RAG1, and any gene in the chromosome 6p21 region; and

(ix) introduced or increased expression in at least one of HLA-E, 41BBL, CD3, CD4, CD8, CD16, CD47, CD113, CD131, CD137, CD80, PDL1, $A_{2A}R$, CAR, TCR, Fc receptor, an engager, and surface triggering receptor for coupling with bi- or multi- specific or universal engagers.

35. The method of manufacturing the cells of claim 34, further comprising (a) knocking out TCR of a clonal iPSC to obtain the genomically engineered TCR^{neg} iPSC, and knocking in, simultaneously or subsequently, one or more polynucleotide encoding one or more exogenous protein; or

(b) reprogramming an invariant NKT cell to iPSC to provide a clonal iPSC comprising iTCRαβ but not T cell-TCR,

to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed; and

(c) optionally genomically engineering the iPSC of (a) or (b) by

(i) knocking out B2M and CIITA, or

(ii) introducing expression of HLA-G or non-cleavable HLA-G, a high affinity non-cleavable CD16 or a variant thereof, a CAR, and/or a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof;

wherein the CAR and the partial or full peptide of a cell surface expressed exogenous cytokine or a receptor thereof are co-expressed in separate constructs or in a bi-cistronic construct.

36. The method of manufacturing the cells of claim 35, wherein the step (a), knocking in one or more polynucleotide encoding one or more exogenous protein to provide cs-CD3, further comprises introducing to the iPSC one of the following:

(i) one or both of a tgTRAC and a tgTRBC encoding polynucleotide, to provide a nb-rTCR when expressed;

(ii) a tgTCRα, and optionally a tgTCRβ, encoding polynucleotide, to provide a d-rTCR when expressed, wherein each of the tgTCRα and the tgTCRβ comprises a respective defined variable region;

(iii) a tgpTCRα, and optionally a tgTRBC or a tgTCRβ, encoding polynucleotide, to provide a p-rTCR, wherein the tgTCRβ comprises a defined variable region;

(iv) one or more polynucleotides encoding one or more of fusion proteins: (1) tgCD3(ε-δ)-TRAC, (2) tgCD3(ε-γ)-TRBC, (3) tgCD3(ε-γ)-TRAC, and/or (4) tgCD3(ε-δ)-TRBC, to provide a nb-rTCR-CD3; wherein the fusion protein comprises full or partial length of ectodomains of CD3ε, CD3δ, CD3γ, and/or a full or partial length of TRAC or TRBC; or

(v) one or more polynucleotides encoding one or more of fusion proteins: (1) tgCD3(ε-γ)-ζ, (2) tgCD3(ε-δ)-ζ, (3) tgCD3(ε- γ/δ)-28ζ, (4) tgCD3(ε- γ/δ)-BBζ, and (5) tgCD3(ε-γ/δ)-(28-BB)ζ, to provide ccCD3; wherein the fusion protein comprising full or partial length of ectodomains of CD3ε, CD3δ and/or CD3γ protein, further comprises a cytoplasmic domain comprising a full or partial length endodomain of CDζ protein, and optionally one or both of a CD28 signaling domain and a 41BB signaling domain.

37. The method of manufacturing the cell of claim 36, wherein the step of introducing to the iPSC one or more polynucleotides encoding fusion protein tgCD3(ε-δ)-TRAC of (iv), further

comprises introducing a polynucleotide encoding tgTRBC or tgTCRβ, to provide the nb-rTCR-CD3; or

wherein the step of introducing to the iPSC one or more polynucleotides encoding fusion protein tgCD3(ε-γ)-TRBC of (iv) further comprises tgTRAC or tgTCRα, to provide the nb-rTCR-CD3; or

wherein in the step of introducing to the iPSC the polynucleotide encoding tgTCRα, and optionally, the polynucleotide encoding tgTCRβ, to provide the d-rTCR, the tgTCRα and the tgTCRβ respectively comprise a TCRα and a TCRβ of an invariant NKT cell.

38. The method of manufacturing the cell of claim 35, wherein the knocking out, the knocking in, or the genomically engineering comprises targeted editing.

39. The method of manufacturing the cell of claim 38, wherein the targeted editing comprises deletion, insertion, or in/del, and wherein the targeted editing is carried out by CRISPR, ZFN, TALEN, homing nuclease, homology recombination, or any other functional variation of these methods.

40. CRISPR mediated editing of clonal iPSCs of any one of claims 1-26, wherein the edited iPSCs are TCR^{neg} and comprise one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, wherein the edited clonal iPSCs comprise at least one of the genotypes listed in Table 1.

41. The CRISPR mediated editing of claim 40, wherein the editing further comprises an insertion of a CAR at a TRAC or a TRBC locus, and/or wherein the CAR is driven by an endogenous promoter of TCR, and/or wherein the TCR is knocked out by the CAR insertion.

42. A method of combinational treatment comprising providing to a subject under the treatment effector cells comprising TCR^{neg}, and one or more polynucleotide encoding one or more exogenous protein to provide a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) when expressed, and a selected multi-specific engager, wherein the effector cells comprise the derivative cells of any one of claims 1-26.

43. The method of claim 42, wherein the selected multi-specific engager is at least one of: (i) a T cell engager; (ii) an NK cell engager; (iii) a bispecific T cell engager (BiTE); (iv) a bispecific

killer cell engager (BiKE); (v) a tri-specific killer cell engager (TriKE); (vi) a CD3 engager; or (vii) a CD16 engager.

44. The method of claim 42, wherein the selected multispecific engager is a CD3 engager, wherein the CD3 engager comprises a first variable segment that binds to a cs-CD3 and a second variable segment that binds to an antigen comprising at least one of:

(i) ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP), fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and/or a pathogen antigen; or

(ii) BCMA, CD19, CD20, CD33, CD38, CD52, CD123, CEA, EGFR, EpCAM, GD2, GPA33, HER2, MICA/B, PDL1, and/or PSMA; or

(iii) CD19, CD33, CD123, CEA, EpCAM, GPA33, HER2, and/or PSMA;

or wherein the CD3 engager comprises at least one of: blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05.

45. The method of claim 44, wherein the CD3 engager is administered to the subject simultaneously or subsequently with the effector cells.

46. The method of claim 42, wherein the effector cells comprise derivative hematopoietic cells comprising derivative NK cells or derivative T cells, wherein the derivative NK cells or derivative T cells comprise a CD38 knockout, a high affinity non-cleavable CD16 or a variant thereof, and optionally comprise:

(i) B2M and CIITA knockout;

(ii) introduced expression of HLA-G or non-cleavable HLA-G, a CAR, and/or a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof; wherein the CAR and a partial or full length peptide of a cell surface expressed exogenous cytokine or a receptor thereof is co-expressed in separate constructs or in a bi-cistronic construct; and/or

(iii) at least one of the genotypes listed in Table 1.

47. A method of reducing or preventing allorejection by recipient T cells against effector cells in an adoptive cell treatment, wherein the method comprises providing to a subject under the treatment (i) an anti-CD3 agent, and (ii) effector cells comprising TCR^{neg}, and a cell surface CD3 complex, or one or more subunits or subdomains thereof (cs-CD3) preloaded with a CD3 engager, wherein the effector cells comprise the derivative cells of any one of claims 1-26,.

48. The method of claim 47, wherein the anti-CD3 agent is CD3 antibody or a CD3-CAR, wherein the CD3-CAR is comprised in a NK cell; and wherein the anti-CD3 agent deactivates recipient T cells, thereby reducing or preventing allorejection.

49. The method of 47, wherein the CD3 engager comprising a first variable segment that binds to a cs-CD3 of the effector cell, comprises a second variable segment that binds to an antigen related to an autoimmune disorder; a hematological malignancy; a solid tumor; cancer, or a virus infection.

50. The method of claim 49, wherein the CD3 engager comprising a second variable segment that binds to an antigen comprises at least one of:

(i) ADGRE2, carbonic anhydrase IX (CAIX), CCRI, CCR4, carcinoembryonic antigen (CEA), CD3, CD5, CD7, CD8, CD10, CD19, CD20, CD22, CD30, CD33, CD34, CD38, CD41, CD44, CD44V6, CD49f, CD56, CD70, CD74, CD99, CD123, CD133, CD138, CDS, CLEC12A, an antigen of a cytomegalovirus (CMV) infected cell, epithelial glycoprotein2 (EGP 2), epithelial glycoprotein-40 (EGP-40), epithelial cell adhesion molecule (EpCAM), EGFRvIII, receptor tyrosine-protein kinases erb- B2,3,4, EGFIR, EGFR-VIII, ERBB folate-binding protein (FBP),

fetal acetylcholine receptor (AChR), folate receptor-a, Ganglioside G2 (GD2), Ganglioside G3 (GD3), human Epidermal Growth Factor Receptor 2 (HER-2), human telomerase reverse transcriptase (hTERT), ICAM-1, Integrin B7, Interleukin-13 receptor subunit alpha-2 (IL-13Rα2), κ-light chain, kinase insert domain receptor (KDR), Lewis A (CA19.9), Lewis Y (LeY), L1 cell adhesion molecule (L1-CAM), LILRB2, melanoma antigen family A 1 (MAGE-A1), MICA/B, Mucin 1 (Muc-1), Mucin 16 (Muc-16), Mesothelin (MSLN), NKCSI, NKG2D ligands, c-Met, cancer-testis antigen NY-ESO-1, oncofetal antigen (h5T4), PRAME, prostate stem cell antigen (PSCA), PRAME prostate-specific membrane antigen (PSMA), tumor- associated glycoprotein 72 (TAG-72), TIM-3, TRBCI, TRBC2, vascular endothelial growth factor R2 (VEGF- R2), Wilms tumor protein (WT-1), and/or a pathogen antigen; or

(ii) BCMA, CD19, CD20, CD33, CD38, CD52, CD123, CEA, EGFR, EpCAM, GD2, GPA33, HER2, MICA/B, PDL1, and/or PSMA; or

(iii) CD19, CD33, CD123, CEA, EpCAM, GPA33, HER2, and/or PSMA;

or wherein the CD3 engager comprises at least one of: blinatumomab, catumaxomab, ertumaxomab, RO6958688, AFM11, MT110/AMG 110, MT111/AMG211/MEDI-565, AMG330, MT112/BAY2010112, MOR209/ES414, MGD006/S80880, MGD007, and/or FBTA05.

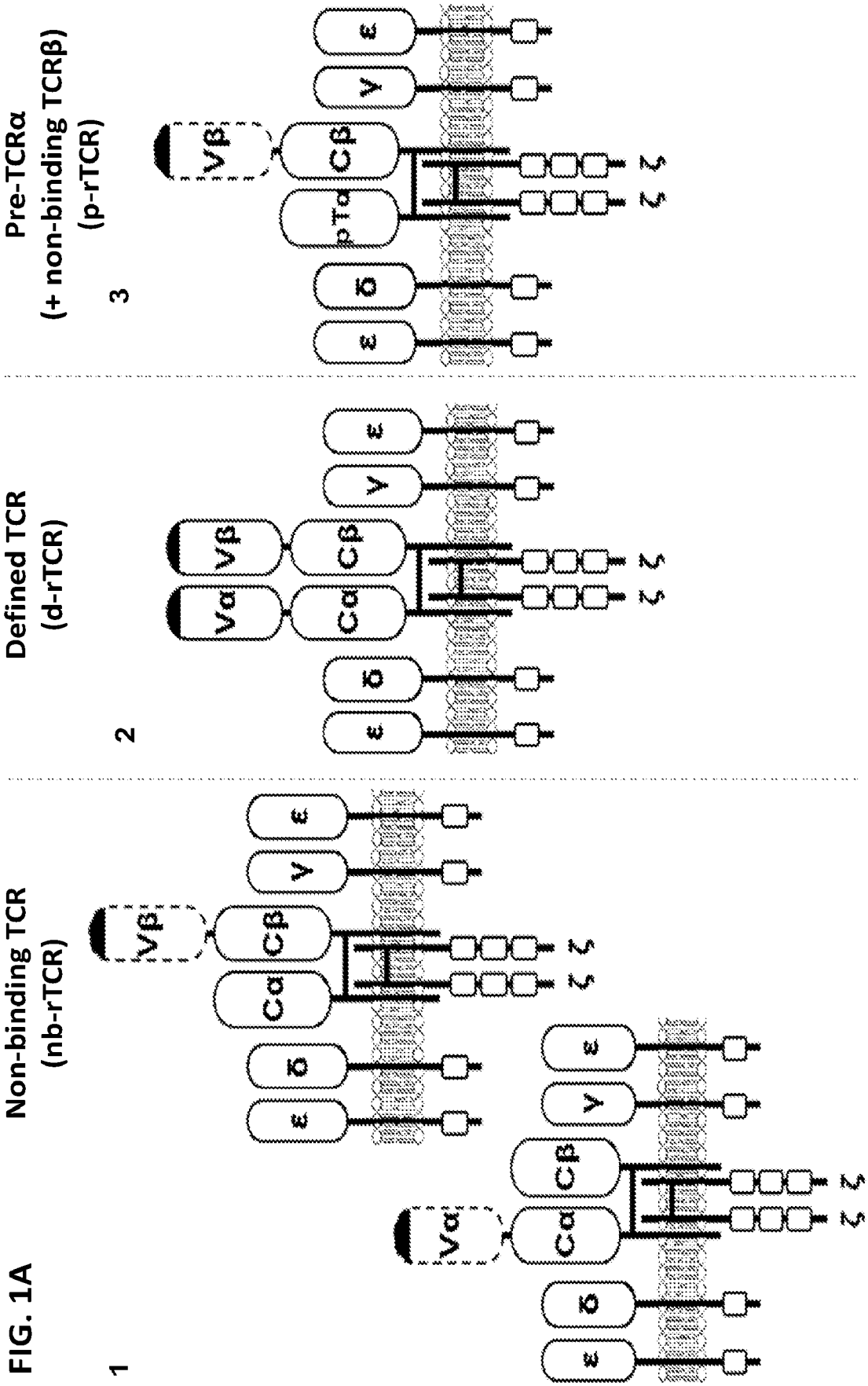

Non-binding TCR
(nb-rTCR)
1
Vβ
Cβ
Vα
Cα
ε
γ
δ
ε
ζ ζ
Defined TCR
(d-rTCR)
2
Vβ
Cβ
Vα
Cα
ε
γ
δ
ε
ζ ζ
Pre-TCRα
(+ non-binding TCRβ)
(p-rTCR)
3
Vβ
Cβ
pTα
ε
γ
δ
ε
ζ ζ

