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(54) **Title:** TREATMENT OF NSCLC PATIENTS WITH TUMOR INFILTRATING LYMPHOCYTE THERAPIES

(57) **Abstract:** The present invention provides improved and/or shortened processes and methods for preparing TILs in order to prepare therapeutic populations of TILs with increased therapeutic efficacy for the treatment of cancer, including for example, non-small cell lung carcinoma (NSCLC), wherein the NSCLC is refractory to treatment with an anti-PD-1 antibody and/or anti-PD-L1 antibody and/or VEGF inhibitor, and/or wherein the cancer, including for example or NSCLC, has a predetermined tumor proportion score (TPS), and including when the TILs for expansion are obtained prior to the patient receiving a cancer treatment.

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TREATMENT OF NSCLC PATIENTS WITH TUMOR INFILTRATING LYMPHOCYTE THERAPIES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 63/328,236, filed April 6, 2022, of which is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0002] A significant unmet need exists for new treatment options for patients with locally advanced or metastatic non-small-cell lung cancer (NSCLC); these patients comprise approximately 70% of newly diagnosed patients with NSCLC (Molina JR, Yang P, Cassivi SD, Schild SE, Adjei AA. Mayo Clin Proc. 2008; 83(5):584-94). Lung cancer is the leading cause of cancer deaths worldwide, with approximately 1.7 million deaths reported in 2015. Of the lung cancer deaths, > 80% were attributed to non-small-cell lung cancer (NSCLC) (21). It was expected that in 2020, there would have been an estimated 228,820 new cases and 135,720 deaths attributed to lung and bronchus cancer in the United States (Siegel RL, 2015. CA Cancer J Clin. 2015; 65(1):5-29). Thus, despite the approval of checkpoint inhibitors (CPIs), which revolutionized NSCLC treatment and outcomes, there remains a significant unmet medical need in NSCLC.

[0003] Overall, in men and women, the lifetime risk of developing lung cancer regardless of smoking status is approximately 1 in 14 and 1 in 17, respectively. However, the risk of developing lung cancer is much higher in smokers vs. nonsmokers, *e.g.*, men who smoke are 23 times more likely to develop cancer; likewise, women who smoke are 13 times more likely to develop lung cancer than those who do not (American Lung Association - Lung cancer fact sheet 2017 [American Lung Association - Lung cancer fact sheet]; available from: the World Wide Web at lung.org/lung-health-and-diseases/lung-disease-lookup/lung-cancer/resource-library/lung-cancer-fact-sheet.html).

[0004] Prior to checkpoint inhibitors, platinum doublet chemotherapy was utilized in the initial treatment of patients with incurable NSCLC (Schiller J. H. et al. 2002 *N Engl J Med* 346 (2):92-8.), and it produced an objective response rate (ORR) of 20% to 30% with limited durability. Pembrolizumab, alone or in combination with cytotoxic therapy, revolutionized the treatment, producing higher response rates that have proven more durable as well (Gandhi Leena et al. 2018 *N Engl J Med* 378 (22):2078-2092; Paz-Ares L. et al. 2018 *N Engl J Med* 379 (21):2040-2051; Viteri S. et al. 2020 *Transl Lung Cancer Res* 9 (3):828-832; Pacheco J. M. 2020 *Transl Lung Cancer Res* 9 (1):148-153; Mok T. S. K. et al. 2019 *Lancet* 393 (10183):1819-1830; Nosaki K. et al. 2019 *Lung Cancer* 135:188-195; Morgensztern D. 2019 *J Thorac Dis* 11 (Suppl 15):S1963-S1965 ; Reck M. et

al. 2016 *N Engl J Med* 375 (19):1823-1833). Other CPIs have demonstrated improved ORR and durability in combination with chemotherapy in the first-line setting for NSCLC (Socinski MA et al 2018 *New Engl J Med* 378:2288-301). Despite these impressive results, there are few complete responses; almost all patients either fail to respond or progress, thus necessitating subsequent therapy.

