

METHODS FOR SELECTIVE EXPANSION OF $\delta\gamma$ T-CELL POPULATIONS AND COMPOSITIONS THEREOF

CROSS-REFERENCE TO RELATED APPLICATION

The present application claims the benefit of priority to U.S. Provisional Appl. No. 62/586,782, filed November 15, 2017, the contents of which are hereby incorporated in the entirety and for all purposes.

BACKGROUND

Antigen recognition by T lymphocytes may be achieved by highly diverse heterodimeric receptors, the T-cell receptors (TCRs). Approximately 95% of human T-cells in blood and lymphoid organs express a heterodimeric $\alpha\beta$ TCR receptor ($\alpha\beta$ T-cell lineage). Approximately 5% of human T-cells in the blood and lymphoid organs express heterodimeric $\gamma\delta$ TCR receptor ($\gamma\delta$ T-cell lineage). These T-cell subsets may be referred to as ' $\alpha\beta$ ' and ' $\gamma\delta$ ' T-cells, respectively. $\alpha\beta$ and $\gamma\delta$ T-cells are different in function. Activation of $\alpha\beta$ T-cells then occurs when an antigen presenting cell (APC) presents an antigen in the context of class I/II MHC. In contrast to $\alpha\beta$ T-cells, $\gamma\delta$ T-cells can recognize an antigen independent of MHC restriction. In addition, $\gamma\delta$ T-cells combine both innate and adoptive immune recognition and responses.

$\gamma\delta$ T cells utilize a distinct set of somatically rearranged variable (V), diversity (D), joining (J), and constant (C) genes. $\gamma\delta$ T cells contain fewer V, D, and J segments than $\alpha\beta$ T cells. Although the number of germline $V\gamma$ and $V\delta$ genes is more limited than the repertoire of $V\alpha$ and $V\beta$ TCR genes, more extensive junctional diversification processes during TCR γ and δ chain rearrangement leads to a potential larger $\gamma\delta$ TCRs repertoire than that of $\alpha\beta$ TCRs (Carding and Egan, Nat Rev Immunol (2002) 2:336).

Human $\gamma\delta$ T-cells use 3 main $V\delta$ ($V\delta 1$, $V\delta 2$, $V\delta 3$) and at most six $V\gamma$ region genes to make their TCRs (Hayday AC., Annu Rev Immunol. 2000;18, 975-1026). Two main $V\delta$ subsets are $V\delta 1$ and $V\delta 2$ $\gamma\delta$ T cells. $V\delta 1$ T cells with different $V\gamma$ predominate in the intraepithelial subset of mucosal $\gamma\delta$ T cells where the TCRs appear to recognize stress molecules on epithelial

cells (Beagley KW, Husband AJ. Crit Rev Immunol. 1998;18(3):237-254). V δ 2 T cells that generally coexpress V γ 9 are abundant in the peripheral blood and lymphatic system.

The ability of $\gamma\delta$ T-cells to recognize an antigen on diseased cells directly and to exhibit inherent ability to kill tumor cells renders $\gamma\delta$ T-cells an attractive therapeutic tool. Adoptive transfer of V γ 9V δ 2 T cells has yielded limited objective clinical responses for investigational treatment of cancer (Kondo et al, Cytotherapy, 10:842- 856, 2008; Lang et al, Cancer Immunology, Immunotherapy: CII, 60: 1447-1460, 2011; Nagamine et al, 2009; Nicol et al, British Journal of Cancer, 105:778-786, 2011; Wilhelm et al, Blood. 2003 Jul 1;102(1):200-6), indicating the need to isolate and test clinically new $\gamma\delta$ T-cell populations.

The ability to selectively expand $\gamma\delta$ T-cell subset populations having potent anti-tumor activity with improved purity and in clinically-relevant levels is highly desirable. Although antibodies and cytokine cocktails have been used to propagate a more diverse set of $\gamma\delta$ T cells, activation of specific $\gamma\delta$ T-cell subsets to sufficient purity and clinically-relevant levels, was not achieved (Dokouhaki et al, 2010; Kang et al, 2009; Lopez et al, 2000; Kress, 2006). Therefore, clinically-relevant methods of expanding specific $\gamma\delta$ T cell subsets *ex vivo*, and the cells produced thereby, are greatly needed.

SUMMARY OF THE INVENTION

The present invention, in one aspect, provides *ex vivo* methods for producing enriched $\gamma\delta$ T cell populations. The enriched $\gamma\delta$ T cell populations can be produced from isolated mixed cell populations by a method comprising contacting the mixed cell population, or a purified fraction thereof, with one or more agents that selectively expand δ 3 T cells by binding to an epitope specific to a δ 3 TCR. The expanded T cell populations can be used, *e.g.*, individually or in combination with other T cell populations, in methods of treatment by administering to a subject in need thereof. In some cases, the agents are antibodies or fragments thereof.

In a first aspect, the present invention provides an agent that selectively binds an epitope specific to a δ 3 $\gamma\delta$ TCR. In some embodiments, the agent is an antibody or a fragment thereof. In some embodiments, the agent is an activating agent that selectively binds an activating epitope specific to a δ 3 $\gamma\delta$ TCR.

In some embodiments, the agent (*e.g.*, antibody or fragment thereof) binds the same epitope, or essentially the same epitope, as (or competes with) an antibody selected from the

group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) binds the same epitope, or essentially the same epitope, as (or competes with) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) comprises the complementarity determining regions of an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) comprises the complementarity determining regions of an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58.

In some embodiments, the agent (*e.g.*, antibody or fragment thereof) competes with binding of antibody $\delta 3$ -23, $\delta 3$ -42, and/or $\delta 3$ -58 to a $\delta 3$ TCR (*e.g.*, a $\gamma 2\delta 3$ TCR). In some embodiments, the agent (*e.g.*, antibody or fragment thereof) competes with binding of antibody $\delta 3$ -08 to a $\delta 3$ TCR (*e.g.*, a $\gamma 2\delta 3$ TCR). In some embodiments, the agent (*e.g.*, antibody or fragment thereof) competes with binding of antibody $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -42, and/or $\delta 3$ -58 to a $\delta 3$ TCR (*e.g.*, a $\gamma 2\delta 3$ TCR). In some embodiments, the agent (*e.g.*, antibody or fragment thereof) competes with binding of antibody $\delta 3$ -31 to a $\delta 3$ TCR (*e.g.*, a $\gamma 2\delta 3$ TCR).

In some embodiments, the agent (*e.g.*, antibody or fragment thereof) selectively expands a $\delta 3 \gamma \delta$ T cell as compared to $\alpha \beta$ T cells in a mixed cell population comprising $\gamma \delta$ T cells and $\alpha \beta$ T cells. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) is bound to a $\delta 3 \gamma \delta$ TCR. In some embodiments, the $\delta 3 \gamma \delta$ TCR is expressed on the surface of an engineered $\delta 3 \gamma \delta$ T cell. In some embodiments, the $\delta 3 \gamma \delta$ TCR is expressed on the surface of a non-engineered $\delta 3 \gamma \delta$ T cell, such as a selectively expanded non-engineered $\delta 3 \gamma \delta$ T cell. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) is bound to a $\delta 3 \gamma \delta$ TCR expressed on the surface of a $\delta 3 \gamma \delta$ T cell. In some cases, the agent (*e.g.*, antibody or fragment thereof) bound to the $\delta 3 \gamma \delta$ TCR expressed on the surface of a $\delta 3 \gamma \delta$ T cell forms an isolated complex with the $\delta 3 \gamma \delta$ T cell, is in a subject, is in an *ex vivo* or *in vitro* culture, or is in a container. In some embodiments, the agent (*e.g.*, antibody or fragment thereof) is bound to a $\delta 3 \gamma \delta$ TCR expressed on the surface of a $\delta 3 \gamma \delta$ T cell in an *ex vivo* expansion culture.

In some embodiments, the agent (*e.g.*, antibody or fragment thereof) is bound to an extracellular surface of an antigen presenting cell (APC). In some embodiments, the agent (*e.g.*, antibody or fragment thereof) is anchored in the membrane of the APC. In some embodiments,

an Fc region of the agent (*e.g.*, antibody or fragment thereof) is bound to an Fc-receptor expressed by the APC. In some cases, the APC is an artificial APC (aAPC). In some cases, the APC is in a subject, isolated, in an *ex vivo* or *in vitro* culture, or is in a container.

In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to a region distal from the γ -chain binding interface of V δ 3. In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to β strand D and E of the V δ 3 of the $\gamma\delta$ TCR according to IMGT nomenclature. In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to β strand C'' and D and a loop between β strands E and F of the V δ 3 of the $\gamma\delta$ TCR according to IMGT nomenclature. In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to β strand A, B, D, and E of the V δ 3 of the $\gamma\delta$ TCR according to IMGT nomenclature.

In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids K79 and H88 of V δ 3 (IMGT nomenclature). In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids R75 and R95 of V δ 3 (IMGT nomenclature). In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids K79, E18, and H88 of V δ 3 (IMGT nomenclature). In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids E67, D70, R75, R95, and E97 of V δ 3 (IMGT nomenclature). In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids K3, K79, and H88 of V δ 3 (IMGT nomenclature). In some cases, the agent (*e.g.*, antibody or fragment thereof) binds to amino acids K79, L82, and H88 of V δ 3 (IMGT nomenclature). Typically, the agent binds the specified amino acids or groups thereof in the context of a V δ 3 $\gamma\delta$ TCR, such as a V δ 3 $\gamma\delta$ TCR expressed on the surface of a V δ 3 $\gamma\delta$ T cell.

In a second aspect, the present invention provides a nucleic acid encoding any one of the foregoing agents (*e.g.*, antibodies or fragments thereof). In some cases, the nucleic acid is operably linked to a heterologous promoter. In a third aspect, the present invention provides a host cell comprising any one of the foregoing agents or any one of the foregoing nucleic acids. In some cases, the host cell is an artificial antigen presenting cell (aAPC).

In a fourth aspect, the present invention provides a method of making an agent (*e.g.*, antibody or fragment thereof) that binds an epitope specific to a δ 3 $\gamma\delta$ TCR, the method comprising culturing any one of the foregoing host cells under conditions sufficient to produce the antibody or fragment thereof.

In a fifth aspect, the present invention provides an *ex vivo* method for producing an enriched $\gamma\delta$ T cell population, comprising contacting a first cell population comprising $\gamma\delta$ T cells with one or more of the foregoing agents (*e.g.*, antibodies or fragments thereof). In some embodiments, the first cell population is an isolated mixed cell population comprising $\alpha\beta$ T cells and $\gamma\delta$ T cells (*e.g.*, $\delta 3 \gamma\delta$ T cells). In some embodiments, the first cell population is selected from a peripheral blood sample, a leukapheresis sample, a cord blood sample, a tumor sample, or a tissue sample. In some cases, the first cell population is a sample isolated from a single donor. In some cases, the first cell population is a sample isolated from multiple donors. In some cases, the first cell population is a PBMC sample. In some cases, the first cell population is a sample of PBMCs isolated from a single donor. In some cases, the first cell population is a sample of PBMCs isolated from multiple donors.

In some embodiments, the method comprises directly contacting the isolated mixed cell population with the one or more of the foregoing agents (*e.g.*, antibodies or fragments thereof). In some embodiments, the first cell population is a population comprising one or more engineered $\gamma\delta$ T cells. In some embodiments, the first cell population is a first population of expanded $\gamma\delta$ T cells. In some embodiments, the method comprises a first $\gamma\delta$ T cell expansion and a second $\gamma\delta$ T cell expansion. In some embodiments, the method comprises producing an enriched $\gamma\delta$ T cell population comprising at least $10^8 \delta 3 \gamma\delta$ T cells. In some embodiments, the enriched $\gamma\delta$ T cell population comprising at least $10^8 \delta 3 \gamma\delta$ T cells is produced within 12 to 21 days. In some embodiments, the method comprises expanding the $\gamma\delta$ T cells in the first cell population at least 1,000-fold. In some embodiments, the at least 1,000-fold expansion is achieved within 12 to 21 days.

In a sixth aspect, the present invention provides an *ex vivo* method for producing an enriched $\gamma\delta$ T cell population, comprising: a) contacting a first cell population comprising $\gamma\delta$ T cells with one or more first activating agents that activate and expand $\gamma\delta$ T cells, thereby producing an expanded first $\gamma\delta$ T cell population; and b) contacting the expanded first $\gamma\delta$ T cell population with one or more second activating agents that activate and expand $\gamma\delta$ T cells, thereby producing the enriched $\gamma\delta$ T cell population, wherein, at least one of the one or more first activating agents or at least one of the one or more second activating agents is an agent (*e.g.*, antibody or fragment thereof) according to the first aspect. In some embodiments, the method comprises isolating the expanded first $\gamma\delta$ T cell population after a) and before b). In some

embodiments, a) comprises culturing the first cell population in the presence of an antigen presenting cell (APC) and the one or more first activating agents. In some embodiments, b) comprises culturing the activated $\gamma\delta$ T cell population in the presence of an antigen presenting cell (APC) and the one or more second activating agents.

In some embodiments, the first cell population is an isolated mixed cell population comprising $\alpha\beta$ T cells and $\gamma\delta$ T cells. In some embodiments, the first cell population is selected from a peripheral blood sample, a leukapheresis sample, a cord blood sample, a tumor sample, or a tissue sample. In some embodiments, the first cell population is a population of engineered $\gamma\delta$ T cells. In some embodiments, the method comprises genetically modifying the expanded first $\gamma\delta$ T cell population or genetically modifying the enriched $\gamma\delta$ T cell population. In some embodiments, the method comprises producing an enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta 3$ $\gamma\delta$ T cells. In some embodiments, the enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta 3$ $\gamma\delta$ T cells is produced within 12 to 21 days.

In some embodiments, the method comprises expanding the $\gamma\delta$ T cells in the first cell population at least 1,000-fold. In some embodiments, the at least 1,000-fold expansion is achieved within 12 to 21 days.

In some embodiments, at least one of the one or more first activating agents is structurally identical to at least one of the one or more second activating agents. In some embodiments, at least one of the one or more first activating agents is structurally different than at least one of the one or more second activating agents. In some embodiments, at least one of the one or more first activating agents or at least one of the one or more second activating agents is immobilized. In some embodiments, the immobilized activating agent is immobilized on a surface of a culture vessel. In some embodiments, the immobilized activating agent is immobilized on a surface of an antigen presenting cell (APC). In some embodiments, the immobilized activating agent is the agent (*e.g.*, antibody or fragment thereof) that binds the epitope specific to a $\delta 3$ $\gamma\delta$ TCR.

In a seventh aspect, the present invention provides an expanded $\gamma\delta$ T cell population (*e.g.*, before positive or negative selection for $\delta 3$ $\gamma\delta$ T cells), wherein greater than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, or 80% of the expanded $\gamma\delta$ T cells are $\delta 3$ $\gamma\delta$ T cells. In some embodiments, from 10% to 80% of the expanded $\gamma\delta$ T cells are $\delta 3$ $\gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3$ $\gamma\delta$ T cells). In some embodiments, from 10% to 60% of the

expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells). In some embodiments, from 10% to 40% of the expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells). In some embodiments, from 20% to 80% of the expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells). In some embodiments, from 20% to 60% of the expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells). In some embodiments, from 20% to 50% of the expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells). In some embodiments, from 20% to 40% of the expanded $\gamma\delta$ T cells are $\delta 3 \gamma\delta$ T cells (*e.g.*, before positive or negative selection for $\delta 3 \gamma\delta$ T cells).

In some embodiments, the expanded $\gamma\delta$ T cell population comprises polyclonal TCR diversity. In some embodiments, greater than 30%, 40%, 50%, 60%, or 70% of the $\delta 3 \gamma\delta$ T cells in the expanded $\gamma\delta$ T cell population express the phenotype CD45RA+/CD27+ and/or CD45RA-/CD27+. In some embodiments, from 20% to 70% of the $\delta 3 \gamma\delta$ T cells in the expanded $\gamma\delta$ T cell population express the phenotype CD45RA+/CD27+ and/or CD45RA-/CD27+. In some embodiments, greater than 30%, 40%, 50%, 60%, or 70% of the $\delta 1^+ \delta 2^- \gamma\delta$ T cells in the expanded $\gamma\delta$ T cell population express the phenotype CD45RA+/CD27+ and/or CD45RA-/CD27+. In some embodiments, from 20% to 70% of the $\delta 1^+ \delta 2^- \gamma\delta$ T cells in the expanded $\gamma\delta$ T cell population express the phenotype CD45RA+/CD27+ and/or CD45RA-/CD27+.

In some embodiments, the expanded $\gamma\delta$ T cell population is derived from a tissue such as skin. In some embodiments, the expanded $\gamma\delta$ T cell population is derived from tumor infiltrating lymphocytes. In some embodiments, the expanded $\gamma\delta$ T cell population comprises $\gamma\delta$ T-cells that express an endogenous or heterologous tumor recognition moiety. In some embodiments, the population comprises a therapeutically effective amount (*e.g.*, $>10^8$) of $\gamma\delta$ T-cells. In some embodiments, the $\gamma\delta$ T cell population comprises anti-tumor cytotoxicity that is independent of NKp30 activity, NKp44 activity, and/or NKp46 activity. In some embodiments, the $\gamma\delta$ T cell population does not comprise NKp30 activity-dependent anti-tumor cytotoxicity, NKp44 activity-dependent anti-tumor cytotoxicity, and/or NKp46 activity-dependent anti-tumor cytotoxicity. In some embodiments, less than 40% of the $\gamma\delta$ T cells express (*e.g.*, as protein or mRNA) a detectable level of NKp30, NKp44, and/or NKp46.

In an eighth aspect, the present invention provides an expanded $\gamma\delta$ T cell population, which is produced by any one of the foregoing methods. In a ninth aspect, the present invention

provides a method of treating cancer, an inflammatory disease, or an autoimmune disease in a subject in need thereof, the method comprising administering a therapeutically effective amount of $\delta 3$ $\gamma\delta$ T cells to the subject, administering a therapeutically effective amount of a $\gamma\delta$ T cell population that is enriched in $\delta 3$ $\gamma\delta$ T cells to the subject, or administering to the subject a therapeutically effective amount of a $\gamma\delta$ T cell population obtained by a method described herein.

In a tenth aspect, the present invention provides a method of treating cancer, an inflammatory disease, or an autoimmune disease in a subject in need thereof, the method comprising: a) providing a therapeutically effective amount of $\delta 3$ $\gamma\delta$ T cells isolated from any one or more of the foregoing expanded $\gamma\delta$ T cell populations; and administering the therapeutically effective amount of $\delta 3$ $\gamma\delta$ T cells to the subject. In some embodiments, the method further comprises admixing the expanded $\gamma\delta$ T cell population with a different expanded $\gamma\delta$ T cell population to form an admixed population and administering the admixed population to the subject.

In some embodiments, the different expanded $\gamma\delta$ T cell population comprises an amount of expanded $\delta 1$ $\gamma\delta$ T cells, and/or an amount of expanded $\delta 2$ $\gamma\delta$ T cells. In some embodiments, the different expanded $\gamma\delta$ T cell population comprises $> 5\%$ $\delta 1$ (e.g., $> 10\%$, 20% , 30% , 40% , 50% , 60% , 70% , 80% , or 90% $\delta 1$) or $> 5\%$ $\delta 2$ (e.g., $> 10\%$, 20% , 30% , 40% , 50% , 60% , 70% , 80% , or 90% $\delta 2$) $\gamma\delta$ T cells. In some embodiments, the different expanded $\gamma\delta$ T cell population comprises from about, or at least about, 60% to about 90% $\delta 1$ $\gamma\delta$ T cells, or from about, or at least about, 60% to about 80% $\delta 1$ $\gamma\delta$ T cells. In some embodiments, the different expanded $\gamma\delta$ T cell population comprises from about, or at least about, 60% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 70% to about 80% $\delta 2$ $\gamma\delta$ T cells, or from about, or at least about, 80% to about 90% $\delta 2$ $\gamma\delta$ T cells.

In some embodiments, the admixed $\gamma\delta$ T cell population comprises an amount of $\delta 1$ $\gamma\delta$ T cells, and/or an amount of $\delta 2$ $\gamma\delta$ T cells, and an amount of $\delta 3$ $\gamma\delta$ T cells. In some embodiments, the admixed $\gamma\delta$ T cell population comprises $> 5\%$ $\delta 1$ (e.g., $> 10\%$, 20% , 30% , 40% , 50% , 60% , 70% , 80% , or 90% $\delta 1$) or $> 5\%$ $\delta 2$ (e.g., $> 10\%$, 20% , 30% , 40% , 50% , 60% , 70% , 80% , or 90% $\delta 2$) $\gamma\delta$ T cells. In some embodiments, the admixed $\gamma\delta$ T cell population comprises $> 5\%$ $\delta 3$ (e.g., $> 10\%$, 20% , 30% , 40% , 50% , 60% , 70% , 80% , or 90% $\delta 3$) $\gamma\delta$ T cells. In some embodiments, the admixed $\gamma\delta$ T cell population comprises from about, or at least about, 5% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 10% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least

about, 20% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 30% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 40% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 50% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 60% to about 90% $\delta 3$ $\gamma\delta$ T cells, from about, or at least about, 70% to about 90% $\delta 3$ $\gamma\delta$ T cells, or from about, or at least about, 80% to about 90% $\delta 3$ $\gamma\delta$ T cells.

In some embodiments, the admixed $\gamma\delta$ T cell population comprises from about, or at least about, 5% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 10% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 20% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 30% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 40% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 50% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 60% to about 90% $\delta 1$ $\gamma\delta$ T cells, from about, or at least about, 70% to about 90% $\delta 1$ $\gamma\delta$ T cells, or from about, or at least about, 80% to about 90% $\delta 1$ $\gamma\delta$ T cells. In some embodiments, the admixed $\gamma\delta$ T cell population comprises from about, or at least about, 5% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 10% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 20% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 30% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 40% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 50% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 60% to about 90% $\delta 2$ $\gamma\delta$ T cells, from about, or at least about, 70% to about 90% $\delta 2$ $\gamma\delta$ T cells, or from about, or at least about, 80% to about 90% $\delta 2$ $\gamma\delta$ T cells.

INCORPORATION BY REFERENCE

All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings (also “figure”

and “Fig.” herein), of which:

Fig. 1 shows variable region sequences of $\delta 3$ -specific anti- $\gamma\delta$ TCR antibodies. **Top** sequence of heavy chain variable regions. **Bottom** sequence of light chain variable regions.

Fig. 2 schematically illustrates a method for treating a subject.

Fig. 3 schematically illustrates a method for administering a population of engineered $\gamma\delta$ T cells to a subject.

Figs. 4A-B illustrate selective expansion of V $\delta 3$ $\gamma\delta$ T cells using a 21-day expansion culture protocol. Fold-expansion is measured on Day 21. **A)** PBMCs are isolated from Donor 1 and directly activated and expanded using the indicated antibody. **B)** PBMCs are isolated from Donor 2 and directly activated and expanded using the indicated antibody.

Figs. 5A-B illustrates the proportion of V $\delta 1^+V\delta 2^-$ $\gamma\delta$ T cells in the expanded cell population illustrated in **Figs. 4A-B**.

Figs. 6A-B illustrates the phenotype of the $\gamma\delta$ T cells in the expanded cell population illustrated in **Figs. 4A-B**. The phenotype of V $\delta 3$ T-cells activated and expanded with the indicated antibodies after 21 days of expansion culture is predominantly (>50%) CD27+CD45RA+ (naïve) and CD27+CD45RA- (central memory).

Fig. 7 illustrates results of a competition assay for binding of the indicated $\delta 3$ $\gamma\delta$ TCR specific antibodies to $\gamma\delta 3$ TCR- hFc recombinant protein.

Figs. 8A-C illustrate selective expansion of V $\delta 3$ $\gamma\delta$ T cells. **A.** Untransduced and anti-CD20 CAR V $\delta 3$ $\gamma\delta$ T cells are expanded approximately 10,000-fold. V $\delta 3$ $\gamma\delta$ T cells are detected as $\delta 1^-$, $\delta 2^-$, and $\delta 3^+$ using antibodies specific for the $\delta 1$, $\delta 2$, and $\delta 3$ sub-types respectively. **B.** Before $\alpha\beta$ T cell depletion, V $\delta 3$ $\gamma\delta$ T cells represent a major fraction of the expanded cell culture. **C.** anti-CD20 CAR construct is expressed on the surface of expanded and transduced V $\delta 3$ $\gamma\delta$ T cells.

Fig. 9 illustrates successful depletion of $\alpha\beta$ T cells from culture of activated expanded V $\delta 3$ $\gamma\delta$ T cells (left cells are transduced with anti-CD20 CAR construct; right cells are untransduced).

Fig. 10 illustrates results from staining an activated, expanded, and $\alpha\beta$ T cell depleted population of $\gamma\delta$ T cells to detect surface expression of V $\delta 1$ and V $\delta 2$ (left panels) or V $\delta 3$ (right panels).

Fig. 11 illustrates cytotoxicity of activated and expanded V $\delta 3$ $\gamma\delta$ T cells against CD20+

Raji cells. Untransduced V δ 3 $\gamma\delta$ T cells exhibited slight cytotoxicity against the CD20+ Raji cells at Effector:Target (E/T) ratios >1 and moderate cytotoxic activity at E/T ratios > 5. Anti-CD20 CAR transduced V δ 3 $\gamma\delta$ T cells exhibited moderate cytotoxic activity at an E/T ratio of 0.5 and strong cytotoxic activity at E/T ratios >0.75.

Fig. 12 illustrates an amino acid sequence of V δ 3, numbered according to IMGT nomenclature.

Fig. 13 illustrates 3 different projections of a 3D model of antigen binding hot spots identified by fine epitope mapping via mutagenesis as described in Example 7.

Figs. 14A-C illustrate IMGT Collier de Perles, with residues shown by fine epitope mapping to contribute to antigen binding highlighted by dark double circles. **A.** K79 and H88 contribute to antigen binding of δ 3-23, δ 3-42, and δ 3-58. **B.** E67 and D70 contribute to antigen binding of δ 3-31; R75 and R95 also contribute to antigen binding of δ 3-31; the combination of E67, D70, R75, R95, and E97 contributes to antigen binding of δ 3-31 and δ 3-42. **C.** E18 contributes to antigen binding of δ 3-58; and K3 contributes to antigen binding of δ 3-08.

DETAILED DESCRIPTION OF THE INVENTION

While various embodiments of the invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions may occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed.

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which the inventions described herein belong. For purposes of interpreting this specification, the following definitions will apply and whenever appropriate, terms used in the singular will also include the plural and vice versa. In the event that any definition set forth conflicts with any document incorporated herein by reference, the definition set forth below shall control.

The term “ $\gamma\delta$ T cells (gamma delta T cells)” as used herein refers to a subset of T-cells that express a distinct T-cell receptor (TCR), $\gamma\delta$ TCR, on their surface, composed of one γ -chain

and one δ -chain. The term “ $\gamma\delta$ T cells” specifically includes all subsets of $\gamma\delta$ T cells and combinations thereof, including, without limitation, V δ 3 $\gamma\delta$ T cells, as well as naïve, effector memory, central memory, and terminally differentiated $\gamma\delta$ T-cells. As a further example, the term “ $\gamma\delta$ T-cells” includes V δ 1, V δ 2, V δ 3, V δ 4, V δ 5, V δ 7, and V δ 8 $\gamma\delta$ T cells, as well as V γ 2, V γ 3, V γ 5, V γ 8, V γ 9, V γ 10, and V γ 11 $\gamma\delta$ T cells. As a further example, the term “ $\gamma\delta$ T-cells” includes V δ 3 γ 2 T cells, and optionally can include or refer to V δ 3 γ 8 T cells.

As used herein, the term “T lymphocyte” or “T cell” refers to an immune cell expressing CD3 (CD3+) and a T Cell Receptor (TCR+). T cells play a central role in cell-mediated immunity.

As used herein, the term “TCR” or “T cell receptor” refers to a dimeric heterologous cell surface signaling protein forming an alpha-beta or gamma-delta receptor. $\alpha\beta$ TCR recognize an antigen presented by an MHC molecule, whereas $\gamma\delta$ TCR recognize an antigen independently of MHC presentation.

The term “MHC” (major histocompatibility complex) refers to a subset of genes that encodes cell-surface antigen-presenting proteins. In humans, these genes are referred to as human leukocyte antigen (HLA) genes. Herein, the abbreviations MHC or HLA are used interchangeably.

As used herein, the term “peripheral blood lymphocyte(s)” or “PBL(s)” is used in the broadest sense and refers to white blood cell(s) comprising T cells and B cells of a range of differentiation and functional stages, plasma cells, monocytes, macrophages, natural killer cells, basocytes, eosinophils, etc. The range of T lymphocytes in peripheral blood is about 20-80%.

As used herein, the term “cell population” refers to a number of cells obtained by isolation directly from a suitable source, usually from a mammal. The isolated cell population may be subsequently cultured *in vitro*. Those of ordinary skill in the art will appreciate that various methods for isolating and culturing cell populations are suitable for use with the present invention and various numbers of cells in a cell population are suitable for use in the present invention. A cell population may be purified to homogeneity, substantial homogeneity, or to deplete one or more cell types (*e.g.*, $\alpha\beta$ T cells) by various culture techniques and/or negative or positive selection for a specified cell type. A cell population may be, for example, a mixed heterogeneous cell population derived (*e.g.*, directly isolated) from a peripheral blood sample, a cord blood sample, a tumor, a stem cell precursor, a tumor biopsy, a tissue, a lymph, skin, a

sample of or containing tumor infiltrating lymphocytes, or from epithelial sites of a subject directly contacting the external milieu, or derived from stem precursor cells. Alternatively, the mixed cell population may be derived from *in vitro* cultures of mammalian cells, established from a peripheral blood sample, a cord blood sample, a tumor, a stem cell precursor, a tumor biopsy, a tissue, a lymph, skin, a sample of or containing tumor infiltrating lymphocytes, or from epithelial sites of a subject directly contacting the external milieu, or derived from stem precursor cells.