FIG. 1A

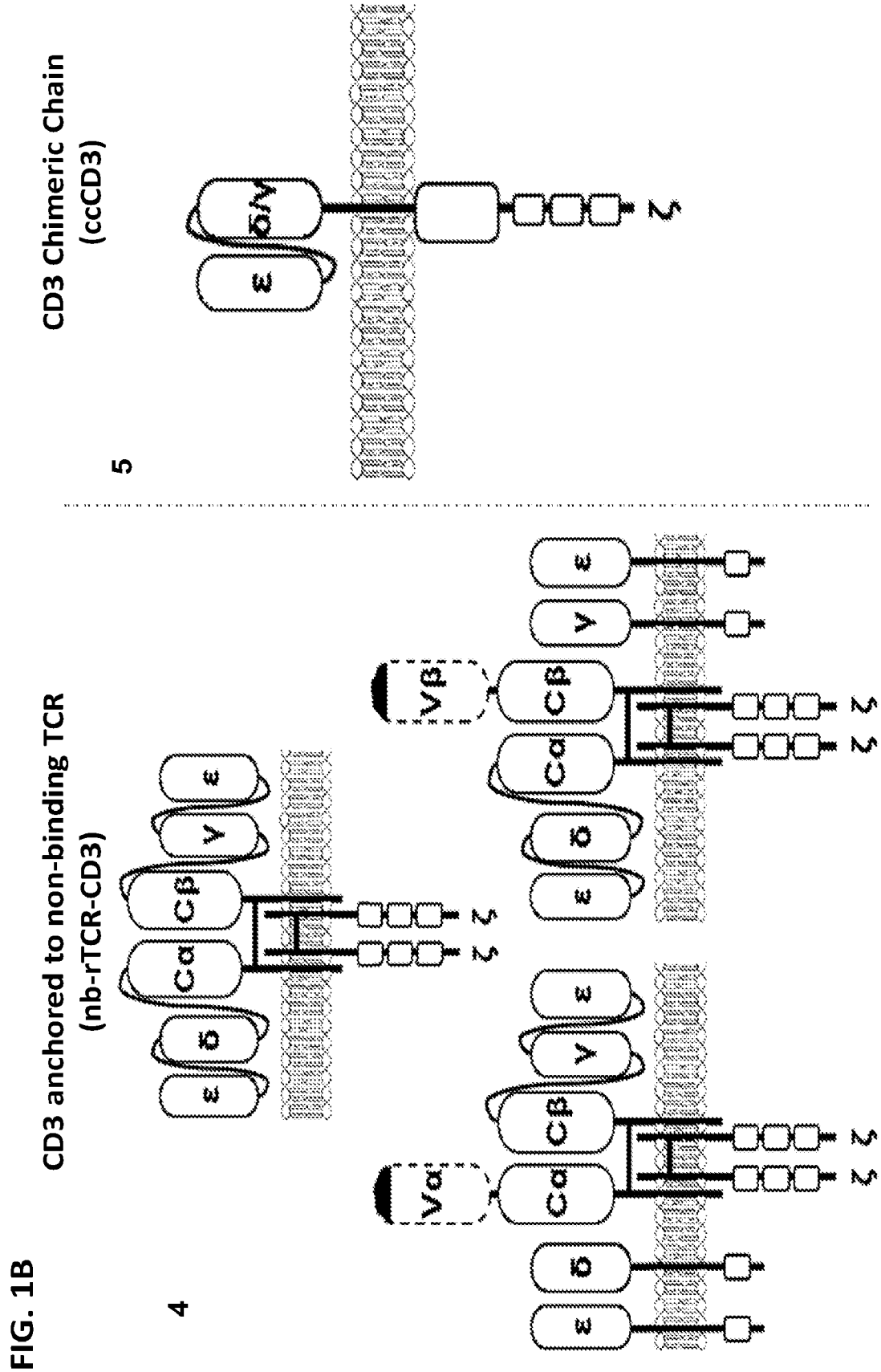
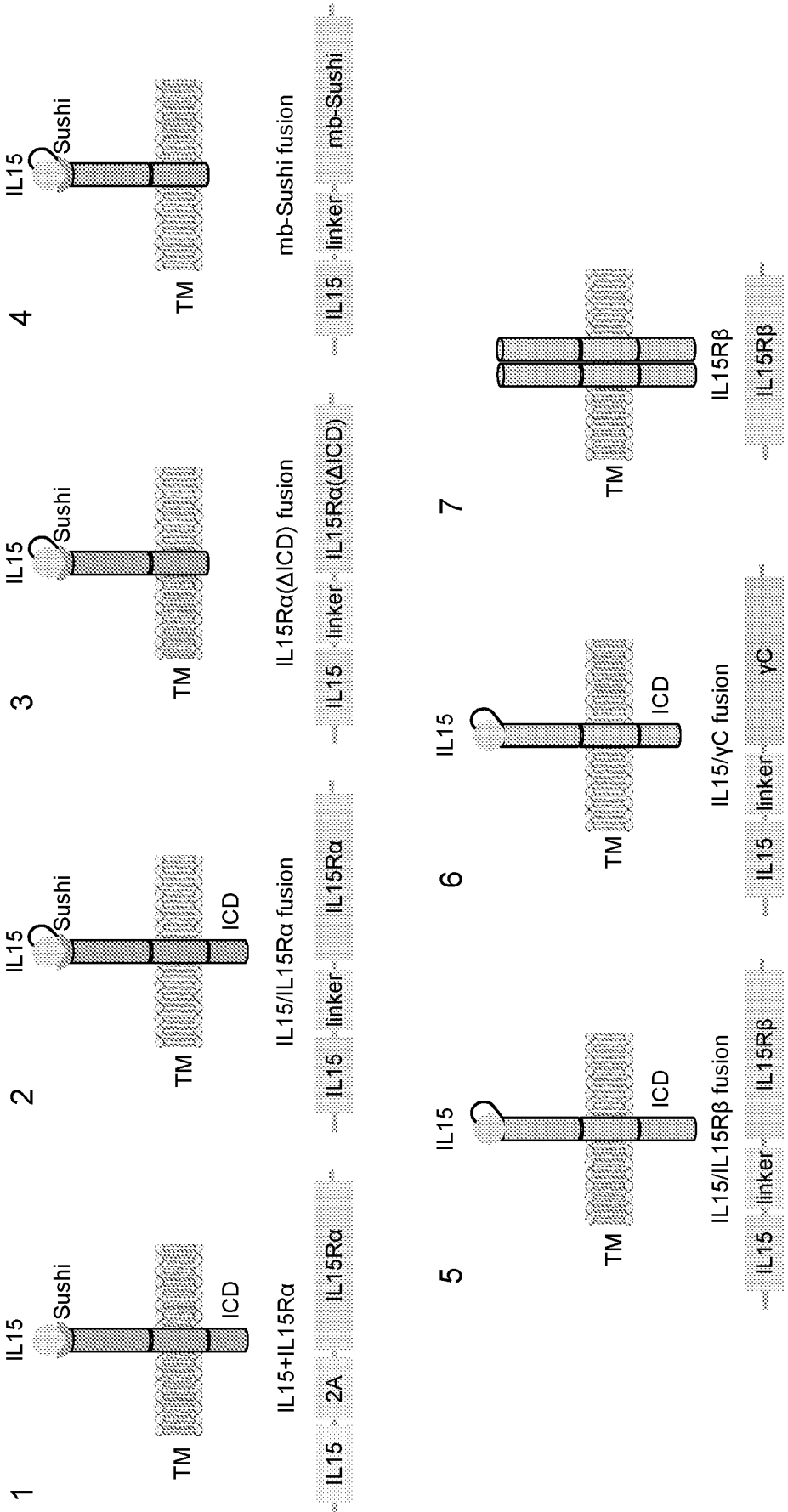

CD3 Chimeric Chain
(ccCD3)
5
δ/γ
ε
ζ
CD3 anchored to non-binding TCR
(nb-rTCR-CD3)
4
Vα
Cα
Cβ
Vβ
ε
γ
δ
ζ

FIG. 1B

FIG. 1C

	1	2	3	4	5
	Non-binding TCR (nb-rTCR)	**Defined TCR (d-rTCR)**	**Pre-TCRα (+ non-binding TCRβ) (p-rTCR)**	**CD3 anchored to non-binding TCR (nb-rTCR-CD3)**	**CD3 Chimeric Chain (ccCD3)**
Endogenous TCR KO	TCR(α or β) KO (+the other optional)	TCRα KO+ TCRβ KO	TCRα KO (+ TCRβ KO)	TCRα KO+ TCRβ KO	TCRα KO
Transgenic/modified protein expression	tgTRAC (+tgTRBC); or tgTRBC (+tgTRAC)	Defined tgTCRα+tgTCRβ	tgpTCRα (+ tgTRBC); or upregulating (down-reg prevention) endogenous pre-TCRα	tgCD3(ε-δ)-TRAC fusion and/or tgCD3(ε-γ)-TRBC fusion	tgCD3(ε- γ/δ)-(28/BB)ζ
Locus/promoter	TCRα (+ TCRβ) or constitutive	TCRα + TCRβ or constitutive	Constitutive	TCRα + TCRβ or constitutive	Constitutive
Peptide-MHC binding	No binding	Defined/No binding	No binding	No binding	No binding
Signaling	Canonical TCR/CD3	Canonical TCR/CD3	Canonical TCR/CD3	CDζ only	z/28z/BBz specific

FIG. 2


1
IL15
Sushi
TM
ICD
IL15+IL15Rα
IL15
2A
IL15Rα
2
IL15
Sushi
TM
ICD
IL15/IL15Rα fusion
IL15
linker
IL15Rα
3
IL15
Sushi
TM
IL15Rα(ΔICD) fusion
IL15
linker
IL15Rα(ΔICD)
4
IL15
Sushi
TM
mb-Sushi fusion
IL15
linker
mb-Sushi
5
IL15
TM
ICD
IL15/IL15Rβ fusion
IL15
linker
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γC
7
TM
IL15Rβ
IL15Rβ