[0005] For NSCLC patients with identified driver mutations, the preferred option is treatment with targeted TKIs directed against the relevant mutation (*e.g.*, osimertinib for epidermal growth factor receptor [EGFR] mutations, ceritinib for ALK mutations or crizotinib for ROS-1 mutations). For previously untreated patients with NSCLC whose tumors express PD-L1, the available treatment options include pembrolizumab monotherapy (commonly used only for patients with tumor proportion score (TPS) for PD-L1 expression of at least 50%) or pembrolizumab in combination with chemotherapy. For patients with NSCLC and PD-L1 expression < 50%, the preferred option is the combination of pemetrexed, carboplatin or cisplatin, and pembrolizumab. Patients with TPS for PD-L1 < 1% and no actionable mutations have no viable treatment options and are not candidates for PD-1 or PD-L1 CPIs. The combination of platinum-based doublet chemotherapy, bevacizumab, and atezolizumab is another potential therapeutic alternative in patients with NSCLC, as is a combination of nivolumab, ipilimumab and cytotoxic therapy (Hellmann et al. 2019 *New Engl J Med* 381:2020-31).

[0006] Once a patient has disease progression on checkpoint inhibitor therapy plus chemotherapy, treatment options are limited and suffer from low efficacy, with objective response rate ~ 10% and short progression-free survival (PFS), as well as high toxicity. The most commonly used agent is docetaxol, though other single agent cytotoxics or cytotoxics combined with VEGF inhibitors are sometimes employed, but all have similar, poor, outcomes. Thus, there is an urgent need for better therapeutic options in the second line treatment following checkpoint inhibitor therapy plus chemotherapy.

[0007] Furthermore, current TIL manufacturing and treatment processes are limited by length, cost, sterility concerns, and other factors described herein such that the potential to treat patients which are refractory to anti-PD-1 and/or anti-PD-L1 and/or VEGF inhibitor treatments and as such have been severely limited. There is an urgent need to provide TIL manufacturing processes and therapies based on such processes that are appropriate for use in treating patients for whom very few or no viable treatment options remain. The present invention meets this need by providing a shortened manufacturing process for use in generating TILs which can then be employed in the treatment of refractory and/or progressive non-small cell lung carcinoma (NSCLC) patients.

BRIEF SUMMARY OF THE INVENTION

[0008] In some embodiments, the present invention provides a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naive to a cancer treatment, the method comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

wherein the patient subsequently receives an ICI treatment and/or a standard of care treatment;

optionally wherein the first population of TILs is further expanded into a therapeutic population of TILs if the patient exhibits progressive disease on or after the ICI and/or standard of care treatment.

[0009] In some embodiments, the present invention provides a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

wherein the patient subsequently resumes the maitnainence therapy;

optionally wherein the first population of TILs is further expanded into a therapeutic population of TILs if the patient exhibits progressive disease on or after the resumption of the maintenance therapy.

[0010] In some embodiments, the present invention provides a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naïve to a cancer treatment, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0011] In some embodiments, the present invention provides a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naïve to a cancer treatment, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first

gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(c) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0012] In some embodiments, the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

[0013] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed

for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0014] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs,

wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0015] In some embodiments, the cancer patient is naïve to any cancer treatment.

[0016] In some embodiments, the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

[0017] In some embodiments, the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after step (a).

[0018] In some embodiments, the patient is in a washout period at initiation of step (a).

[0019] In some embodiments, step of thawing and the subsequent steps are performed after the patient receives the cancer treatment or resumes the maintenance therapy and the patient exhibits progressive disease.

[0020] In some embodiments, the patient exhibits progressive disease at least about 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 month, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 25 months, 26 months, 27 months, 28 months, 29 months, 30 months, 31 months, 32 months, 33 months, 34 months, 35 months, 36 months, after the step (b) of cryopreserving.

[0021] In some embodiments, the patient receives or is going to receive a first-line ICI treatment and/or standard treatment.

[0022] In some embodiments, the patient receives or is going to receive a second-line ICI treatment and/or standard treatment.

[0023] In some embodiments, the patient is diagnosed with NSCLC.

[0024] In some embodiments, the patient is diagnosed with metastatic stage IV NSCLC.