An "enriched" cell population or preparation refers to a cell population derived from a starting mixed cell population that contains a greater percentage of a specific cell type than the percentage of that cell type in the starting population. For example, a starting mixed cell population can be enriched for a specific $\gamma\delta$ T-cell population. In one embodiment, the enriched $\gamma\delta$ T-cell population contains a greater percentage of $\delta 3$ cells than the percentage of that cell type in the starting population. As another example, an enriched $\gamma\delta$ T-cell population can contain a greater percentage of both $\delta 1$ cells and a greater percentage of $\delta 3$ cells than the percentage of that cell type in the starting population. As yet another example, an enriched $\gamma\delta$ T-cell population can contain a greater percentage of both $\delta 3$ cells and a greater percentage of $\delta 4$ cells than the percentage of that cell type in the starting population. As yet another example, an enriched $\gamma\delta$ T-cell population can contain a greater percentage of $\delta 1$ T cells, $\delta 3$ T cells, $\delta 4$ T cells, and $\delta 5$ T cells than the percentage of that cell type in the starting population. In another embodiment, the enriched $\gamma\delta$ T cell population contains a greater percentage of $\delta 2$ T cells and $\delta 3$ T cells than the percentage of that cell type in the starting population. In yet another embodiment, the enriched $\gamma\delta$ T cell population contains a greater percentage of $\delta 1$ T cells $\delta 2$ T cells and $\delta 3$ T cells than the percentage of that cell type in the starting population. In all embodiments, the enriched $\gamma\delta$ T cell population contains a lesser percentage of $\alpha\beta$ T cells than the percentage of $\alpha\beta$ T cells in the starting population.

By "expanded" as used herein is meant that the number of the desired or target cell type (*e.g.*, $\delta 3$ T cells) in the enriched preparation is higher than the number in the initial or starting cell population. By "selectively expand" is meant that the target cell type (*e.g.*, $\delta 3$ T cells) are preferentially expanded over one or more other non-target cell types, *e.g.*, $\alpha\beta$ T-cells, NK cells, and/or one or more $\gamma\delta$ T cell sub-populations not expanded by a selective activating agent used in the selective expansion. In certain embodiments, the activating agents of the invention

selectively expand, *e.g.*, engineered or non-engineered, $\delta 3$ T-cells without, or without significant, expansion of $\alpha\beta$ T cells. In certain embodiments, the activating agents of the invention selectively expand, *e.g.*, engineered or non-engineered, $\delta 3$ T-cells without, or without significant, expansion of $\delta 1$ T cells. In other embodiments, the activating agents of the invention selectively expand, *e.g.*, engineered or non-engineered, $\delta 3$ T cells without, or without significant, expansion of $\delta 2$ T cells. In certain embodiments, the activating agents of the invention selectively expand, *e.g.*, engineered or non-engineered, $\delta 3$ T-cells without, or without significant, expansion of $\delta 1$ T cells and $\delta 2$ T cells. In certain embodiments, the activating agents of the invention selectively expand, *e.g.*, engineered or non-engineered, $\delta 1$ and $\delta 3$ T cells without, or without significant, expansion of $\delta 2$ T cells. In this context, the term "without significant expansion of" means that the preferentially expanded cell population are expanded at least 10-fold, preferably 100-fold, and more preferably 1,000-fold more than the reference cell population.

The term "admixture" as used herein refers to a combination of two or more isolated, enriched cell populations derived from a mixed, heterogeneous cell population. According to certain embodiments, the cell populations of the present invention are isolated $\gamma\delta$ T cell populations.

The term "isolated," as applied to a cell population, refers to a cell population, isolated from the human or animal body, which is substantially free of one or more cell populations that are associated with said cell population *in vivo* or *in vitro*.

The term "contacting" in the context of a cell population, as used here refers to incubation of an isolated cell population with a reagent, such as, for example, an antibody, cytokine, ligand, mitogen, or co-stimulatory molecule that can be linked either to beads or to cells. The antibody or cytokine can be in a soluble form, or it can be immobilized. In one embodiment, the immobilized antibody or cytokine is tightly bound or covalently linked to a bead or plate. In one embodiment, the antibody is immobilized on Fc-coated wells. In one embodiment, the antibody is immobilized on a surface of a cell such as an antigen presenting cell (APC) or an artificial antigen presenting cell (aAPC). In desirable embodiments, the contact occurs *ex vivo* (*e.g.*, *in vitro*) or *in vivo*.

As used herein, the term "antibody" refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. By "specifically

bind” or “immunoreacts with” or “directed against” is meant that the antibody reacts with one or more antigenic determinants of the desired antigen and does not react with other polypeptides or binds at much lower affinity ($K_D > 10^{-6}$ molar). Antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, sdAb (heavy or light single domain antibody), single chain, F_{ab} , $F_{ab'}$ and $F_{(ab')_2}$ fragments, scFvs, diabodies, minibodies, nanobodies, and F_{ab} expression library.

The basic antibody structural unit is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. In general, antibody molecules obtained from humans relate to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.

The term “Fab” refers to an antibody fragment that consists of an entire L chain (V_L and C_L) along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain ($CH1$). Papain digestion of an intact antibody can be used to produce two Fab fragments, each of which contains a single antigen-binding site. Typically, the L chain and H chain fragment of the Fab produced by papain digestion are linked by an interchain disulfide bond.

The term “Fc” refers to an antibody fragment that comprises the carboxy-terminal portions of both H chains ($CH2$ and $CH3$) and a portion of the hinge region held together by disulfide bonds. The effector functions of antibodies are determined by sequences in the Fc region; this region is also the part recognized by Fc receptors (FcR) found on certain types of cells. One Fc fragment can be obtained by papain digestion of an intact antibody.

The term “ $F(ab')_2$ ” refers to an antibody fragment produced by pepsin digestion of an intact antibody. $F(ab')_2$ fragments contain two Fab fragments and a portion of the hinge region held together by disulfide bonds. $F(ab')_2$ fragments have divalent antigen-binding activity and are capable of cross-linking antigen.

The term Fab' refers to an antibody fragment that is the product of reduction of an F(ab')₂ fragment. Fab' fragments differ from Fab fragments by having a few additional residues at the carboxy terminus of the CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group.

The term "Fv" refers to an antibody fragment that consists of a dimer of one heavy-chain variable region and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although often at a lower affinity than the entire binding site.

The term "single-chain Fv" also abbreviated as "sFv" or "scFv" refer to antibody fragments that comprise the VH and VL antibody domains connected into a single polypeptide chain. Typically, the scFv polypeptide further comprises a polypeptide linker between the VH and VL domains, which enables the scFv to form the desired structure for antigen binding. For a review of scFv, see, *e.g.*, Pluckthun, The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); and Malmberg *et al.*, J. Immunol. Methods 183:7-13, 1995.

The expression "linear antibody" is used to refer to a polypeptide comprising a pair of tandem V_H-C_H1 segments (V_H-C_H1-V_H-C_H1) which form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific and are described, for example, by Zapata *et al.*, *Protein Eng.* 8(10):1057-1062 (1995).

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a beta-sheet configuration, connected by three hypervariable regions, which form loops

connecting, and in some cases forming part of, the beta-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al (1991) Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md.). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "antigen-binding site" or "binding portion" refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains, referred to as "hypervariable regions," are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus, the term "FR" refers to amino acid sequences which are naturally found between, and adjacent to, hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs." The assignment of amino acids to each domain is in accordance with the definitions of Kabat Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia & Lesk J. Mol. Biol. 196:901-917 (1987), Chothia *et al.* Nature 342:878-883 (1989).

The term "hypervariable region," "HVR," or "HV," refers to the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops. Generally, antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3). In native antibodies, H3 and L3 display the most diversity of the six HVRs, and H3 in particular is believed to play a unique role in conferring fine specificity to antibodies. See, *e.g.*, Xu *et al.*, *Immunity* 13:37-45 (2000); Johnson and Wu, in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, N.J., 2003). Indeed, naturally occurring camelid antibodies consisting of a heavy chain only are functional and stable in the absence of light

chain. See, *e.g.*, Hamers-Casterman *et al.*, *Nature* 363:446-448 (1993); Sheriff *et al.*, *Nature Struct. Biol.* 3:733-736 (1996).

“Framework regions” (FR) are those variable domain residues other than the CDR residues. Each variable domain typically has four FRs identified as FR1, FR2, FR3, and FR4. If the CDRs are defined according to Kabat, the light chain FR residues are positioned at about residues 1-23 (LCFR1), 35-49 (LCFR2), 57-88 (LCFR3), and 98-107 (LCFR4) and the heavy chain FR residues are positioned about at residues 1-30 (HCFR1), 36-49 (HCFR2), 66-94 (HCFR3), and 103-113 (HCFR4) in the heavy chain residues. If the CDRs comprise amino acid residues from hypervariable loops, the light chain FR residues are positioned about at residues 1-25 (LCFR1), 33-49 (LCFR2), 53-90 (LCFR3), and 97-107 (LCFR4) in the light chain and the heavy chain FR residues are positioned about at residues 1-25 (HCFR1), 33-52 (HCFR2), 56-95 (HCFR3), and 102-113 (HCFR4) in the heavy chain residues. In some instances, when the CDR comprises amino acids from both a CDR as defined by Kabat and those of a hypervariable loop, the FR residues will be adjusted accordingly. For example, when CDRH1 includes amino acids H26-H35, the heavy chain FR1 residues are at positions 1-25 and the FR2 residues are at positions 36-49.

A “human consensus framework” is a framework that represents the most commonly occurring amino acid residues in a selection of human immunoglobulin VL or VH framework sequences. Generally, the selection of human immunoglobulin VL or VH sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat. In certain instances, for the VL, the subgroup is subgroup kappa I as in Kabat. In certain instances, for the VH, the subgroup is subgroup III as in Kabat.

An antibody described herein can be humanized. “Humanized” forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These

modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See also the following review articles and references cited therein: Vaswani and Hamilton, *Ann. Allergy, Asthma and Immunol.*, 1:105-115 (1998); Harris, *Biochem. Soc. Transactions*, 23:1035-1038 (1995); Hurlle and Gross, *Curr. Op. Biotech.*, 5:428-433 (1994).

A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies as disclosed herein. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues. Human antibodies can be produced using various techniques known in the art, including phage-display libraries. Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991). Also available for the preparation of human monoclonal antibodies are methods described in Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); Boerner et al., *J. Immunol.*, 147(1):86-95 (1991). See also van Dijk and van de Winkel, *Curr. Opin. Pharmacol.*, 5: 368-74 (2001). Human antibodies can be prepared by administering the antigen to a transgenic animal that has been modified to produce such antibodies in response to antigenic challenge, but whose endogenous loci have been disabled, e.g., immunized xenomice (see, e.g., U.S. Pat. Nos. 6,075,181 and 6,150,584 regarding XENOMOUSE™ technology). See also, for example, Li et al., *Proc. Natl. Acad. Sci. USA*, 103:3557-3562 (2006) regarding human antibodies generated via a human B-cell hybridoma technology.

As used herein, the "K_d" or "K_d value" refers to a dissociation constant measured by using surface plasmon resonance assays, for example, using a BIAcore.TM.-2000 or a BIAcore.TM.-3000 (BIAcore, Inc., Piscataway, N.J.) at 25 °C. with CM5 chips immobilized with antigen or antibody at about 10 response units (RU). For divalent or other multivalent antibodies, typically the antibody is immobilized to avoid avidity-induced interference with

measurement of the dissociation constant. For further details see, *e.g.*, Chen *et al.*, *J. Mol. Biol.* 293:865-881 (1999).

“Or better” when used herein to refer to binding affinity refers to a stronger binding between a molecule and its binding partner. “Or better” when used herein refers to a stronger binding, represented by a smaller numerical K_D value. For example, an antibody which has an affinity for an antigen of “0.6 nM or better”, the antibody's affinity for the antigen is ≤ 0.6 nM, i.e. 0.59 nM, 0.58 nM, 0.57 nM *etc.* or any value less than or equal to 0.6 nM.

The term “epitope” includes any protein determinant, lipid or carbohydrate determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of active surface groupings of molecules such as amino acids, lipids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. An antibody is said to specifically bind an antigen when the equilibrium dissociation constant (K_D) is within the range of $10^{-6} - 10^{-12}$ M, or better. Specific binding can refer to binding to a target epitope with at least a 10-fold; preferably 100-fold; or more preferably 1,000-fold tighter dissociation constant (lower K_D), as compared to the dissociation constant for binding to other non-target epitopes. In some cases, the target epitope is an epitope of a delta-3 chain of a delta-3 TCR. In some cases, the non-target epitope is an $\alpha\beta$ TCR. In some cases, the non-target epitope is a delta chain of a δ -TCR that is not delta-3. For example, in some cases, the non-target epitope can be a delta-1, delta-2, delta-4, delta-5, or delta-8 chain of a δ -TCR. Specificity of binding can be determined in the context of binding to a extracellular region of a $\gamma\delta$ -TCR and/or $\alpha\beta$ -TCR (*e.g.*, as an Fc fusion immobilized on an ELISA plate or as expressed on a cell).

An “activating epitope” is capable of activation of the specific $\gamma\delta$ T-cell population upon binding. T cell proliferation indicates T cell activation and expansion.

An antibody binds “essentially the same epitope” as a reference antibody, when the two antibodies recognize identical or sterically overlapping epitopes. The most widely used and rapid methods for determining whether two epitopes bind to identical or sterically overlapping epitopes are competition assays, which can be configured in a number of different formats, using either labeled antigen or labeled antibody. In some embodiments, the antigen is immobilized on a 96-well plate, and the ability of unlabeled antibodies to block the binding of labeled antibodies is measured using radioactive or enzyme labels. Alternatively, the competition studies, using

labelled and unlabeled antibodies, are performed using flow cytometry on antigen-expressing cells.

“Epitope mapping” is the process of identifying the binding sites, or epitopes, of antibodies on their target antigens. Antibody epitopes may be linear epitopes or conformational epitopes. Linear epitopes are formed by a continuous sequence of amino acids in a protein. Conformational epitopes are formed of amino acids that are discontinuous in the protein sequence, but which are brought together upon folding of the protein into its three-dimensional structure.

“Epitope binning”, as defined herein, is the process of grouping antibodies based on the epitopes they recognize. More particularly, epitope binning comprises methods and systems for discriminating the epitope recognition properties of different antibodies, combined with computational processes for clustering antibodies based on their epitope recognition properties and identifying antibodies having distinct binding specificities.

The term "chimeric antigen receptors (CARs)," as used herein, may refer to artificial T-cell receptors, T-bodies, single-chain immunoreceptors, chimeric T-cell receptors, or chimeric immunoreceptors, for example, and encompass engineered receptors that graft an artificial specificity onto a particular immune effector cell. CARs may be employed to impart the specificity of a monoclonal antibody onto a T cell, thereby allowing a large number of specific T cells to be generated, for example, for use in adoptive cell therapy. In specific embodiments, CARs direct specificity of the cell to a tumor associated antigen, for example. In some embodiments, CARs comprise an intracellular activation domain (allowing the T cell to activate upon engagement of targeting moiety with target cell, such as a target tumor cell), a transmembrane domain, and an extracellular domain that may vary in length and comprises a disease- or disorder-associated, *e.g.*, a tumor-antigen binding region. In particular aspects, CARs comprise fusions of single-chain variable fragments (scFv) derived from monoclonal antibodies, fused to CD3-zeta a transmembrane domain and endodomain. The specificity of other CAR designs may be derived from ligands of receptors (*e.g.*, peptides) or from pattern-recognition receptors, such as Dectins. In certain cases, the spacing of the antigen-recognition domain can be modified to reduce activation-induced cell death. In certain cases, CARs comprise domains for additional co-stimulatory signaling, such as CD3-zeta, FcR, CD27, CD28, CD137, DAP 10/12, and/or OX40, ICOS, TLRs, etc. In some cases, molecules can be co-expressed with the CAR,

including co-stimulatory molecules, reporter genes for imaging (e.g., for positron emission tomography), gene products that conditionally ablate the T cells upon addition of a pro-drug, homing receptors, chemokines, chemokine receptors, cytokines, and cytokine receptors.

An “agent” or “compound” according to the present invention comprises small molecules, polypeptides, proteins, antibodies or antibody fragments. Small molecules, in the context of the present invention, mean in one embodiment chemicals with molecular weight smaller than 1000 Daltons, particularly smaller than 800 Daltons, more particularly smaller than 500 Daltons. The term “therapeutic agent” refers to an agent that has biological activity. The term “anti-cancer agent” refers to an agent that has biological activity against cancer cells.

As used herein, the term “cell culture” refers to any *in vitro* culture of cells. Included within this term are continuous cell lines (e.g., with an immortal phenotype), primary cell cultures, finite cell lines (e.g., non-transformed cells), and any other cell population maintained *in vitro*, including stem cells, blood cells, embryonic cord blood cells, tumor cells, transduced cells, etc.

The terms “treat” or “treatment” refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) an undesired physiological change or disorder. Beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease (e.g., decrease of tumor size, tumor burden, or tumor distribution), stabilized (i.e., not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. “Treatment” can also mean prolonging survival, as compared to expected survival if not receiving treatment. Those in need of treatment include those already with the condition or disorder as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

Administration “in combination with” one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

The term “identical,” as used herein, refers to two or more sequences or subsequences that are the same. In addition, the term “substantially identical,” as used herein, refers to two or more sequences which have a percentage of sequential units which are the same when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using comparison algorithms or by manual alignment and visual inspection. By way of

example only, two or more sequences may be “substantially identical” if the sequential units are about 60% identical, about 65% identical, about 70% identical, about 75% identical, about 80% identical, about 85% identical, about 90% identical, or about 95% identical over a specified region. Such percentages to describe the “percent identity” of two or more sequences. The identity of a sequence can exist over a region that is at least about 75-100 sequential units in length, over a region that is about 50 sequential units in length, or, where not specified, across the entire sequence. This definition also refers to the complement of a test sequence. In addition, by way of example only, two or more polynucleotide sequences are identical when the nucleic acid residues are the same, while two or more polynucleotide sequences are “substantially identical” if the nucleic acid residues are about 60% identical, about 65% identical, about 70% identical, about 75% identical, about 80% identical, about 85% identical, about 90% identical, or about 95% identical over a specified region. The identity can exist over a region that is at least about 75 to about 100 nucleic acids in length, over a region that is about 50 nucleic acids in length, or, where not specified, across the entire sequence of a polynucleotide sequence.

The term “pharmaceutically acceptable”, as used herein, refers to a material, including but not limited, to a salt, carrier or diluent, which does not abrogate the biological activity or properties of the compound, and is relatively nontoxic, i.e., the material may be administered to an individual without causing undesirable biological effects or interacting in a deleterious manner with any of the components of the composition in which it is contained.

The term “subject,” or “patient”, as used herein, refers to a vertebrate. In certain embodiments, the vertebrate is a mammal. Mammals include, but are not limited to, humans, non-human primates, farm animals (such as cows), sport animals, and pets (such as cats, dogs, and horses). In certain embodiments, a mammal is a human.

The term “therapeutically effective amount,” as used herein, refers to the amount of a composition containing the expanded cell populations and/or admixtures of the present invention administered to a subject, *e.g.*, a human patient, already suffering from a disease, condition or disorder, sufficient to cure or at least partially arrest, or relieve to some extent one or more of the symptoms of the disease, disorder or condition being treated. The effectiveness of such compositions depend conditions including, but not limited to, the severity and course of the disease, disorder or condition, previous therapy, the patient’s health status and response to the drugs, and the judgment of the treating physician. By way of example only, therapeutically

effective amounts may be determined by routine experimentation, including but not limited to a dose escalation clinical trial.

The term antigen presenting cell (APC) refers to a wild-type APC, or an engineered or artificial antigen presenting cell (aAPC). APCs can be provided as an irradiated population of APCs. APCs can be provided from a immortalized cell line (e.g., K562 or an engineered aAPC derived from an immortalized cell line) or as a fraction of cells from a donor (e.g., PBMCs).

As used herein, the terms “structurally different” and “structurally distinct,” in reference to a protein or polypeptide fragment thereof, such as an antibody or an epitope, refer to a covalent (*i.e.*, structural) difference between at least two different proteins, polypeptide fragments thereof, or epitopes. For example, two structurally different proteins (e.g., antibodies) can refer to two proteins that have different primary amino acid sequences. In some cases, structurally different activating agents bind structurally different epitopes, such as epitopes having a different primary amino acid sequence.

As used herein, the term “anti-tumor cytotoxicity” that is “independent of” a specified receptor activity (*e.g.*, NKp30 activity, NKp44 activity, and/or NKp46 activity), refers to anti-tumor cytotoxicity that is exhibited whether or not the specified receptor or specified combination of receptors is expressed by the cell or is functional to mediate cytolysis. As such, a $\gamma\delta$ T cell that exhibits anti-tumor cytotoxicity that is independent of NKp30 activity, NKp44 activity, and/or NKp46 activity can also exhibit NKp30 activity-dependent anti-tumor cytotoxicity, NKp44 activity -dependent anti-tumor cytotoxicity, and/or NKp46 activity-dependent anti-tumor cytotoxicity.

As used herein, the terms “NKp30 activity-dependent anti-tumor cytotoxicity,” “NKp44 activity-dependent anti-tumor cytotoxicity,” and “NKp46 activity-dependent anti-tumor cytotoxicity” refer to anti-tumor cytotoxicity that requires functional expression of the specified receptor. The presence or absence of such receptor dependent anti-tumor cytotoxicity can be determined by performing standard *in vitro* cytotoxicity assays in the presence or absence of an antagonist to the specified receptor. For example, presence or absence of NKp30 activity-dependent anti-tumor cytotoxicity can be determined by comparing the results of an *in vitro* cytotoxicity assays in the presence of an anti-NKp30 antagonist to the results obtained in the absence of an anti-NKp30 antagonist.

As used herein, a $\gamma\delta$ T-cell population that comprises anti-tumor cytotoxicity, wherein at least a specified “%” of the anti-tumor cytotoxicity is “independent of” a specified receptor activity (*e.g.*, NKp30 activity, NKp44 activity, and/or NKp46 activity), refers to a cell where blocking specified receptor reduces measured anti-tumor cytotoxicity by no more than the numerical % value. Thus, a $\gamma\delta$ T-cell population that comprises anti-tumor cytotoxicity, wherein at least 50% of the anti-tumor cytotoxicity is independent of NKp30 activity would exhibit a reduction of 50% or less of *in vitro* anti-tumor cytotoxicity in the presence of an NKp30 antagonist as compared to in the absence of the NKp30 antagonist.

Overview

In humans, $\gamma\delta$ T-cell(s) are a subset of T-cells that provide a link between the innate and adaptive immune responses. These cells undergo V-(D)-J segment rearrangement to generate antigen-specific $\gamma\delta$ T-cell receptors ($\gamma\delta$ TCRs), and $\gamma\delta$ T-cell(s) and can be directly activated via the recognition of an antigen by either the $\gamma\delta$ TCR or other, non-TCR proteins, acting independently or together to activate $\gamma\delta$ T-cell effector functions. $\gamma\delta$ T-cells represent a small fraction of the overall T-cell population in mammals, approximately 1-5% of the T-cells in peripheral blood and lymphoid organs, and they appear to reside primarily in epithelial cell-rich compartments like skin, liver, digestive, respiratory, and reproductive tracts. Unlike $\alpha\beta$ TCRs, which recognize antigens bound to major histocompatibility complex molecules (MHC), $\gamma\delta$ TCRs can directly recognize bacterial antigens, viral antigens, stress antigens expressed by diseased cells, and tumor antigens in the form of intact proteins or non-peptide compounds.

$\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58 can activate and expand $\gamma\delta$ T cells, and in some embodiments can be used to preferentially activate and expand $\delta 3$ $\gamma\delta$ T cells, *e.g.*, to clinically relevant levels. Without being bound by theory, different levels of activation and expansion of cultures originating from different donors may be due to the donor $\gamma\delta$ variable TCR repertoire and the specificity of the antibody binding epitope. It has been discovered that not every agent which binds to specific $\gamma\delta$ T-cell subsets is capable of activating the specific $\gamma\delta$ T-cell and particularly activating and expanding the specific $\gamma\delta$ T-cell population to clinically-relevant levels, *i.e.*, $>10^8$ target $\gamma\delta$ T cells in an enriched culture. Similarly, not every binding epitope of a $\gamma\delta$ T-cell population is an activating epitope, *i.e.*, capable of activation of the specific $\gamma\delta$ T-cell population upon binding.

The inventors of the present invention have identified specific $\gamma\delta$ TCR binding regions associated with potent activation and expansion of the $\delta 3$ $\gamma\delta$ T cell subtype. In some cases, the binding regions are within, or overlap with, a $\delta 3$ variable region. Thus, agents that bind these activating regions can be developed and used to selectively activate and expand the $\delta 3$ $\gamma\delta$ T cell subtype. Exemplary activating agents are described herein. Thus, the present invention enables the specific activation and expansion of the $\delta 3$ $\gamma\delta$ T cell subtype which produces clinically relevant levels of highly enriched $\delta 3$ $\gamma\delta$ T-cell populations with increased purity, and admixtures thereof, that can be administered to patients. Such admixtures can include admixtures of other expanded $\gamma\delta$ T cell subpopulations, such as $\delta 1$ and/or $\delta 2$ $\gamma\delta$ T cells. Novel activating ligands, including antibodies, which specifically bind the activating epitopes capable of inducing enhanced activation and expansion of $\delta 3$ $\gamma\delta$ T cell subtypes are also contemplated and further described herein. The activating ligands, methods, and compositions described herein can be used in combination with the activating ligands, methods, and compositions described in PCT/US17/32530, herein incorporated by reference in the entirety, to obtain and use expanded $\gamma\delta$ T cell populations, and admixtures, and/or purified fractions thereof comprising essentially any desired proportion of $\delta 1$, $\delta 2$, $\delta 3$, $\delta 4$, and/or $\delta 8$ (e.g., $\delta 1$, $\delta 2$, and $\delta 3$) engineered or non-engineered $\gamma\delta$ T cells by *ex vivo* expansion and/or post-expansion isolation. For example, one or more of the $\delta 3$ specific $\gamma\delta$ T cell activating ligands described herein can be used in a culture medium in combination with one or more of the $\delta 1$ specific and/or $\delta 2$ specific $\gamma\delta$ T cell activating ligands described in PCT/US17/32530 for *ex vivo* expansion. As another example, activating ligands, methods or compositions described herein can be used in a first or second *ex vivo* $\gamma\delta$ T cell expansion step and activating ligands, methods or compositions described in PCT/US17/32530 can be used in a subsequent or previous *ex vivo* $\gamma\delta$ T cell expansion step. Activating ligands can also be used for purification of specified $\gamma\delta$ T cell populations by positive or negative selection.

In some cases, the production of clinically relevant levels (i.e., $>10^8$) of $\gamma\delta$ T cells using the methods of the present invention can be obtained with relatively small volumes of culture medium. For example, in some embodiments, the clinically relevant levels of $\gamma\delta$ T cells can be obtained from expansion of a population of cells (e.g., an isolated mixed population of cells), in a final culture volume of approximately 25 L; 20 L; 10 L; 5 L; 3 L; 2 L; 1,500 mL; 1,000 mL; 500 mL; 200 mL; 150 mL; 100 mL, or less (e.g., from about 10 mL to about 100 mL, from about 100

mL to about 500 mL, from about 500 mL to about 5,000 mL, or from about 5 L to about 25 L). As another example, in some embodiments, the clinically relevant levels of $\gamma\delta$ T cells can be obtained under conditions such that the expansion from an isolated mixed population of cells obtained from a donor, or multiple donors can be achieved using a total volume of culture media of less than about 50 L, 25L, 20L, 10 L, 5L, 1 L, or 750 mL (*e.g.*, from about 750 mL to less than about 50 L, from about 100 mL to about 750 mL, from about 750 mL to about 5 L, from about 1 L to about 10 L, from about 10L to about 50 L, or from about 10 L to about 25 L).

Described herein are methods for the selective activation and expansion of $\gamma\delta$ T cell subtypes (*e.g.*, $\delta\beta$ $\gamma\delta$ T cells) directly from isolated mixed cell populations, *e.g.*, without prior depletion of non-target cell types, providing clinically-relevant levels of enriched $\gamma\delta$ T cell population(s) having cytotoxic properties. Activating $\gamma\delta$ variable TCR epitopes of specific $\gamma\delta$ cell population(s) are also described. The present invention also provides methods of treatment with compositions comprising the enriched $\gamma\delta$ T cell population(s) of the invention.

Described herein are methods of producing or providing clinically relevant levels ($>10^8$) of engineered or non-engineered $\gamma\delta$ T cells, including one or more specific subsets of $\gamma\delta$ T cells (*e.g.*, $\delta\beta$ $\gamma\delta$ T cells). Such methods can be used to produce such clinically relevant levels from a single donor, including from a single sample of a single donor. Moreover, such methods can be used to produce significantly greater than 10^8 engineered or non-engineered $\gamma\delta$ T cells. For example, in some embodiments about, or at least about, 10^9 , 10^{10} , 10^{11} , or 10^{12} engineered or non-engineered $\gamma\delta$ T cells, including one or more specific subsets of $\gamma\delta$ T cells (*e.g.*, $\delta\beta$ $\gamma\delta$ T cells), can be produced in the methods described herein. In some cases, such population sizes can be achieved in as few as 14-30 days, 19-30 days, or 21-30 days, and/or with a total volume of culture media used of less than about 1L.

Isolation of $\gamma\delta$ T-cells

In some aspects, the instant invention provides *ex vivo* methods for expansion of engineered or non-engineered $\gamma\delta$ T cells. In some cases, the methods employ one or more (*e.g.*, first and/or second) expansion steps that do not include a cytokine that favors expansion of a specific population of $\gamma\delta$ T cells, such as IL-4, IL-2, or IL-15, or a combination thereof. In some embodiments, the instant invention provides *ex vivo* methods for producing enriched $\gamma\delta$ T cell populations from isolated mixed cell populations, comprising contacting the mixed cell

population with one or more agents which selectively expand $\delta 3$ T cells by binding to an epitope specific to a $\delta 3$ TCR (*e.g.*, a $\delta 3 \gamma \delta$ TCR) to provide an enriched $\gamma \delta$ T cell population.