FIG. 3

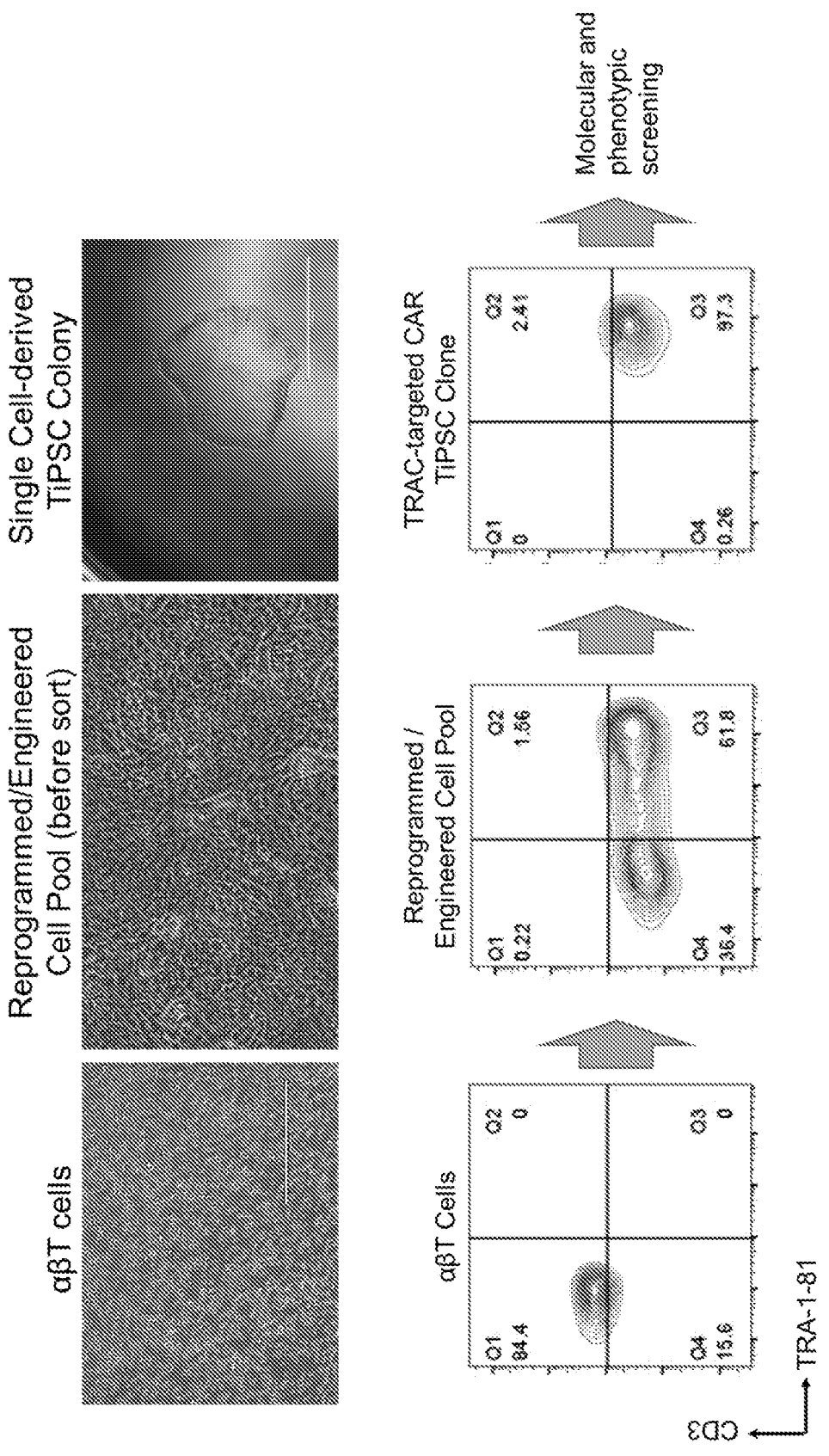
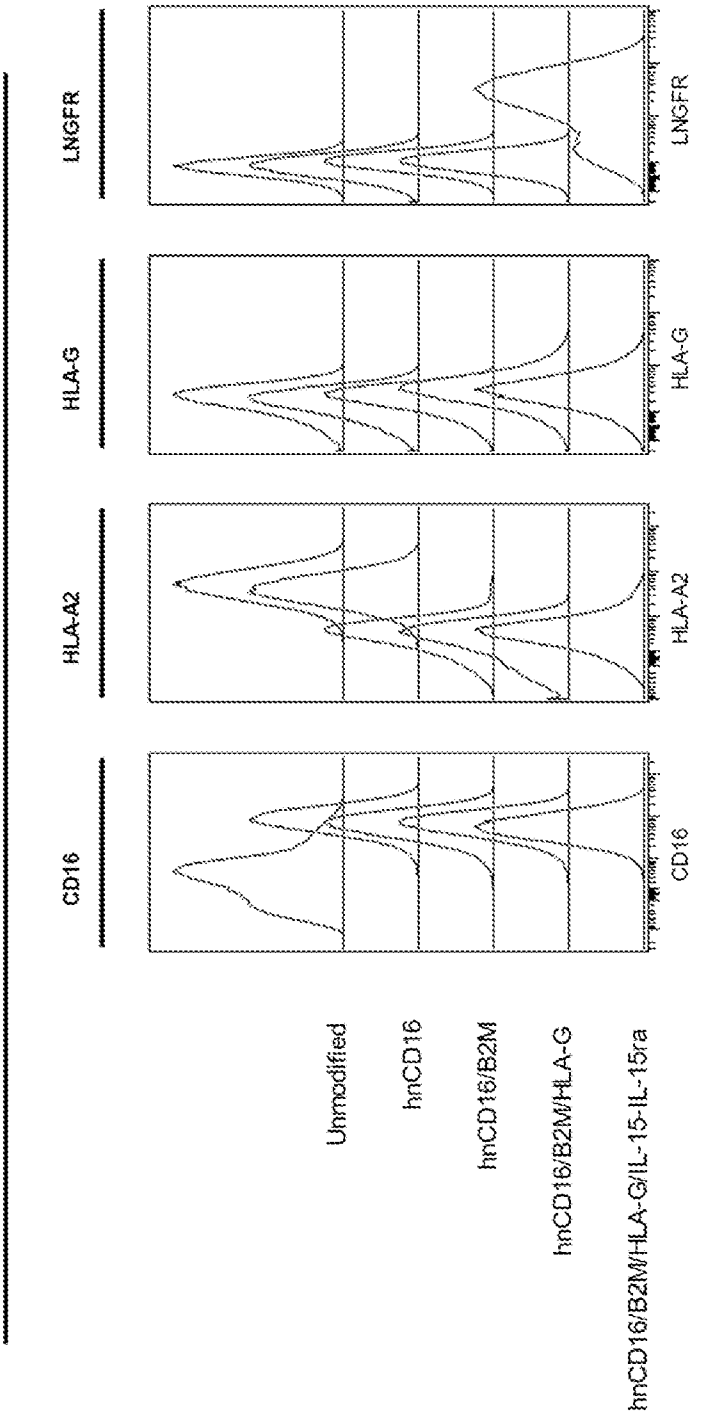

A
αβT cells
Reprogrammed/Engineered Cell Pool (before sort)
Single Cell-derived TiPSC Colony
B
αβT Cells
Q1 84.4
Q2 0
Q4 15.6
Q3 0
Reprogrammed / Engineered Cell Pool
Q1 0.22
Q2 1.56
Q4 36.4
Q3 61.8
TRAC-targeted CAR TiPSC Clone
Q1 0
Q2 2.41
Q4 0.26
Q3 97.3
Molecular and phenotypic screening
CD3
TRA-1-81

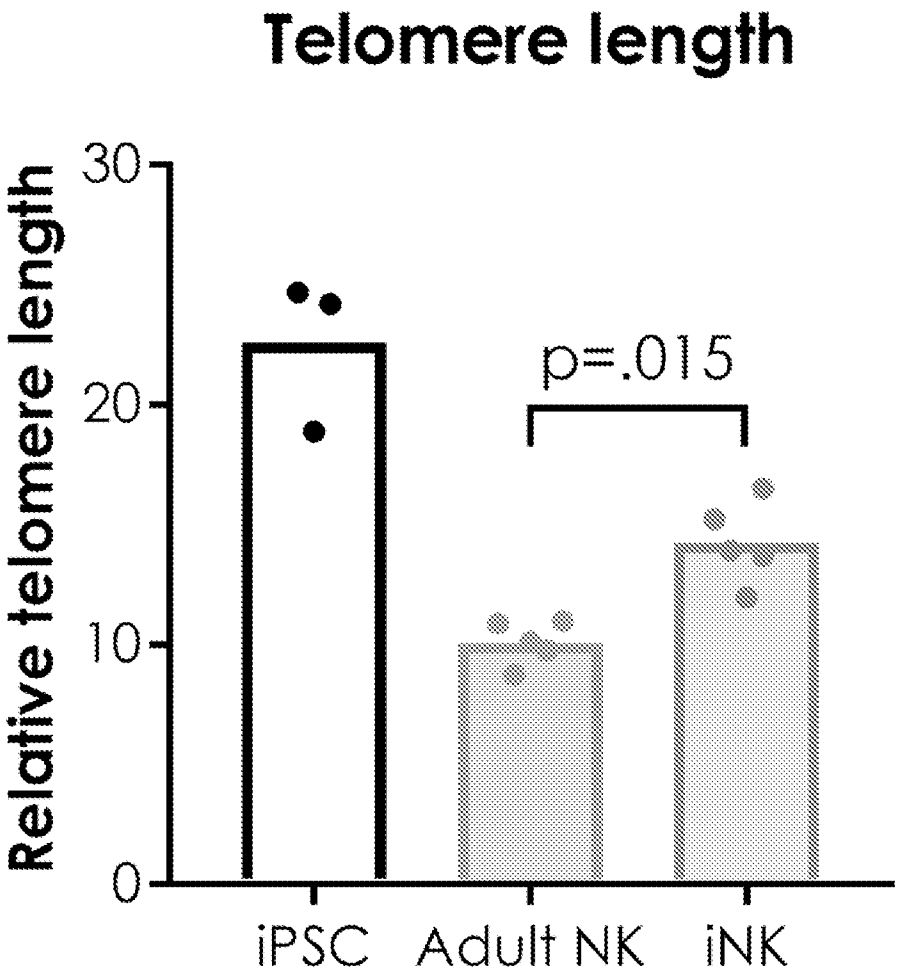
FIG. 4



	CD16	HLA-A2	HLA-G	LNGFR
Unmodified	1	19.41	1.17	1
hnCD16	12.14	15.63	1	1.11
hnCD16/B2M	9.41	1.52	1.25	1.64
hnCD16/B2M/HLA-G	9.34	1	2.33	1.58
hnCD16/B2M/HLA-G/IL-15-IL-15ra	8.66	1.9	2.13	48.13

Calculated Fold of Means by Column's Minimum using X-Axis channel(s): Panel/Channel Values

FIG. 5


Telomere length
Relative telomere length
30
20
10
0
p=.015
iPSC
Adult NK
iNK

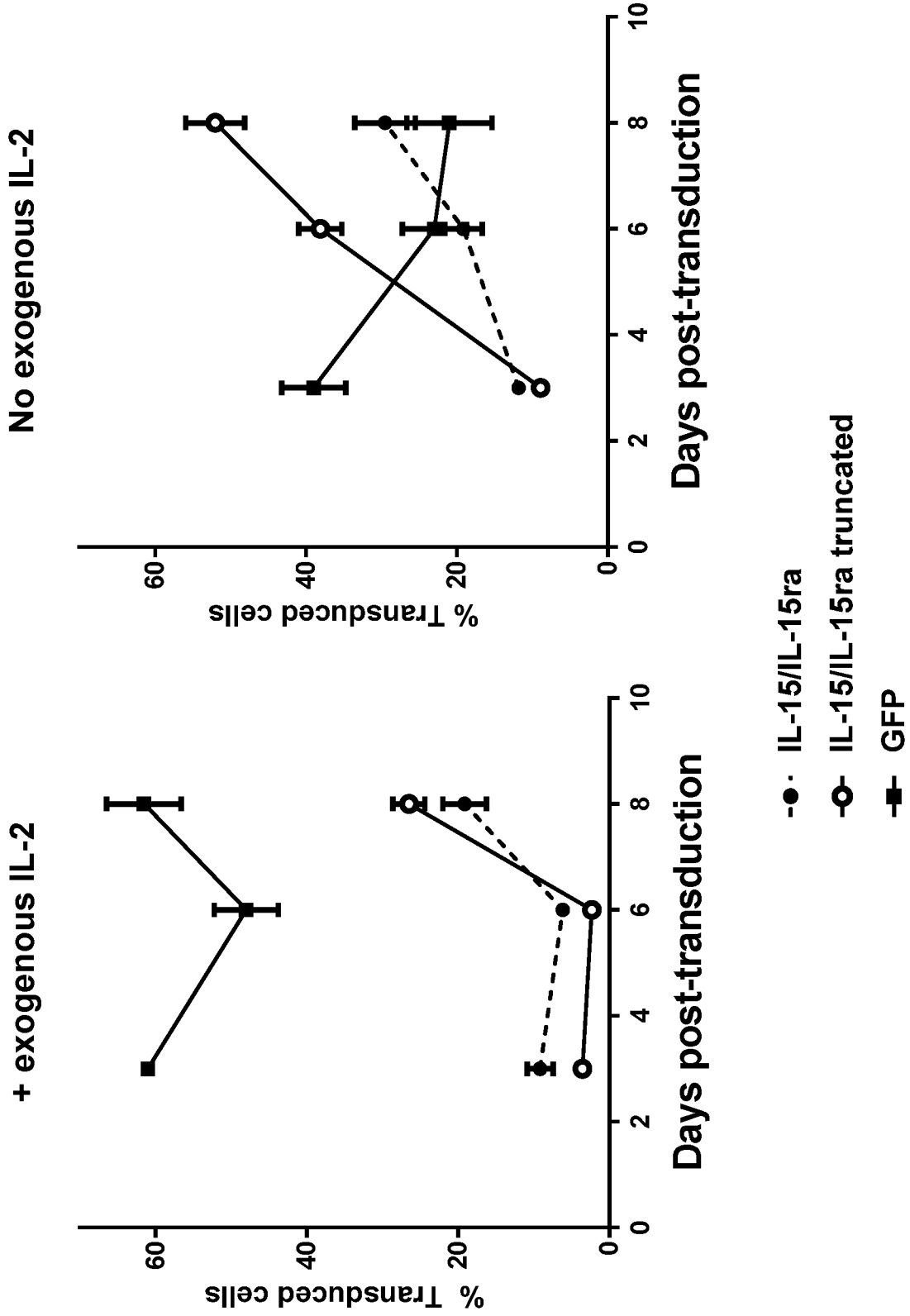

No exogenous IL-2
+ exogenous IL-2
% Transduced cells
Days post-transduction
0
20
40
60
0
2
4
6
8
10
IL-15/IL-15ra
IL-15/IL-15ra truncated
GFP