[0025] In some embodiments, the subject or patient has at least one of:

i) a predetermined tumor proportion score (TPS) of PD-L1 of < 1%,

ii) a TPS score of PD-L1 of 1%-49%, or

iii) a predetermined absence of one or more driver mutations.

[0026] In some embodiments, the patient or subject has a TPS of PD-L1 of 1%-49%.

[0027] In some embodiments, the patient or subject has a TPS of PD-L1 of < 1% and has a predetermined absence of one or more driver mutations.

[0028] In some embodiments, the one or more driver is selected from the group consisting of an EGFR mutation, an EGFR insertion, EGFR exon20, a KRAS mutation, a BRAF-mutation, a BRAF V600 mutation, an ALK-mutation, a c-ROS-mutation (ROS1-mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation, a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation.

[0029] In some embodiments, the patient or subject has a TPS of < 1% and has a NSCLC that is not indicated for treatment by an EGFR inhibitor, a BRAF inhibitor, an ALK inhibitor, a c-Ros inhibitor, a RET inhibitor, an ERBB2 inhibitor, BRCA inhibitor, a MAP2K1 inhibitor, PIK3CA inhibitor, CDKN2A inhibitor, a PTEN inhibitor, an UMD inhibitor, an NRAS inhibitor, a KRAS inhibitor, an NF1 inhibitor, MET inhibitor a TP53 inhibitor, a CREBBP inhibitor, a KMT2C inhibitor, a KMT2D mutation, an ARID1A mutation, a RB1 inhibitor, an ATM inhibitor, a SETD2 inhibitor, a FLT3 inhibitor, a PTPN11 inhibitor, a FGFR1 inhibitor, an EP300 inhibitor, a MYC inhibitor, an EZH2 inhibitor, a JAK2 inhibitor, a FBXW7 inhibitor, a CCND3 inhibitor, and a GNA11 inhibitor.

[0030] In some embodiments, the one or more driver mutations comprises a genomic alteration of EGFR, ALK, or ROS.

[0031] In some embodiments, the one or more driver mutations consists of a genomic alteration of EGFR, ALK, or ROS.

[0032] In some embodiments, the NSCLC has low or no expression of PD-L1.

[0033] In some embodiments, the patient has a predetermined absence of one or more driver mutations.

[0034] In some embodiments, the NSCLC is refractory or resistant to treatment with a chemotherapeutic agent.

[0035] In some embodiments, the NSCLC is refractory or resistant to treatment with a VEGF-A In some embodiments, the NSCLC has been treated with a chemotherapeutic agent but is not being currently treated with a chemotherapeutic agent.

[0036] In some embodiments, the NSCLC has been treated with a chemotherapeutic agent but is not being currently treated with a chemotherapeutic agent and has a TPS of < 1%.

[0037] In some embodiments, the NSCLC has been treated with a VEGF-A inhibitor but is not being currently treated with a VEGF-A inhibitor.

[0038] In some embodiments, the NSCLC has been treated with a VEGF-A inhibitor but is not being In some embodiments, the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor, but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0039] In some embodiments, the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor and has a TPS of < 1%.

[0040] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody.

[0041] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0042] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0043] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a VEGF-A inhibitor but is not being currently treated with a VEGF-A inhibitor.

[0044] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0045] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has low or no expression of PD-L1.

[0046] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor and has a TPS of < 1%.

[0047] In some embodiments, the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 and/or anti-PD-L2 antibody.

[0048] In some embodiments, the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0049] In some embodiments, the NSCLC is refractory or resistant to treatment with an anti-PD-1 and/or anti-PD-L1 antibody.

[0050] In some embodiments, the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment.

[0051] In some embodiments, the NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment, or the NSCLC has been previously treated with an anti-PD-1 antibody and the tumor proportion score was determined prior to the anti-PD-1 antibody treatment.

[0052] In some embodiments, the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

[0053] In some embodiments, the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has bulky disease at baseline.

[0054] In some embodiments, the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has bulky disease at baseline.

[0055] In some embodiments, the NSCLC has been treated with a chemotherapeutic agent and has bulky disease at baseline.

[0056] In some embodiments, the NSCLC has been treated with a chemotherapeutic agent and/or VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or VEGF-A inhibitor and has bulky disease at baseline.