In other aspects, the present disclosure provides methods for the genetic engineering of $\gamma \delta$ T cells that have been isolated from a subject. Methods of enrichment, activation, expansion, or genetic engineering can be performed singly or in combination, in any order. In one embodiment, $\gamma \delta$ T cells can be isolated, genetically engineered, and then activated and expanded. In a preferred embodiment, $\gamma \delta$ T cells can be isolated, the isolated cells can be directly activated and expanded, optionally purified, and then optionally genetically engineered. In some embodiments, such activated and expanded and then genetically engineered $\gamma \delta$ T cells can be further activated and/or expanded and/or purified.

An, *e.g.*, non-engineered, $\gamma \delta$ T cell population can be expanded from a complex sample of a subject. A complex sample can be a peripheral blood sample (*e.g.*, PBLs or PBMCs), a leukapheresis sample, a cord blood sample, a tumor, a stem cell precursor, a tumor biopsy, a tissue, a lymph, or from epithelial sites of a subject directly contacting the external milieu, or derived from stem precursor cells. In some cases, the present disclosure provides methods for selective expansion of $V\delta 3^+$ cells. In some cases, the present disclosure provides methods for expansion of $V\delta 3^+$ cells in combination with expansion of, $V\delta 1^+$ cells, $V\delta 2^+$ cells, $V\delta 1^+$ cells and $V\delta 3^+$ cells, $V\delta 1^+$ cells and $V\delta 4^+$ cells, $V\delta 1^+$ cells, $V\delta 3^+$ cells, $V\delta 4^+$ cells, and $V\delta 5^+$ cells, or any grouping thereof.

Peripheral blood mononuclear cells can be collected from a subject, for example, with an apheresis machine, including the Ficoll-Paque™ PLUS (GE Healthcare) system, or another suitable device/system. $\gamma \delta$ T cell(s), or a desired subpopulation of $\gamma \delta$ T cell(s), can be purified from the collected sample with, for example, flow cytometry techniques. Cord blood cells can also be obtained from cord blood during the birth of a subject. See WO 2016/081518, incorporated by reference herein in its entirety for all purposes including but not limited to methods and compositions for PBMC isolation, $\gamma \delta$ T cell activation and expansion, and making and using $\gamma \delta$ T cell activation agents.

A $\gamma \delta$ T cell may be expanded from an isolated complex sample or mixed cell population that is cultured *in vitro* by contacting the mixed cell population with one or more agents which expand $\gamma \delta$ T cell by specifically binding to an epitope of a $\delta 3 \gamma \delta$ TCR to provide an enriched $\gamma \delta$ T cell population, *e.g.*, in a first enrichment step. In some embodiments, $\gamma \delta$ T cells comprised in

a whole PBMC population, without prior depletion of one or more specific cell populations such as one or more or all of the following non- $\gamma\delta$ T cell monocytes: $\alpha\beta$ T cells, B cells, and NK cells, can be activated and expanded, resulting in an enriched $\gamma\delta$ T cell population. In some aspects, activation and expansion of $\gamma\delta$ T cells are performed without the presence of native or engineered APCs. In some aspects, activation and expansion of $\gamma\delta$ T cells are performed in the presence of native or engineered APCs. In some aspects, activation and expansion of $\gamma\delta$ T cells are performed in the presence of native or engineered APCs in a first or second step, and activation and expansion are also performed in a step (first or second) without native or engineered APCs. In some aspects, isolation and expansion of $\gamma\delta$ T cells from, *e.g.*, tumor specimens, can be performed using immobilized $\gamma\delta$ T cell mitogens, including antibodies specific to activating epitopes of a $\gamma\delta$ TCR (*e.g.*, $\delta 3^+$ TCR), and other activating agents, including lectins, which can, *e.g.*, bind the activating epitopes of a $\gamma\delta$ TCR provided herein.

In certain embodiments, the isolated mixed cell population is contacted with one or more agents which expand (*e.g.*, selectively expand) $\delta 3$ $\gamma\delta$ T cells for about, or at least about, 2 days, about 3 days, about 4 days, about 5 days, about 6 days, about 7 days, about 8 days, about 9 days, about 10 days, about 11 days, about 12 days, about 13 days, about 14 days, about 15 days, about 17 days, about 19 days, about 21 days, about 25 days, about 29 days, about 30 days, or any range therein. For example, the isolated mixed cell population is contacted with one or more agents which expand (*e.g.*, selectively expand) $\delta 3$ $\gamma\delta$ T cells for about 1 to about 4 days, about 2 to about 4 days, about 2 to about 5 days, about 3 to about 5 days, about 5 to about 21 days, about 5 to about 19 days, about 5 to about 15 days, about 5 to about 10 days, or about 5 to about 7 days, to provide a first enriched $\gamma\delta$ T cell population. As another example, the isolated mixed cell population is contacted with one or more agents which expand (*e.g.*, selectively expand) $\delta 3$ $\gamma\delta$ T cells for about 7 to about 21 days, about 7 to about 19 days, about 7 to about 23 days, or about 7 to about 15 days to provide a first enriched $\gamma\delta$ T-cell population.

In some cases, a purification or isolation step is performed between a first and second expansion step. In some cases, the isolation step includes removal of one or more activating agents. In some cases, the isolation step includes specific isolation of $\gamma\delta$ T cells, or a subtype thereof (*e.g.*, $\delta 3$ $\gamma\delta$ T cells). In some cases, one or more (*e.g.*, all) activating agents (*e.g.*, all activating agents that are not common components of cell culture media such as serum components and/or IL-2)) are removed between first and second expansion steps, but $\gamma\delta$ T-cells

are not specifically isolated from other cell types ($\alpha\beta$ T-cells). In some cases, one or more (*e.g.*, all) soluble activating agents are removed between first and second expansion steps, but $\gamma\delta$ T-cells are not specifically isolated from other cell types ($\alpha\beta$ T-cells).

In some embodiments, following the activation and expansion of $\gamma\delta$ T cells using activating agents which bind to an activating epitope of a $\gamma\delta$ TCR, in a first enrichment step, and optionally a second enrichment step, the, *e.g.*, first, enriched $\gamma\delta$ T cell population(s) of the invention may be further enriched or purified using techniques known in the art to obtain a second or further enriched $\gamma\delta$ T cell population(s) in a second, third, fourth, fifth, etc. enrichment step. For example, the, *e.g.*, first, enriched $\gamma\delta$ T cell population(s) may be depleted of $\alpha\beta$ T cells, B cells and NK cells. Positive and/or negative selection of cell surface markers expressed on the collected $\gamma\delta$ T cell(s) can be used to directly isolate a $\gamma\delta$ T cell, or a population of $\gamma\delta$ T cell(s) expressing similar cell surface markers from the, *e.g.*, first, enriched $\gamma\delta$ T-cell population(s). For instance, a $\gamma\delta$ T cell can be isolated from an enriched $\gamma\delta$ T cell population (*e.g.*, after a first and/or second step of expansion) based on positive or negative expression of markers such as CD2, CD3, CD4, CD8, CD24, CD25, CD44, Kit, TCR α , TCR β , TCR γ (including one or more TCR γ sub-types), TCR δ (including one or more TCR δ sub-types), NKG2D, CD70, CD27, CD28, CD30, CD16, OX40, CD46, CD161, CCR7, CCR4, NKp30, NKp44, NKp46, DNAM-1, CD242, JAML, and other suitable cell surface markers.

In some embodiments, after a first step of expansion (*e.g.*, after an isolation step performed subsequent to the first step of expansion), the expanded cells are, optionally diluted, and cultured in a second step of expansion. In preferred embodiments, the second step of expansion is performed under conditions in which culture media is replenished about every 1-2, 1-3, 1-4, 1-5, 2-5, 2-4, or 2-3 days in a second expansion step. In some embodiments, the second step of expansion is performed under conditions in which the cells are diluted or adjusted to a density that supports further $\gamma\delta$ T cell expansion 1, 2, 3, 4, 5, 6, or more times. In some cases, the cell density adjustment is performed contemporaneously with (*i.e.*, on the same day as, or at the same time as) replenishment of culture media. For example, cell density can be adjusted every 1-2, 1-3, 1-4, 1-5, 2-5, 2-4, or 2-3 days in a second expansion step. Typical cell densities that support further $\gamma\delta$ T cell expansion include, but are not limited to, about 1×10^5 , 2×10^5 , 3×10^5 , 4×10^5 , 5×10^5 , 6×10^5 , 7×10^5 , 8×10^5 , 9×10^5 , 1×10^6 , 2×10^6 , 3×10^6 , 4×10^6 , 5×10^6

cells/mL, 10×10^6 cells/mL, 15×10^6 cells/mL, 20×10^6 cells/mL, or 30×10^6 cells/mL of culture.

In some embodiments, cell density is adjusted to a density of from about 0.5×10^6 to about 1×10^6 cells/mL, from about 0.5×10^6 to about 1.5×10^6 cells/mL, from about 0.5×10^6 to about 2×10^6 cells/mL, from about 0.75×10^6 to about 1×10^6 cells/mL, from about 0.75×10^6 to about 1.5×10^6 cells/mL, from about 0.75×10^6 to about 2×10^6 cells/mL, from about 1×10^6 to about 2×10^6 cells/mL, or from about 1×10^6 to about 1.5×10^6 cells/mL, from about 1×10^6 to about 2×10^6 cells/mL, from about 1×10^6 to about 3×10^6 cells/mL, from about 1×10^6 to about 4×10^6 cells/mL, from about 1×10^6 to about 5×10^6 cells/mL, from about 1×10^6 to about 10×10^6 cells/mL, from about 1×10^6 to about 15×10^6 cells/mL, from about 1×10^6 to about 20×10^6 cells/mL, or from about 1×10^6 to about 30×10^6 cells/mL.

In some embodiments, the second step of expansion is performed under conditions in which the cells are monitored and maintained at a predetermined cell density (or density interval) and/or maintained in culture medium having a predetermined glucose content. For example, the cells can be maintained at a viable cell density of from about 0.5×10^6 to about 1×10^6 cells/mL, from about 0.5×10^6 to about 1.5×10^6 cells/mL, from about 0.5×10^6 to about 2×10^6 cells/mL, from about 0.75×10^6 to about 1×10^6 cells/mL, from about 0.75×10^6 to about 1.5×10^6 cells/mL, from about 0.75×10^6 to about 2×10^6 cells/mL, from about 1×10^6 to about 2×10^6 cells/mL, or from about 1×10^6 to about 1.5×10^6 cells/mL, from about 1×10^6 to about 3×10^6 cells/mL, from about 1×10^6 to about 4×10^6 cells/mL, from about 1×10^6 to about 5×10^6 cells/mL, from about 1×10^6 to about 10×10^6 cells/mL, from about 1×10^6 to about 15×10^6 cells/mL, from about 1×10^6 to about 20×10^6 cells/mL, from about 1×10^6 to about 30×10^6 cells/mL.

In some cases, the cells can be maintained at a higher concentration for at least a portion of the expansion. For example, for a first portion of a first or second expansion, cells viability may be enhanced at a higher cell concentration. As another example, for a final portion of a first or second expansion culture volume may be most efficiently utilized at a higher cell concentration. Thus, in some embodiments, cells can be maintained at a viable cell density of from about 1×10^6 cells/mL to about 20×10^6 cells/mL for at least a portion of a first or second expansion culture or all of a first or second expansion culture.

As another example, the cells can be maintained in culture medium having a glucose content of from about 0.5 g/L to about 1 g/L, from about 0.5 g/L to about 1.5 g/L, from about 0.5 g/L to about 2 g/L, from about 0.75 g/L to about 1 g/L, from about 0.75 g/L to about 1.5 g/L, from about 0.75 g/L to about 2 g/L, from about 1 g/L to about 1.5 g/L, from about 1 g/L to about 2 g/L, from 1 g/L to 3 g/L, or from 1 g/L to 4 g/L.. In some embodiments, the cells can be maintained in culture medium having a glucose content of about 1.25 g/L. In some cases, such as where a high cell density culture is maintained, cells can be maintained in culture medium having a glucose content of about 1 g/L to about 5 g/L, from about 1 g/L to about 4 g/L, from about 2 g/L to about 5 g/L, or from about 2 g/L to about 4 g/L.

Typically glucose content is maintained by addition of fresh serum containing or serum free culture medium to the culture. In some embodiments, the cells can be maintained at a predetermined viable cell density interval and in a culture medium having a predetermined glucose content interval, *e.g.*, by monitoring each parameter and adding fresh media to maintain the parameters within the predetermined limits. In some embodiments, glucose content is maintained by adding fresh serum containing or serum free culture medium in the culture while removing spent medium in a perfusion bioreactor while retaining the cells inside. In some embodiments, additional parameters including, without limitation, one or more of: pH, partial pressure of O₂, O₂ saturation, partial pressure of CO₂, CO₂ saturation, lactate, glutamine, glutamate, ammonium, sodium, potassium, and calcium, are monitored and/or maintained during a $\gamma\delta$ T cell expansion (*e.g.*, selective $\gamma\delta$ T cell expansion) or during a first or second step of $\gamma\delta$ T cell expansion (*e.g.*, selective $\gamma\delta$ T cell expansion) described herein.

A $\delta\delta$ $\gamma\delta$ T cell population may be selectively expanded from an isolated complex sample or mixed cell population that is cultured *in vitro* by contacting the mixed cell population with one or more agents which selectively expand $\delta\delta$ T-cells by specifically binding to an epitope of a $\delta\delta$ TCR to provide an enriched $\gamma\delta$ T-cell population, *e.g.*, in a first enrichment step. In some cases, the one or more agents specifically bind to a $\delta\delta$ J1, $\delta\delta$ J2, or $\delta\delta$ J3 TCR, $\delta\delta$ J4 TCR, or two thereof, or three thereof, or all thereof.

In some embodiments, $\delta\delta$ $\gamma\delta$ cells in a whole PBMC population, without prior depletion of specific cell populations such as monocytes, $\alpha\beta$ T cells, B cells, and NK cells, can be activated and expanded, resulting in an enriched $\gamma\delta$ T cell population (*e.g.*, an enriched $\delta\delta$ $\gamma\delta$ T cell population). In some aspects, activation and expansion of $\delta\delta$ $\gamma\delta$ T cells are performed without

the presence of native or engineered APCs. In some aspects, isolation and expansion of $\gamma\delta$ T cells from tumor specimens can be performed using immobilized $\gamma\delta$ T cell mitogens, including antibodies specific to activating epitopes specific to a $\delta 3$ TCR; a $\delta 1$ TCR; a $\delta 1$, $\delta 3$, $\delta 4$, and $\delta 5$ TCR, a $\delta 1$ and $\delta 4$ TCR; or a $\delta 2$ TCR, and other activating agents, including lectins, which, *e.g.*, bind the activating epitopes specific to a $\delta 3$ TCR; a $\delta 1$ TCR; a $\delta 1$, $\delta 3$, $\delta 4$ and $\delta 5$ TCR; a $\delta 1$ and $\delta 4$ TCR; or a $\delta 2$ TCR provided herein.

In certain embodiments, the isolated mixed cell population is contacted with one or more agents which selectively expand $\delta 3$ T cells for about 5 days, 6 days, about 7 days, about 8 days, about 9 days, about 10 days, about 11 days, about 12 days, about 13 days, about 14 days, about 15 days, or any range therein. For example, the isolated mixed cell population is contacted with one or more agents which selectively expand $\delta 3$ T cells for about 1 to about 3 days, about 1 to about 4 days, about 1 to about 5 days, about 2 to about 3 days, about 2 to about 4 days, about 2 to about 5 days, about 3 to about 4 days, about 3 to about 5 days, about 4 to about 5 days, about 5 to about 15 days, or about 5 to about 7 days, to provide a first enriched $\gamma\delta$ T-cell population. In some embodiments selectively expanded $\gamma\delta$ T cells are further expanded in a second step of expansion as described herein.

In certain embodiments, the starting isolated mixed cell population, *e.g.*, peripheral blood sample, comprises T lymphocytes in the range of about 20-80%. In certain embodiments, the percent of residual $\alpha\beta$ T cells and NK cells in enriched $\gamma\delta$ T-cell population(s) of the invention is about, or less than about, 2.5% and 1 %, respectively. In certain embodiments, the percent of residual $\alpha\beta$ T cells or NK cells in enriched $\gamma\delta$ T-cell population(s) of the invention is about, or less than about, 1%, 0.5%, 0.4%, 0.2%, 0.1%, or 0.01%. In certain embodiments, the percent of residual $\alpha\beta$ T cells in enriched $\gamma\delta$ T cell population(s) of the invention is about, or less than about, 0.4%, 0.2%, 0.1%, or 0.01% (*e.g.*, after a step of positive selection for $\gamma\delta$ T cells or a sub-type thereof such as $\delta 3$ $\gamma\delta$ T cells or after depletion of $\alpha\beta$ T cells). In some embodiments, $\alpha\beta$ T cells are depleted, but NK cells are not depleted before or after a first and/or second $\gamma\delta$ T-cell expansion. In certain aspects, the isolated mixed cell population is derived from a single donor. In other aspects, the isolated mixed cell population is derived from more than one donor or multiple donors (*e.g.*, 2, 3, 4, 5, or from 2-5, 2-10, or 5-10 donors, or more).

As such, in some embodiments, the methods of the present invention can provide a clinically relevant number ($>10^8$, $>10^9$, $>10^{10}$, $>10^{11}$, or $>10^{12}$, or from about 10^8 to about 10^{12})

of expanded $\gamma\delta$ T-cells from as few as one donor. In some cases, the methods of the present invention can provide a clinically relevant number ($>10^8$, $>10^9$, $>10^{10}$, $>10^{11}$, or $>10^{12}$, or from about 10^8 to about 10^{12}) of expanded $\gamma\delta$ T-cells within less than 19, 21, or 30 days from the time of obtaining a donor sample.

Following the specific activation and expansion of the specific $\gamma\delta$ T cell subsets using activating agents which bind to an activating epitope specific to a $\delta\beta$ TCR, in a first enrichment step, the first enriched $\gamma\delta$ T cell population(s) of the invention may be further enriched or purified using techniques known in the art to obtain a second or further enriched $\gamma\delta$ T cell population(s) in a second, third, fourth, fifth, etc. enrichment step. For example, the first enriched $\gamma\delta$ T cell population(s) may be depleted of $\alpha\beta$ T cells, B cells and/or NK cells. Positive and/or negative selection of cell surface markers expressed on the collected $\gamma\delta$ T cell(s) can be used to directly isolate a $\gamma\delta$ T cell, or a population of $\gamma\delta$ T cell(s) expressing similar cell surface markers from the first enriched $\gamma\delta$ T cell population(s). For instance, a $\gamma\delta$ T cell can be isolated from a first enriched $\gamma\delta$ T cell population based on positive or negative expression of markers such as CD2, CD3, CD4, CD8, CD24, CD25, CD44, Kit, TCR α , TCR β , TCR γ (or one or more subtypes thereof), TCR δ (or one or more subtypes thereof), NKG2D, CD70, CD27, CD28, CD30, CD16, OX40, CD46, CD161, CCR7, CCR4, DNAM-1, JAML, and other suitable cell surface markers.

In some embodiments, following the first $\gamma\delta$ T cell expansion, first enrichment step, second $\gamma\delta$ T-cell expansion, and/or second enrichment step, of the invention, the enriched $\gamma\delta$ T cell population comprises clinically-relevant levels of $\gamma\delta$ T cell subsets of $>10^8$ cells, e.g., in a culture volume of less than 10 mL, 25 mL, 50 mL, 100 mL, 150 mL, 200 mL, 500 mL, 750 mL, 1 L, 2 L, 3 L, 4 L, 5 L, 10 L, 20 L, or 25 L. For example, the methods of the present invention can provide clinically-relevant levels of $\gamma\delta$ T cell subsets of $>10^8$ cells in an expansion culture having a volume of from 10-100 mL; from 25-100 mL; from 50-100 mL; from 75-100mL; from 10-150 mL; from 25-150 mL; from 50-150 mL; from 75-150 mL; from 100-150 mL; from 10-200 mL; from 25-200 mL; from 50-200 mL; from 75-200 mL, from 100-200 mL; from 10-250 mL; from 25-250 mL; from 50-250 mL; from 75-250 mL, from 100-250 mL; from 150-250 mL; from 5-1,000 mL; from 10-1,000 mL, or from 100-1,000 mL; from 150-1,000 mL; from 200-1,000 mL; from 250-1,000 mL, 400 mL to 1L, 1 L to 2 L, 2 L to 5 L, 2 L to 10 L, 4 L to 10 L, 4 L to 15 L, 4 L to 20 L, or 4 L to 25 L. In other embodiments, following the second, third, fourth,

fifth, etc. enrichment step of the invention, the enriched $\gamma\delta$ T-cell population comprises clinically-relevant levels $>10^8$ of one or more $\gamma\delta$ T cell subsets (*e.g.*, $>10^8$ $\delta 3$ $\gamma\delta$ T cells).

In some embodiments, $\gamma\delta$ T cell(s) can rapidly expand in response to contact with one or more antigens. Some $\gamma\delta$ T cell(s), such as $V\gamma 9V\delta 2^+$ $\gamma\delta$ T cell(s) rapidly expand *in vitro* in response to contact with some antigens, like prenyl-pyrophosphates, alkyl amines, and metabolites or microbial extracts during tissue culture. In addition, some wild-type $\gamma\delta$ T cell(s), such as $V\gamma 2V\delta 2^+$ $\gamma\delta$ T cell(s) rapidly expand *in vivo* in humans in response to certain types of vaccination(s). Stimulated $\gamma\delta$ T cells can exhibit numerous antigen-presentation, co-stimulation, and adhesion molecules that can facilitate the isolation of a $\gamma\delta$ T-cell(s) from a complex sample. A $\gamma\delta$ T-cell(s) within a complex sample can be stimulated *in vitro* with at least one antigen for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, about 5-15 days, 5-10 days, or 5-7 days, or another suitable period of time, *e.g.*, in combination with, before, or after expansion with a selective $\gamma\delta$ T-cell expansion agent described herein such as an antibody or an immobilized antibody. Stimulation of the $\gamma\delta$ T cell with a suitable antigen can expand the $\gamma\delta$ T cell population *ex vivo* or *in vitro*.

Non-limiting examples of antigens that may be used to stimulate the expansion of $\gamma\delta$ T-cell(s) from a complex sample *in vitro* include, prenyl-pyrophosphates, such as isopentenyl pyrophosphate (IPP), alkyl-amines, metabolites of human microbial pathogens, metabolites of commensal bacteria, -methyl-3-butenyl-1-pyrophosphate (2M3B1PP), (e)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate (HMB-PP), ethyl pyrophosphate (EPP), farnesyl pyrophosphate (FPP), dimethylallyl phosphate (DMAP), dimethylallyl pyrophosphate (DMAPP), ethyl-adenosine triphosphate (EPPPA), geranyl pyrophosphate (GPP), geranylgeranyl pyrophosphate (GGPP), isopentenyl-adenosine triphosphate (IPPPA), monoethyl phosphate (MEP), monoethyl pyrophosphate (MEPP), 3-formyl-1-butyl-pyrophosphate (TUBAg 1), X-pyrophosphate (TUBAg 2), 3-formyl-1-butyl-uridine triphosphate (TUBAg 3), 3-formyl-1-butyl-deoxythymidine triphosphate (TUBAg 4), monoethyl alkylamines, allyl pyrophosphate, crotoyl pyrophosphate, dimethylallyl- γ -uridine triphosphate, crotoyl- γ -uridine triphosphate, allyl- γ -uridine triphosphate, ethylamine, isobutylamine, sec-butylamine, iso-amylamine and nitrogen containing bisphosphonates.

Activation and expansion of $\gamma\delta$ T-cells can be performed using activation and co-stimulatory agents described herein to trigger specific $\gamma\delta$ T cell proliferation and persistent

populations. In some embodiments, activation and expansion of $\gamma\delta$ T cells from different cultures can achieve distinct clonal or mixed polyclonal population subsets by using different culture conditions such as different activating agents or mixtures thereof. In some cases, the distinct populations subsets can be purified and/or admixed to produce additional clonal or mixed polyclonal population subsets. In some embodiments, different agonist agents can be used to identify agents that provide specific $\gamma\delta$ T cell activating signals. In one aspect, agents that provide specific $\gamma\delta$ T cell activating signals can be different monoclonal antibodies (MAbs) directed against the $\gamma\delta$ TCRs.

In one aspect, the MAbs can bind to different epitopes on the constant or variable regions of δ TCR and/or γ TCR. In one aspect, the MAbs can include pan $\gamma\delta$ TCR MAbs. In one aspect, the pan $\gamma\delta$ TCR MAbs may recognize domains shared by different γ and δ TCRs on either the γ or δ chain or both, including $\delta 3^+$ cell populations. In one aspect, the antibodies may be 5A6.E9 (Thermo scientific), B1 (Biolegend), IMMU510 and/or 11F2 (11F2) (Beckman Coulter). In one aspect, the MAbs can be directed to specific domains unique to the variable regions of the γ chain (7A5 Mab, directed to V γ 9 TCR (Thermo Scientific #TCR1720)), or domains on V δ 1 variable region (Mab TS8.2 (Thermo scientific #TCR1730; Mab TS-1 (ThermoFisher #TCR 1055), Mab R9.12 (Beckman Coulter #IM1761)), or V δ 2 chain (Mab 15D (Thermo Scientific #TCR1732 or Life technologies #TCR2732) B6 (Biolegend #331402), one or more of the δ 1-# antibodies described in PCT/US17/32530, one or more of the δ 2-# antibodies described in PCT/US17/32530, or one or more of δ 3-08, δ 3-20, δ 3-23, δ 3-31, δ 3-42, δ 3-47 and δ 3-58.

In some embodiments, antibodies against different domains of the $\gamma\delta$ TCR (pan antibodies and antibodies recognizing specific variable region epitopes on subset populations) can be combined to evaluate or make use of their ability to enhanced activation and expansion of $\gamma\delta$ T cells and/or one or more subpopulations thereof. In some embodiments, $\gamma\delta$ T cell activators can include $\gamma\delta$ TCR-binding agents such as MICA, an agonist antibody to NKG2D, an, *e.g.*, Fc tag, fusion protein of MICA, ULBP1, or ULBP3 (R&D systems Minneapolis, MN) ULBP2, or ULBP6 (Sino Biological Beijing, China). In some embodiments, companion co-stimulatory agents to assist in triggering specific $\gamma\delta$ T cell proliferation without induction of cell anergy and apoptosis can be identified or used in the methods and compositions of the present invention. These co-stimulatory agents can include ligands to receptors expressed on $\gamma\delta$ cells, such as ligand(s) to one or more of the following: NKG2D, CD161, CD70, JAML, DNAX, CD81

accessory molecule-1 (DNAM-1) ICOS, CD27, CD196, CD137, CD30, HVEM, SLAM, CD122, DAP, and CD28. In some aspects, co-stimulatory agents can be antibodies specific to unique epitopes on CD2 and CD3 molecules. CD2 and CD3 can have different conformation structures when expressed on $\alpha\beta$ or $\gamma\delta$ T cells (s), and in some cases, specific antibodies to CD3 and CD2 can lead to selective activation and expansion of $\gamma\delta$ T-cells.

A population of $\gamma\delta$ T cells (*e.g.*, a population comprising $\delta 3$ $\gamma\delta$ T cells) may be expanded *ex vivo* prior to engineering of the $\gamma\delta$ T cells. Non-limiting example of reagents that can be used to facilitate the expansion of a $\gamma\delta$ T cell population *in vitro* include anti-CD3 or anti-CD2, anti-CD27, anti-CD30, anti-CD70, anti-OX40 antibodies, IL-2, IL-4, IL-7, IL-9, IL-12, IL-15, IL-18, IL-19, IL-21, IL 23, IL-33, IFN γ , granulocyte-macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), CD70 (CD27 ligand), concavalin A (ConA), pokeweed (PWM), protein peanut agglutinin (PNA), soybean agglutinin (SBA), Les Culinaris Agglutinin (LCA), Pisum Sativum Agglutinin (PSA), Helix pomatia agglutinin (HPA), Vicia graminea Lectin (VGA), Phaseolus Vulgaris Erythroagglutinin (PHA-E), Phaseolus Vulgaris Leucoagglutinin (PHA-L), Sambucus Nigra Lectin (SNA, EBL), Maackia Amurensis, Lectin II (MAL II), Sophora Japonica Agglutinin (SJA), Dolichos Biflorus Agglutinin (DBA), Lens Culinaris Agglutinin (LCA), Wisteria Floribunda Lectin (WFA, WFL) or another suitable mitogen capable of stimulating T cell proliferation.

Genetic engineering of the $\gamma\delta$ T cell(s) may comprise stably integrating a construct expressing a tumor recognition moiety, such as an $\alpha\beta$ TCR, a $\gamma\delta$ TCR, a CAR encoding an antibody, an antigen binding fragment thereof, and/or a lymphocyte activation domain into the genome of the isolated $\gamma\delta$ T-cells, a cytokine (*e.g.*, IL-15, IL-12, IL-2, IL-7, IL-21, IL-18, IL-19, IL-33, IL-4, IL-9, IL-23, or IL-1 β) to enhance T-cell proliferation, survival, and function *ex vivo* and *in vivo*. Genetic engineering of the isolated $\gamma\delta$ T-cell may also comprise deleting or disrupting gene expression from one or more endogenous genes in the genome the isolated $\gamma\delta$ T-cell, such as the MHC locus (loci).

Ex-vivo Expansion of $\gamma\delta$ T-cells

In other aspects, the present disclosure provides methods for the *ex vivo* expansion of a population of non-engineered and engineered $\gamma\delta$ T cells for adoptive transfer therapy. A non-

engineered or engineered $\gamma\delta$ T cell of the disclosure may be expanded *ex vivo*. A non-engineered or engineered $\gamma\delta$ T cell of the disclosure can be expanded *in vitro* without activation by APCs, or without co-culture with APCs and/or aminophosphonates. Additionally, or alternatively, a non-engineered or engineered $\gamma\delta$ T cell of the disclosure can be expanded *in vitro* with at least one expansion step that includes activation by or co-culture with APCs and/or with one or more aminophosphonates.