FIG. 6

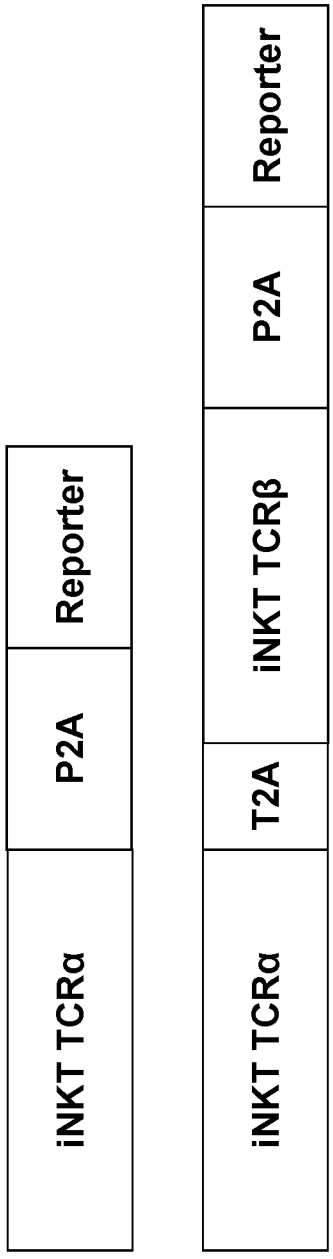

iTCRα
iNKT TCRα
P2A
Reporter
iTCRαβ
iNKT TCRα
T2A
iNKT TCRβ
P2A
Reporter

FIG. 7

FIG. 8A

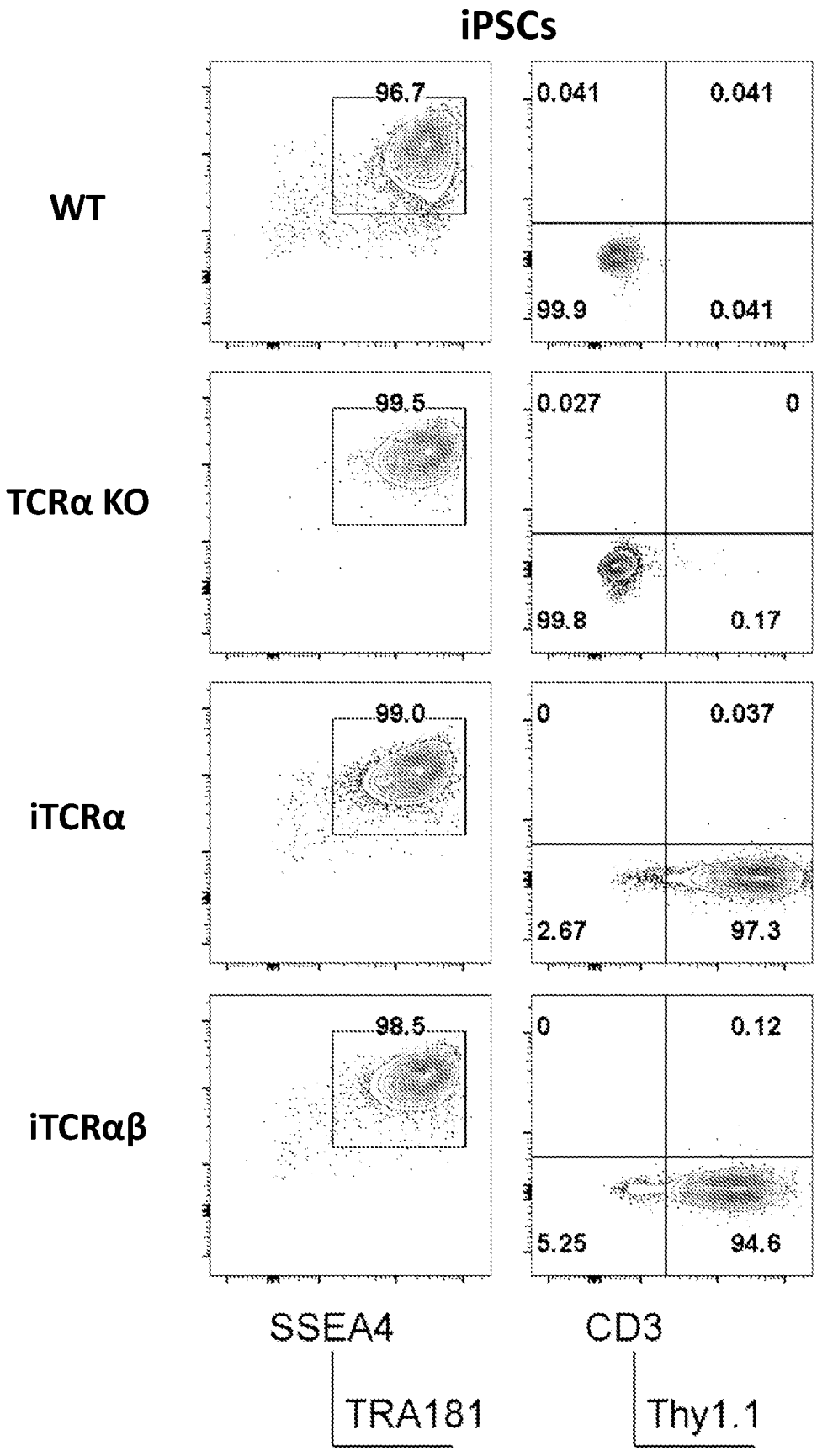

iPSCs
WT
96.7
0.041
0.041
99.9
0.041
TCRα KO
99.5
0.027
0
99.8
0.17
iTCRα
99.0
0
0.037
2.67
97.3
iTCRαβ
98.5
0
0.12
5.25
94.6
SSEA4
TRA181
CD3
Thy1.1

FIG. 8B

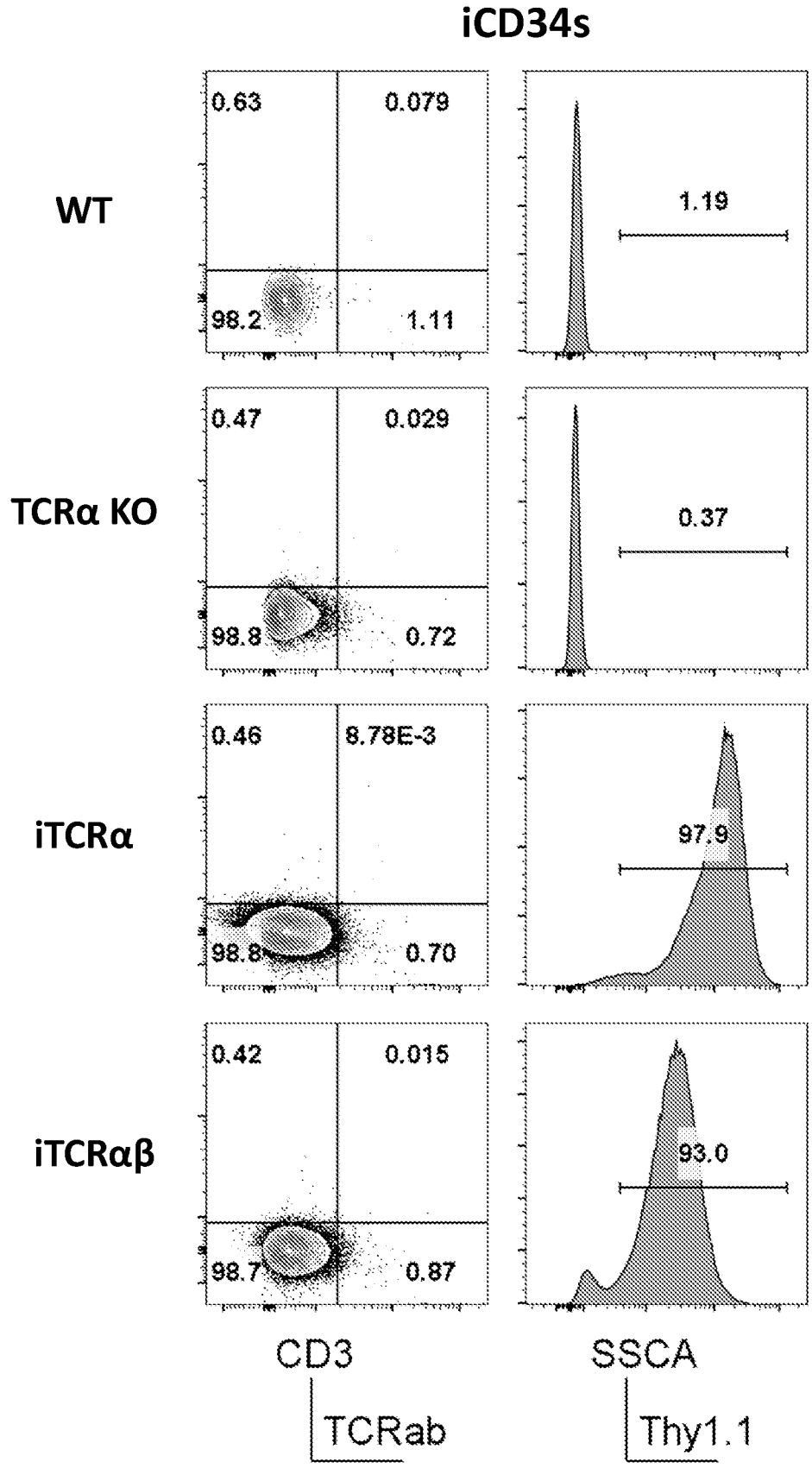

iCD34s
WT
TCRα KO
iTCRα
iTCRαβ
0.63
0.079
98.2
1.11
1.19
0.47
0.029
98.8
0.72
0.37
0.46
8.78E-3
98.8
0.70
97.9
0.42
0.015
98.7
0.87
93.0
CD3
TCRab
SSCA
Thy1.1