[0057] In some embodiments, bulky disease is indicated where the maximal tumor diameter is greater than 7 cm measured in either the transverse or coronal plane or swollen lymph nodes with a short-axis diameter of 20 mm or greater.

[0058] In some embodiments, the NSCLC is refractory or resistant to at least two prior systemic treatment courses, not including neo-adjuvant or adjuvant therapies.

[0059] In some embodiments, the NSCLC is refractory or resistant to an anti-PD-1 or an anti-PD-L1 antibody selected from the group consisting of nivolumab, pembrolizumab, JS001, TSR-042, pidilizumab, BGB-A317, SHR-1210, REGN2810, MDX-1106, PDR001, anti-PD-1 from clone: RMP1-14, anti-PD-1 antibodies disclosed in U.S. Patent No. 8,008,449, durvalumab, atezolizumab, avelumab, and fragments, derivatives, variants, as well as biosimilars thereof.

[0060] In some embodiments, the NSCLC is refractory or resistant to pembrolizumab or a biosimilar thereof.

[0061] In some embodiments, the NSCLC is refractory or resistant to nivolumab or a biosimilar thereof.

[0062] In some embodiments, the NSCLC is refractory or resistant to an anti-CTLA-4 antibody.

[0063] In some embodiments, the NSCLC is refractory or resistant to an anti- CTLA -4 antibody and pembrolizumab or a biosimilar thereof.

[0064] In some embodiments, the NSCLC is refractory or resistant to an anti- CTLA -4 antibody, and nivolumab or a biosimilar thereof.

[0065] In some embodiments, the anti-CTLA-4 antibody is ipilimumab or a biosimilar thereof.

[0066] In some embodiments, the NSCLC is refractory or resistant to durvalumab or a biosimilar thereof.

[0067] In some embodiments, the NSCLC is refractory or resistant to atezolizumab or a biosimilar thereof.

[0068] In some embodiments, the NSCLC is refractory or resistant to avelumab or a biosimilar thereof.

[0069] In some embodiments, the chemotherapeutic agent is a platinum doublet chemotherapeutic agent(s).

[0070] In some embodiments, the platinum doublet chemotherapeutic agent therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

[0071] In some embodiments, the chemotherapeutic agent, including the first and/or second chemotherapeutic agent, is in combination with pemetrexed.

[0072] In some embodiments, the NSCLC is refractory or resistant to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, and cisplatin.

[0073] In some embodiments, the NSCLC is refractory or resistant to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, cisplatin, nivolumab, and ipilimumab.

[0074] In some embodiments, the NSCLC is refractory or resistant to a VEGF-A inhibitor.

[0075] In some embodiments, the NSCLC is refractory or resistant to a VEGF-A inhibitor selected from the group consisting of bevacizumab, ranibizumab, and icrucumab.

[0076] In some embodiments, the NSCLC is refractory or resistant to bevacizumab.

[0077] In some embodiments, the NSCLC has been analyzed for the absence or presence of one or more driver mutations.

[0078] In some embodiments, one or more driver mutations are not present.

[0079] T In some embodiments, he method of any one of Claims 64 to 65, wherein the NSCLC treatment is independent of the presence or absence of one or more driver mutations.

[0080] In some embodiments, the one or more driver mutations is selected from the group consisting of an EGFR mutation, an EGFR insertion, a KRAS mutation, a BRAF-mutation, an ALK-mutation, a c-ROS-mutation a c-ROS-mutation, EML4-ALK, and MET mutation.

[0081] In some embodiments, the EGFR mutation results in tumor transformation from NSCLC to small cell lung cancer (SCLC).

[0082] In some embodiments, the NSCLC treatment is independent of the presence or absence of high-tumor mutational burden (high-TMB) and/or microsatellite instability-high (MSI-high) status.

[0083] In some embodiments, the NSCLC exhibits high-TMB and/or MSI-high status.

[0084] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(f) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0085] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(f) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0086] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(f) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0087] In some embodiments, the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

[0088] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(f) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[0089] In some embodiments, the patient is naïve to any cancer treatment.