In some embodiments, a non-engineered or engineered $\gamma\delta$ T cell of the disclosure can be expanded *in vitro* without activation by APC in a first $\gamma\delta$ T cell expansion, and then expanded *in vitro* with activation by APC in a second $\gamma\delta$ T cell expansion. In some cases, the first $\gamma\delta$ T cell expansion includes contacting the $\gamma\delta$ T cells with one or more agents which (a) expand $\gamma\delta$ T cells, or (b) selectively expand $\delta 3$ T cells by binding to an activating epitope specific to a $\delta 3$ TCR.

In some cases, the second $\gamma\delta$ T cell expansion is performed in a culture medium that is free of the one or more agents used in the first $\gamma\delta$ T cell expansion, or free of one of the one or more agents used in the first $\gamma\delta$ T cell expansion. In some cases, the second $\gamma\delta$ T cell expansion is performed in a culture medium that contains one or more second agents that (a) expand T cells, (b) selectively expand $\gamma\delta$ T cells (*e.g.*, compared to $\alpha\beta$ T cells, B cells, or NK cells), or (c) selectively expand $\delta 3$ T cells by binding to an activating epitope specific to a $\delta 3$ TCR.

In some cases, the second agents are different (*e.g.*, have a different primary amino acid sequence and/or bind a structurally different $\gamma\delta$ TCR epitope) as compared to the agents used in the first $\gamma\delta$ T cell expansion. In some cases, the second agents bind an overlapping $\gamma\delta$ TCR epitope, the same $\gamma\delta$ TCR epitope, or can compete for binding to $\gamma\delta$ TCR with one or more of the agents used in the first $\gamma\delta$ T-cell expansion. In some cases, the second agents are expressed on the cell surface of an APC. In some cases, the second agents are bound to the surface of an APC, *e.g.*, by a binding interaction between a constant region of the second agent and an Fc-receptor on the surface of the APC. In some cases, the second agents are soluble. In some cases, the second $\gamma\delta$ T cell expansion is performed in a culture medium containing soluble second agents and APCs, optionally wherein the APC express on their cell surface or bind to their cell surface an agent that expands or selectively expands a $\gamma\delta$ T cell population. The soluble second agents

and the agent expressed on the surface or bound to the surface of the APC can be the same or different, *e.g.*, bind the same or different epitope on a $\gamma\delta$ TCR.

In some cases, the first $\gamma\delta$ T cell expansion is performed without an APC, and the second $\gamma\delta$ T cell expansion is performed with an APC. In some cases, the second $\gamma\delta$ T cell expansion is performed with an APC and one or more second agents that (a) expand T cells, (b) selectively expand $\gamma\delta$ T cells, or (c) selectively expand $\delta 3$ T cells by binding to an activating epitope specific to a $\delta 3$ TCR.

One of skill in the art will appreciate that, in certain embodiments, the methods of the second expansion step described herein can be performed as a first expansion step and methods of the first step described herein can be performed as a second expansion step. As an example, and without limitation, in some embodiments, a mixed population of cells (*e.g.*, PBMC) can be expanded by contacting with an APC in a first step, and then expanded in the absence of an APC, *e.g.*, by contacting the expanded population from the first expansion step with an immobilized agent that selectively expands $\delta 3$ T-cells by binding to an activating epitope specific to a $\delta 3$ TCR. In some embodiments, a method of the invention can expand various $\gamma\delta$ T cell populations, such as a $V\gamma 1^+$, a $V\gamma 2^+$, or $V\gamma 3^+$ $\gamma\delta$ T-cell population.

In some instances, a $\gamma\delta$ T cell population can be expanded *in vitro* in fewer than 36 days, fewer than 35 days, fewer than 34 days, fewer than 33 days, fewer than 32 days, fewer than 31 days, fewer than 30 days, fewer than 29 days, fewer than 28 days, fewer than 27 days, fewer than 26 days, fewer than 25 days, fewer than 24 days, fewer than 23 days, fewer than 22 days, fewer than 21 days, fewer than 20 days, fewer than 19 days, fewer than 18 days, fewer than 17 days, fewer than 16 days, fewer than 15 days, fewer than 14 days, fewer than 13 days, fewer than 12 days, fewer than 11 days, fewer than 10 days, fewer than 9 days, fewer than 8 days, fewer than 7 days, fewer than 6 days, fewer than 5 days, fewer than 4 days, or fewer than 3 days.

In some aspects, provided are methods for selectively expanding various $\gamma\delta$ T cells, including engineered and non-engineered $\gamma\delta$ T cells by contacting the $\gamma\delta$ T cells from the mixed cell population with an activation agent. In some cases, the activation agent binds to a specific epitope on a cell-surface receptor of a $\gamma\delta$ T cell. The activation agent can be an antibody, such as a monoclonal antibody. The activation agent, or combinations thereof, can specifically activate the expansion of one or more types of $\gamma\delta$ T-cells, such as $\delta 3$, $\delta 2$, $\delta 1$, $\delta 4$, or $\delta 1$ and $\delta 3$ cell

populations. In some embodiments the activation agent specifically activates the expansion of $\delta 3$ cell populations to provide an enriched $\delta 3$ T cell population.

An activation agent may stimulate the expansion of engineered and non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) at a fast rate of growth. For instance, an agent can stimulate an expansion of the $\gamma\delta$ T-cell population at a mean rate of 1 cell division in less than 30 hours, 1 cell division in less than 29 hours, 1 cell division in less than 28 hours, 1 cell division in less than 27 hours, 1 cell division in less than 26 hours, 1 cell division in less than 25 hours, 1 cell division in less than 24 hours, 1 cell division in less than 23 hours, 1 cell division in less than 22 hours, 1 cell division in less than 21 hours, 1 cell division in less than 20 hours, 1 cell division in less than 19 hours, 1 cell division in less than 18 hours, 1 cell division in less than 17 hours, 1 cell division in less than 16 hours, 1 cell division in less than 15 hours, 1 cell division in less than 14 hours, 1 cell division in less than 13 hours, 1 cell division in less than 12 hours, 1 cell division in less than 11 hours, 1 cell division in less than 10 hours, 1 cell division in less than 9 hours, 1 cell division in less than 8 hours, 1 cell division in less than 7 hours, 1 cell division in less than 6 hours, 1 cell division in less than 5 hours, 1 cell division in less than 4 hours, 1 cell division in less than 3 hours, 1 cell division in less than 2 hours. In some cases, the fast rate of expansion can be maintained for at least about 8 hours of culture (e.g., 8 to 24 hours, or 1-3, 1-4, 1-8, 2-3, 2-4, or 2-8 days, or less than about 19, 21, or 30 days).

In some cases, an activation agent may stimulate the expansion of engineered and non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) at a mean rate of about 1 division per about 4 hours, a mean rate of about 1 division per about 5 hours, a mean rate of about 1 division per about 6 hours, a mean rate of about 1 division per about 7 hours, a mean rate of about 1 division per about 8 hours, a mean rate of about 1 division per about 9 hours, a mean rate of about 1 division per about 10 hours, a mean rate of about 1 division per about 11 hours, a mean rate of about 1 division per about 12 hours, a mean rate of about 1 division per about 13 hours, a mean rate of about 1 division per about 14 hours, a mean rate of about 1 division per about 15 hours, a mean rate of about 1 division per about 16 hours, a mean rate of about 1 division per about 17 hours, a mean rate of about 1 division per about 18 hours, a mean rate of about 1 division per about 19 hours, a mean rate of about 1 division per about 20 hours, a mean rate of about 1 division per about 21 hours, a rate of about 1 division per about 22 hours, a rate of about 1 division per about 23 hours, a mean rate of about 1 division per about 24 hours, a mean rate of about 1 division per

about 25 hours, a mean rate of about 1 division per about 26 hours, a mean rate of about 1 division per about 27 hours, a rate of about 1 division per about 28 hours, a rate of about 1 division per about 29 hours, a mean rate of about 1 division per about 30 hours, a mean rate of about 1 division per about 31 hours, a mean rate of about 1 division per about 32 hours, a mean rate of about 1 division per about 33 hours, a rate of about 1 division per about 34 hours, a rate of about 1 division per about 35 hours, a mean rate of about 1 division per about 36 hours. In some cases, the fast rate of expansion can be maintained for at least about 8 hours of culture (*e.g.*, 8 to 24 hours, or 1-3, 1-4, 1-8, 2-3, 2-4, or 2-8 days, or less than about 19, 21, or 30 days).

In some cases, an activation agent may stimulate the rapid expansion of engineered and/or non-engineered $\gamma\delta$ T cells (*e.g.*, $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture (*e.g.*, $\delta 3 \gamma\delta$ T cell expansion culture), wherein the rapid expansion is at any one of the foregoing mean rates of cell division and is maintained for between about 1 contiguous day and about 19 contiguous days, between about 1 contiguous day and about 14 contiguous days, between about 1 contiguous day and about 7 contiguous days, between about 1 contiguous day and about 5 contiguous days, between about 2 contiguous days and about 19 contiguous days, between about 2 contiguous days and about 14 contiguous days, between about 2 contiguous days and about 7 contiguous days, between about 2 contiguous days and about 5 contiguous days, between about 4 contiguous days and about 19 contiguous days, between about 4 contiguous days and about 14 contiguous days, between about 4 contiguous days and about 7 contiguous days, or between about 4 contiguous days and about 5 contiguous days.

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (*e.g.*, $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture (*e.g.*, $\delta 3 \gamma\delta$ T cell expansion culture) that has been maintained for between about 2 and about 7 contiguous days, or between about 2 and about 5 contiguous days, at a mean rate of about 1 division per about 12 hours (*e.g.*, 10-12 hours), a mean rate of about 1 division per about 13 hours (*e.g.*, 10-13 hours), a mean rate of about 1 division per about 14 hours (*e.g.*, 10-14 hours), a mean rate of about 1 division per about 15 hours (*e.g.*, 10-15 hours), a mean rate of about 1 division per about 16 hours (*e.g.*, 10-16 hours), a mean rate of about 1 division per about 17 hours (*e.g.*, 10-17 hours or 12-17 hours), a mean rate of about 1 division per about 18 hours (*e.g.*, 10-18 hours or 12-18 hours), a mean rate of about 1 division per about 19 hours (*e.g.*, 10-19 hours or 12-19 hours), a mean rate of about 1 division per about 20 hours (*e.g.*, 12-20 hours, 16-20 hours or 18-20 hours),

a mean rate of about 1 division per about 21 hours (e.g., 12-21 hours, 16-21 hours or 18-21 hours), a rate of about 1 division per about 22 hours (e.g., 12-22 hours, 16-22 hours or 18-22 hours), a rate of about 1 division per about 23 hours or less (e.g., 12-23 hours, 16-23 hours or 18-23 hours), a mean rate of about 1 division per about 24 hours (e.g., 12-24 hours, 16-24 hours or 18-24 hours).

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture (e.g., $\delta 3 \gamma\delta$ T cell expansion culture) that has been maintained for between about 2 and about 7 contiguous days, or between about 2 and about 5 contiguous days at a mean rate of about 1 division per about 25 hours (e.g., 12-25 hours, 16-25 hours 18-25 hours, or 20-25 hours), a mean rate of about 1 division per about 26 hours (e.g., 12-26 hours, 16-26 hours 18-26 hours, or 20-26 hours), a mean rate of about 1 division per about 27 hours (e.g., 12-27 hours, 16-27 hours 18-27 hours, or 20-27 hours), a rate of about 1 division per about 28 hours (e.g., 12-28 hours, 16-28 hours 18-28 hours, 20-28 hours, or 22-28 hours), a rate of about 1 division per about 29 hours (e.g., 16-29 hours 18-29 hours, 20-29 hours, or 22-29 hours), a mean rate of about 1 division per about 30 hours (e.g., 16-30 hours 18-30 hours, 20-30 hours, or 22-30 hours), a mean rate of about 1 division per about 31 hours (e.g., 16-31 hours 18-31 hours, 20-31 hours, 22-31 hours, or 24-31 hours), a mean rate of about 1 division per about 32 hours (e.g., 18-32 hours, 20-32 hours, 22-32 hours, or 24-32 hours), a mean rate of about 1 division per about 33 hours (e.g., 18-33 hours, 20-33 hours, 22-33 hours, or 24-33 hours), a rate of about 1 division per about 34 hours (e.g., 18-34 hours, 20-34 hours, 22-34 hours, or 24-34 hours), a rate of about 1 division per about 35 hours (e.g., 18-35 hours, 20-35 hours, 22-35 hours, or 24-35 hours), a mean rate of about 1 division per about 36 hours (e.g., 18-36 hours, 20-36 hours, 22-36 hours, or 24-36 hours).

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture (e.g., $\delta 3 \gamma\delta$ T cell expansion culture) that has been maintained for at least 14 contiguous days at a mean rate of about 1 division per about 12 hours (e.g., 10-12 hours), a mean rate of about 1 division per about 13 hours (e.g., 10-13 hours), a mean rate of about 1 division per about 14 hours (e.g., 10-14 hours), a mean rate of about 1 division per about 15 hours (e.g., 10-15 hours), a mean rate of about 1 division per about 16 hours (e.g., 10-16 hours), a mean rate of about 1 division per about 17 hours (e.g., 10-17 hours or 12-17 hours), a mean rate of about 1 division per about 18 hours

(e.g., 10-18 hours or 12-18 hours), a mean rate of about 1 division per about 19 hours (e.g., 10-19 hours or 12-19 hours), a mean rate of about 1 division per about 20 hours (e.g., 12-20 hours, 16-20 hours or 18-20 hours), a mean rate of about 1 division per about 21 hours (e.g., 12-21 hours, 16-21 hours or 18-21 hours), a rate of about 1 division per about 22 hours (e.g., 12-22 hours, 16-22 hours or 18-22 hours), a rate of about 1 division per about 23 hours or less (e.g., 12-23 hours, 16-23 hours or 18-23 hours), a mean rate of about 1 division per about 24 hours (e.g., 12-24 hours, 16-24 hours or 18-24 hours).

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture that has been maintained for at least 14 contiguous days at a mean rate of about 1 division per about 25 hours (e.g., 12-25 hours, 16-25 hours 18-25 hours, or 20-25 hours), a mean rate of about 1 division per about 26 hours (e.g., 12-26 hours, 16-26 hours 18-26 hours, or 20-26 hours), a mean rate of about 1 division per about 27 hours (e.g., 12-27 hours, 16-27 hours 18-27 hours, or 20-27 hours), a rate of about 1 division per about 28 hours (e.g., 12-28 hours, 16-28 hours 18-28 hours, 20-28 hours, or 22-28 hours), a rate of about 1 division per about 29 hours (e.g., 16-29 hours 18-29 hours, 20-29 hours, or 22-29 hours), a mean rate of about 1 division per about 30 hours (e.g., 16-30 hours 18-30 hours, 20-30 hours, or 22-30 hours), a mean rate of about 1 division per about 31 hours (e.g., 16-31 hours 18-31 hours, 20-31 hours, 22-31 hours, or 24-31 hours), a mean rate of about 1 division per about 32 hours (e.g., 18-32 hours, 20-32 hours, 22-32 hours, or 24-32 hours), a mean rate of about 1 division per about 33 hours (e.g., 18-33 hours, 20-33 hours, 22-33 hours, or 24-33 hours), a rate of about 1 division per about 34 hours (e.g., 18-34 hours, 20-34 hours, 22-34 hours, or 24-34 hours), a rate of about 1 division per about 35 hours (e.g., 18-35 hours, 20-35 hours, 22-35 hours, or 24-35 hours), a mean rate of about 1 division per about 36 hours (e.g., 18-36 hours, 20-36 hours, 22-36 hours, or 24-36 hours).

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture that has been maintained for at least 19 contiguous days at a mean rate of about 1 division per about 12 hours (e.g., 10-12 hours), a mean rate of about 1 division per about 13 hours (e.g., 10-13 hours), a mean rate of about 1 division per about 14 hours (e.g., 10-14 hours), a mean rate of about 1 division per about 15 hours (e.g., 10-15 hours), a mean rate of about 1 division per about 16 hours (e.g., 10-16 hours), a mean rate of about 1 division per about 17 hours (e.g., 10-17 hours or

12-17 hours), a mean rate of about 1 division per about 18 hours (e.g., 10-18 hours or 12-18 hours), a mean rate of about 1 division per about 19 hours (e.g., 10-19 hours or 12-19 hours), a mean rate of about 1 division per about 20 hours (e.g., 12-20 hours, 16-20 hours or 18-20 hours), a mean rate of about 1 division per about 21 hours (e.g., 12-21 hours, 16-21 hours or 18-21 hours), a rate of about 1 division per about 22 hours (e.g., 12-22 hours, 16-22 hours or 18-22 hours), a rate of about 1 division per about 23 hours or less (e.g., 12-23 hours, 16-23 hours or 18-23 hours), a mean rate of about 1 division per about 24 hours (e.g., 12-24 hours, 16-24 hours or 18-24 hours).

In some cases, an activation agent may stimulate the expansion of engineered and/or non-engineered $\gamma\delta$ T cells (e.g., $\delta 3 \gamma\delta$ T cells) in a $\gamma\delta$ T cell expansion culture (e.g., $\delta 3 \gamma\delta$ T cell expansion culture) that has been maintained for at least 19 contiguous days at a mean rate of about 1 division per about 25 hours (e.g., 12-25 hours, 16-25 hours 18-25 hours, or 20-25 hours), a mean rate of about 1 division per about 26 hours (e.g., 12-26 hours, 16-26 hours 18-26 hours, or 20-26 hours), a mean rate of about 1 division per about 27 hours (e.g., 12-27 hours, 16-27 hours 18-27 hours, or 20-27 hours), a rate of about 1 division per about 28 hours (e.g., 12-28 hours, 16-28 hours 18-28 hours, 20-28 hours, or 22-28 hours), a rate of about 1 division per about 29 hours (e.g., 16-29 hours 18-29 hours, 20-29 hours, or 22-29 hours), a mean rate of about 1 division per about 30 hours (e.g., 16-30 hours 18-30 hours, 20-30 hours, or 22-30 hours), a mean rate of about 1 division per about 31 hours (e.g., 16-31 hours 18-31 hours, 20-31 hours, 22-31 hours, or 24-31 hours), a mean rate of about 1 division per about 32 hours (e.g., 18-32 hours, 20-32 hours, 22-32 hours, or 24-32 hours), a mean rate of about 1 division per about 33 hours (e.g., 18-33 hours, 20-33 hours, 22-33 hours, or 24-33 hours), a rate of about 1 division per about 34 hours (e.g., 18-34 hours, 20-34 hours, 22-34 hours, or 24-34 hours), a rate of about 1 division per about 35 hours (e.g., 18-35 hours, 20-35 hours, 22-35 hours, or 24-35 hours), a mean rate of about 1 division per about 36 hours (e.g., 18-36 hours, 20-36 hours, 22-36 hours, or 24-36 hours).

An activation agent may stimulate the expansion of sub-populations of engineered or non-engineered $\gamma\delta$ T-cells at different rates of growth. For instance, an agent may stimulate the growth of a $\delta 3$ cell population at a faster rate such that over a period of time from 1 day to 90 days of culture (e.g., about 1 day to about 19, 21, or 23 days of culture) the expansion results in greater than about 10-fold, 100-fold, 200-fold, 300-fold, 400-fold, 500-fold, 600-fold, 700-fold,

800-fold, 900-fold, 1,000-fold, 10,000-fold, 20,000-fold, 30,000-fold, 50,000-fold, 70,000-fold, 100,000-fold or 1,000,000-fold expansion over another $\gamma\delta$ T cell population, such as a $\delta 1$ or $\delta 2$ population; over a starting number of $\gamma\delta$ T cells before the expansion; over a starting number of $\gamma\delta 3$ T cells before the expansion; or over an $\alpha\beta$ T cell population in the culture.

In some aspects, the disclosure provides an engineered or non-engineered $\gamma\delta$ T cell population (*e.g.*, $\delta 3$ $\gamma\delta$ T cell population), in contact with an agent that stimulates an expansion of the $\gamma\delta$ T cell population at a rapid rate, such as a rate of about 1 cell division per 30 hours or faster. In some cases, the agent selectively stimulates the proliferation of $\delta 3$ T cells. A $\gamma\delta$ T cell population can comprise an amount of non-engineered $\gamma\delta$ T-cells and an amount of engineered $\gamma\delta$ T cells. In some cases, the $\gamma\delta$ T cell population comprises different percentages of $\delta 1$, $\delta 2$, $\delta 3$, and/or $\delta 4$ T-cells. In some cases, the $\gamma\delta$ T cell population comprises different percentages of $\delta 1$, $\delta 2$, $\delta 3$, and/or $\delta 4$ T-cells, contains more $\delta 3$ $\gamma\delta$ T cells than any other $\gamma\delta$ T cell subpopulation, and/or contains predominantly (>50%) $\delta 3$ $\gamma\delta$ T cells. An engineered or non-engineered $\gamma\delta$ T-cell population can comprise, for example, fewer than 90% $\delta 3$ T-cells, fewer than 80% $\delta 3$ T-cells, fewer than 70% $\delta 3$ T-cells, fewer than 60% $\delta 3$ T-cells, fewer than 50% $\delta 3$ T-cells, fewer than 40% $\delta 3$ T-cells, fewer than 30% $\delta 3$ T-cells, fewer than 20% $\delta 3$ T-cells, fewer than 10% $\delta 3$ T-cells, or fewer than 5% $\delta 3$ T-cells. Alternatively, an engineered or non-engineered $\gamma\delta$ T-cell population can comprise greater than 5% $\delta 3$ T-cells, greater than 10% $\delta 3$ T-cells, greater than 20% $\delta 3$ T-cells, greater than 30% $\delta 3$ T-cells, greater than 40% $\delta 3$ T-cells, greater than 50% $\delta 3$ T-cells, greater than 60% $\delta 3$ T-cells, greater than 70% $\delta 3$ T-cells, greater than 80% $\delta 3$ T-cells, or greater than 90% $\delta 3$ T-cells. In some cases, the agent is one of the selective expansion agents described herein. In some cases, the agent is immobilized on a surface such as a cell culture surface, or a surface of an APC (*e.g.*, expressed on the surface of the APC or bound to an Fc receptor expressed on the surface of the APC).

An engineered or non-engineered $\gamma\delta$ T cell population can comprise, for example, fewer than 90% $\delta 2$ T-cells, fewer than 80% $\delta 2$ T-cells, fewer than 70% $\delta 2$ T-cells, fewer than 60% $\delta 2$ T-cells, fewer than 50% $\delta 2$ T-cells, fewer than 40% $\delta 2$ T-cells, fewer than 30% $\delta 2$ T-cells, fewer than 20% $\delta 2$ T-cells, fewer than 10% $\delta 2$ T-cells, or fewer than 5% $\delta 2$ T-cells. Alternatively, an engineered or non-engineered $\gamma\delta$ T-cell population can comprise greater than 5% $\delta 2$ T-cells, greater than 10% $\delta 2$ T-cells, greater than 20% $\delta 2$ T-cells, greater than 30% $\delta 2$ T-cells, greater

than 40% $\delta 2$ T-cells, greater than 50% $\delta 2$ T-cells, greater than 60% $\delta 2$ T-cells, greater than 70% $\delta 2$ T-cells, greater than 80% $\delta 2$ T-cells, or greater than 90% $\delta 2$ T-cells.

An engineered or non-engineered $\gamma\delta$ T-cell population can comprise, for example, fewer than 90% $\delta 1$ and $\delta 4$ T-cells, fewer than 80% $\delta 1$ and $\delta 4$ T-cells, fewer than 70% $\delta 1$ and $\delta 4$ T-cells, fewer than 60% $\delta 1$ and $\delta 4$ T-cells, fewer than 50% $\delta 1$ and $\delta 4$ T-cells, fewer than 40% $\delta 1$ and $\delta 4$ T-cells, fewer than 30% $\delta 1$ and $\delta 4$ T-cells, fewer than 20% $\delta 1$ and $\delta 4$ T-cells, fewer than 10% $\delta 1$ and $\delta 4$ T-cells, or fewer than 5% $\delta 1$ and $\delta 4$ T-cells. Alternatively, an engineered or non-engineered $\gamma\delta$ T-cell population can comprise greater than 5% $\delta 1$ and $\delta 4$ T-cells, greater than 10% $\delta 1$ and $\delta 4$ T-cells, greater than 20% $\delta 1$ and $\delta 4$ T-cells, greater than 30% $\delta 1$ and $\delta 4$ T-cells, greater than 40% $\delta 1$ and $\delta 4$ T-cells, greater than 50% $\delta 1$ and $\delta 4$ T-cells, greater than 60% $\delta 1$ and $\delta 4$ T-cells, greater than 70% $\delta 1$ and $\delta 4$ T-cells, greater than 80% $\delta 1$ and $\delta 4$ T-cells, or greater than 90% $\delta 1$ and $\delta 4$ T-cells.

An engineered or non-engineered $\gamma\delta$ T-cell population can comprise, for example, fewer than 90% $\delta 4$ T-cells, fewer than 80% $\delta 4$ T-cells, fewer than 70% $\delta 4$ T-cells, fewer than 60% $\delta 4$ T-cells, fewer than 50% $\delta 4$ T-cells, fewer than 40% $\delta 4$ T-cells, fewer than 30% $\delta 4$ T-cells, fewer than 20% $\delta 4$ T-cells, fewer than 10% $\delta 4$ T-cells, or fewer than 5% $\delta 4$ T-cells. Alternatively, an engineered or non-engineered $\gamma\delta$ T-cell population can comprise greater than 5% $\delta 1$ and $\delta 4$ T-cells, greater than 10% $\delta 1$ and $\delta 4$ T-cells, greater than 20% $\delta 1$ and $\delta 4$ T-cells, greater than 30% $\delta 1$ and $\delta 4$ T-cells, greater than 40% $\delta 1$ and $\delta 4$ T-cells, greater than 50% $\delta 1$ and $\delta 4$ T-cells, greater than 60% $\delta 1$ and $\delta 4$ T-cells, greater than 70% $\delta 1$ and $\delta 4$ T-cells, greater than 80% $\delta 1$ and $\delta 4$ T-cells, or greater than 90% $\delta 1$ and $\delta 4$ T-cells. An engineered or non-engineered $\gamma\delta$ T-cell population can comprise, for example, fewer than 90% $\delta 1$ and $\delta 4$ T-cells, fewer than 80% $\delta 1$ and $\delta 4$ T-cells, fewer than 70% $\delta 1$ and $\delta 4$ T-cells, fewer than 60% $\delta 1$ and $\delta 4$ T-cells, fewer than 50% $\delta 1$ and $\delta 4$ T-cells, fewer than 40% $\delta 1$ and $\delta 4$ T-cells, fewer than 30% $\delta 1$ and $\delta 4$ T-cells, fewer than 20% $\delta 1$ and $\delta 4$ T-cells, fewer than 10% $\delta 1$ and $\delta 4$ T-cells, or fewer than 5% $\delta 1$ and $\delta 4$ T-cells.

In certain embodiments, the present invention provides admixtures of expanded $\gamma\delta$ T-cell populations comprising 10-90% $\delta 3$ T-cells and 90-10% $\delta 2$ T-cells. In certain embodiments, the present invention provides admixtures of expanded $\gamma\delta$ T-cell populations comprising 10-90% $\delta 3$ T-cells and 90-10% $\delta 1$ T-cells. In certain embodiments, the present invention provides

admixture of expanded $\gamma\delta$ T-cell populations comprising 10-90% $\delta 1$ and $\delta 3$ T-cells and 90-10% $\delta 2$ T-cells. In certain embodiments, the present invention provides admixtures of expanded $\gamma\delta$ T-cell populations comprising 10-90% $\delta 3$ and $\delta 2$ T-cells and 90-10% $\delta 1$ T-cells. In certain embodiments, the present invention provides admixtures of expanded $\gamma\delta$ T-cell populations comprising 10-90% $\delta 1$, $\delta 3$, $\delta 4$ and $\delta 5$ T-cells and 90-10% $\delta 2$ T-cells.

One or more activation agent can contact the $\gamma\delta$ T cells (for example an activator that binds a receptor on the surface of a $\gamma\delta$ T cell, such as a $\gamma\delta$ TCR) and thereafter a costimulatory molecule can contact the $\gamma\delta$ T cells to provide further stimulation and to expand the $\gamma\delta$ T cells. In some embodiments, the activation agent and/or costimulatory agent can be lectins of plant or non-plant origin, monoclonal antibodies that activate $\gamma\delta$ T-cells, and other non-lectin/ non-antibody agents. In other cases, the plant lectin can be concanavalin A (ConA) although other plant lectins such as may be used. Other examples of lectins include protein peanut agglutinin (PNA), soybean agglutinin (SBA), les culinaris agglutinin (LCA), pisum sativum agglutinin (PSA), Helix pomatia agglutinin (HPA), Vicia graminea Lectin (VGA), Phaseolus Vulgaris Erythroagglutinin (PHA-E), Phaseolus Vulgaris Leucoagglutinin (PHA-L), Sambucus Nigra Lectin (SNA, EBL), Maackia Amurensis, Lectin II (MAL II), Sophora Japonica Agglutinin (SJA), Dolichos Biflorus Agglutinin (DBA), Lens Culinaris Agglutinin (LCA), and Wisteria Floribunda Lectin (WFA, WFL).

Non-limiting examples of activating agents and costimulatory molecules include any one or more antibodies selective for a δ or γ -chain or subtypes thereof described herein, antibodies such as 5A6.E9, B1, TS8.2, 15D, B6, B3, TS-1, $\gamma 3.20$, 7A5, IMMU510, R9.12, 11F2, or a combination thereof. Other examples of activating agents and costimulatory molecules include zoledronate, phorbol 12-myristate-13-acetate (TPA), mezerein, staphylococcal enterotoxin A (SEA), streptococcal protein A, or a combination thereof.