FIG. 9A

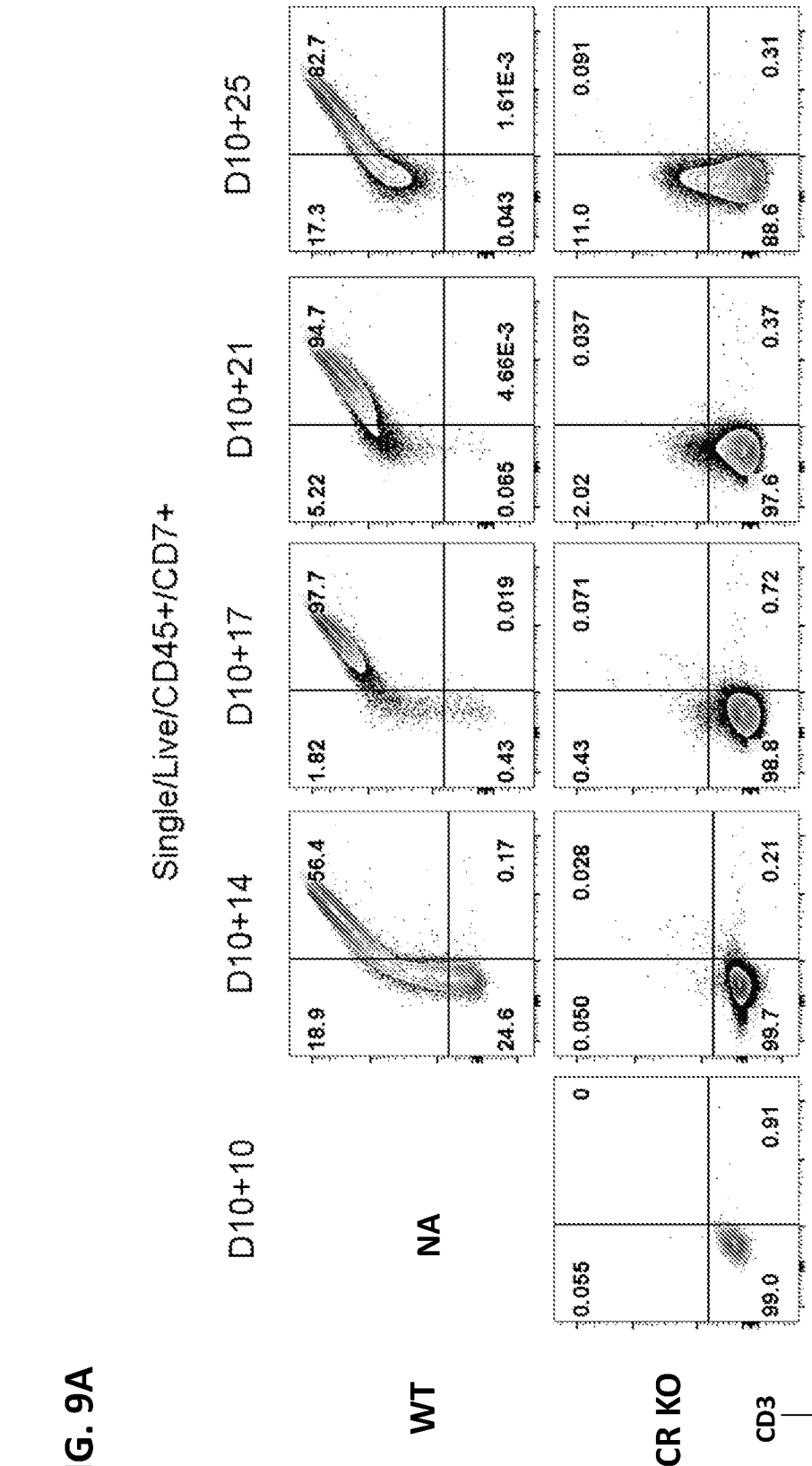

Single/Live/CD45+/CD7+
D10+10
D10+14
D10+17
D10+21
D10+25
NA
WT
TCR KO
CD3
TCRαβ
0.055
0
18.9
56.4
1.82
97.7
5.22
84.7
17.3
82.7
99.0
0.91
24.6
0.17
0.43
0.019
0.065
4.66E-3
0.043
1.61E-3
0.050
0.028
0.43
0.071
2.02
0.037
11.0
0.091
99.7
0.21
98.8
0.72
97.6
0.37
88.6
0.31

FIG. 9B

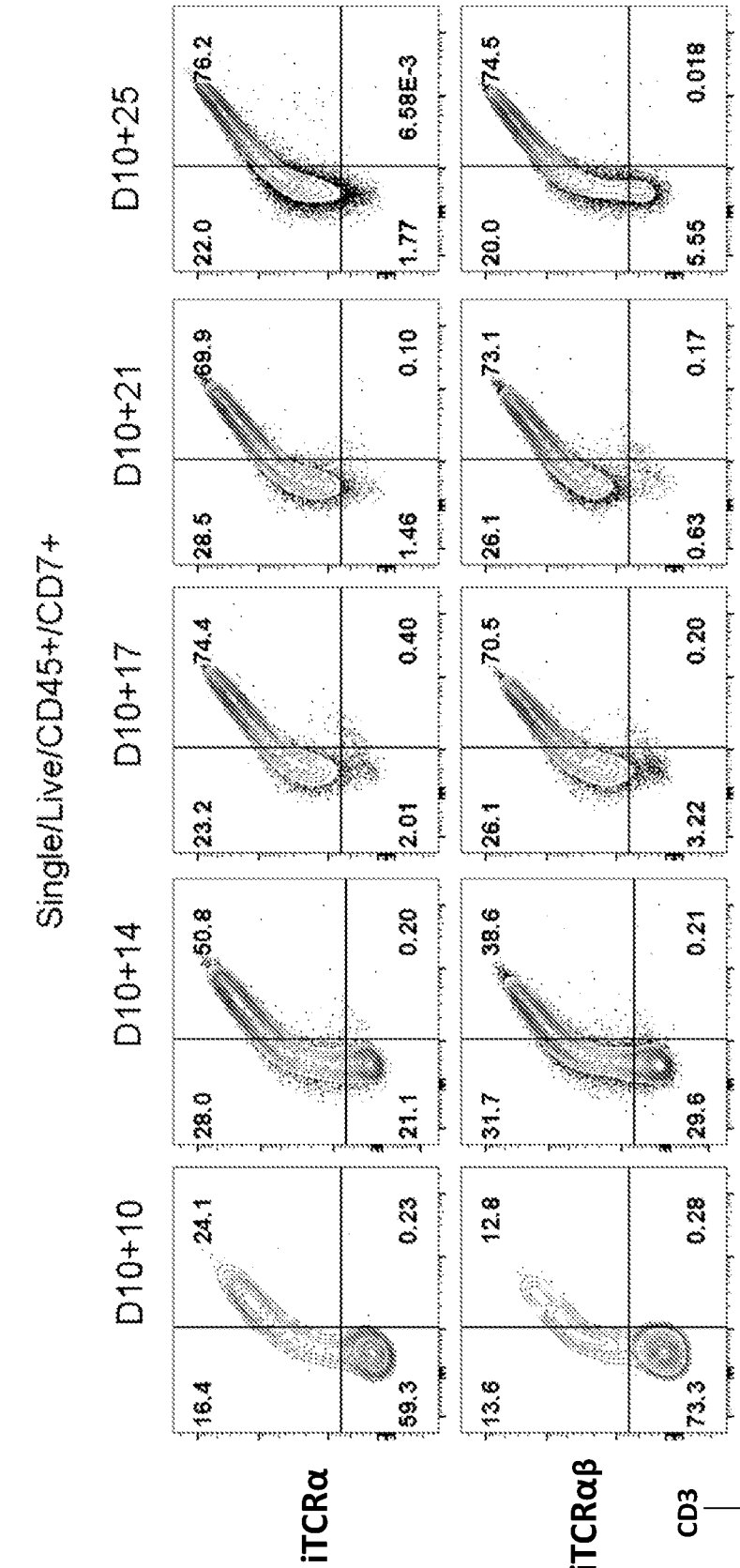
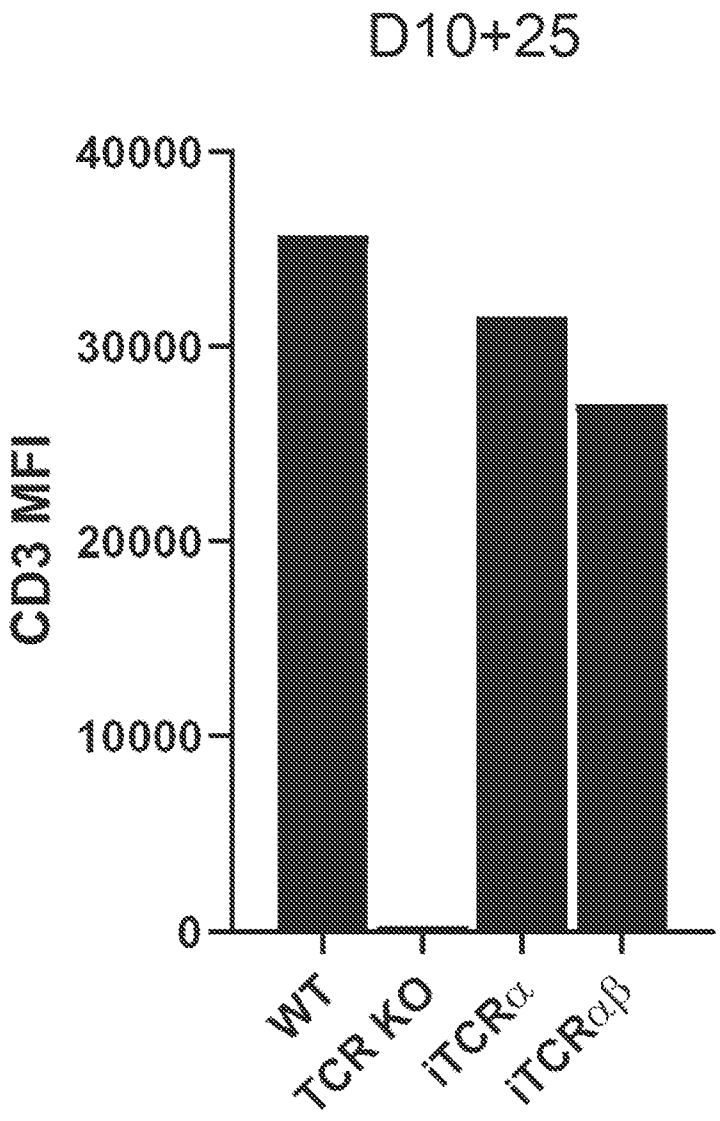

Single/Live/CD45+/CD7+
D10+10
D10+14
D10+17
D10+21
D10+25
iTCRα
iTCRαβ
CD3
TCRαβ
16.4
24.1
59.3
0.23
28.0
50.8
21.1
0.20
23.2
74.4
2.01
0.40
28.5
69.9
1.46
0.10
22.0
76.2
1.77
6.58E-3
13.6
12.8
73.3
0.28
31.7
38.6
29.6
0.21
26.1
70.5
3.22
0.20
26.1
73.1
0.63
0.17
20.0
74.5
5.55
0.018