[0090] In some embodiments, the patient receives a first-line ICI treatment and/or standard treatment.

[0091] In some embodiments, the patient receives a second-line ICI treatment and/or standard treatment.

[0092] In some embodiments, step (b) comprises flash freezing of the tumor fragments or tumor digest.

[0093] In some embodiments, the flash freezing comprises:

i) incubating the tumor fragments or tumor digest in a cryopreservation medium; optionally incubating for about 30 minutes to about 60 minutes at about 2°C to about 8°C in a cryopreservation medium comprising 10% v/v DMSO, and

ii) freezing the tumor wherein the freezing is flash freezing using the vapor phase of liquid nitrogen.

[0094] In some embodiments, step (b) comprises controlled-rate freezing of the tumor fragments or tumor digest.

[0095] In some embodiments, the controlled-rate freezing comprises:

i) adding cryopreservation medium to a closable vessel;

ii) pre-cooling the closable vessel in a controlled-rate freezing device;

iii) placing the tumor in the closable vessel comprising cryopreservation medium and closing the vessel;

iv) incubating the closed vessel comprising the tumor and cryopreservation medium at a temperature of about 2-8C for a time period of about 30 to 60 minutes; and

v) slow-freezing the vessel in a controlled-rate freezing device.

[0096] In some embodiments, the cancer patient is naïve to any cancer treatment.

[0097] In some embodiments, the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

[0098] In some embodiments, the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after step (a).

[0099] In some embodiments, the patient receives a first-line ICI treatment and/or standard treatment.

[00100] In some embodiments, the patient receives a second-line ICI treatment and/or standard treatment.

[00101] In some embodiments, the patient is diagnosed with NSCLC.

[00102] In some embodiments, the patient is diagnosed with metastatic stage IV NSCLC.

[00103] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system;

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process;

[00104] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00105] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00106] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a tumor in the subject or patient,

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a

second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

[00107] (f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00108] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, resecting a tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a tumor;

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (e) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00109] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00110] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from the subject or patient;

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and contacting the first population of TILs with a first cell culture medium in a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (g) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

[00111] In some embodiments, the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

[00112] In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL in the first cell culture medium, when present.

[00113] In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL and the OKT-3 antibody is present at an initial concentration of about 30 ng/mL in the second wherein the initial expansion, when present, is performed using a gas permeable container.

[00114] In some embodiments, the rapid expansion, when present, is performed using a gas permeable container.

[00115] In some embodiments, the first cell culture medium, when present, further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof.

[00116] In some embodiments, the second cell culture medium, when present, further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof.

[00117] In some embodiments, the harvested population of TILs comprises a therapeutically effective population of TILs, and wherein a therapeutically effective population of TILs comprises from about 2.3×1010 to about 13.7×1010 TILs.

[00118] In some embodiments, the initial expansion is performed over a period of 21 days or less.

[00119] In some embodiments, the initial expansion is performed over a period of 7 days or less.

[00120] In some embodiments, the rapid expansion is performed over a period of 7 days or less.

[00121] In some embodiments, the first expansion and the second expansion are each individually performed within a period of 11 days.

[00122] In some embodiments, step of performing the first expansion through the setp of harvesting are performed in about 10 days to about 24 days.

[00123] In some embodiments, step of performing the first expansion through the setp of harvesting are performed in about 10 days to about 22 days.

[00124] In some embodiments, the method further comprising a step of modifying a portion of the TILs at any time prior to the harvesting such that each of the modified TILs comprises an immunomodulatory composition associated with its surface membrane.

[00125] In some embodiments, the step of modifying comprises gene-editing the TILs to effect transfer of at least one gene editing system selected from the group consisting of a TALEN system, a CRISPR system and zinc finger system, into the modified TILs.

[00126] In some embodiments, during the step of modifying the cell membranes of the modified TILs are temporarily disrupted to effect transfer of the at least one gene editing system by using a microfluidic platform or sterile electroporation.

[00127] In some embodiments, the microfluidic platform is a SQZ platform.

[00128] In some embodiments, immunomodulatory composition comprises one or more membrane anchored immunomodulatory fusion proteins each comprising one or more immunomodulatory agents and a cell membrane anchor moiety.