In other cases, the activation agent and/or costimulatory agent can be, antibodies or ligands to α TCR, β TCR, γ TCR, δ TCR, CD277, CD28, CD46, CD81, CTLA4, ICOS, PD-1, CD30, NKG2D, NKG2A, HVEM, 4-1 BB (CD137), OX40 (CD134), CD70, CD80, CD86, DAP, CD122, GITR, Fc ϵ RI γ , CD1, CD16, CD161, DNAX, accessory molecule-1 (DNAM-1), one or more NCRs (*e.g.*, NKp30, NKp44, NKp46), SLAM, Coxsackie virus and adenovirus receptor or a combination thereof.

Engineered $\gamma\delta$ T cells

Engineered $\gamma\delta$ T cells (*e.g.*, $\delta 3$ $\gamma\delta$ T cells) may be generated with various methods known in the art. An engineered $\gamma\delta$ T-cell may be designed to stably express a particular tumor recognition moiety. A polynucleotide encoding an expression cassette that comprises a tumor recognition, or another type of recognition moiety, can be stably introduced into the $\gamma\delta$ T-cell by a transposon/transposase system or a viral-based gene transfer system, such as a lentiviral or a retroviral system, or another suitable method, such as transfection, electroporation, transduction, lipofection, calcium phosphate (CaPO_4), nanoengineered substances, such as Ormosil, viral delivery methods, including adenoviruses, retroviruses, lentiviruses, adeno-associated viruses, or another suitable method. An antigen specific TCR, either $\alpha\beta$ or $\gamma\delta$, can be introduced into the engineered $\gamma\delta$ T-cell by stably inserting a polynucleotide comprising a genetic code for the antigen specific TCR into the genome of the $\gamma\delta$ T-cell. A polynucleotide encoding a CAR with a tumor recognition moiety may be introduced into the engineered $\gamma\delta$ T-cell by stably inserting the polynucleotide into the genome of the $\gamma\delta$ T-cell. In some cases, the engineered tumor recognition moiety is an engineered T-cell receptor, and the expression cassette incorporated into the genome of an engineered $\gamma\delta$ T-cell comprises a polynucleotide encoding an engineered TCR α (TCR alpha) gene, an engineered TCR β (TCR beta) gene, an TCR δ (TCR delta) gene, or an engineered TCR γ (TCR gamma) gene. In some cases, the expression cassette incorporated into the genome of the engineered $\gamma\delta$ T-cell comprises a polynucleotide encoding an antibody fragment or an antigen binding portion thereof. In some cases, the antibody fragment or antigen binding fragment thereof is a polynucleotide encoding a whole antibody, an antibody fragment, a single-chain variable fragment (scFv), a single domain antibody (sdAb), a Fab, F(ab)_2 , an Fc, the light or heavy chains on an antibody, the variable or the constant region of an antibody, or any combination thereof that binds to a cell surface tumor antigen as part of the Chimeric Antigen Receptor (CAR) construct, or a bi-specific construct, comprising a CAR and a T-cell receptor (TCR), or CARs with antibodies directed to different antigens. In some cases, the polynucleotide is derived from a human or from another species. An antibody fragment or antigen binding fragment polynucleotide that is derived from a non-human species can be modified to increase their similarity to antibody variants produced naturally in humans, and an antibody fragment or antigen binding fragment can be partially or fully humanized. An antibody fragment or antigen binding fragment polynucleotide can also be chimeric, for example a mouse-

human antibody chimera. An engineered $\gamma\delta$ T-cell that expresses a CAR can also be engineered to express a ligand to the antigen recognized by the tumor recognition moiety.

Various techniques known in the art can be used to introduce a cloned, or synthetically engineered, nucleic acid comprising the genetic code for a tumor recognition moiety into a specific location within the genome of an engineered $\gamma\delta$ T-cell. The RNA-guided Cas9 nuclease from the microbial clustered regularly interspaced short palindromic repeats (CRISPR) system, zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and meganuclease technologies, as described, respectively by WO201409370, WO2003087341, WO2014134412, and WO2011090804, each of which is incorporated by reference herein in its entirety, can be used to provide efficient genome engineering in $\gamma\delta$ T-cell(s). The technologies described herein can also be used to insert the expression cassette into a genomic location that simultaneously provides a knock-out of one gene and a knock-in of another gene. For example, a polynucleotide comprising an expression cassette of the disclosure can be inserted into a genomic region that encodes for an MHC gene. Such engineering can simultaneously provide the knock-in of one or more genes, e.g. the genes comprised in the expression cassette, and a knock-out of another gene, e.g. an MHC locus.

In one case, a Sleeping Beauty transposon that includes a nucleic acid coding for the tumor recognition moiety is introduced into the cell $\gamma\delta$ T-cell that is being engineered. A mutant Sleeping Beauty transposase that provides for enhanced integration as compared to the wild-type Sleeping Beauty, such as the transposase described in US 7,985,739, which is incorporated by reference herein in its entirety, may be used to introduce a polynucleotide in the engineered $\gamma\delta$ T-cell.

In some cases, a viral method is used to introduce a polynucleotide comprising a tumor recognition moiety into the genome of an engineered $\gamma\delta$ T-cell. A number of viral methods have been used for human gene therapy, such as the methods described in WO 1993020221, which is incorporated herein in its entirety. Non-limiting examples of viral methods that can be used to engineer a $\gamma\delta$ T-cell include retroviral, adenoviral, lentiviral, herpes simplex virus, vaccinia virus, pox virus, or adeno-virus associated viral methods.

A polynucleotide containing the genetic code for a tumor recognition moiety may comprise mutations or other transgenes that affect the growth, proliferation, activation status of the engineered $\gamma\delta$ T-cell or an antigen specific to tumor cells such as testis-specific cancer

antigens. A $\gamma\delta$ T-cell of the disclosure may be engineered to express a polynucleotide comprising an activation domain that is linked to the antigen recognition moiety, such as a molecule in TCR-CD3 complex or a co-stimulatory factor. An engineered $\gamma\delta$ T-cell can express an intracellular signaling domain that is a T-lymphocyte activation domain. The $\gamma\delta$ T-cell may be engineered to express an intracellular activation domain gene or an intracellular signaling domain. The intracellular signaling domain gene, may be, for example CD3 ζ , CD28, CD2, ICOS, JAML, CD27, CD30, OX40, NKG2D, CD4, OX40/CD134, 4-1BB/CD137, Fc ϵ RI γ , IL-2RB/CD 122, IL-2RG/CD132, DAP molecules, CD70, cytokine receptor, CD40, or any combination thereof. In some cases, the engineered $\gamma\delta$ T-cell is also engineered to express a cytokine, an antigen, a cellular receptor, or other immunomodulatory molecule.

The appropriate tumor recognition moiety to be expressed by the engineered $\gamma\delta$ T-cell can be selected based on the disease to be treated. For example, in some cases a tumor recognition moiety is a TCR. In some cases, a tumor recognition moiety is a receptor to a ligand that is expressed on a cancer cell. Non-limiting examples of suitable receptors include NKG2D, NKG2A, NKG2C, NKG2F, LIT1, AICL, CD26, NKRP1, CD244 (2B4), DNAM-1, NKp30, NKp44, NKp46, and NKp80. In some cases, a tumor recognition moiety can include a ligand, *e.g.* IL-13 ligand, or a ligand mimetic to the tumor antigen, such as the IL-13 mimetic to IL13R.

A $\gamma\delta$ T-cell may be engineered to express a chimeric tumor recognition moiety comprising a ligand binding domain derived from NKG2D, NKG2A, NKG2C, NKG2F, LIT1, AICL, CD26, NKRP1, CD244 (2B4), DNAM-1, or an anti-tumor antibody such as anti-Her2neu or anti-EGFR and a signaling domain obtained from CD3- ζ , Dap 10, Dap 12, CD28, 41BB, and CD40L. In some examples, the chimeric receptor binds MICA, MICB, Her2neu, EGFR, EGFRvIII, mesothelin, CD38, CD20, CD19, BCMA, PSA, RON, CD30, CD22, CD37, CD38, CD56, CD33, CD138, CD123, CD79b, CD70, CD75, CA6, GD2, alphafetoprotein (AFP), CS1, carcinoembryonic antigen (CEA), CEACAM5, CA-125, MUC-16, 5T4, NaPi2b, ROR1, ROR2, PLIF, Her2/Neu, EGFRvIII, GPMNB, LIV-1, glycolipidF77, fibroblast activation protein (FAP), PSMA, STEAP-1, STEAP-2, c-Met, CSPG4, CD44v6, PVRL-4, VEGFR2, C4.4a, PSCA, folate binding protein/receptor, SLC44A4, Cripto, CTAG1B, AXL, IL-13R α 2, IL-3R, EPHA3, SLTRK6, gp100, MART1, Tyrosinase, SSX2, SSX4, NYESO-1, epithelial tumor antigen (ETA), MAGEA family genes (such as MAGEA3, MAGEA4), KKLC1, mutated ras (H,

N, K), BRAf, p53, β catenin, EGFR T790, MHC class I chain-related molecule A (MICA), or MHC class I chain-related molecule B (MICB), or one or more antigens of HPV, CMV, or EBV.

In some cases, the tumor recognition moiety targets an MHC class I molecule (HLA-A, HLA-B, or HLA-C) in complex with a tumor-associated peptide. Methods and compositions for generating and using tumor recognition moieties that target a tumor-associated peptide in complex with a MHC class I molecule include those described in Weidanz *et al.*, Int. Rev. Immunol. 30:328-40, 2011; Scheinberg *et al.*, Oncotarget. 4(5):647-8, 2013; Cheever *et al.*, Clin. Cancer Res. 15(17):5323-37, 2009; Dohan & Reiter Expert Rev Mol Med. 14:e6, 2012; Dao *et al.*, Sci Transl Med. 2013 Mar 13;5(176):176ra33; U.S. 9,540,448; and WO 2017/011804. In some embodiments, the targeted tumor-associated peptide of the peptide MHC complex is a peptide of Wilms' tumor protein 1 (WT1), human telomerase reverse transcriptase (hTERT), survivin, mouse double minute 2 homolog (MDM2), cytochrome P450 (CYP1B), KRAS, or BRAF.

Two or more tumor recognition moieties may be expressed in the $\gamma\delta$ T-cell from genetically different, substantially different, or substantially identical, $\alpha\beta$ TCR polynucleotides stably expressed from the engineered $\gamma\delta$ T-cell or from genetically distinct $\alpha\beta$ TCR polynucleotides stably incorporated in the engineered $\gamma\delta$ T-cell. In the case of genetically distinct $\alpha\beta$ TCR(s), $\alpha\beta$ TCR(s) recognizing different antigens associated with the same condition may be utilized. In one preferred embodiment, a $\gamma\delta$ T-cell is engineered to express different TCRs, from human or mouse origin, from one or more expression cassettes that recognize the same antigen in the context of different MHC haplotypes. In another preferred embodiment, a $\gamma\delta$ T-cell is engineered to express one TCR and two or more antibodies directed to the same or different peptides from a given antigen complexed with different MHC haplotypes. In some cases, expression of a single TCR by an engineered $\gamma\delta$ T-cell facilitates proper TCR pairing. An engineered $\gamma\delta$ T-cell that expresses different TCRs can provide a universal allogeneic engineered $\gamma\delta$ T-cell. In a second preferred embodiment, a $\gamma\delta$ T-cell is engineered to express one or more different antibodies directed to peptide-MHC complexes, each directed to the same or different peptide complexed with the same or different MHC haplotypes. In some cases, a tumor recognition moiety can be an antibody that binds to peptide-MHC complexes.

A $\gamma\delta$ T-cell can be engineered to express TCRs from one or more expression cassettes that recognize the same antigen in the context of different MHC haplotypes. In some cases, an

engineered $\gamma\delta$ T-cell is designed to express a single TCR, or a TCR in combination with a CAR to minimize the likelihood of TCR mispairing within the engineered cell. The tumor recognition moieties expressed from two or more expression cassettes preferably have different polynucleotide sequences, and encode tumor recognition moieties that recognize different epitopes of the same target, *e.g.*, in the context of different HLA haplotypes. An engineered $\gamma\delta$ T-cell that expresses such different TCRs or CARs can provide a universal allogeneic engineered $\gamma\delta$ T-cell.

In some cases, a $\gamma\delta$ T-cell is engineered to express one or more tumor recognition moieties. Two or more tumor recognition moieties may be expressed from genetically identical, or substantially identical, antigen-specific chimeric (CAR) polynucleotides engineered in the $\gamma\delta$ T-cell. Two or more tumor recognition moieties may be expressed from genetically distinct CAR polynucleotides engineered in the $\gamma\delta$ T-cell. The genetically distinct CAR(s) may be designed to recognize different antigens associated with the same condition.

A $\gamma\delta$ T-cell may alternatively be bi-specific. A bi-specific engineered $\gamma\delta$ T-cell can express two or more tumor recognition moieties. A bi-specific engineered $\gamma\delta$ T-cell can express both TCR and CAR tumor recognition moieties. A bi-specific engineered $\gamma\delta$ T-cell can be designed to recognize different antigens associated with the same condition. An engineered $\gamma\delta$ T-cell can express two or more CAR/TCR(s) bi-specific polynucleotides that recognize an identical or substantially identical antigen. An engineered $\gamma\delta$ T-cell can express two or more CAR/TCR(s) bi-specific constructs that recognize distinct antigens. In some cases, a bi-specific construct of the disclosure binds to an activating and an inactivating domain of a target cell, thereby providing increased target specificity. The $\gamma\delta$ T-cell may be engineered to express at least 1 tumor recognition moiety, at least 2 tumor recognition moieties, at least 3 tumor recognition moieties, at least 4 tumor recognition moieties, at least 5 tumor recognition moieties, at least 6 tumor recognition moieties, at least 7 tumor recognition moieties, at least 8 tumor recognition moieties, at least 9 tumor recognition moieties, at least 10 tumor recognition moieties, at least 11 tumor recognition moieties, at least 12 tumor recognition moieties, or another suitable number of tumor recognition moieties.

Proper TCR function may be enhanced by two functioning ζ (zeta) proteins comprising ITAM motifs. Proper TCR function may also be enhanced by expression of $\alpha\beta$ or $\gamma\delta$ activation domains, such as CD3 ζ , CD28, CD2, CTLA4, ICOS, JAML, PD-1, CD27, CD30, 41-BB, OX40,

NKG2D, HVEM, CD46, CD4, FcεRIγ, IL-2RB/CD122, IL-2RG/CD132, DAP molecules, and CD70. The expressed polynucleotide may include the genetic code for a tumor recognition moiety, a linker moiety, and an activation domain. Translation of the polynucleotide by the engineered γδ T-cell may provide a tumor recognition moiety and an activation domain linked by a protein linker. Often, the linker comprises amino acids that do not obstruct the folding of the tumor recognition moiety and the activation domain. A linker molecule can be at least about 5 amino acids, about 6 amino acids, about 7 amino acids, about 8 amino acids, about 9 amino acids, about 10 amino acids, about 11 amino acids, about 12 amino acids, about 13 amino acids, about 14 amino acids, about 15 amino acids, about 16 amino acids, about 17 amino acids, about 18 amino acids, about 19 amino acids, or about 20 amino acids in length. In some cases, at least 50%, at least 70% or at least 90% of the amino acids in the linker are serine or glycine.

In some cases, an activation domain can comprise one or more mutations. Suitable mutations may be, for example, mutations that render an activation domain constitutively active. Altering the identity of one or more nucleic acids changes the amino acid sequence of the translated amino acid. A nucleic acid mutation can be made such that the encoded amino acid is modified to a polar, non-polar, basic or acidic amino acid. A nucleic acid mutation can be made such that the tumor recognition moiety is optimized to recognize an epitope from a tumor. The engineered tumor recognition moiety, an engineered activation domain, or another engineered component of a γδ T-cell may include more than 1 amino acid mutation, 2 amino acid mutations, 3 amino acid mutations, 4 amino acid mutations, 5 amino acid mutations, 6 amino acid mutations, 7 amino acid mutations, 8 amino acid mutations, 9 amino acid mutations, 10 amino acid mutations, 11 amino acid mutations, 12 amino acid mutations, 13 amino acid mutations, 14 amino acid mutations, 15 amino acid mutations, 16 amino acid mutations, 17 amino acid mutations, 18 amino acid mutations, 19 amino acid mutations, 20 amino acid mutations, 21 amino acid mutations, 22 amino acid mutations, 23 amino acid mutations, 24 amino acid mutations, 25 amino acid mutations, 26 amino acid mutations, 27 amino acid mutations, 28 amino acid mutations, 29 amino acid mutations, 30 amino acid mutations, 31 amino acid mutations, 32 amino acid mutations, 33 amino acid mutations, 34 amino acid mutations, 35 amino acid mutations, 36 amino acid mutations, 37 amino acid mutations, 38 amino acid mutations, 39 amino acid mutations, 40 amino acid mutations, 41 amino acid mutations, 42 amino acid mutations, 43 amino acid mutations, 44 amino acid mutations, 45 amino acid

mutations, 46 amino acid mutations, 47 amino acid mutations, 48 amino acid mutations, 49 amino acid mutations, or 50 amino acid mutations.

In some cases, a $\gamma\delta$ T-cell of the disclosure does not express one or more MHC molecules. Deletion of one or more MHC loci in an engineered $\gamma\delta$ T-cell can decrease the likelihood that the engineered $\gamma\delta$ T-cell will be recognized by the host immune system. The human Major Histocompatibility Complex (MHC) loci, known as the human leukocyte antigen (HLA) system, comprises a large gene family that is expressed in antigen presenting cells, including $\gamma\delta$ T-cells. The HLA-A, HLA-B, and HLA-C molecules function to present intracellular peptides as antigens to antigen presenting cells. The HLA-DP, HLA-DM, HLA-DOA, HLA-DOB, HLA-DQ, and HLA-DR molecules function to present extracellular peptides as antigens to antigen presenting cells. Some alleles of the HLA genes have been associated with GVHD, autoimmune disorders, and cancer. An engineered $\gamma\delta$ T-cell described herein can be further engineered to lack, or to disrupt gene expression of one or more HLA genes. An engineered $\gamma\delta$ T-cell described herein can be further engineered to lack, or to disrupt gene expression of one or more components of the MHC complex, such as complete deletion of one or more of the MHC genes, deletion of specific exons, or deletion of the β_2 microglobulin (B2m). Genetic excision or genetic disruption of at least one HLA gene can provides a clinically therapeutic $\gamma\delta$ T-cell that can be administered to a subject with any HLA haplotype without causing host-versus-graft disease. An engineered $\gamma\delta$ T-cell as described herein can be a universal donor for a human subject with any HLA haplotype.

A $\gamma\delta$ T-cell can be engineered to lack one or various HLA locus (loci). An engineered $\gamma\delta$ T-cell can be engineered to lack an HLA-A allele, an HLA-B allele, an HLA-C allele, an HLA-DR allele, an HLA-DQ allele, or an HLA-DP allele. In some cases, an HLA allele is associated with a human condition, such as an auto-immune condition. For instance, the HLA-B27 allele has been associated with arthritis and uveitis, the HLA-DR2 allele has been associated with systemic lupus erythematosus, and multiple sclerosis, the HLA-DR3 allele has been associated with 21-hydroxylase deficiency, the HLA-DR4 has been associated with rheumatoid arthritis and type 1 diabetes. An engineered $\gamma\delta$ T-cell that lacks, for example, the HLA-B27 allele can be administered to a subject afflicted with arthritis without being readily recognized the immune system of the subject. In some cases, deletion of one or more HLA loci provides an engineered $\gamma\delta$ T-cell that is a universal donor for any subject with any HLA haplotype.

In some cases, engineering a $\gamma\delta$ T-cell requires the deletion of a portion of the $\gamma\delta$ T-cell genome. In some cases, the deleted portion of the genome comprises a portion of the MHC locus (loci). In some instances, the engineered $\gamma\delta$ T-cell is derived from a wild-type human $\gamma\delta$ T-cell, and the MHC locus is an HLA locus. In some cases, the deleted a portion of the genome comprises a portion of a gene corresponding to a protein in the MHC complex. In some cases, the deleted portion of the genome comprises the $\beta 2$ microglobulin gene. In some instances, the deleted portion of the genome comprises an immune checkpoint gene, such as PD-1, CTLA-4, LAG3, ICOS, BTLA, KIR, TIM3, A2aR, B7-H3, B7-H4, and CECAM-1. In some cases, an engineered $\gamma\delta$ T-cell can be designed to express an activation domain that enhances T-cell activation and cytotoxicity. Non-limiting examples of activation domains that can be expressed by an engineered $\gamma\delta$ T-cell include: CD2, ICOS, 4-1 BB (CD137), OX40 (CD134), CD27, CD70, CD80, CD86, DAP molecules, CD122, GITR, Fc ϵ RI γ .

Any portion of the genome of an engineered $\gamma\delta$ T-cell can be deleted to disrupt the expression of an endogenous $\gamma\delta$ T-cell gene. Non-limiting examples of genomic regions that can be deleted or disrupted in the genome of an $\gamma\delta$ T-cell include a promoter, an activator, an enhancer, an exon, an intron, a non-coding RNA, a micro-RNA, a small-nuclear RNA, variable number tandem repeats (VNTRs), short tandem repeat (STRs), SNP patterns, hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, or simple sequence repeats. In some cases, the deleted a portion of the genome ranges between 1 nucleic acid to about 10 nucleic acids, 1 nucleic acid to about 100 nucleic acids, 1 nucleic acid to about 1,000 nucleic acids, 1 nucleic acid to about 10,000 nucleic acids, 1 nucleic acid to about 100,000 nucleic acids, 1 nucleic acid to about 1,000,000 nucleic acids, or other suitable range.

HLA gene expression in an engineered $\gamma\delta$ T-cell can also be disrupted with various techniques known in the art. In some cases, large loci gene editing technologies are used to excise a gene from the engineered $\gamma\delta$ T-cell genome, or to disrupt gene expression of at least one HLA locus in the engineered $\gamma\delta$ T-cell. Non-limiting examples of gene editing technologies that can be used to edit a desired locus on a genome of an engineered $\gamma\delta$ T-cell include Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-Cas, zinc finger nucleases (ZFNs), Transcription activator-like effector nucleases (TALENs), and meganuclease technologies, as described, respectively by WO201409370, WO2003087341, WO2014134412, and WO 2011090804, and each of which is incorporated by reference herein in its entirety.

A $\gamma\delta$ T-cell may be engineered from an isolated non-engineered $\gamma\delta$ T-cell that already expresses a tumor recognition moiety. The engineered $\gamma\delta$ T-cell can retain a tumor cell recognition moiety that is endogenously expressed by the isolated wild-type $\gamma\delta$ T-cell, *e.g.*, isolated from tumor infiltrating lymphocytes of a tumor sample. In some cases, the engineered $\gamma\delta$ T-cell tumor cell recognition moiety replaces the wild-type $\gamma\delta$ TCR.

A $\gamma\delta$ T-cell can be engineered to express one or more homing molecules, such as a lymphocyte homing molecule. Homing molecules can be, for instance, lymphocyte homing receptors or cell adhesion molecules. A homing molecule can help an engineered $\gamma\delta$ T-cell to migrate and infiltrate a solid tumor, including a targeted solid tumor upon administration of the engineered $\gamma\delta$ T-cell to the subject. Non-limiting examples of homing receptors include members of the CCR family, *e.g.* CCR2, CCR4, CCR7, CCR8, CCR9, CCR10, CLA, CD44, CD103, CD62L, E-selectin, P-selectin, L-selectin, integrins, such as VLA-4 and LFA-1. Non-limiting examples of cell adhesion molecules include ICAM, N-CAM, VCAM, PE-CAM, L1-CAM, Nectins (PVRL1, PVRL2, PVRL3), LFA-1, integrin $\alpha\text{X}\beta\text{2}$, $\alpha\text{h}\beta\text{7}$, macrophage-1 antigen, CLA-4, glycoprotein IIb/IIIa. Additional examples of cell adhesion molecules include calcium dependent molecules, such as T-cadherin, and antibodies to matrix metalloproteinases (MMPs) such as MMP9 or MMP2.

The steps involved in T-cell maturation, activation, proliferation, and function may be regulated through co-stimulatory and inhibitory signals through immune checkpoint proteins. Immune checkpoints are co-stimulatory and inhibitory elements intrinsic to the immune system. Immune checkpoints aid in maintaining self-tolerance and modulating the duration and amplitude of physiological immune responses to prevent injury to tissues when the immune system responds to disease conditions, such as cell transformation or infection. The equilibrium between the co-stimulatory and inhibitory signals used to control the immune response from either $\gamma\delta$ and $\alpha\beta$ T-cells can be modulated by immune checkpoint proteins. Immune checkpoint proteins, such as PD1 and CTLA4 are present on the surface of T-cells and can be used to turn an immune response “on” or “off.” Tumors can dysregulate checkpoint protein function as an immune-resistance mechanism, particularly against T-cells that are specific for tumor antigens. An engineered $\gamma\delta$ T-cell of the disclosure can be further engineered to lack one or more immune checkpoint locus (loci), such as PD-1, CTLA-4, LAG3, ICOS, BTLA, KIR, TIM3, A2aR, CEACAM1, B7-H3, and B7-H4. Alternatively, the expression of an endogenous immune check

point gene in an engineered $\gamma\delta$ T-cell of the disclosure can be disrupted with gene editing technologies.

Immunological checkpoints can be molecules that regulate inhibitory signaling pathways (exemplified by CTLA4, PD1, and LAG3) or molecules that regulate stimulatory signaling pathways (exemplified by ICOS) in an engineered $\gamma\delta$ T-cell of the disclosure. Several proteins in the extended immunoglobulin superfamily can be ligands for immunological checkpoints. Non-limiting examples of immune checkpoint ligand proteins include B7-H4, ICOSL, PD-L1, PD-L2, MegaCD40L, MegaOX40L, and CD137L. In some cases, immune checkpoint ligand proteins are antigens expressed by a tumor. In some cases, the immune checkpoint gene is a CTLA-4 gene. In some cases, the immune checkpoint gene is a PD-1 gene.

PD1 is an inhibitory receptor belonging to the CD28/CTLA4 family and is expressed on activated T lymphocytes, B cells, monocytes, DCs, and T-regs. There are two known ligands for PD1, PD-L1 and PD-L2, which are expressed on T cells, APCs, and malignant cells function to suppress self-reactive lymphocytes and to inhibit the effector function of TAA-specific cytotoxic T lymphocytes (CTLs). Accordingly, an engineered $\gamma\delta$ T-cell that lacks PD1 can retain its cytotoxic activity regardless of expression of PD-L1 and PD-L2 by tumor cells. In some cases, an engineered $\gamma\delta$ T-cell of the disclosure lacks the gene locus for the PD-1 gene. In some cases, expression of the PD-1 gene in an engineered $\gamma\delta$ T-cell is disrupted by gene editing technologies.

CTLA4 (cytotoxic T-lymphocyte antigen 4) is also known as CD152 (Cluster of differentiation 152). CTLA4 shares sequence homology and ligands (CD80/B7-1 and CD86/B7-2) with the costimulatory molecule CD28, but differs by delivering inhibitory signals to T-cells expressing CTLA4 as a receptor. CTLA4 has a much higher overall affinity for both ligands and can out-compete CD28 for binding when ligand densities are limiting. CTLA4 is often expressed on the surface of CD8⁺ effector T-cells, and plays a functional role in the initial activation stages of both naive and memory T-cells. CTLA4 counteracts the activity of CD28 via increased affinity for CD80 and CD86 during the early stages of T-cell activation. The major functions of CTLA4 include down-modulation of helper T-cells and enhancement of regulatory T-cell immunosuppressive activity. In some instances, an engineered $\gamma\delta$ T-cell of the disclosure lacks the CTLA4 gene. In some cases, expression of the CTLA4 gene in an engineered $\gamma\delta$ T-cell is disrupted by gene editing technologies.

LAG3 (Lymphocyte-activation gene 3) is expressed on activated antigen-specific cytotoxic T-cells, and can enhance the function of regulatory T-cells and independently inhibit CD8⁺ effector T-cell activity. LAG3 is a CD-4-like negative regulatory protein with a high affinity binding to MHC Class II proteins, which are upregulated on some epithelial cancers, leading to tolerance of T cell proliferation and homeostasis. Reduction of the LAG-3/Class II interaction using a LAG-3-IG fusion protein may enhance antitumor immune responses. In some cases, an engineered $\gamma\delta$ T-cell of the disclosure lacks the gene locus for the LAG3 gene. In some instances, expression of the LAG3 gene in an engineered $\gamma\delta$ T-cell is disrupted by gene editing technologies.

Phenotype of Non-Engineered and Engineered $\gamma\delta$ T-cells

An engineered $\gamma\delta$ T-cell may home to a specific physical location in a subject's body. Migration and homing of engineered $\gamma\delta$ T cells, can be dependent on the combined expression and actions of specific chemokines and/or adhesion molecules. Homing of engineered $\gamma\delta$ T cells can be controlled by the interactions between chemokines and their receptors. For example, cytokines including but not limited to CXCR3 (whose ligands are represented by IP-10/CXCL10 and 6CKine/SLC/CCL21) CCR4⁺ CXCR5⁺ (receptor for RANTES, MIP-1 α , MIP-1 β), CCR6⁺ and CCR7 may affect homing of engineered $\gamma\delta$ T cells. In some cases, an engineered $\gamma\delta$ T-cell may home to sites of inflammation and injury, and to diseased cells to perform repair functions. In some cases, an engineered $\gamma\delta$ T-cell can home to a cancer. In some cases, an engineered $\gamma\delta$ T-cell may home to a thymus, a bone marrow, a skin, a larynx, a trachea, pleurae, a lung, an esophagus, an abdomen, a stomach, a small intestine, a large intestine, a liver, a pancreas, a kidney, a urethra, a bladder, a testis, a prostate, a ductus deferens, an ovary, an ureter, a mammary gland, a parathyroid gland, a spleen or another site in a subject's body. An engineered $\gamma\delta$ T-cell can express one or more homing moieties, such as particular TCR allele and/or a lymphocyte homing molecule.