FIG. 9C


D10+25
CD3 MFI
40000
30000
20000
10000
0
WT
TCR KO
iTCRα
iTCRαβ

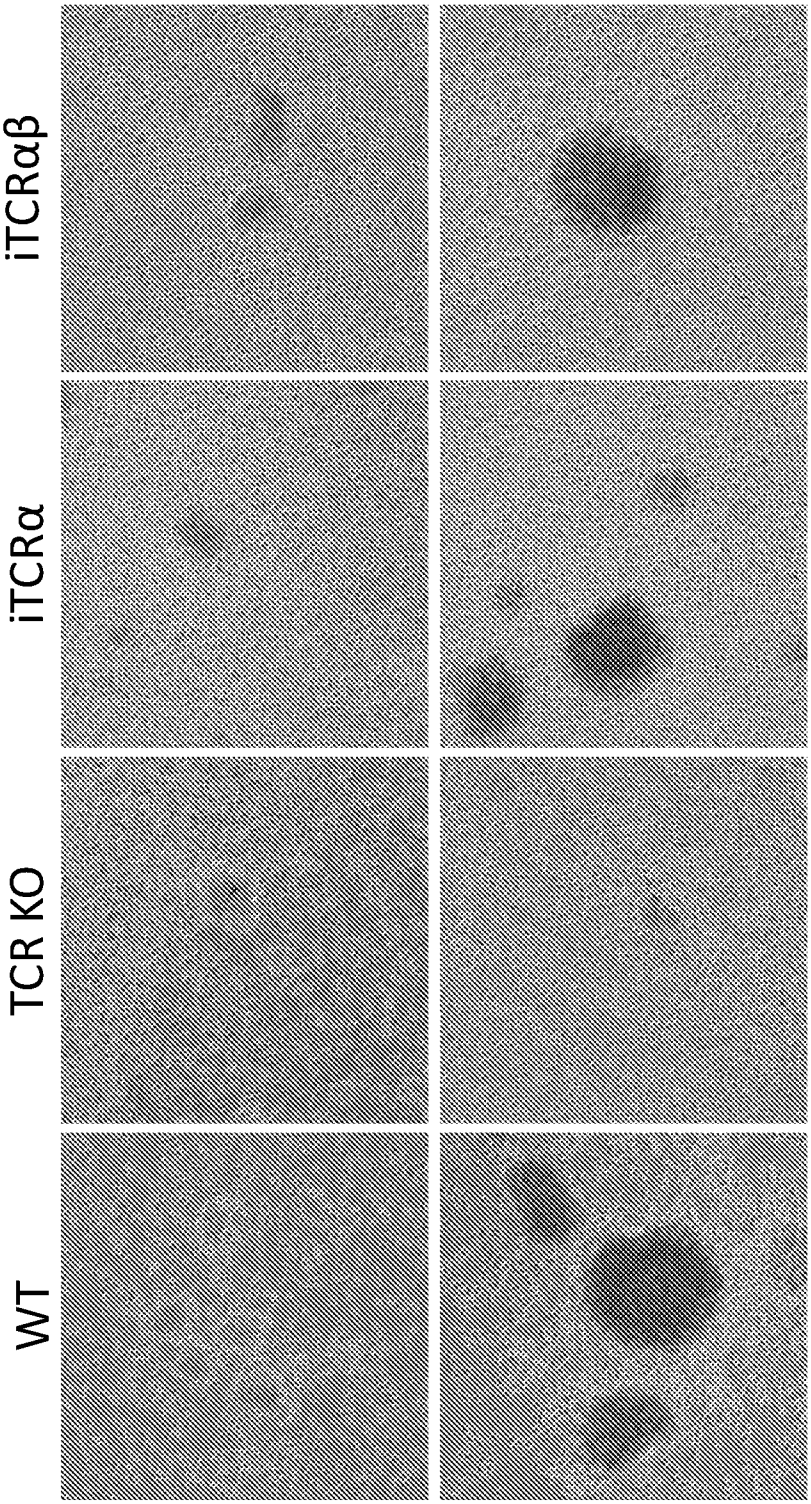

WT
TCR KO
iTCRα
iTCRαβ
Control
+ Tetramer
72hrs post stimulation

FIG. 10

FIG. 11

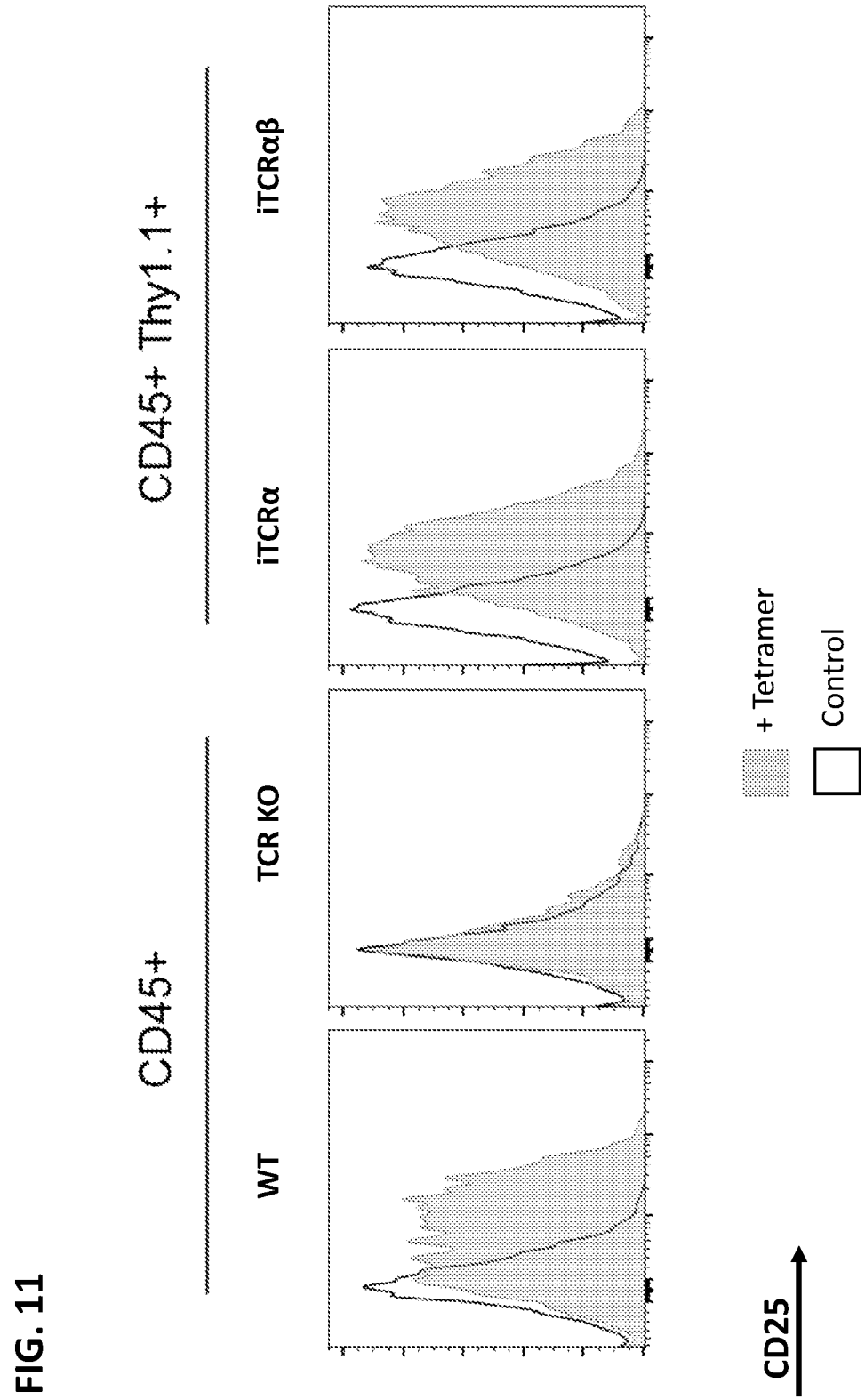

CD45+
CD45+ Thy1.1+
WT
TCR KO
iTCRα
iTCRαβ
+ Tetramer
Control
CD25

FIG. 12A

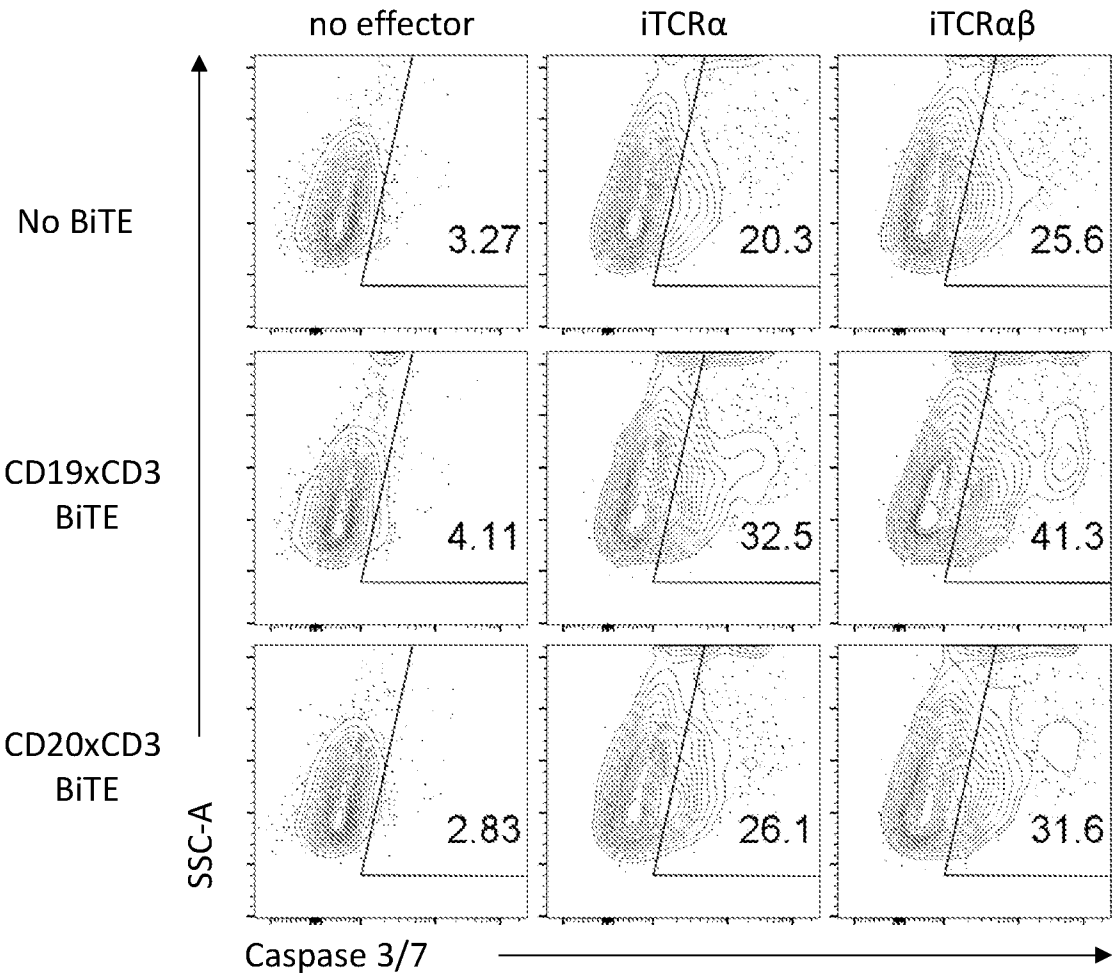
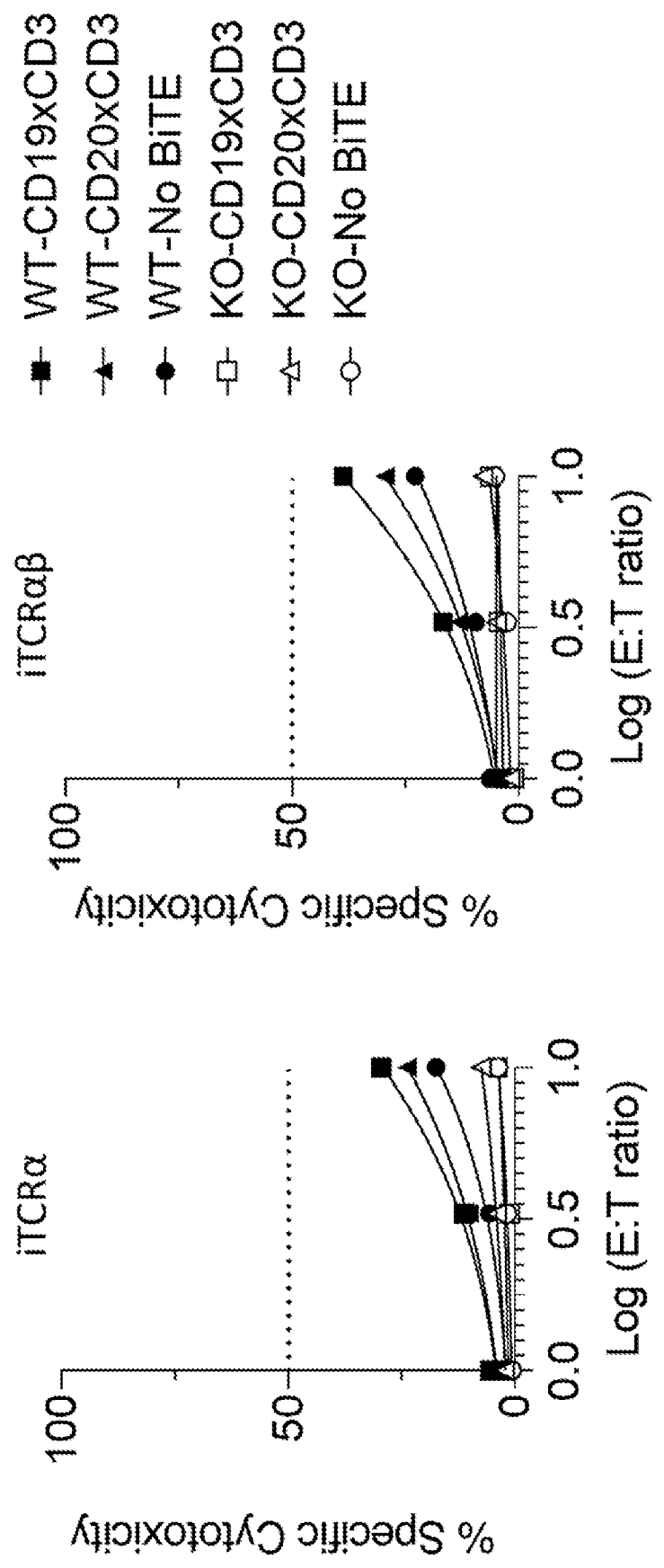

no effector
iTCRα
iTCRαβ
No BiTE
CD19xCD3 BiTE
CD20xCD3 BiTE
3.27
20.3
25.6
4.11
32.5
41.3
2.83
26.1
31.6
SSC-A
Caspase 3/7

FIG. 12B



EC50	No BiTE	CD19xCD3 BiTE	CD20xCD3 BiTE
iTCRα	46.59	24.68	38.80
iTCRαβ	51.44	15.52	25.24

SEQUENCE LISTING

<110> Fate Therapeutics, Inc.