[00129] In some embodiments, the immunomodulatory composition comprises two or more different membrane anchored immunomodulatory fusion proteins, wherein each of the different membrane anchored immunomodulatory fusion proteins each comprises a different immunomodulatory agent.

[00130] In some embodiments, immunomodulatory composition comprises a fusion protein comprising one or more immunomodulatory agents linked to a TIL surface antigen binding domain.

[00131] In some embodiments, immunomodulatory composition comprises a nanoparticle comprising a plurality of immunomodulatory agents.

[00132] In some embodiments, the immunomodulatory agents comprise one or more cytokines.

[00133] In some embodiments, the one or more cytokines comprise IL-2, IL-6, IL-7, IL-9, IL-12, IL-15, IL-18, IL-21, IL-23, IL-27, IFN gamma, TNFa, IFN alpha, IFN beta, GM-CSF, or GCSF or a variant thereof.

[00134] In some embodiments, the immunomodulatory agents comprise a CD40 agonist.

[00135] In some embodiments, the membrane anchored immunomodulatory fusion protein is according to the formula, from N- to C-terminus: S-IA-L-C, wherein S is a signal peptide, IA is an immunomodulatory agent, L is a linker and C is a cell membrane anchor moiety.

[00136] In some embodiments, the cell membrane anchor moiety comprises a CD8a transmembrane-intracellular domain, a B7-1 transmembrane domain, a B7-2 transmembrane domain, or a CD8a transmembrane domain.

[00137] In some embodiments, the one or more immunomodulatory agents comprise one or more cytokines.

[00138] In some embodiments, the one or more cytokines comprises IL-2, IL-6, IL-7, IL-9, IL-12, IL-15, IL-18, IL-21, IL-23, IL-27, IFN gamma, TNFa, IFN alpha, IFN beta, GM-CSF, or GCSF or a variant thereof.

[00139] In some embodiments, the TIL surface antigen binding domain comprises an antibody variable heavy domain and variable light domain.

[00140] In some embodiments, the TIL surface antigen binding domain comprises an antibody or fragment thereof.

[00141] In some embodiments, the TIL surface antigen binding domain exhibits an affinity for one or more of following TIL surface antigens: CD45, CD4, CD8, CD3, CDlla, CDllb, CDllc, CD18, CD25, CD127, CD19, CD20, CD22, HLA-DR, CD197, CD38, CD27, CD196, CXCR3, CXCR4, CXCR5, CD84, CD229, CCR1, CCR5, CCR4, CCR6, CCR8, CCR10, CD 16, CD56, CD 137, OX40, or GITR.

[00142] In some embodiments, the nanoparticle is a liposome, a protein nanogel, a nucleotide nanogel, a polymer nanoparticle, or a solid nanoparticle.

[00143] In some embodiments, the nanoparticle is a nanogel.

[00144] In some embodiments, the nanoparticle further comprises an antigen binding domain that binds to one or more of the following antigens: CD45, CDlla (integrin alpha- L), CD 18 (integrin beta-2), CD1lb, CD1lc, CD25, CD8, or CD4.

[00145] In some embodiments, the modifying comprises introducing a heterologous nucleic acid encoding the fusion protein into the portion of TILs and expressing the fusion protein on the surface of the modified TILs.

[00146] In some embodiments, the heterologous nucleic acid is introduced into the genome of the modified TIL using one or more methods selected from a CRISPR method, a TALE method, a zinc finger method, and a combination thereof.

[00147] In some embodiments, the modifying comprises incubating the fusion protein with the portion of TILs under conditions to permit the binding of the fusion protein to the portion of TILs.

[00148] In some embodiments, the modifying comprises attaching the immunomodulatory composition to the surface of the portion of TILs.

[00149] In some embodiments, the modifying is carried out on TILs from the first expansion, or TILs from the second expansion, or both.

[00150] In some embodiments, the modifying is carried out on TILs from the priming first expansion, or TILs from the rapid second expansion, or both.

[00151] In some embodiments, the modifying is carried out after the first expansion and before the second expansion.