An engineered $\gamma\delta$ T-cell may have a particular phenotype and a phenotype can be described in terms of cell-surface marker expression. Various types of $\gamma\delta$ T-cells can be engineered as described herein. In preferred embodiments, the engineered $\gamma\delta$ T-cell is derived

from a human, but the engineered $\gamma\delta$ T-cell may also be derived from a different source, such as a mammal or a synthetic cell.

The immunophenotype of the expanded cell populations may be determined using markers including but not limited to CD27, CD45RA, CD45RO, CCR7 and CD62L (Klebanoff et al., Immunol Rev.211: 214 2006). CD45RA is expressed on naïve T lymphocytes, replaced by CD45RO upon antigen encounter, but re-expressed in late effector cells (Michie et al., Nature 360, 264 - 265 (1992); CD62L is a cell adhesion molecule that acts as a homing molecule to enter secondary lymphoid tissues and is lost after T-cell activation, when T-cells acquire effector functions (Sallusto et al., Nature. 401:708 (1999); CD27 is costimulation markers that are lost during T-cell differentiations (Appay et al., Nat Med.8:379 (2002); Klebanoff et al., Immunol Rev.211: 214 2006).

Antigens

The invention disclosed herein provides an engineered $\gamma\delta$ T-cell that expresses an antigen recognition moiety, wherein the antigen recognition moiety recognizes a disease-specific epitope. An antigen may be a molecule that provokes an immune response. This immune response may involve either antibody production, the activation of specific immunologically-competent cells, or both. An antigen may be, for example, a peptide, a protein, a hapten, a lipid, a carbohydrate, bacteria, a pathogen, or a virus. An antigen may be a tumor antigen. A tumor epitope may be presented by the MHC I or MHC II complexes on the surface of tumor cells. An epitope can be the portion of the antigen that is expressed on the cell surface and recognized by the tumor recognition moiety.

Non-limiting examples of antigens recognized by an engineered $\gamma\delta$ T-cell include CD19, CD20, CD30, CD22, CD37, CD38, CD56, CD33, CD138, CD123, CD79b, CD70, CD75, CA6, GD2, alphafetoprotein (AFP), carcinoembryonic antigen (CEA), RON, CEACAM5, CA-125, MUC-16, 5T4, NaPi2b, ROR1, ROR2, PLIF, Her2/Neu, EGFRvIII, GPMNB, LIV-1, glycolipidF77, fibroblast activation protein (FAP), PSMA, STEAP-1, STEAP-2, mesothelin, c-Met, CSPG4, PVRL-4, VEGFR2, PSCA, CLEC12a, L1CAM, GPC2, GPC3, folate binding protein/receptor, SLC44A4, Cripto, CTAG1B, AXL, IL-13R, IL-3R α 2, SLTRK6, gp100, MART1, Tyrosinase, SSX2, SSX4, NYESO-1, WT-1, PRAME, epithelial tumor antigen (ETA), MAGEA family genes (such as MAGEA3, MAGEA4), KKLC1, mutated

ras, Raf, p53, MHC class I chain-related molecule A (MICA), or MHC class I chain-related molecule B (MICB), or one or more antigens of HPV, CMV, or EBV.

An antigen can be expressed in the intracellular or the extracellular compartment of a cell and an engineered $\gamma\delta$ T-cell can recognize an intracellular or an extracellular tumor antigen. In some cases, an $\alpha\beta$ TCR in the engineered $\gamma\delta$ T-cell recognizes a peptide derived from either an intracellular or an extracellular tumor antigen. For example, an antigen may be a protein intracellularly or extracellularly produced by a cell infected with a virus, such as an HIV, an EBV, a CMV, or an HPV protein. An antigen may also be a protein intracellularly or extracellularly expressed by a cancerous cell.

An antigen recognition moiety may recognize an antigen from a cell in distress, such as a cancerous cell or a cell that has been infected with a virus. For instance, the human MHC class I chain-related genes (MICA and MICB) are located within the HLA class I region of chromosome 6. MICA and MICB proteins are considered to be markers of “stress” in the human epithelia, and act as ligands for cells expressing a common natural killer-cell receptor (NKG2D). As stress markers, MICA and MICB can be highly expressed from cancerous cells. An engineered $\gamma\delta$ T-cell can recognize a MICA or a MICB tumor epitope.

A tumor recognition moiety may be engineered to recognize an antigen with certain avidity. For instance, a tumor recognition moiety encoded by a TCR or CAR construct may recognize an antigen with a dissociation constant of at least at least 10 fM, at least 100 fM, at least 1 picomolar (pM), at least 10 pM, at least 20 pM, at least 30 pM, at least 40 pM, at least 50 pM, at least 60 pM, at least 70 pM, at least 80 pM, at least 90 pM, at least 100 pM, at least 200 pM, at least 300 pM, at least 400 pM, at least 500 pM, at least 600 pM, at least 700 pM, at least 800 pM, at least 900 pM, at least 1 nanomolar (nM), at least 2 nM, at least 3 nM, at least 4 nM, at least 5 nM, at least 6 nM, at least 7 nM, at least 8 nM, at least 9 nM, at least 10 nM, at least 20 nM, at least 30 nM, at least 40 nM, at least 50 nM, at least 60 nM, at least 70 nM, at least 80 nM, at least 90 nM, at least 100 nM, at least 200 nM, at least 300 nM, at least 400 nM, at least 500 nM, at least 600 nM, at least 700 nM, at least 800 nM, at least 900 nM, at least 1 μ M, at least 2 μ M, at least 3 μ M, at least 4 μ M, at least 5 μ M, at least 6 μ M, at least 7 μ M, at least 8 μ M, at least 9 μ M, at least 10 μ M, at least 20 μ M, at least 30 μ M, at least 40 μ M, at least 50 μ M, at least 60 μ M, at least 70 μ M, at least 80 μ M, at least 90 μ M, or at least 100 μ M.

In some instances, a tumor recognition moiety may be engineered to recognize an antigen with a dissociation constant of at most 10 fM, at most 100 fM, at most 1 picomolar (pM), at most 10 pM, at most 20 pM, at most 30 pM, at most 40 pM, at most 50 pM, at most 60 pM, at most 7 pM, at most 80 pM, at most 90 pM, at most 100 pM, at most 200 pM, at most 300 pM, at most 400 pM, at most 500 pM, at most 600 pM, at most 700 pM, at most 800 pM, at most 900 pM, at most 1 nanomolar (nM), at most 2 nM, at most 3 nM, at most 4 nM, at most 5 nM, at most 6 nM, at most 7 nM, at most 8 nM, at most 9 nM, at most 10 nM, at most 20 nM, at most 30 nM, at most 40 nM, at most 50 nM, at most 60 nM, at most 70 nM, at most 80 nM, at most 90 nM, at most 100 nM, at most 200 nM, at most 300 nM, at most 400 nM, at most 500 nM, at most 600 nM, at most 700 nM, at most 800 nM, at most 900 nM, at most 1 μ M, at most 2 μ M, at most 3 μ M, at most 4 μ M, at most 5 μ M, at most 6 μ M, at most 7 μ M, at most 8 μ M, at most 9 μ M, at most 10 μ M, at most 20 μ M, at most 30 μ M, at most 40 μ M, at most 50 μ M, at most 60 μ M, at most 70 μ M, at most 80 μ M, at most 90 μ M, or at most 100 μ M.

Novel Activating Agents

The inventors of the present invention have identified activation agents that bind specific subtypes of $\gamma\delta$ TCRs and thereby activate and expand specific populations of $\gamma\delta$ T cells. In one aspect, the invention provides novel activating agents which bind the novel activating epitopes identified and described herein in Examples 1 and 2, and **Fig. 1**. Activation agents include, but are not limited to MAbs $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58. In certain embodiments the activating agent (*e.g.*, antibody) expands and/or activates one or more $\gamma\delta$ T-cell populations (*e.g.*, $\delta 3$ T cells).

These activation agents further include, but are not limited to activation agents that bind the same epitope or compete with one or more MAbs selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58.

These activation agents further include, but are not limited to activation agents that contain the complementarity determining regions (CDRs) and/or variable regions of a MAb selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58.

The present invention also provides a nucleic acid encoding an activation agent that: (i) contains the complementarity determining regions (CDRs) and/or variable regions of; (ii) binds the same epitope as or competes with; or (iii) is a MAb selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58. In some cases, the nucleic acid is in a host cell

(*e.g.*, a heterologous host cell). In some cases, the nucleic acid is operably linked to a heterologous promoter or operably linked to a nucleic acid encoding a heterologous polypeptide. As used herein, the term “heterologous” refers to two components that do not naturally exist together in nature.

The present invention also provides methods of producing one or more of the foregoing activation agents. For example, a host cell containing a nucleic acid encoding an activation agent can be cultured to produce one or more of the foregoing activation agents.

APCs

Also described herein are APCs for expansion of engineered or non-engineered $\gamma\delta$ T-cells, such as one or more subpopulations of $\gamma\delta$ T-cells. In some embodiments, described herein is an APC that contains a heterologous nucleic acid encoding one or more of the foregoing activation agents. In some embodiments, described herein is an APC that expresses one or more of the foregoing activation agents on a cell surface. In some embodiments, described herein is an APC that expresses one or more Fc receptors on its cell surface, wherein the Fc receptor(s) are in contact with and/or bound to one or more of the foregoing activation agents.

In some cases, the APCs (*e.g.*, APCs having one or more of the foregoing activation agents expressed, on or bound to an Fc receptor expressed on, the cell surface) do not express, or exhibit reduced expression of, HLA class I, HLA class II, invariant chain, and/or HLA-DM. In some cases, the APCs express adhesion molecules such as intercellular adhesion molecule-1, CD11a, CD18, CD54, and/or leukocyte function-associated antigen-3. In some cases, the APCs express an Fc receptor, such as an Fc receptor that is specific for an isotype of an activation agent used in a $\gamma\delta$ T-cell expansion method described herein. In some cases, the APCs express one or more Fc receptors selected from the group consisting of CD64, CD32A, CD32B, CD32C, CD16A, CD16B, FcRn, TRIM21, or CD307, or an engineered variant thereof having a higher affinity or altered specificity.

Also described herein cultures comprising one or more of the foregoing APCs. The culture can further contain expanded or unexpanded, engineered or non-engineered, $\gamma\delta$ T-cells. The culture can additionally or alternatively contain a selective or non-selective $\gamma\delta$ T-cell activation agent including any one of the $\gamma\delta$ T-cell activation agents described herein. In some cases, the culture does not contain IL-21. In some cases, the culture does not contain IL-4, IL-2,

or IL-15, or a combination thereof. In some cases, the culture does not contain a cytokine that selectively expands a sub-population of $\gamma\delta$ T cells.

Epitope Identification

The inventors of the present invention have identified binding regions within the epitope of $\gamma\delta$ TCR activating MAbs $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58. Exemplary epitopes include, but are not limited to, the epitopes of $\gamma\delta$ TCR activating MAbs $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58. In some embodiments, the epitope is an epitope specifically bound by one or more of $\gamma\delta$ TCR activating MAbs $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58.

In one aspect, the disclosure provides a method for identifying the epitope of an agent that stimulates the expansion of engineered and non-engineered $\gamma\delta$ T-cells at a fast rate of growth. An epitope can include at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids in a unique spatial conformation. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids can be typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding can be typically lost on treatment with denaturing solvents.

Epitope mapping can be performed to identify the linear or non-linear, discontinuous amino acid sequence(s), i.e. the epitope, that is (e.g., specifically) recognized by an activating agent of interest, such as the $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58, antibodies. A general approach for epitope mapping can require the expression of the full-length polypeptide sequence that is recognized by an antibody or ligand of interest, as well as various fragments, i.e., truncated forms of the polypeptide sequence, generally in a heterologous expression system. These various recombinant polypeptide sequences or fragments thereof (e.g., fused with an N-terminal protein (e.g., GFP)) can then be used to determine if the antibody or ligand of interest is capable of binding to one or more of the truncated forms of the polypeptide sequence.

In some embodiments, the recombinant polypeptide sequences are chimeras containing joined fragments of two or more homologous parental polypeptides, wherein at least one parental polypeptide binds to the activating agent of interest and at least one parental polypeptide does not bind to the activating agent of interest. For example, segments of a human $\delta 3$ chain gene can be joined with segments of a homologous dolphin (or other non-human animal) δ chain gene,

and tested for the ability to generate a chimeric TCR in a recombinant expression system. As another segments of a human $\delta 3$ chain gene can be joined with segments of a different δ chain subtype. Chimeric TCR genes that form a TCR, as *e.g.*, indicated by detection with a pan- $\gamma\delta$ -TCR antibody on a cell surface, can then be tested for binding to the activation agent of interest.

Through the use of reiterative truncation and the generation of recombinant polypeptide sequences with overlapping amino acid regions, it is possible to identify the region of the polypeptide sequence that is recognized by the antibody of interest (see, *e.g.*, Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, Glenn E. Morris, Ed (1996)). The methods rely on the ability of an agent such as an antibody of interest to bind to sequences that have been recreated from epitope libraries, such as epitope libraries derived from, synthetic peptide arrays on membrane supports, combinatorial phage display peptide libraries. The epitope libraries then provide a range of possibilities that are screened against an antibody. Additionally, site specific mutagenesis, or random Ala scan, targeting one or more residues of an epitope can be pursued to confirm the identity of an epitope.

A library of epitopes can be created by synthetically designing various possible recombinations of a $\gamma\delta$ T-cell receptor ($\gamma\delta$ TCR) as cDNA constructs and expressing them in a suitable system. For instance, a plurality of V $\delta 3$ gene segments differing in their J δ region can be synthetically designed, including J $\delta 1$, J $\delta 2$ and J $\delta 3$ gene segments. Such, V $\delta 3$ J segments can, *e.g.*, be ordered as synthetic genes and cloned into suitable vectors. A plurality of synthetically cloned $\delta 3$ TCR chains, such as V $\delta 3$ J1, V $\delta 3$ J2, V $\delta 3$ J3, or V $\delta 3$ J4 chains can be co-transfected into a host system with synthetically cloned γ TCR chains such as V $\gamma 2$, V $\gamma 3$, V $\gamma 4$, V $\gamma 5$, V $\gamma 8$, V $\gamma 9$ and V $\gamma 10$ synthetically designed gene segments. In other cases, δ TCR chains, can be amplified out of Total RNA extracted from human PBMCs or $\gamma\delta$ T-cells isolated from human normal and malignant tissue.

The host system can be any suitable expression system such as 293 cells, insect cells, or a suitable in-vitro translation system. The plurality of various possible combinations of synthetically designed $\gamma\delta$ T-cell segments transfected into a host system can provide, for instance, more than 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, or 90 possible pairing combinations of $\gamma\delta$ TCRs. The binding of an agent to one of the epitopes in the previously described library can be detected by contacting a labeled antibody, such as $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58, with an epitope of the library and detecting a signal from the

label. Alternatively, the binding of the agent can be detected using a labeled secondary antibody such as an anti-mouse antibody.

For epitope mapping, computational algorithms have also been developed which have been shown to map conformational discontinuous epitopes. Conformational epitopes can be identified by determining spatial conformation of amino acids with methods that include, e.g., x-ray crystallography and 2-dimensional nuclear magnetic resonance. Some epitope mapping methods, such as, x-ray analyses of crystals of antigen:antibody complexes can provide atomic resolution of the epitope. In other cases, computational combinatorial methods for epitope mapping can be employed to model a potential epitope based on the sequence of the antibody, such as $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 or $\delta 3$ -58 antibody. In such cases, the antigen binding portion of the antibody is sequenced, and computation models are used to reconstruct and predict a potential binding site of the antibody.

In some cases the disclosure provides a method of determining an epitope of a $\gamma\delta$ T-cell receptor, comprising: (a) preparing a library of epitopes from the $\gamma\delta$ T-cell receptor; (b) contacting the library of epitopes with an antibody; and (c) identifying the amino acid sequence of at least one epitope in the library of epitopes that is bound by the antibody. In some cases, the antibody is selected from the group consisting of, $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58, antibodies. In one instance, the antibody is attached to a solid support. The library of epitopes can comprise sequences that correspond to continuous and discontinuous epitopes of a T-cell receptor, such as a γ TCR or a δ TCR. In some cases, the library of epitopes comprises fragments from a $\gamma\delta$ T-cell receptor ranging from about 10 amino acids to about 30 amino acids in length, from about 10 amino acids to about 20 amino acids in length, or from about 5 amino acids to about 12 amino acids in length. In some cases, the antibody is labeled and the label is a radioactive molecule, a luminescent molecule, a fluorescent molecule, an enzyme, or biotin.

$\delta 3$ Epitope Bins

In some embodiments, the activating agent of interest competes with the binding to $\gamma\delta 3$ TCR of one or more Bin 1A antibodies $\delta 3$ -23, $\delta 3$ -42, and/or $\delta 3$ -58. In some embodiments, the activating agent of interest competes with the binding to $\gamma\delta 3$ TCR of Bin 1B antibody $\delta 3$ -08. In some embodiments, the activating agent of interest competes with the binding to $\gamma\delta 3$ TCR of one or more Bin 1 (Bin1A and Bin1B) antibodies $\delta 3$ -23, $\delta 3$ -42, $\delta 3$ -58, and/or $\delta 3$ -08. In some

embodiments, the activating agent of interest competes with the binding to $\gamma\delta 3$ TCR of Bin 2 antibody $\delta 3$ -31.

Generally, the $\delta 3$ -specific antibodies described herein recognize a conformational epitope in the context of a $\gamma\delta$ -TCR. In some cases, the $\delta 3$ -specific antibodies described herein are specific for one or more pairs of $\gamma\delta 3$ -TCRs respectively. For example, in some cases, the $\delta 3$ -specific antibodies described herein are specific for a $\gamma\delta 3$ -TCR.

Methods of Treatment

Pharmaceutical compositions containing a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, as described herein may be administered for prophylactic and/or therapeutic treatments. In therapeutic applications, the compositions can be administered to a subject already suffering from a disease or condition in an amount sufficient to cure or at least partially arrest the symptoms of the disease or condition. A non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can also be administered to lessen a likelihood of developing, contracting, or worsening a condition. Effective amounts of a population of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, for therapeutic use can vary based on the severity and course of the disease or condition, previous therapy, the subject's health status, weight, and/or response to the drugs, and/or the judgment of the treating physician.

A non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and /or admixtures thereof, of the disclosure can be used to treat a subject in need of treatment for a condition. Examples of conditions include cancer, infectious disease, autoimmune disorder and sepsis. Subjects can be humans, non-human primates such as chimpanzees, and other apes and monkey species; farm animals such as cattle, horses, sheep, goats, swine; domestic animals such as rabbits, dogs, and cats; laboratory animals including rodents, such as rats, mice and guinea pigs, and the like. A subject can be of any age. Subjects can be, for example, elderly adults, adults, adolescents, pre-adolescents, children, toddlers, or infants.

A method of treating a condition (e.g., ailment) in a subject with an enriched $\gamma\delta$ T-cell population of the instant invention may comprise administering to the subject a therapeutically-effective amount of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$

T-cell population, and/or admixtures thereof. An enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be administered at various regimens (e.g., timing, concentration, dosage, spacing between treatment, and/or formulation). A subject can also be preconditioned with, for example, chemotherapy, radiation, or a combination of both, prior to receiving a an enriched $\gamma\delta$ T-cell population and/or admixtures thereof, of the disclosure. As part of a treatment, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, may be administered to a subject at a first regimen and the subject may be monitored to determine whether the treatment at the first regimen meets a given level of therapeutic efficacy. In some cases, the engineered $\gamma\delta$ T-cell or another engineered $\gamma\delta$ T-cell may be administered to the subject at a second regimen. **FIG. 2** schematically illustrates a method for treating a subject. In a first operation **201**, at least one engineered $\gamma\delta$ T-cell is administered to a subject that has or is suspected of having a given condition (e.g., cancer). The engineered $\gamma\delta$ T-cell may be administered at a first regimen. In a second operation **202**, the subject may be monitored, for example by a healthcare provider (e.g., treating physician or nurse). In some examples, the subject is monitored to determine or gauge an efficacy of the engineered $\gamma\delta$ T-cell in treating the condition of the subject. In some situations, the subject may also be monitored to determine the *in vivo* expansion of a $\gamma\delta$ T-cell population in the subject. Next, in a third operation **203**, at least one other engineered $\gamma\delta$ T-cell is administered to the subject at a second regimen. The second regimen may be the same as the first regimen or different than the first regimen. In some situations, the third operation **203** is not performed, for example, if the administration of the engineered $\gamma\delta$ T-cell in the first operation **201** is found to be effective (e.g., a single round of administration may be sufficient to treat the condition). Due to their allogeneic and universal donor characteristics, a population of engineered $\gamma\delta$ T-cells may be administered to various subjects, with different MHC haplotypes. An engineered $\gamma\delta$ T-cell may be frozen or cryopreserved prior to being administered to a subject.

A enriched population of $\gamma\delta$ T-cells (*i.e.*, engineered or non-engineered) and/or admixtures thereof, may also be frozen or cryopreserved prior to being administered to a subject. In certain embodiments, a population of engineered, enriched $\gamma\delta$ T-cells can comprise two or more cells that express identical, different, or a combination of identical and different tumor recognition moieties. For instance, a population of engineered, enriched $\gamma\delta$ T-cells can comprises several distinct engineered $\gamma\delta$ T-cells that are designed to recognize different antigens, or

different epitopes of the same antigen. For example, human cells afflicted with melanoma can express the NY-ESO-1 oncogene. Infected cells within the human can process the NY-ESO-1 oncoprotein into smaller fragments and present various portions of the NY-ESO-1 protein for antigen recognition. A population of engineered, enriched $\gamma\delta$ T-cells can comprise various engineered $\gamma\delta$ T-cells that express different tumor recognition moieties designed to recognize different portions of the NY-ESO-1 protein. **FIG. 3** schematically illustrates a method for treating a subject with a population of engineered $\gamma\delta$ T-cells that recognizes different epitopes of the melanoma antigen NY-ESO-1. In a first operation **301**, a population of engineered $\gamma\delta$ T-cells that recognize different epitopes of the same antigen is selected. For example, the population of engineered $\gamma\delta$ T-cells may comprise two or more cells that expressing different tumor recognition moieties that recognize different portions of the NY-ESO-1 protein. In a second operation **302**, The population of engineered $\gamma\delta$ T-cells may be administered at a first regimen. In a second operation **303**, the subject may be monitored, for example by a healthcare provider (e.g., treating physician or nurse).

An enriched $\gamma\delta$ T-cell population, *i.e.*, non-engineered or engineered, and/or admixtures thereof, of the disclosure may be used to treat various conditions. In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be used to treat a cancer, including solid tumors and hematologic malignancies. Non-limiting examples of cancers include: acute lymphoblastic leukemia, acute myeloid leukemia, adrenocortical carcinoma, AIDS-related cancers, AIDS-related lymphoma, anal cancer, appendix cancer, astrocytomas, neuroblastoma, basal cell carcinoma, bile duct cancer, bladder cancer, bone cancers, brain tumors, such as cerebellar astrocytoma, cerebral astrocytoma/malignant glioma, ependymoma, medulloblastoma, supratentorial primitive neuroectodermal tumors, visual pathway and hypothalamic glioma, breast cancer, bronchial adenomas, Burkitt lymphoma, carcinoma of unknown primary origin, central nervous system lymphoma, cerebellar astrocytoma, cervical cancer, childhood cancers, chronic lymphocytic leukemia, chronic myelogenous leukemia, chronic myeloproliferative disorders, colon cancer, cutaneous T-cell lymphoma, desmoplastic small round cell tumor, endometrial cancer, ependymoma, esophageal cancer, Ewing's sarcoma, germ cell tumors, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumor, gliomas, hairy cell leukemia, head and neck cancer, heart cancer, hepatocellular (liver)

cancer, Hodgkin lymphoma, Hypopharyngeal cancer, intraocular melanoma, islet cell carcinoma, Kaposi sarcoma, kidney cancer, laryngeal cancer, lip and oral cavity cancer, liposarcoma, liver cancer, lung cancers, such as non-small cell and small cell lung cancer, lymphomas, leukemias, macroglobulinemia, malignant fibrous histiocytoma of bone/osteosarcoma, medulloblastoma, melanomas, mesothelioma, metastatic squamous neck cancer with occult primary, mouth cancer, multiple endocrine neoplasia syndrome, myelodysplastic syndromes, myeloid leukemia, nasal cavity and paranasal sinus cancer, nasopharyngeal carcinoma, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, osteosarcoma/malignant fibrous histiocytoma of bone, ovarian cancer, ovarian epithelial cancer, ovarian germ cell tumor, pancreatic cancer, pancreatic cancer islet cell, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pineal astrocytoma, pineal germinoma, pituitary adenoma, pleuropulmonary blastoma, plasma cell neoplasia, primary central nervous system lymphoma, prostate cancer, rectal cancer, renal cell carcinoma, renal pelvis and ureter transitional cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcomas, skin cancers, skin carcinoma merkel cell, small intestine cancer, soft tissue sarcoma, squamous cell carcinoma, stomach cancer, T-cell lymphoma, throat cancer, thymoma, thymic carcinoma, thyroid cancer, trophoblastic tumor (gestational), cancers of unknown primary site, urethral cancer, uterine sarcoma, vaginal cancer, vulvar cancer, Waldenström macroglobulinemia, and Wilms tumor.

In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be used to treat an infectious disease. An infectious disease may be caused, for example, by a pathogenic bacterium or by a virus. Various pathogenic proteins, nucleic acids, lipids, or fragments thereof can be expressed by a diseased cell. An antigen presenting cell can internalize such pathogenic molecules, for instance with phagocytosis or by receptor-mediated endocytosis, and display a fragment of the antigen bound to an appropriate MHC molecule. For instance, various 9 mer fragments of a pathogenic protein may be displayed by an APC. Engineered, enriched $\gamma\delta$ T-cell populations of the disclosure may be designed to recognize various antigens and antigen fragments of a pathogenic bacterium or a virus. Non-limiting examples of pathogenic bacteria can be found in the: a) *Bordetella* genus, such as *Bordetella pertussis* species; b) *Borrelia* genus, such *Borrelia burgdorferi* species; c) *Brucella* genus, such as *Brucella abortus*, *Brucella canis*,

Brucella meliteris, and/or Brucella suis species; d) Campylobacter genus, such as Campylobacter jejuni species; e) Chlamydia and Chlamydophila genuses, such as Chlamydia pneumonia, Chlamydia trachomatis, and/or Chlamydophila psittaci species; f) Clostridium genus, such as Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Clostridium tetani species; g) Corynebacterium genus, such as Corynebacterium diphtheria species; h) Enterococcus genus, such as Enterococcus faecalis, and/or Enterococcus faecium species; i) Escherichia genus, such as Escherichia coli species; j) Francisella genus, such as Francisella tularensis species; k) Haemophilus genus, such as Haemophilus influenza species; l) Helicobacter genus, such as Helicobacter pylori species; m) Legionella genus, such as Legionella pneumophila species; n) Leptospira genus, such as Leptospira interrogans species; o) Listeria genus, such as Listeria monocytogenes species; p) Mycobacterium genus, such as Mycobacterium leprae, mycobacterium tuberculosis, and/or mycobacterium ulcerans species; q) Mycoplasma genus, such as Mycoplasma pneumonia species; r) Neisseria genus, such as Neisseria gonorrhoeae and/or Neisseria meningitidis species; s) Pseudomonas genus, such as Pseudomonas aeruginosa species; t) Rickettsia genus, such as Rickettsia rickettsii species; u) Salmonella genus, such as Salmonella typhi and/or Salmonella typhimurium species; v) Shigella genus, such as Shigella sonnei species; w) Staphylococcus genus, such as Staphylococcus aureus, Staphylococcus epidermidis, and/or Staphylococcus saprophyticus species; x) Streptococcus genus, such as Streptococcus agalactiae, Streptococcus pneumonia, and/or Streptococcus pyogenes species; y) Treponema genus, such as Treponema pallidum species; z) Vibrio genus, such as Vibrio cholera; and/or aa) Yersinia genus, such as Yersinia pestis species.

In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be used to treat an infectious disease, an infectious disease may be caused a virus. Non-limiting examples of viruses can be found in the following families of viruses and are illustrated with exemplary species: a) Adenoviridae family, such as Adenovirus species; b) Herpesviridae family, such as Herpes simplex type 1, Herpes simplex type 2, Varicella-zoster virus, Epstein-barr virus, Human cytomegalovirus, Human herpesvirus type 8 species; c) Papillomaviridae family, such as Human papillomavirus species; d) Polyomaviridae family, such as BK virus, JC virus species; e) Poxviridae family, such as Smallpox species; f) Hepadnaviridae family, such as Hepatitis B virus species; g) Parvoviridae family, such as Human bocavirus, Parvovirus B19 species; h)

Astroviridae family, such as Human astrovirus species; i) Caliciviridae family, such as Norwalk virus species; j) Flaviviridae family, such as Hepatitis C virus (HCV), yellow fever virus, dengue virus, West Nile virus species; k) Togaviridae family, such as Rubella virus species; l) Hepeviridae family, such as Hepatitis E virus species; m) Retroviridae family, such as Human immunodeficiency virus (HIV) species; n) Orthomyxoviridae family, such as Influenza virus species; o) Arenaviridae family, such as Guanarito virus, Junin virus, Lassa virus, Machupo virus, and/or Sabiá virus species; p) Bunyaviridae family, such as Crimean-Congo hemorrhagic fever virus species; q) Filoviridae family, such as Ebola virus and/or Marburg virus species; Paramyxoviridae family, such as Measles virus, Mumps virus, Parainfluenza virus, Respiratory syncytial virus, Human metapneumovirus, Hendra virus and/or Nipah virus species; r) Rhabdoviridae genus, such as Rabies virus species; s) Reoviridae family, such as Rotavirus, Orbivirus, Coltivirus and/or Borna disease virus species. In some examples, a virus is unassigned to a viral family, such as Hepatitis D.