<120> CD3 RECONSTITUTION IN ENGINEERED iPSC AND IMMUNE EFFECTOR CELLS

<130> 056932-518001WO

<150> US 62/832,622
<151> 2019-04-11

<160> 45

<170> PatentIn version 3.5

<210> 1
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> a construct expressing constant region of TCR-beta (TRBC)

<400> 1

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
1 5 10 15

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
20 25 30

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
35 40 45

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
50 55 60

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
65 70 75 80

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
85 90 95

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
100 105 110

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
115 120 125

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 2
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> a construct expressing constant region of TCR-beta(TRBC1)

<400> 2

Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
1 5 10 15

Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
20 25 30

Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
35 40 45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
50 55 60

Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
65 70 75 80

Asn His Phe Arg Cys Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Gln
85 90 95

Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
100 105 110

Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
115 120 125

Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala
130 135 140

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
145 150 155 160

Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Phe
165 170 175

<210> 3
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> TRBC2

<400> 3

Asp Leu Lys Asn Val Phe Pro Pro Lys Val Ala Val Phe Glu Pro Ser
1 5 10 15

Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
20 25 30

Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly

35 40 45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
50 55 60

Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
65 70 75 80

Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
85 90 95

Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
100 105 110

Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
115 120 125

Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
130 135 140

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
145 150 155 160

Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
165 170 175

Arg Gly

<210> 4
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Exemplary signal peptide for the construct encoding TCR-beta constant region (tgTRBC) - CD8asp

<400> 4

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala

<210> 5
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary signal peptide for the construct encoding TCR-beta constant region (tgTRBC) - IgKsp

<400> 5

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg
20

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker peptide for the construct encoding TCR-beta constant region (tgTRBC) - FLAG

<400> 6

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 7
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> 340 a.a. CD64 domain-based construction

<400> 7

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe

130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
275 280 285

Val Trp Phe His Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu
290 295 300

Phe Ala Val Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg
305 310 315 320

Ser Ser Thr Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp
325 330 335

Pro Gln Asp Lys
340

<210> 8
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> 336 a.a. CD64 exon-based construction

<400> 8

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg

100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Phe Phe Pro Pro Gly
275 280 285

Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp
290 295 300

Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg
305 310 315 320

Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
325 330 335

<210> 9
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> 335 a.a. CD64 exon-based construction

<400> 9

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile

85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Phe Phe Pro Pro Gly Tyr
275 280 285

Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr
290 295 300

Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp
305 310 315 320

Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
325 330 335

<210> 10
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplifying sequence encoding 340 a.a. CD64 domain-based construction

<400> 10
cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa 60

gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag 120

gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg 180

tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt 240

gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata 300

cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa 360

ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt 420

tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg 480

aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac 540

acatcagcag gaatatctgt cactgtgaaa gagctatttc agctccagt gctgaatgca 600

tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg 660

ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg 720

cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg 780

ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg 840

gagcttcaag tgcttggcct ccagttacca actcctgtct ggtttcatta ccaagtctct 900

ttctgcttgg tgatggtact ccttttgca gtggacacag gactatattt ctctgtgaag 960

acaaacattc gaagctcaac aagagactgg aaggaccata aatttaaatg gagaaaggac 1020

c c t c a a g a c a a 1032

<210> 11
<211> 1020
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> exemplifying sequence encoding 336 a.a. CD64 exon-based

construction

<400> 11
cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa
60

gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag
120

gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg
180

tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt
240

gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata
300

cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa
360

ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt
420

tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg
480

aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac
540

acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca
600

tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg
660

ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg
720

cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg
780

ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg
840

gagcttcaag tgcttggttt gttctttcca cctgggtacc aagtctcttt ctgcttggtg 900

atggtactcc tttttgcagt ggacacagga ctatatttct ctgtgaagac aaacattcga 960

agctcaacaa gagactggaa ggaccataaa tttaaatgga gaaaggaccc tcaagacaaa 1020

<210> 12
<211> 1005
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> exemplifying sequence encoding 335 a.a. CD64 exon-based construction

<400> 12
atgtggttct tgacaactct gctcctttgg gttccagttg atgggcaagt ggacaccaca 60

aaggcagtga tcactttgca gcctccatgg gtcagcgtgt tccaagagga aaccgtaacc 120

ttgcactgtg aggtgctcca tctgcctggg agcagctcta cacagtggtt tctcaatggc 180

acagccactc agacctcgac ccccagctac agaatcacct ctgccagtgt caatgacagt 240

ggtgaataca ggtgccagag aggtctctca gggcgaagtg accccataca gctggaaatc 300

cacagaggct ggctactact gcaggtctcc agcagagtct tcacggaagg agaacctctg 360

gccttgaggt gtcatgcgtg gaaggataag ctggtgtaca atgtgcttta ctatcgaaat 420

ggcaaagcct ttaagttttt ccactggaac tctaacctca ccattctgaa aaccaacata 480

agtcacaatg gcacctacca ttgctcaggc atgggaaagc atcgctacac atcagcagga 540

atatctgtca ctgtgaaaga gctatttcca gctccagtgc tgaatgcatc tgtgacatcc 600

ccactcctgg aggggaatct ggtcaccctg agctgtgaaa caaagttgct cttgcagagg 660

cctggtttgc agctttactt ctccttctac atgggcagca agaccctgcg aggcaggaac 720

acatcctctg aataccaaat actaactgct agaagagaag actctgggtt atactggtgc 780

gaggctgcca cagaggatgg aaatgtcctt aagcgcagcc ctgagttgga gcttcaagtg 840

cttggcttct ttccacctgg gtaccaagtc tctttctgct tggtgatggt actccttttt 900

gcagtggaca caggactata tttctctgtg aagacaaaca ttcgaagctc aacaagagac 960

tggaaggacc ataaatttaa atggagaaag gaccctcaag acaaa 1005

<210> 13
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> 153 a.a. CD28 co-stim + CD3-zeta-ITAM

<400> 13

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser

35 40 45

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
50 55 60

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
65 70 75 80

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
85 90 95

Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe
100 105 110

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
115 120 125

Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala
130 135 140

Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 14
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 219 a.a. CD28 hinge + CD28 TM + CD28 co-stim + CD3-zeta-ITAM

<400> 14

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
20 25 30

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
35 40 45

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
50 55 60

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
65 70 75 80

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
85 90 95

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
100 105 110

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
115 120 125

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
130 135 140

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
145 150 155 160

Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
165 170 175

Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
180 185 190

His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe

195 200 205

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
210 215

<210> 15
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> 263 a.a NKG2D TM + 2B4 + CD3-zeta

<400> 15

Ser Asn Leu Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg
1 5 10 15

Ile Gly Met Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp
20 25 30

Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe
35 40 45

Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His
50 55 60

Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met
65 70 75 80

Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr
85 90 95

Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg
100 105 110

Asn His Ser Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys
115 120 125

Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu
130 135 140

Glu Asn Phe Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
145 150 155 160

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
165 170 175

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
180 185 190

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
195 200 205

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
210 215 220

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
225 230 235 240

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
245 250 255

Met Gln Ala Leu Pro Pro Arg
260

<210> 16
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> 308 a.a CD8 hinge + NKG2D TM + 2B4 + CD3-zeta

<400> 16

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1   5   10   15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ser Asn Leu
        35   40   45

Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg Ile Gly Met
    50   55   60

Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp Arg Arg Lys
65   70   75   80

Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe Leu Thr Ile
                85   90   95

Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His Glu Gln Glu
            100   105   110

Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met Ile Gln Ser
        115   120   125

Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr Leu Tyr Ser
    130   135   140

Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg Asn His Ser
145   150   155   160

Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys Ser Gln Pro
165 170 175

Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu Glu Asn Phe
180 185 190

Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
195 200 205

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
210 215 220

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
225 230 235 240

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
245 250 255

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
260 265 270

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
275 280 285

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
290 295 300

Leu Pro Pro Arg
305

<210> 17
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> construct mimicking trans-presentation of IL15 (design 3)

<400> 17

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
50 55 60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65 70 75 80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
85 90 95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
100 105 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
115 120 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
130 135 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
165 170 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
180 185 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
195 200 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
210 215 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225 230 235 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr
245 250 255

Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser
260 265 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala
275 280 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser
290 295 300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly
305 310 315 320

Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala
325 330 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr

340 345 350

Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val
355 360 365

Ser Leu Leu Ala Cys Tyr Leu Lys Ser Arg Gln
370 375

<210> 18
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> an exemplary nucleic acid sequence encoding construct mimicking
trans-presentation of IL15 (design 3)

<400> 18
atggactgga cctggattct gttcctggtc gcggctgcaa cgcgagtcca tagcggtatc 60

catgttttta ttcttgggtg tttttctgct gggctgccta agaccgaggc caactgggta 120

aatgtcatca gtgacctcaa gaaaatagaa gaccttatac aaagcatgca cattgatgct 180

actctctaca ctgagtcaga tgtacatccc tcatgcaaag tgacggccat gaaatgtttc 240

ctcctcgaac ttcaagtcat atctctggaa agtggcgacg cgtccatcca cgacacggtc 300

gaaaacctga taatactcgc taataatagt ctctcttcaa atggtaacgt aaccgagtca 360

ggttgcaaag agtgcgaaga gttggaagaa aaaaacataa aggagttcct gcaaagtttc 420

gtgcacattg tgcagatgtt cattaatacc tctagcggcg gaggatcagg tggcggtgga 480

agcggaggtg gaggctccgg tggaggaggt agtggcggag gttctcttca aataacttgt 540

cctccaccga tgtccgtaga acatgcggat atttgggtaa aatcctatag cttgtacagc 600

cgagagcggt atatctgcaa cagcggcttc aagcggaagg ccggcacaag cagcctgacc 660

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccctag cctgaagtgc 720

atcagagatc ccgccctggt gcatcagcgg cctgcccctc caagcacagt gacaacagct 780

ggcgtgaccc cccagcctga gagcctgagc ccttctggaa aagagcctgc cgccagcagc 840

cccagcagca acaatactgc cgccaccaca gccgccatcg tgcctggatc tcagctgatg 900

cccagcaaga gccctagcac cggcaccacc gagatcagca gccacgagtc tagccacggc 960

accccatctc agaccaccgc caagaactgg gagctgacag ccagcgcctc tcaccagcct 1020

ccaggcgtgt accctcaggg ccacagcgat accacagtgg ccatcagcac ctccaccgtg 1080

ctgctgtgtg gactgagcgc cgtgtcactg ctggcctgct acctgaagtc cagacagtga 1140

<210> 19
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> fused IL15/mb-Sushi construct (design 4)

<400> 19

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
50 55 60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65 70 75 80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
85 90 95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
100 105 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
115 120 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
130 135 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
165 170 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp

180 185 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
195 200 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
210 215 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225 230 235 240

Ile Arg

<210> 20
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> an exemplary nucleic acid sequence encoding fused IL15/mb-Sushi
construct (design 4)

<400> 20
atggactgga cctggattct gttcctggtc gcggctgcaa cgcgagtcca tagcggtatc 60

catgttttta ttcttgggtg tttttctgct gggctgccta agaccgaggc caactgggta 120

aatgtcatca gtgacctcaa gaaaatagaa gaccttatac aaagcatgca cattgatgct 180

actctctaca ctgagtcaga tgtacatccc tcatgcaaag tgacggccat gaaatgtttc 240

ctcctcgaac ttcaagtcat atctctggaa agtggcgacg cgtccatcca cgacacggtc 300

gaaaacctga taatactcgc taataatagt ctctcttcaa atggtaacgt aaccgagtca 360

ggttgcaaag agtgcgaaga gttggaagaa aaaaacataa aggagttcct gcaaagtttc 420

gtgcacattg tgcagatgtt cattaatacc tctagcggcg gaggatcagg tggcggtgga 480

agcggaggtg gaggctccgg tggaggaggt agtggcggag gttctcttca aataacttgt 540

cctccaccga tgtccgtaga acatgcggat atttgggtaa aatcctatag cttgtacagc 600

cgagagcggt atatctgcaa cagcggcttc aagcggaagg ccggcacaag cagcctgacc 660

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccctag cctgaagtgc 720

a t c a g a 726

<210> 21
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> protein construct further modified from SEQ ID NO. 17

<400> 21

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
    50   55   60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65   70   75   80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
                85   90   95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
            100   105   110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
        115   120   125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
    130   135   140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145   150   155   160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
                165   170   175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
            180   185   190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
        195   200   205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
    210   215   220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225 230 235 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr
245 250 255

Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser
260 265 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala
275 280 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser
290 295 300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly
305 310 315 320

Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala
325 330 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
340 345 350

Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val
355 360 365

Ser Leu Leu Ala Cys Tyr Leu
370 375

<210> 22
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> non-limiting exemplary signal peptide for the construct encoding
tgpTCR-alpha

<400> 22

Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly
20

<210> 23
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding tgpTCR-alpha (tgpTCR-alpha with TM)

<400> 23

Thr Pro Phe Pro Ser Leu Ala Pro Pro Ile Met Leu Leu Val Asp Gly
1 5 10 15

Lys Gln Gln Met Val Val Val Cys Leu Val Leu Asp Val Ala Pro Pro
20 25 30

Gly Leu Asp Ser Pro Ile Trp Phe Ser Ala Gly Asn Gly Ser Ala Leu
35 40 45

Asp Ala Phe Thr Tyr Gly Pro Ser Pro Ala Thr Asp Gly Thr Trp Thr
50 55 60

Asn Leu Ala His Leu Ser Leu Pro Ser Glu Glu Leu Ala Ser Trp Glu
65 70 75 80

```
Pro Leu Val Cys His Thr Gly Pro Gly Ala Glu Gly His Ser Arg Ser
                85                  90                  95

Thr Gln Pro Met His Leu Ser Gly Glu Ala Ser Thr Ala Arg Thr Cys
            100                 105                 110

Pro Gln Glu Pro Leu Arg Gly Gly Cys Gly Leu Leu Arg Ala Pro Glu
        115                 120                 125

Arg Phe Leu Leu Ala Gly Thr Pro Gly Gly Ala Leu Trp Leu Gly Val
    130                 135                 140

Leu Arg Leu Leu Leu Phe Lys Leu Leu Leu Phe Asp Leu Leu Leu Thr
145                 150                 155                 160

Cys Ser Cys Leu Cys Asp Pro Ala Gly Pro Leu Pro Ser Pro Ala Thr
                165                 170                 175

Thr Thr Arg Leu Arg Ala Leu Gly Ser His Arg Leu His Pro Ala Thr
            180                 185                 190

Glu Thr Gly Gly Arg Glu Ala Thr Ser Ser Pro Arg Pro Gln Pro Arg
        195                 200                 205

Asp Arg Arg Trp Gly Asp Thr Pro Pro Gly Arg Lys Pro Gly Ser Pro
    210                 215                 220

Val Trp Gly Glu Gly Ser Tyr Leu Ser Ser Tyr Pro Thr Cys Pro Ala
225                 230                 235                 240

Gln Ala Trp Cys Ser Arg Ser Ala Leu Arg Ala Pro Ser Ser Ser Leu
                245                 250                 255
```

Gly Ala Phe Phe Ala Gly Asp Leu Pro Pro Pro Leu Gln Ala Gly Ala
260 265 270

Ala

<210> 24
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> partial length of a construct encoding tgpTCR-alpha (Truncated
tgpTCR-alpha with TM)

<400> 24

Thr Pro Phe Pro Ser Leu Ala Pro Pro Ile Met Leu Leu Val Asp Gly
1 5 10 15

Lys Gln Gln Met Val Val Val Cys Leu Val Leu Asp Val Ala Pro Pro
20 25 30

Gly Leu Asp Ser Pro Ile Trp Phe Ser Ala Gly Asn Gly Ser Ala Leu
35 40 45

Asp Ala Phe Thr Tyr Gly Pro Ser Pro Ala Thr Asp Gly Thr Trp Thr
50 55 60

Asn Leu Ala His Leu Ser Leu Pro Ser Glu Glu Leu Ala Ser Trp Glu
65 70 75 80

Pro Leu Val Cys His Thr Gly Pro Gly Ala Glu Gly His Ser Arg Ser
85 90 95

Thr Gln Pro Met His Leu Ser Gly Glu Ala Ser Thr Ala Arg Thr Cys
100 105 110

Pro Gln Glu Pro Leu Arg Gly Gly Cys Gly Leu Leu Arg Ala Pro Glu
115 120 125

Arg Phe Leu Leu Ala Gly Thr Pro Gly Gly Ala Leu Trp Leu Gly Val
130 135 140

Leu Arg Leu Leu Leu Phe Lys Leu Leu Leu Phe Asp Leu Leu Leu Thr
145 150 155 160

Cys Ser Cys Leu Cys Asp Pro Ala Gly Pro Leu Pro Ser Pro Ala Thr
165 170 175

Thr Thr Arg Leu Arg Ala Leu Gly Ser His Arg Leu His Pro Ala Thr
180 185 190

Glu Thr Gly Gly Arg Glu Ala Thr Ser Ser Pro Arg Pro Gln Pro Arg
195 200 205

Asp Arg Arg Trp Gly Asp Thr Pro Pro Gly Arg Lys Pro Gly Ser Pro
210 215 220

Val
225

<210> 25
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding a full or partial length of CD3-epsilon ectodomain

<400> 25

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
35 40 45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Cys Glu Asn Cys Met Glu Met Asp
100

<210> 26
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding a full or partial length of CD3-delta ectodomain

<400> 26

Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1 5 10 15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
20 25 30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
35 40 45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
50 55 60

Val Gln Val His Tyr Arg Met Cys Gln Ser Cys Val Glu Leu Asp Pro
65 70 75 80

Ala Thr Val Ala

<210> 27
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding a full or partial length of CD3-gamma ectodomain

<400> 27

Gln Ser Ile Lys Gly Asn His Leu Val Lys Val Tyr Asp Tyr Gln Glu
1 5 10 15

Asp Gly Ser Val Leu Leu Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr
20 25 30

Trp Phe Lys Asp Gly Lys Met Ile Gly Phe Leu Thr Glu Asp Lys Lys
35 40 45

Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln
50 55 60

Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg
65 70 75 80

Met Cys Gln Asn Cys Ile Glu Leu Asn Ala Ala Thr Ile Ser
85 90

<210> 28
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length
of CD3-epsilon ectodomain

<400> 28

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln
20

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length
of CD3-delta ectodomain

<400> 29

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

Ser Gln Val Ser Pro
            20

<210> 30
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length
       of CD3-gamma ectodomain

<400> 30

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
1   5   10   15

Leu Gln Gly Thr Leu Ala
            20

<210> 31
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence polynucleotide encoding
       tgCD3(epsilon-delta)-TRAC fusion protein

<400> 31

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1   5   10   15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20   25   30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu

```
        35                  40                  45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50                  55                  60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65                  70                  75                  80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85                  90                  95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
            100                 105                 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Phe Lys Ile Pro Ile Glu
        115                 120                 125

Glu Leu Glu Asp Arg Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp
    130                 135                 140

Val Glu Gly Thr Val Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp
145                 150                 155                 160

Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly
                165                 170                 175

Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg
            180                 185                 190

Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
    210                 215                 220
```

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
225 230 235 240

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
245 250 255

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
260 265 270

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
275 280 285

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
290 295 300

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
305 310 315 320

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
325 330 335

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
340 345

<210> 32
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence polynucleotide encoding
tgCD3(epsilon-delta)-TRAC fusion protein

<400> 32

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
35 40 45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
100 105 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Gln Ser Ile Lys Gly Asn
115 120 125

His Leu Val Lys Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu
130 135 140

Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys
145 150 155 160

Met Ile Gly Phe Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser
165 170 175

Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn

180 185 190

Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Gly Gly Gly Gly Ser
195 200 205

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu Asn Lys Val Phe
210 215 220

Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His
225 230 235 240

Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp
245 250 255

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
260 265 270

Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp
275 280 285

Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp
290 295 300

Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu
305 310 315 320

Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln
325 330 335

Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser
340 345 350

Val Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile
355 360 365

Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val
    370   375   380

Leu Met Ala Met Val Lys Arg Lys Asp Phe
385   390

<210> 33
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence to the polynucleotide encoding
       tgCD3(epsilon-delta)-TRAC fusion protein (G4S linker)

<400> 33

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
1   5   10   15

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser
            20   25

<210> 34
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence to the polynucleotide encoding
       tgCD3(epsilon-delta)-TRAC fusion protein (G4S linker)

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 35

<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence encoding a full or partial length of CD3-zeta
endodomain

<400> 35

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
1 5 10 15

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
85 90 95

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
100 105 110

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
115 120 125

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
130 135 140

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
145 150 155 160

Pro Pro Arg

<210> 36
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM1 sequence

<400> 36

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
1 5 10 15

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
20 25

<210> 37
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM2 sequence

<400> 37

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
1 5 10 15

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
20 25

<210> 38
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM3 sequence

<400> 38

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
1 5 10 15

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
20 25

<210> 39
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence from which any one or two CD3-zeta ITAMs may
be removed

<400> 39

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
35 40 45

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
50 55 60

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
65 70 75 80

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
85 90 95

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
100 105 110

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
115 120 125

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
130 135 140

Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 40
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence CD3 chimeric chain with 41BB signaling domain
from which any one or two CD3-zeta ITAMs may be removed

<400> 40

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
35 40 45

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
50 55 60

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
65 70 75 80

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
85 90 95

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
100 105 110

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
115 120 125

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
130 135 140

Ala Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 41
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of polynucleotide encoding a full or partial
length of 28BB-zeta endodomain

<400> 41

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
35 40 45

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
50 55 60

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
65 70 75 80

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
85 90 95

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
100 105 110

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
115 120 125

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
130 135 140

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
145 150 155 160

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
165 170 175

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu

180 185 190

Pro Pro Arg
195

<210> 42
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of polynucleotide encoding a full or partial
length of 28BB-zeta endodomain

<400> 42

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
35 40 45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
100 105 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Gln Ser Ile Lys Gly Asn
115 120 125

His Leu Val Lys Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu
130 135 140

Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys
145 150 155 160

Met Ile Gly Phe Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser
165 170 175

Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn
180 185 190

Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Arg Ala Ala Ala Ile
195 200 205

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
210 215 220

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
225 230 235 240

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
245 250 255

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
260 265 270

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
275 280 285

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
290 295 300

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
305 310 315 320

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
325 330 335

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
340 345 350

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
355 360 365

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
370 375 380

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
385 390 395 400

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
405 410 415

Ala Leu His Met Gln Ala Leu Pro Pro Arg
420 425

<210> 43
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide encoding construct tgCD3(epsilon-delta)-(28/BB)-zeta

<400> 43

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
35 40 45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
100 105 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Phe Lys Ile Pro Ile Glu
115 120 125

Glu Leu Glu Asp Arg Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp
130 135 140

Val Glu Gly Thr Val Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp
145 150 155 160

Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly
165 170 175

Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg
180 185 190

Met Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp
195 200 205

Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu
210 215 220

Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu
225 230 235 240

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
245 250 255

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
260 265 270

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
275 280 285

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
290 295 300

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
305 310 315 320

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
325 330 335

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
340 345 350

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
355 360 365

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
370 375 380

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
385 390 395 400

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
405 410 415

<210> 44
<211> 276
<212> PRT
<213> Homo sapiens

<400> 44

Met Lys Lys His Leu Thr Thr Phe Leu Val Ile Leu Trp Leu Tyr Phe
1 5 10 15

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

Ile Ile Leu Glu Gly Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val
35 40 45

Ser Pro Phe Ser Asn Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly
50 55 60

Pro Val Ser Leu Thr Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn
65 70 75 80

Gly Arg Tyr Thr Ala Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu

85 90 95

His Ile Thr Ala Ser Gln Leu Ser Asp Ser Ala Ser Tyr Ile Cys Val
100 105 110

Val Ser Asp Arg Gly Ser Thr Leu Gly Arg Leu Tyr Phe Gly Arg Gly
115 120 125

Thr Gln Leu Thr Val Trp Pro Asp Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
180 185 190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
275

<210> 45
<211> 289
<212> PRT
<213> Homo sapiens

<400> 45

Met Thr Ile Arg Leu Leu Cys Tyr Met Gly Phe Tyr Phe Leu Gly Ala
1 5 10 15

Gly Leu Met Glu Ala Asp Ile Tyr Gln Thr Pro Arg Tyr Leu Val Ile
20 25 30

Gly Thr Gly Lys Lys Ile Thr Leu Glu Cys Ser Gln Thr Met Gly His
35 40 45

Asp Lys Met Tyr Trp Tyr Gln Gln Asp Pro Gly Met Glu Leu His Leu
50 55 60

Ile His Tyr Ser Tyr Gly Val Asn Ser Thr Glu Lys Gly Asp Leu Ser
65 70 75 80

Ser Glu Ser Thr Val Ser Arg Ile Arg Thr Glu His Phe Pro Leu Thr
85 90 95

Leu Glu Ser Ala Arg Pro Ser His Thr Ser Gln Tyr Leu Cys Ala Ser
100 105 110

Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
115 120 125

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
130 135 140

Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
145 150 155 160

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
165 170 175

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
180 185 190

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
195 200 205

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
210 215 220

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
225 230 235 240

Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
245 250 255

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
260 265 270

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
275 280 285

Phe