In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be used to treat an immune disease, such as an autoimmune disease. Inflammatory diseases, including autoimmune diseases are also a class of diseases associated with B- cell disorders. Examples of immune diseases or conditions, including autoimmune conditions, include: rheumatoid arthritis, rheumatic fever, multiple sclerosis, experimental autoimmune encephalomyelitis, psoriasis, uveitis, diabetes mellitus, systemic lupus erythematosus (SLE), lupus nephritis, eczema, scleroderma, polymyositis/scleroderma, polymyositis/dermatomyositis, ulcerative proctitis, severe combined immunodeficiency (SCID), DiGeorge syndrome, ataxia-telangiectasia, seasonal allergies, perennial allergies, food allergies, anaphylaxis, mastocytosis, allergic rhinitis, atopic dermatitis, Parkinson's, Alzheimer's, hypersplenism, leukocyte adhesion deficiency, X-linked lymphoproliferative disease, X-linked agammaglobulinemia, selective immunoglobulin A deficiency, hyper IgM syndrome, HIV, autoimmune lymphoproliferative syndrome, Wiskott-Aldrich syndrome, chronic granulomatous disease, common variable immunodeficiency (CVID), hyperimmunoglobulin E syndrome, Hashimoto's thyroiditis, acute idiopathic thrombocytopenic purpura, chronic idiopathic thrombocytopenia purpura, dermatomyositis, Sydenham's chorea, myasthenia gravis, polyglandular syndromes, bullous pemphigoid, Henoch-Schonlein purpura, poststreptococcal nephritis, erythema nodosum, erythema multiforme, glomerulonephropathy,

Takayasu's arteritis, Addison's disease, sarcoidosis, ulcerative colitis, polyarteritis nodosa, ankylosing spondylitis, Goodpasture's syndrome, thromboangitis obliterans, Sjogren's syndrome, primary biliary cirrhosis, Hashimoto's thyroiditis, thyrotoxicosis, chronic active hepatitis, polychondritis, pemphigus vulgaris, Wegener's granulomatosis, membranous nephropathy, amyotrophic lateral sclerosis, tabes dorsalis, giant cell arteritis, polymyalgia, pernicious anemia, rapidly progressive glomerulonephritis, psoriasis, fibrosing alveolitis, and cancer.

Treatment with a $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure may be provided to the subject before, during, and after the clinical onset of the condition. Treatment may be provided to the subject after 1 day, 1 week, 6 months, 12 months, or 2 years after clinical onset of the disease. Treatment may be provided to the subject for more than 1 day, 1 week, 1 month, 6 months, 12 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more after clinical onset of disease. Treatment may be provided to the subject for less than 1 day, 1 week, 1 month, 6 months, 12 months, or 2 years after clinical onset of the disease. Treatment may also include treating a human in a clinical trial. A treatment can comprise administering to a subject a pharmaceutical composition comprising a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixture thereof, of the disclosure.

In some cases, administration of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixture thereof, of the disclosure to a subject modulates the activity of endogenous lymphocytes in a subject's body. In some cases, administration of the non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, to a subject provides an antigen to an endogenous T-cell and may boost an immune response. In some cases, the memory T-cell is a $CD4^+$ T-cell. In some cases, the memory T-cell is a $CD8^+$ T-cell. In some cases, administration of the non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, to a subject activates the cytotoxicity of another immune cell. In some cases, the other immune cell is a $CD8^+$ T-cell. In some cases, the other immune cell is a Natural Killer T-cell. In some cases, administration of the non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, to a subject suppress a regulatory T-cell. In some cases, the regulatory T-cell is a $Fox3^+$ Treg cell. In some cases, the regulatory T-cell is a $Fox3^-$ Treg cell. Non-limiting examples of cells whose activity can be

modulated by a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure include: hematopoietic stem cells; B cells; CD4; CD8; red blood cells; white blood cells; dendritic cells, including dendritic antigen presenting cells; leukocytes; macrophages; memory B cells; memory T-cells; monocytes; natural killer cells; neutrophil granulocytes; T-helper cells; and T-killer cells.

During most bone marrow transplants, a combination of cyclophosphamide with total body irradiation is conventionally employed to prevent rejection of the hematopoietic stem cells (HSC) in the transplant by the subject's immune system. In some cases, incubation of donor bone marrow with interleukin-2 (IL-2) *ex vivo* is performed to enhance the generation of killer lymphocytes in the donor marrow. Interleukin-2 (IL-2) is a cytokine that is necessary for the growth, proliferation, and differentiation of wild-type lymphocytes. Current studies of the adoptive transfer of $\gamma\delta$ T-cells into humans may require the co-administration of $\gamma\delta$ T-cells and interleukin-2. However, both low- and high- dosages of IL-2 can have highly toxic side effects. IL-2 toxicity can manifest in multiple organs/systems, most significantly the heart, lungs, kidneys, and central nervous system. In some cases, the disclosure provides a method for administering a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, to a subject without the co-administration of a cytokine, such as IL-2, IL-15, IL-12, or IL-21. In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be administered to a subject without co-administration with IL-2. In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, is administered to a subject during a procedure, such as a bone marrow transplant without the co-administration of IL-2.

Methods of Administration

One or multiple non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be administered to a subject in any order or simultaneously. If simultaneously, the multiple non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be provided in a single, unified form, such as an intravenous injection, or in multiple forms, for example, as multiple intravenous infusions, s.c. injections or pills. The non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or

admixtures thereof, of the invention can be packed together or separately, in a single package or in a plurality of packages. One or all of the non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be given in multiple doses. If not simultaneous, the timing between the multiple doses may vary to as much as about a week, a month, two months, three months, four months, five months, six months, or about a year. In some cases, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can expand within a subject's body, *in vivo*, after administration to a subject. Non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be frozen to provide cells for multiple treatments with the same cell preparation. Non-engineered, enriched $\gamma\delta$ T-cell population, engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure, and pharmaceutical compositions comprising the same, can be packaged as a kit. A kit may include instructions (e.g., written instructions) on the use of the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, and compositions comprising the same.

In some cases, a method of treating a cancer comprises administering to a subject a therapeutically-effective amount of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, wherein the administration treats the cancer. In some embodiments the therapeutically-effective amount of the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, is administered for at least about 10 seconds, 30 seconds, 1 minute, 10 minutes, 30 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 12 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, or 1 year. In some embodiments the therapeutically-effective amount of the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, is administered for at least one week. In some embodiments the therapeutically-effective amount of the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, is administered for at least two weeks.

A non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, described herein can be administered before, during, or

after the occurrence of a disease or condition, and the timing of administering a pharmaceutical composition containing a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can vary. For example, the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be used as a prophylactic and can be administered continuously to subjects with a propensity to conditions or diseases in order to lessen a likelihood of the occurrence of the disease or condition. The non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be administered to a subject during or as soon as possible after the onset of the symptoms. The administration of the non-engineered, enriched $\gamma\delta$ T-cell population, the engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be initiated immediately within the onset of symptoms, within the first 3 hours of the onset of the symptoms, within the first 6 hours of the onset of the symptoms, within the first 24 hours of the onset of the symptoms, within 48 hours of the onset of the symptoms, or within any period of time from the onset of symptoms. The initial administration can be via any route practical, such as by any route described herein using any formulation described herein. In some examples, the administration of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the disclosure is an intravenous administration. One or multiple dosages of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be administered as soon as is practicable after the onset of a cancer, an infectious disease, an immune disease, sepsis, or with a bone marrow transplant, and for a length of time necessary for the treatment of the immune disease, such as, for example, from about 24 hours to about 48 hours, from about 48 hours to about 1 week, from about 1 week to about 2 weeks, from about 2 weeks to about 1 month, from about 1 month to about 3 months. For the treatment of cancer, one or multiple dosages of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be administered years after onset of the cancer and before or after other treatments. In some examples, a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, can be administered for at least about 10 minutes, 30 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 12 hours, 24 hours, at least 48 hours, at least 72 hours, at least 96 hours, at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 1 month, at least 2 months, at least 3

months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months, at least 10 months, at least 11 months, at least 12 months, at least 1 year, at least 2 years at least 3 years, at least 4 years, or at least 5 years. The length of treatment can vary for each subject.

Dosages

A non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, as disclosed herein may be formulated in unit dosage forms suitable for single administration of precise dosages. In some cases, the unit dosage forms comprise additional lymphocytes. In unit dosage form, the formulation is divided into unit doses containing appropriate quantities of one or more compounds. The unit dosage can be in the form of a package containing discrete quantities of the formulation. Non-limiting examples are packaged tablets or capsules, and powders in vials or ampoules. Aqueous suspension compositions can be packaged in single-dose non-reclosable containers. Multiple-dose reclosable containers can be used, for example, in combination with a preservative or without a preservative. In some examples, the pharmaceutical composition does not comprise a preservative. Formulations for parenteral injection can be presented in unit dosage form, for example, in ampoules, or in multi-dose containers with a preservative.

A non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, as described herein may be present in a composition in an amount of at least 5 cells, at least 10 cells, at least 20 cells, at least 30 cells, at least 40 cells, at least 50 cells, at least 60 cells, at least 70 cells, at least 80 cells, at least 90 cells, at least 100 cells, at least 200 cells, at least 300 cells, at least 400 cells, at least 500 cells, at least 600 cells, at least 700 cells, at least 800 cells, at least 900 cells, at least 1×10^3 cells, at least 2×10^3 cells, at least 3×10^3 cells, at least 4×10^3 cells, at least 5×10^3 cells, at least 6×10^3 cells, at least 7×10^3 cells, at least 8×10^3 cells, at least 9×10^3 cells, at least 1×10^4 cells, at least 2×10^4 cells, at least 3×10^4 cells, at least 4×10^4 cells, at least 5×10^4 cells, at least 6×10^4 cells, at least 7×10^4 cells, at least 8×10^4 cells, at least 9×10^4 cells, at least 1×10^5 cells, at least 2×10^5 cells, at least 3×10^5 cells, at least 4×10^5 cells, at least 5×10^5 cells, at least 6×10^5 cells, at least 7×10^5 cells, at least 8×10^5 cells, at least 9×10^5 cells, at least 1×10^6 cells, at least 2×10^6 cells, at least 3×10^6 cells, at least 4×10^6 cells, at least 5×10^6 cells, at least 6×10^6 cells, at least 7×10^6 cells, at least 8×10^6 cells, at least 9×10^6 cells, at least 1×10^7 cells, at least 2×10^7 cells,

at least 3×10^7 cells, at least 4×10^7 cells, at least 5×10^7 cells, at least 6×10^7 cells, at least 7×10^7 cells, at least 8×10^7 cells, at least 9×10^7 cells, at least 1×10^8 cells, at least 2×10^8 cells, at least 3×10^8 cells, at least 4×10^8 cells, at least 5×10^8 cells, at least 6×10^8 cells, at least 7×10^8 cells, at least 8×10^8 cells, at least 9×10^8 cells, at least 1×10^9 cells, or more.

The therapeutically effective dose of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be from about 1 cell to about 10 cells, from about 1 cell to about 100 cells, from about 1 cell to about 10 cells, from about 1 cell to about 20 cells, from about 1 cell to about 30 cells, from about 1 cell to about 40 cells, from about 1 cell to about 50 cells, from about 1 cell to about 60 cells, from about 1 cell to about 70 cells, from about 1 cell to about 80 cells, from about 1 cell to about 90 cells, from about 1 cell to about 100 cells, from about 1 cell to about 1×10^3 cells, from about 1 cell to about 2×10^3 cells, from about 1 cell to about 3×10^3 cells, from about 1 cell to about 4×10^3 cells, from about 1 cell to about 5×10^3 cells, from about 1 cell to about 6×10^3 cells, from about 1 cell to about 7×10^3 cells, from about 1 cell to about 8×10^3 cells, from about 1 cell to about 9×10^3 cells, from about 1 cell to about 1×10^4 cells, from about 1 cell to about 2×10^4 cells, from about 1 cell to about 3×10^4 cells, from about 1 cell to about 4×10^4 cells, from about 1 cell to about 5×10^4 cells, from about 1 cell to about 6×10^4 cells, from about 1 cell to about 7×10^4 cells, from about 1 cell to about 8×10^4 cells, from about 1 cell to about 9×10^4 cells, from about 1 cell to about 1×10^5 cells, from about 1 cell to about 2×10^5 cells, from about 1 cell to about 3×10^5 cells, from about 1 cell to about 4×10^5 cells, from about 1 cell to about 5×10^5 cells, from about 1 cell to about 6×10^5 cells, from about 1 cell to about 7×10^5 cells, from about 1 cell to about 8×10^5 cells, from about 1 cell to about 9×10^5 cells, from about 1 cell to about 1×10^6 cells, from about 1 cell to about 2×10^6 cells, from about 1 cell to about 3×10^6 cells, from about 1 cell to about 4×10^6 cells, from about 1 cell to about 5×10^6 cells, from about 1 cell to about 6×10^6 cells, from about 1 cell to about 7×10^6 cells, from about 1 cell to about 8×10^6 cells, from about 1 cell to about 9×10^6 cells, from about 1 cell to about 1×10^7 cells, from about 1 cell to about 2×10^7 cells, from about 1 cell to about 3×10^7 cells, from about 1 cell to about 4×10^7 cells, from about 1 cell to about 5×10^7 cells, from about 1 cell to about 6×10^7 cells, from about 1 cell to about 7×10^7 cells, from about 1 cell to about 8×10^7 cells, from about 1 cell to about 9×10^7 cells, from about 1 cell to about 1×10^8 cells, from about 1 cell to about 2×10^8 cells, from about 1 cell to about 3×10^8 cells, from about 1 cell to about 4×10^8

cells, from about 1 cell to about 5×10^8 cells, from about 1 cell to about 6×10^8 cells, from about 1 cell to about 7×10^8 cells, from about 1 cell to about 8×10^8 cells, from about 1 cell to about 9×10^8 cells, or from about 1 cell to about 1×10^9 cells.

In some cases, the therapeutically effective dose of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be from about 1×10^3 cells to about 2×10^3 cells, from about 1×10^3 cells to about 3×10^3 cells, from about 1×10^3 cells to about 4×10^3 cells, from about 1×10^3 cells to about 5×10^3 cells, from about 1×10^3 cells to about 6×10^3 cells, from about 1×10^3 cells to about 7×10^3 cells, from about 1×10^3 cells to about 8×10^3 cells, from about 1×10^3 cells to about 9×10^3 cells, from about 1×10^3 cells to about 1×10^4 cells, from about 1×10^3 cells to about 2×10^4 cells, from about 1×10^3 cells to about 3×10^4 cells, from about 1×10^3 cells to about 4×10^4 cells, from about 1×10^3 cells to about 5×10^4 cells, from about 1×10^3 cells to about 6×10^4 cells, from about 1×10^3 cells to about 7×10^4 cells, from about 1×10^3 cells to about 8×10^4 cells, from about 1×10^3 cells to about 9×10^4 cells, from about 1×10^3 cells to about 1×10^5 cells, from about 1×10^3 cells to about 2×10^5 cells, from about 1×10^3 cells to about 3×10^5 cells, from about 1×10^3 cells to about 4×10^5 cells, from about 1×10^3 cells to about 5×10^5 cells, from about 1×10^3 cells to about 6×10^5 cells, from about 1×10^3 cells to about 7×10^5 cells, from about 1×10^3 cells to about 8×10^5 cells, from about 1×10^3 cells to about 9×10^5 cells, from about 1×10^3 cells to about 1×10^6 cells, from about 1×10^3 cells to about 2×10^6 cells, from about 1×10^3 cells to about 3×10^6 cells, from about 1×10^3 cells to about 4×10^6 cells, from about 1×10^3 cells to about 5×10^6 cells, from about 1×10^3 cells to about 6×10^6 cells, from about 1×10^3 cells to about 7×10^6 cells, from about 1×10^3 cells to about 8×10^6 cells, from about 1×10^3 cells to about 9×10^6 cells, from about 1×10^3 cells to about 1×10^7 cells, from about 1×10^3 cells to about 2×10^7 cells, from about 1×10^3 cells to about 3×10^7 cells, from about 1×10^3 cells to about 4×10^7 cells, from about 1×10^3 cells to about 5×10^7 cells, from about 1×10^3 cells to about 6×10^7 cells, from about 1×10^3 cells to about 7×10^7 cells, from about 1×10^3 cells to about 8×10^7 cells, from about 1×10^3 cells to about 9×10^7 cells, from about 1×10^3 cells to about 1×10^8 cells, from about 1×10^3 cells to about 2×10^8 cells, from about 1×10^3 cells to about 3×10^8 cells, from about 1×10^3 cells to about 4×10^8 cells, from about 1×10^3 cells to about 5×10^8 cells, from about 1×10^3 cells to about 6×10^8 cells, from about 1×10^3 cells to about 7×10^8 cells, from about 1×10^3 cells to about 8×10^8

cells, from about 1×10^3 cells to about 9×10^8 cells, or from about 1×10^3 cells to about 1×10^9 cells.

In some cases, the therapeutically effective dose of a non-engineered, enriched $\gamma\delta$ T-cell population, an engineered, enriched $\gamma\delta$ T-cell population, and/or admixtures thereof, of the invention can be from about 1×10^6 cells to about 2×10^6 cells, from about 1×10^6 cells to about 3×10^6 cells, from about 1×10^6 cells to about 4×10^6 cells, from about 1×10^6 cells to about 5×10^6 cells, from about 1×10^6 cells to about 6×10^6 cells, from about 1×10^6 cells to about 7×10^6 cells, from about 1×10^6 cells to about 8×10^6 cells, from about 1×10^6 cells to about 9×10^6 cells, from about 1×10^6 cells to about 1×10^7 cells, from about 1×10^6 cells to about 2×10^7 cells, from about 1×10^6 cells to about 3×10^7 cells, from about 1×10^6 cells to about 4×10^7 cells, from about 1×10^6 cells to about 5×10^7 cells, from about 1×10^6 cells to about 6×10^7 cells, from about 1×10^6 cells to about 7×10^7 cells, from about 1×10^6 cells to about 8×10^7 cells, from about 1×10^6 cells to about 9×10^7 cells, from about 1×10^6 cells to about 1×10^8 cells, from about 1×10^6 cells to about 2×10^8 cells, from about 1×10^6 cells to about 3×10^8 cells, from about 1×10^6 cells to about 4×10^8 cells, from about 1×10^6 cells to about 5×10^8 cells, from about 1×10^6 cells to about 6×10^8 cells, from about 1×10^6 cells to about 7×10^8 cells, from about 1×10^6 cells to about 8×10^8 cells, from about 1×10^6 cells to about 9×10^8 cells, from about 1×10^6 cells to about 1×10^9 cells, from about 1×10^6 cells to about 2×10^9 cells, from about 1×10^6 cells to about 3×10^9 cells, from about 1×10^6 cells to about 4×10^9 cells, from about 1×10^6 cells to about 5×10^9 cells, from about 1×10^6 cells to about 6×10^9 cells, from about 1×10^6 cells to about 7×10^9 cells, from about 1×10^6 cells to about 8×10^9 cells, from about 1×10^6 cells to about 9×10^9 cells, from about 1×10^7 cells to about 1×10^9 cells, from about 1×10^7 cells to about 2×10^9 cells, from about 1×10^7 cells to about 3×10^9 cells, from about 1×10^7 cells to about 4×10^9 cells, from about 1×10^7 cells to about 5×10^9 cells, from about 1×10^7 cells to about 6×10^9 cells, from about 1×10^7 cells to about 7×10^9 cells, from about 1×10^7 cells to about 8×10^9 cells, from about 1×10^7 cells to about 9×10^9 cells, from about 1×10^8 cells to about 1×10^9 cells, from about 1×10^8 cells to about 2×10^9 cells, from about 1×10^8 cells to about 3×10^9 cells, from about 1×10^8 cells to about 4×10^9 cells, from about 1×10^8 cells to about 5×10^9 cells, from about 1×10^8 cells to about 6×10^9 cells, from about 1×10^8 cells to about 7×10^9 cells, from about 1×10^8 cells to about 8×10^9 cells,

cells, from about 1×10^8 cells to about 9×10^9 cells, or from about 1×10^9 cells to about 1×10^{10} cells.

Preservation

In some embodiments, enriched $\gamma\delta$ T cell populations, and/or admixtures thereof, may be formulated in freezing media and placed in cryogenic storage units such as liquid nitrogen freezers (-195°C) or ultra-low temperature freezers (-65°C , -80°C or -120°C) for long-term storage of at least about 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, 2 years, 3 years, or at least 5 years. The freeze media can contain dimethyl sulfoxide (DMSO), and/or sodium chloride (NaCl), and/or dextrose, and/or dextran sulfate and/or hydroxyethyl starch (HES) with physiological pH buffering agents to maintain pH between about 6.0 to about 6.5, about 6.5 to about 7.0, about 7.0 to about 7.5, about 7.5 to about 8.0 or about 6.5 to about 7.5. The cryopreserved $\gamma\delta$ T cells can be thawed and further processed by stimulation with antibodies, proteins, peptides, and/or cytokines as described herein. The cryopreserved $\gamma\delta$ T cells can be thawed and genetically modified with viral vectors (including retroviral and lentiviral vectors) or non-viral means (including RNA, DNA, and proteins) as described herein. Alternatively, non-engineered $\gamma\delta$ T cells can be expanded by the methods described herein, genetically modified, and cryopreserved.

Thus, genetically engineered and/or non-engineered $\gamma\delta$ T cells can be further cryopreserved to generate cell banks in quantities of at least about 1, 5, 10, 100, 150, 200, 500 vials at about at least 10^1 , 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , or at least about 10^{10} cells per mL in freeze media. The cryopreserved cell banks may retain their functionality and can be thawed and further stimulated and expanded. In some aspects, thawed cells can be stimulated and expanded in suitable closed vessels such as cell culture bags and/or bioreactors to generate quantities of cells as allogeneic cell product. Cryopreserved $\gamma\delta$ T cells can maintain their biological functions for at least about 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 15 months, 18 months, 20 months, 24 months, 30 months, 36 months, 40 months, 50 months, or at least about 60 months under cryogenic storage condition. In some aspects, no preservatives are used in the formulation. The cryopreserved $\gamma\delta$ T cells can be thawed and infused into multiple patients as allogeneic off-the-shelf cell product.

All publications and patents mentioned herein are incorporated herein by reference in their entirety for the purpose of describing and disclosing, for example, the constructs and

methodologies that are described in the publications, which might be used in connection with the presently described inventions. The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors described herein are not entitled to antedate such disclosure by virtue of prior invention or for any other reason.

The present invention is explained in more detail by the following non-limiting examples.

EXAMPLES

Example 1. Generation of Antibodies that Specifically Bind $\delta 3$ TCR

$\gamma\delta$ TCR activators in the form of murine antibodies were produced by immunization of recombinant human soluble $\gamma 2\delta 3$ TCR- FC, comprising the mature ECD of the $\gamma\delta$ TCR chains fused to human IgG1FC. Three strains of mice (Balb/c, CD-1 and FVB) were inoculated with human recombinant $\gamma\delta$ TCR to provide hybridomas secreting high affinity, murine monoclonal antibody activators.

The $\gamma\delta$ TCR-Fc fusion construct was generated by PCR amplification. $\gamma 2\delta 3$ TCR chains were amplified from RNA isolated from tumor infiltrating $\gamma\delta$ lymphocytes extracted from a fresh specimen of malignant ovary cells from a metastasis to the omentum. Soluble $\delta 3$ TCR-FC was purified from the supernatant of transiently transfected HEK 293 cells. 10 μ g of soluble TCR was emulsified with an equal volume of TITERMAX® Gold (Sigma Aldrich) or Imject Alum Adjuvant (Thermo Fisher) and used for the immunization of each mouse. The resulting emulsions were then injected into three mice (1 each: Balb/c, CD-1 and FVB) via the footpad route.

Solid-phase ELISA assays were used to screen mouse sera for mouse IgG antibodies specific for human $\gamma\delta 3$ TCR. Briefly, 96 well plates (VWR International, Cat. #610744) were coated with recombinant $\gamma\delta 3$ TCR- at 1 μ g/ml in ELISA coating buffer overnight. After washing with PBS containing 0.02% (v/v) Tween 20, the wells were blocked with 3% (w/v) BSA in PBS, 200 μ L/well for 1 hour at room temperature (RT). Mouse serum was titrated (1:100, 1:200, 1:400, and 1:800) and added to the $\gamma\delta$ TCR coated plates at 50 μ L/well and incubated at RT for 1 hour. The plates are washed and then incubated with 50 μ L/well HRP-labeled goat anti-mouse IgG diluted 1:10,000 in 3% BSA-PBS or 2% FCS in PBS for 1 hour at RT. Again the plates were washed and 40 μ L/well of a TMB substrate solution (Thermo Scientific 34028) was added

for 15 minutes at RT. After developing, an equal volume of 2N H₂SO₄ was added to stop substrate development and the plates were analyzed by spectrophotometer at OD 450.

Sera-positive immunized mice were sacrificed and draining lymph nodes (popliteal and inguinal) were dissected out and used as a source for antibody producing cells. A single cell suspension of B cells (766×10⁶ cells) was fused with non-secreting P3×63Ag8.653 myeloma cells (ATCC #CRL-1580) at a ratio of 1:1 by electrofusion. Electrofusion was performed using the BTX Hybrimmune™ System, (BTX Harvard Apparatus) as per the manufacturer's directions. After the fusion, the cells were resuspended in hybridoma selection medium supplemented with Azaserine (Sigma #A9666), high glucose DMEM medium with sodium pyruvate (Cellgro cat#15-017-CM) containing 15% Fetal Clone I serum (Hyclone), 10% BM Condimed (Roche Applied Sciences), 4 mM L-glutamine, 100 IU Penicillin-Streptomycin and 50 μM 2-mercaptoethanol and then plated in three T150 flasks in 50 mL selection medium per flask. The flasks were then placed in a humidified 37 °C. incubator containing 5% CO₂ and 95% air for 6-7 days.

After six days of growth the library consisting of the cells grown in bulk in the T150 flask was plated at 1 cell per well in Falcon 384 well flat-bottom plates using the Aria II cell sorter. The selected hybridomas were then grown in 90 μL of culture medium containing 15% Fetal Clone I serum (Hyclone), 10% BM-Condimed (Roche Applied Sciences), 1 mM sodium pyruvate, 4 mM L-glutamine, 100 IU Penicillin-Streptomycin, 50 μM 2-mercaptoethanol, and 100 μM hypoxanthine. Any remaining unused hybridoma library cells were frozen for future library testing. After ten days of growth supernatants from each well of the plated cells were assayed for antibodies reactive for δ3 TCR by ELISA.

High bond ELISA 96 well plates were coated with soluble γδ TCR proteins generated by panning the following γδ TCR chains: γ8δ1, γ2δ1, and γ2δ3. Soluble TCRs were diluted and used at 1 μg/ml in sodium carbonate buffer overnight at 4 °C. The plates were washed and blocked with 3% BSA in PBS/Tween for one hour at 37 °C. and used immediately or kept at 4 °C. Undiluted hybridoma supernatants were incubated on the plates for one hour at RT. The plates were washed and probed with HRP labeled goat anti-mouse IgG diluted 1:10,000 in 3% BSA-PBS for one hour at RT. The plates were then incubated with substrate solution as described above and read at OD 450. Wells containing immunoglobulin that preferentially bound human δ3 TCR chain as determined by a signal above background, were transferred and expanded.

The resulting $\delta 3$ TCR specific clonal hybridomas were cryopreserved in CS-10 freezing medium (Biolife Solutions) and stored in liquid nitrogen

Example 2. Sequencing of Murine Antibodies that Specifically Bind $\delta 3$ TCR

Based on ELISA binding assays a number of exemplary distinct monoclonal antibodies that specifically bind to $\delta 3$ soluble TCR were selected for sequencing and further analysis. As shown in a tabular fashion in **Fig. 1**, sequence analysis of the light chain variable regions (FIG.) and heavy chain variable regions (FIG.) of selected monoclonal antibodies generated in Example 1 confirmed novel complementarity determining regions and display of novel VDJ arrangements. The complementarity determining regions set forth in **Fig. 1** as defined by Kabat.

Total RNA was extracted from selected hybridoma cells using the RNeasy isolation kit (RNeasy Mini Kit Qiagen # 74106). 10^4 hybridoma cells were lysed in 350 μ L RLT Buffer, an equal volume of 70% ethanol was added, and the sample was loaded to RNeasy Mini spin column. Column was washed twice and RNA was eluted by 100 μ L of RNase-free water loaded directly to the spin column membrane. The quality of the RNA preparations was determined by fractionating 3 μ L in a 1% agarose gel before being stored at -80°C . until used.

The variable region of the Ig heavy chain of each hybridoma was amplified using a 5' primer mix comprising thirty-two mouse specific leader sequence primers, designed to target the complete mouse VH repertoire, in combination with a 3' mouse C γ primer specific for all mouse Ig isotypes. A 400 bp PCR fragment of the VH was sequenced from both ends using the same PCR primers. Similarly, a mix of thirty-two 5' V κ leader sequence primers designed to amplify each of the V κ mouse families combined with a single reverse primer specific to the mouse kappa constant region were used to amplify and sequence the kappa light chain. The VH and VL transcripts were amplified from 100 ng total RNA using reverse transcriptase polymerase chain reaction (RT-PCR).

A total of eight RT-PCR reactions were run for each hybridoma: four for the V κ light chain and four for the V γ heavy chain. The One Step OneStep Ahead RT-PCR kit was used for amplification (Qiagen # 220213). This kit provides a blend of Sensiscript and Omniscript Reverse Transcriptases, QuantiNova HotStarTaq DNA Polymerase, dNTP mix, buffer and Q-Solution, a novel additive that enables efficient amplification of any RNA template. Reaction mixtures were prepared that included 5 μ L of RNA, 0.5 of 100 μ M of either heavy chain or kappa light chain primers (custom synthesized by IDT), 12.5 μ L of master mix with DNA

polymerases, buffer, dNTPs, 1 μ L of enzyme mix containing reverse transcriptase and DNA polymerase, and 0.4 μ L of ribonuclease inhibitor RNasin (1 unit). The reaction mixture contains all of the reagents required for both reverse transcription and PCR. The thermal cycler program was set for an RT step 50 °C. for 10 minutes, 95 °C. for 5 minutes, followed by 30 cycles of PCR (95 °C. for 30 seconds, 58 °C. for 30 seconds, 72 °C. for one minute). There was then a final incubation at 72 °C. for 10 minutes.

To prepare the PCR products for direct DNA sequencing, they were purified using the QIAquick™ PCR Purification Kit (Qiagen) according to the manufacturer's protocol. The DNA was eluted from the spin column using 50 μ L of sterile water and then sequenced directly from both strands. The extracted PCR products were directly sequenced using specific V region primers. Nucleotide sequences were analyzed using VBase2 to identify germline V, D and J gene members with the highest sequence homology.

Annotated sequences are set forth in **Fig. 1**. More specifically, **Fig. 1 (top)** depicts the contiguous amino acid sequences of 7 novel murine heavy chain variable regions from $\delta 3$ TCR specific antibodies, and **Fig. 1 (bottom)** depicts the contiguous amino acid sequences of the corresponding light chain variable regions from the $\delta 3$ TCR specific antibodies

Taken together **Fig. 1** provides the annotated sequences of seven murine anti $\delta 3$ TCR antibodies (termed $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47 and $\delta 3$ -58).

Example 3. $\gamma\delta$ T cell Expansion with $\delta 3$ -specific Antibodies

24-well plates (Corning) were coated with 300 μ L of goat anti-mouse IgG antibodies at 5 μ g/mL overnight. The next day wells were washed once with PBS and blocked with 5% FBS in PBS for 1h at 37 °C. V $\delta 3$ antibodies were prepared at 1 μ g/mL in PBS containing 2% FBS. 300 μ L of antibody solution was dispensed into each well and incubated for 2 h at room temperature for capture.

Human PBMCs from healthy individuals were plated into wells with captured V $\delta 3$ antibodies at 1×10^6 /mL/well in RPMI-1640 media containing 10% FBS, 2mM Glutamine, 100 IU/mL of rhIL-2 and supplemented with antibiotics. Cells in culture were fed every 2-3 days by media replenishment. On Day 7 cells were harvested and re-plated at 1×10^6 /mL into new plates without activating antibodies and further expanded by feeding every 2-3 days. Cells were re-plated on Day 14 to 1×10^6 /mL cell density. Cell analysis (counts and flow cytometry) was performed on Day 21 to determine purity and fold expansion of non-V $\delta 1$ (as determined with R9

Vd1 specific antibody, Beckman-Coulter) and non-Vδ2 (as determined with B6 Vd2 specific antibody, BioLegend) cells. **Fig. 4A-B** shows fold expansion of non-Vδ1/non-Vδ2 cells in PBMC cultures of two donors. Vδ3 specific antibodies induced expansion of up to 8531 fold (donor 1) and up to 6621 fold (donor 2) depending on Vδ3 antibody.

Purity of non-Vδ1/non-Vδ2 cells in the expanded cultures on Day 21 is shown in **Fig 5A-B** for the two donors. Up to 41% of the cell culture on Day 21 was comprised of non-Vδ1/non-Vδ2 γδ T cells for Donor 1 PBMCs expanded with the δ3-23 antibody.

Phenotype of expanded δ1⁺/δ2⁺ T cells on Day 21 was evaluated by CD27 and CD45 surface marker expression. **Fig. 6A-B** shows that phenotype of δ1⁺/δ2⁺ T-cells activated with of MAbs on Day 21 is predominantly (>50%) CD27⁺CD45RA⁺ (naïve) and CD27⁺CD45RA⁻ (central memory).

Example 4. Epitope grouping of Vδ3 antibodies by competition binding to γ2δ3TCR-hFc

Selected Vδ3 antibodies were grouped into epitope bins based on paired competition patterns using ForteBio Octet instrument and anti-human Fc AHC biosensors (ForteBio, Pall Corporation, Fremont, CA). Briefly, γ2δ3TCR- hFc recombinant protein and all Vδ3 antibodies were diluted to 5 μg/mL in HBS-PB buffer (10 mM HEPES, 150 mM NaCl, 0.005% Tween-20, pH 7.4) containing 20 μg/mL of BSA. All samples (300 μl) were arranged in the 96-well plate and competition experiment was performed using Octet 384 instrument as per manufacturer's suggestion. First, the γ2δ3TCR- hFc was captured on anti-human Fc biosensors for 5 minutes. Then, pairs of Vδ3 antibodies were allowed to bind to γ2δ3TCR-hFc to saturation in succession (10 min each association phase) to determine if pairs of antibodies compete for binding sites on γ2δ3TCR- hFc. If the second antibody did not bind, the two antibodies were considered to be in the same epitope bin and recognize the same, very similar, or largely overlapping, epitopes. ForteBio HT9.0 data analysis tool was applied to determine competition between Vδ3 antibodies.

The competition pattern of five anti-Vδ3 antibodies is presented in **Fig. 7**. The tested anti-Vδ3 antibodies were grouped into 3 epitope bins. δ3-23, δ3-42 and δ3-58 were all found to compete with each other in a paired binding assay and constitute one epitope bin designated 1A. δ3-31 did not compete with any of the antibodies tested that placed it into a separate Bin 2. δ3-08 antibody, did not compete with δ3-31 antibody, but appeared to be displaced by δ3-23, δ3-42 and

$\delta 3$ -58, suggesting that $\delta 3$ -08 antibody likely has an overlapping epitope but $\delta 3$ -08 affinity may be lower. Epitope of $\delta 3$ -08 is designated Bin 1B.

Example 5. Activation, Transduction, and Selective Expansion of V $\delta 3$ $\gamma\delta$ T cells

12-well plates (Corning, CellBIND®) were directly coated overnight with purified $\delta 3$ -08 or $\delta 3$ -23 antibodies at 1 $\mu\text{g/mL}$ in PBS at 600 $\mu\text{L/well}$, 4°C. The next day wells were washed with PBS and PBMCs (2×10^6 total cells) from two donors (Donor 3 and Donor 4) were added for activation at 1×10^6 cells/mL in RPMI-1640 media supplemented with 10% FBS, 2mM Glutamine, 100 IU/mL of rhIL-2 (Peprotech). Starting PBMCs were characterized by flow cytometry for the content of V $\delta 1$, V $\delta 2$, and the non-V $\delta 1$ /V $\delta 2$ $\gamma\delta$ T (DN, double negative) fraction containing the V $\delta 3$ cells. The non-V $\delta 1$ /V $\delta 2$ $\gamma\delta$ T cells content was $<0.5\%$ of total cells. Cell cultures were fed with fresh media supplemented with rhIL-2 by demi-exchange on day 2 and day 4.

On day 5, cells were washed in HBSS and transduced with retroviral construct encoding an anti-CD20 (Rituxan) chimeric antigen receptor ACT2 (scFv linked to CD28 transmembrane, co-stimulatory domains and CD3 ζ). Briefly, wells of 12-well non-tissue culture treated plates were pre-coated with Retronectin® (TaKaRa Bio) at 10 $\mu\text{g/mL}$ and 2×10^6 activated PBMCs were added to the wells (per donor, per activating antibody) followed by appropriate volume of viral supernatant to achieve MOI=1. Total volume of media was brought to 2 mL to achieve a cell concentration of 1×10^6 cells/mL and rhIL-2 was supplemented to 100 IU/mL. A portion of cells were not transduced but had undergone the same manipulation as CAR transduced cells (untransduced, mock transduction).

The next day cells were transferred to a 6-well plate for expansion and maintained for additional 11 days by feeding every other day by media demi-exchange. At the end of the expansion, cells were harvested, washed and analyzed by flow cytometry for V $\delta 3$ fold expansion, purity, and CAR expression (**Fig. 8 A-C**). Briefly, cells were stained with antibodies to TCR $\alpha\beta$ (Clone IP26), anti-TCR $\gamma\delta$ (Immuno510, Beckman Coulter), anti-V $\delta 2$ (B6, Biolegend), anti-V $\delta 1$ (R9.12, Beckman Coulter), anti-CD16 and anti-CD56 (both BioLegend) and analyzed on BD FACS Canto II. To determine anti-CD20 CAR transduction efficiency, cells were stained with rat anti-Rituximab-FITC conjugate (BioRad, **Fig. 8C**). Data were analyzed using FlowJo software. $\alpha\beta$ T cells in the culture were depleted using $\alpha\beta$ T cell depletion kit (Miltenyi Biotec) using a manual procedure with LS columns. Purity and CAR expression after $\alpha\beta$ T cell depletion

were confirmed by flow cytometry and cells were used for cytotoxicity assay. The percentage of residual $\alpha\beta$ T cells was $< 1\%$ in all samples; and, the purity of V $\delta 3$ cells was $> 70\%$ depending on donor and antibody used for V $\delta 3$ cell expansion (**Fig. 9**).

Untransduced cells from Donor 4 expanded using both $\delta 3$ -08 and $\delta 3$ -23 MAbs were depleted of residual $\alpha\beta$ T cells and stained with $\delta 3$ -23 MAb as well as other T cell markers (TCR $\alpha\beta$, anti-V $\delta 1$, anti-V $\delta 2$). As shown in **Fig. 10**, majority of cells after $\alpha\beta$ T cell depletion ($\geq 90\%$) are non-V $\delta 1$ /non-V $\delta 2$ cells (left panels), of which $\geq 95\%$ are stained positive for V $\delta 3$ with $\delta 3$ -23 MAb (right panels).

Example 6. Cytotoxicity Assay with Engineered V $\delta 3$ $\gamma\delta$ T cells

Human PBMCs from Donor 3 were activated and transduced with CD20 CAR construct using $\delta 3$ -08 and $\delta 3$ -23 MAbs as described in Example 5. As described in Example 5, at the end of the expansion, cells were characterized for purity and transduction efficiency, and depleted of $\alpha\beta$ T cells. The $\alpha\beta$ T cell depleted cultures were then used in cytotoxicity assays against CD20+ Raji-NucLight Red cells. CD20+ Raji-NucLight Red cells have been transduced with IncuCyte® NucLight Red lentiviral particles allowing fluorescent detection of Raji cells on IncuCyte® platform.

CD20 CAR-transduced or untransduced V $\delta 3$ cells were co-incubated with Raji-NucLight Red cells at various E/T ratios for 6 hours in 384 well plates in RPMI-1640 media supplemented with 10% FBS, 2mM Glutamine. Raji-NucLight Red cell viability was assessed as total fluorescence quantified from the entire well at 6 hour time point. As shown in **Fig. 11**, both anti-CD20 CAR transduced and untransduced V $\delta 3$ cells expanded from Donor 3 using $\delta 3$ -08 (A) or $\delta 3$ -23 (B) MAbs exhibited cytotoxicity against CD20+ Raji-NucLight Red cells. Transduced V $\delta 3$ cells significantly augmented cytotoxicity against CD20+ Raji-NucLight Red cells as compared to untransduced expanded V $\delta 3$ cells.

Example 7. Fine Epitope Mapping of anti-V $\delta 3$ Antibodies by Mutagenesis

To determine amino acid residues in the variable V $\delta 3$ region of the human $\gamma\delta$ TCR that are critical for binding of V $\delta 3$ antibodies, several point mutations, or combination of thereof, were introduced into the $\delta 3$ chain and MAb binding was assessed using Luminex. Briefly, a computer model of V $\delta 3$ V $\gamma 9$ dimer molecule was created using crystal structures of V $\delta 2$ V $\gamma 9$ TCR deposited in PDB (Accession NOs 1HXM and 1TVD). Substitutions were introduced into the wild type sequence of the V $\delta 3$ chain based on potential immunogenicity as shown in Table 1. Residue numbering of V $\delta 3$ amino acids is as shown in **Fig. 12**. The mutated V $\delta 3$ chains indicated in Table 1 were co-expressed with V $\gamma 2$ chain as human-Fc heterodimer fusion proteins

in 293 Expi cells as described in Example 1 and purified using affinity chromatography on Protein A. Mutant and wt $\delta\gamma 2$ -hFc proteins were captured on Luminex® beads conjugated with goat-anti-human Fc polyclonal antibodies and EC₅₀ binding of various V $\delta 3$ antibodies was determined. Loss or drop in EC₅₀ binding to a particular mutant $\delta\gamma 2$ -TCR fusion was monitored to determine contribution of the mutated amino acid to antigen binding. Without wishing to be bound by theory, it is hypothesized that the residues exhibiting a decrease in binding upon mutation are in contact with the $\delta 3$ -specific antibody when bound to a V $\delta 3$ $\gamma\delta$ TCR.

Table 1:

Mutations in V $\delta 3$ chain	Mutant Sequence ##	V $\delta 3$ MAb (EC ₅₀ , nM)				
		$\delta 3$ -08	$\delta 3$ -23	$\delta 3$ -31	$\delta 3$ -42	$\delta 3$ -58
Wild type $\gamma\delta 3$	WT	0.06	0.04	0.05	0.05	0.03
D10N	S1	0.08	0.04	0.06	0.07	0.02
D26N, K85L	S2	0.07	0.04	0.05	0.17	0.03
K79L, H88F	S3	0.05	137.10*	0.05	105.70*	508.30*
E18Q	S4	0.06	0.06	0.05	0.05	0.02
D70N, E67Q	S5	0.05	0.04	4.99	0.08	0.02
R75Q, R95Q	S6	0.06	0.04	44.35*	0.13	0.02
D57N, R65Q	S7	0.07	0.04	0.05	0.15	0.04
K79L, E18Q, H88F	S8	0.04	95.78*	0.06	258.00*	3366.00*
E67Q, D70N, R75Q, R95Q, E97Q	S9	0.07	0.05	37.66*	49.29*	0.05
K3A, K79L, H88T	S10	2.50	117.00*	0.08	449.00*	336.00*
K79L, L82K, H88F	S11	0.03	112.30*	0.06	198.70*	135.70*

* - extrapolated values; no saturation achieved

Close grouping of selected residues indicated to contribute to antigen binding by the fine epitope mapping described herein is illustrated in **Fig. 13** and **Figs. 14A-C**, suggesting that the $\delta 3$ -specific epitopes recognized by the antibodies described herein can be at least partially, or entirely, conformational and/or non-linear. As indicated by **Fig. 13**, $\delta 3$ -specific $\gamma\delta$ TCR binding antibodies can bind an epitope that of V $\delta 3$ that is distal from the γ -chain binding interface of V $\delta 3$.

As shown in Table 1 and **Figs. 13-14C**, the $\delta 3$ -specific antibodies can be grouped into 2 major epitope binding groups, where $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58 form the first group and $\delta 3$ -

31 forms the second group. The first major group can be separated into two sub-groups with $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58 forming sub-group 1A and $\delta 3$ -08 forming sub-group 1B. These results are in good agreement with the competition binding data illustrated in **Fig. 7**. However, in addition to highlighting specific residues involved in antigen binding, the fine mapping uncovers a third grouping formed by antibodies $\delta 3$ -31 and $\delta 3$ -42, which both show a reduction in binding to an E67Q, D70N, R75Q, R95Q, E97Q mutant V $\delta 3$ $\gamma\delta$ TCR.

Figs. 14A-C also highlight β sheet strands D and E (IMGT nomenclature) as hot spots for antigen binding of $\delta 3$ -specific antibodies. Thus, in some cases, $\delta 3$ -specific antibodies can include those that bind a residue in β sheet strands D and E of V $\delta 3$ (IMGT nomenclature); those that additionally or alternatively, bind a residue in β sheet strand C'' and D and a residue in the loop between β strands E and F of V $\delta 3$ of V $\delta 3$ (IMGT nomenclature); and/or those that bind a residue in β sheet strand A, B, D, and E of V $\delta 3$ (IMGT nomenclature).

At the amino acid level, it is hypothesized that some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues K79 and H88 of V $\delta 3$ (IMGT nomenclature). Additionally, or alternatively, some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues R75 and R95 of V $\delta 3$ (IMGT nomenclature). Additionally, or alternatively, some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues K79, E18, and H88 of V $\delta 3$ (IMGT nomenclature). Additionally, or alternatively, some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues E67, D70, R75, R95, and E97 of V $\delta 3$ (IMGT nomenclature). Additionally, or alternatively, some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues K3, K79, and H88 of V $\delta 3$ (IMGT nomenclature). Additionally, or alternatively, some $\delta 3$ $\gamma\delta$ TCR specific antibodies bind to residues K79, L82, and H88 of V $\delta 3$ (IMGT nomenclature).

CLAIMS

What is claimed is:

1. An antibody or fragment thereof that binds an epitope specific to a $\delta 3$ $\gamma\delta$ TCR.
2. The antibody or fragment thereof of claim 1, wherein the antibody or fragment thereof binds essentially the same epitope as:
 - a) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - b) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - c) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;
 - d) an antibody selected from the group consisting of $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;
 - e) an antibody selected from the group consisting of $\delta 3$ -31 and $\delta 3$ -42;
 - f) antibody $\delta 3$ -08; or
 - g) antibody $\delta 3$ -31.
3. The antibody or fragment thereof of claim 1, wherein the antibody or fragment thereof binds the same epitope as :
 - a) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - b) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - c) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;
 - d) an antibody selected from the group consisting of $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;

- e) an antibody selected from the group consisting of $\delta 3$ -31 and $\delta 3$ -42;
 - f) antibody $\delta 3$ -08; or
 - g) antibody $\delta 3$ -31.
4. The antibody or fragment thereof of claim 1, wherein the antibody or fragment thereof comprises the complementarity determining regions of:
- a) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -20, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - b) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -31, $\delta 3$ -42, $\delta 3$ -47, and $\delta 3$ -58;
 - c) an antibody selected from the group consisting of $\delta 3$ -08, $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;
 - d) an antibody selected from the group consisting of $\delta 3$ -23, $\delta 3$ -42, and $\delta 3$ -58;
 - e) an antibody selected from the group consisting of $\delta 3$ -31 and $\delta 3$ -42;
 - f) antibody $\delta 3$ -08; or
 - g) antibody $\delta 3$ -31.
5. The antibody or fragment thereof of claim 1, wherein the antibody or fragment thereof specifically binds to V $\delta 3$ of a $\gamma\delta$ TCR.
6. The antibody of claim 5, wherein the antibody binds to a region distal from the γ -chain binding interface of V $\delta 3$.
7. The antibody of claim 5, wherein the antibody binds to β strand D and E of the V $\delta 3$ of the $\gamma\delta$ TCR according to IMGT nomenclature.
8. The antibody of claim 5, wherein the antibody binds to β strand C'' and D and a loop between β strands E and F of the V $\delta 3$ of the $\gamma\delta$ TCR according to IMGT nomenclature.

9. The antibody of claim 5, wherein the antibody binds to β strand A, B, D, and E of the V δ 3 of the $\gamma\delta$ TCR according to IMGT nomenclature.
10. The antibody or fragment thereof of any one of claims 1-9, wherein the antibody or fragment thereof selectively expands a δ 3 $\gamma\delta$ T cell as compared to $\alpha\beta$ T cells in a mixed cell population comprising $\gamma\delta$ T cells and $\alpha\beta$ T cells.
11. The antibody or fragment thereof of any one of claims 1-10, wherein the antibody or fragment thereof is bound to a δ 3 $\gamma\delta$ TCR.
12. The antibody or fragment thereof of claim 11, wherein the δ 3 $\gamma\delta$ TCR is expressed on the surface of a δ 3 $\gamma\delta$ T cell.
13. The antibody or fragment thereof any one of claims 1-12, wherein the antibody or fragment thereof is bound to an extracellular surface of an antigen presenting cell (APC), such as an artificial antigen presenting cell (aAPC).
14. The antibody or fragment thereof of claim 13, wherein the antibody or fragment thereof is anchored in the membrane of the APC or aAPC.
15. The antibody or fragment thereof of claim 13, wherein an Fc region of the antibody or fragment thereof is bound to an Fc-receptor expressed by the APC or aAPC.
16. The antibody or fragment thereof of any one of claims 1-15, wherein the antibody or fragment thereof competes for binding to:
 - a) an antibody selected from the group consisting of δ 3-08, δ 3-20, δ 3-23, δ 3-31, δ 3-42, δ 3-47, and δ 3-58;
 - b) an antibody selected from the group consisting of δ 3-08, δ 3-23, δ 3-31, δ 3-42, δ 3-47, and δ 3-58;
 - c) an antibody selected from the group consisting of δ 3-08, δ 3-23, δ 3-42, and δ 3-58;
 - d) an antibody selected from the group consisting of δ 3-23, δ 3-42, and δ 3-58;

- e) an antibody selected from the group consisting of $\delta 3$ -31 and $\delta 3$ -42;
 - f) antibody $\delta 3$ -08; or
 - g) antibody $\delta 3$ -31.
17. The antibody or fragment thereof of any one of claims 1-16, wherein the antibody or fragment thereof is a specific activator of $\delta 3$ $\gamma \delta$ T cells.
 18. A nucleic acid encoding any one of the antibodies or fragments thereof according to claims 1-17, wherein the nucleic acid is operably linked to a heterologous promoter.
 19. A host cell comprising any one of the antibodies or fragments thereof according to claims 1-17 or a nucleic acid according to claim 18.
 20. The host cell of claim 19, wherein the host cell is an artificial antigen presenting cell (aAPC).
 21. A method of making an antibody or fragment thereof that binds an epitope specific to a $\delta 3$ $\gamma \delta$ TCR, the method comprising culturing the host cell of claim 19 under conditions sufficient to produce the antibody or fragment thereof.
 22. An *ex vivo* method for producing an enriched $\gamma \delta$ T cell population, comprising contacting a first cell population comprising $\gamma \delta$ T cells with one or more antibodies or fragments thereof according to claims 1-17.
 23. The method of claim 22, wherein the first cell population is an isolated mixed cell population comprising $\alpha \beta$ T cells and $\gamma \delta$ T cells.
 24. The method of claim 23, wherein the first cell population comprises, or is, a sample of peripheral blood mononuclear cells (PBMCs).
 25. The method of claim 23, wherein the first cell population is selected from a peripheral blood sample, a leukapheresis sample, a cord blood sample, a tumor sample, or a tissue sample.

26. The method of any one of claims 23 to 25, wherein the first cell population comprises less than 1% $\delta\gamma$ T cells.
27. The method of any one of claims 22-26, wherein the first cell population comprises uncultured primary cells or unpassaged primary cells.
28. The method of any one of claims 23-27, wherein the method comprises directly contacting the isolated mixed cell population with the one or more antibodies or fragments thereof.
29. The method of claim 22, wherein the first cell population is a population comprising one or more engineered $\gamma\delta$ T cells.
30. The method of any one of claims 22 or 29, wherein the first cell population is a first population of expanded $\gamma\delta$ T cells.
31. The method of claim 30, wherein the method comprises a first $\gamma\delta$ T cell expansion and a second $\gamma\delta$ T cell expansion.
32. The method of any one of claims 22 to 31, wherein the method comprises producing an enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta\gamma$ T cells.
33. The method of claim 32, wherein the enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta\gamma$ T cells is produced within 12 to 21 days.
34. The method of any one of claims 22 to 33, wherein the method comprises expanding the $\delta\gamma$ T cells in the first cell population at least 1,000-fold, preferably at least 5,000-fold, more preferably at least, or about, or at least about, 10,000 fold.
35. The method of claim 34, wherein the specified -fold expansion is achieved within 12 to 21 days.
36. An *ex vivo* method for producing an enriched $\gamma\delta$ T cell population, comprising:

- a) contacting a first cell population comprising $\gamma\delta$ T cells with one or more first activating agents that activate and expand $\gamma\delta$ T cells, thereby producing an expanded first $\gamma\delta$ T cell population; and
- b) contacting the expanded first $\gamma\delta$ T cell population with one or more second activating agents that activate and expand $\gamma\delta$ T cells, thereby producing the enriched $\gamma\delta$ T cell population,

wherein, at least one of the one or more first activating agents or at least one of the one or more second activating agents is an antibody or fragment thereof according to any one of claims 1-17.

- 37. The method of claim 36, wherein the method comprises isolating the expanded first $\gamma\delta$ T cell population after a) and before b).
- 38. The method of claim 36 or 37, wherein a) comprises culturing the first cell population in the presence of an antigen presenting cell (APC) and the one or more first activating agents.
- 39. The method of claim 36 or 37, wherein b) comprises culturing the expanded first $\gamma\delta$ T cell population in the presence of an antigen presenting cell (APC) and the one or more second activating agents.
- 40. The method of any one of claims 36-39, wherein the first cell population is an isolated mixed cell population comprising $\alpha\beta$ T cells and $\gamma\delta$ T cells.
- 41. The method of claim 40, wherein the first cell population is selected from a peripheral blood sample, a leukapheresis sample, a cord blood sample, a tumor sample, or a tissue sample.
- 42. The method of claim 40, wherein the first cell population comprises, or is, a sample of peripheral blood mononuclear cells (PBMCs).
- 43. The method of any one of claims 36-42, wherein the first cell population comprises uncultured primary cells, unpassaged primary cells.

44. The method of any one of claims 36-39, wherein the first cell population is a population of engineered $\gamma\delta$ T cells.
45. The method of any one of claims 36-44, wherein the method comprises genetically modifying the expanded first $\gamma\delta$ T cell population or genetically modifying the enriched $\gamma\delta$ T cell population.
46. The method of any one of claims 36-45, wherein the method comprises producing an enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta 3$ $\gamma\delta$ T cells.
47. The method of claim 46, wherein the enriched $\gamma\delta$ T cell population comprising at least 10^8 $\delta 3$ $\gamma\delta$ T cells is produced within 12 to 21 days.
48. The method of any one of claims 36-47, wherein the method comprises expanding the $\delta 3$ $\gamma\delta$ T cells in the first cell population at least 1,000-fold, preferably at least 5,000-fold, more preferably at least, or about, or at least about, 10,000 fold.
49. The method of claim 48, wherein the specified -fold expansion is achieved within 12 to 21 days.
50. The method of any one of claims 36-49, wherein at least one of the one or more first activating agents is structurally identical to at least one of the one or more second activating agents.
51. The method of any one of claims 36-50, wherein at least one of the one or more first activating agents is structurally different than at least one of the one or more second activating agents.
52. The method of any one of claims 36-51, wherein at least one of the one or more first activating agents or at least one of the one or more second activating agents is immobilized.
53. The method of claim 52, wherein the immobilized activating agent is immobilized on a surface of a culture vessel.

54. The method of claim 52, wherein the immobilized activating agent is immobilized on a surface of an antigen presenting cell (APC) or an artificial antigen presenting cell (aAPC).
55. The method of any one of claims 52-54, wherein immobilized activating agent is the antibody or fragment thereof that binds the epitope specific to a $\delta\delta$ $\gamma\delta$ TCR.
56. A method according to any one of claims 22-35 or 36-55, wherein the method achieves greater than 30% $\delta\delta$ $\gamma\delta$ T cells prior to, or in the absence of, $\alpha\beta$ T cell depletion, preferably greater than 40%.
57. An expanded $\gamma\delta$ T cell population, wherein greater than 30% of the expanded $\gamma\delta$ T cells are $\delta\delta$ $\gamma\delta$ T cells, preferably greater than 40%, more preferably greater than 60%, yet more preferably greater than 70%, even more preferably greater than 80%.
58. The expanded $\gamma\delta$ T cell population of claim 57, wherein the expanded $\gamma\delta$ T cell population comprises polyclonal TCR diversity.
59. The expanded $\gamma\delta$ T cell population of claim 58, wherein greater than 60% or 70% the $\delta\delta$ T-cells express the phenotype CD45RA+/CD27+ and/or CD45RA-/CD27+.
60. The expanded $\gamma\delta$ T cell population of any one of claims 57-59, which is derived from tumor infiltrating lymphocytes.
61. The expanded $\gamma\delta$ T cell population of any one of claims 57-60, wherein the $\gamma\delta$ T-cells express an endogenous or heterologous tumor recognition moiety.
62. The expanded $\gamma\delta$ T cell population of any one of claims 57-61, wherein the population comprises a therapeutically effective amount of $\gamma\delta$ T-cells.
63. The expanded $\gamma\delta$ T cell population of any one of claims 57-62, wherein the $\gamma\delta$ T cell population comprises anti-tumor cytotoxicity that is independent of NKp30 activity, NKp44 activity, and/or NKp46 activity.

64. The expanded $\gamma\delta$ T cell population of claim 63, wherein the $\gamma\delta$ T cell population does not comprise NKp30 activity-dependent anti-tumor cytotoxicity, NKp44 activity-dependent anti-tumor cytotoxicity, and/or NKp46 activity-dependent anti-tumor cytotoxicity.
65. The expanded $\gamma\delta$ T cell population of any one of claims 57-63, wherein less than 40% of the $\gamma\delta$ T cells express a detectable level of NKp30, NKp44, and/or NKp46.
66. An expanded $\gamma\delta$ T cell population, which is produced by:
- a) a method according to any one of claims 22-35; or
 - b) a method according to any one of claims 36-56.
67. A method of treating cancer, an inflammatory disease, or an autoimmune disease in a subject in need thereof, the method comprising administering a therapeutically effective amount of $\delta\gamma$ $\gamma\delta$ T cells to the subject.
68. A method of treating cancer, an inflammatory disease, or an autoimmune disease in a subject in need thereof, the method comprising:
- a) providing a therapeutically effective amount of $\delta\gamma$ $\gamma\delta$ T cells according to any one of claims 57-66; and
 - b) administering the therapeutically effective amount of $\delta\gamma$ $\gamma\delta$ T cells to the subject.
69. The method of claim 68, wherein the method further comprises admixing the expanded $\gamma\delta$ T cell population with a second expanded $\gamma\delta$ T cell population to form an admixed population and administering the admixed population to the subject.
70. The method of claim 69, wherein the second expanded $\gamma\delta$ T cell population comprises $> 60\%$ $\delta 1$ or $> 60\%$ $\delta 2$ $\gamma\delta$ T cells.
71. The method of claim 69, wherein the admixed $\gamma\delta$ T cell population comprises $> 60\%$ $\delta 1$ or $> 60\%$ $\delta 2$ $\gamma\delta$ T cells.

72. The method of claim 69, wherein the admixed $\gamma\delta$ T cell population comprises $> 60\%$ $\delta 3$ $\gamma\delta$ T cells.