[00152] In some embodiments, the modifying is carried out after the priming first expansion and before the rapid second expansion, or both.

[00153] In some embodiments, the modifying is carried out after the second expansion.

[00154] In some embodiments, the modifying is carried out after the rapid second expansion.

[00155] In some embodiments, the modifying is carried out after the harvesting.

[00156] In some embodiments, the modified TILs further comprise a genetic modification that causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs.

[00157] In some embodiments, said one or more immune checkpoint genes is/are selected from the group comprising PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00158] In some embodiments, said one or more immune checkpoint genes is/are selected from the group comprising PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, and PKA.

[00159] In some embodiments, the modified TILs further comprises a genetic modification that causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs, the immune checkpoint gene(s) being selected from the group comprising CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[00160] In some embodiments, the genetic modification is produced using a programmable nuclease that mediates the generation of a double-strand or single-strand break at said one or more immune checkpoint genes.

[00161] In some embodiments, the genetic modification is produced using one or more methods selected from a CRISPR method, a TALE method, a zinc finger method, and a combination thereof.

[00162] In some embodiments, the modified TILs are modified to transiently express the immunomodulatory composition on the cell surface.

[00163] In some embodiments, the immunomodulatory composition comprises one or more membrane anchored immunomodulatory fusion proteins, wherein each fusion protein comprises one or more immunomodulatory agents and a cell membrane anchor moiety.

[00164] In some embodiments, the modified TILs are modified by transfecting the TILs with a nucleic acid encoding the fusion protein.

[00165] In some embodiments, the nucleic acid is an RNA.

[00166] In some embodiments, the RNA is a mRNA.

[00167] In some embodiments, the TILs are transfected with the mRNA by a SQZ platform or electroporation.

[00168] In some embodiments, the TILs are transfected with the mRNA by a SQZ platform or electroporation after the first expansion and before the second expansion.

[00169] In some embodiments, the TILs are transfected with the mRNA by a SQZ platform or electroporation before the first expansion.

[00170] In some embodiments, the modified TILs are transfected with the nucleic acid encoding the fusion protein using a microfluidic device to temporarily disrupt the cell membranes of the TILs, thereby allowing transfection of the nucleic acid.

[00171] In some embodiments, the method further comprises activating the TILs by incubation with an anti-CD3 agonist before transfecting the TILs with the mRNA.

[00172] In some embodiments, the anti-CD3 agonist is OKT-3.

[00173] In some embodiments, the TILs are activated by incubating the TILs with the anti-CD3 agonist for about 1 to 3 days before transfecting the TILs with the mRNA.

[00174] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00175] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00176] In some embodiments, the enzymatic media comprises a DNase.

[00177] In some embodiments, the enzymatic media comprises a collagenase.

[00178] In some embodiments, the enzymatic media comprises a neutral protease.

[00179] In some embodiments, the enzymatic media comprises a hyaluronidase.

[00180] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(g) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide an expanded number of TILs.

[00181] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(h) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide an expanded number of TILs.

[00182] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00183] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00184] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(f) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00185] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;

(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(g) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00186] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00187] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(e) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(g) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00188] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(g) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00189] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(e) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(h) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00190] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 8 days;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-6 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00191] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) subsequent to the cancer progression, performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 8 days;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(e) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00192] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 8 days;

(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-6 days, to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(g) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00193] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 8 days;

(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(f) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises

IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00194] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and adding the tumor tissue into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or CD3 agonist and CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the fifth population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(g) harvesting the therapeutic population of TILs obtained from step (f), wherein each of steps (c) to (g) is performed in a closed, sterile system, and wherein the transition from step (c) to step (d), the transition from step (d) to step (e), the transition from step (e) to step (f) and/or the transition from step (f) to step (g) occurs without opening the system.

[00195] In some embodiments, the present disclosures provide a method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintenance therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;

(b) digesting the sample of tumor tissue in an enzymatic media to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and adding the tumor digest into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or CD3 agonist and CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the fifth population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(g) harvesting the therapeutic population of TILs obtained from step (f), wherein each of steps (d) to (g) is performed in a closed, sterile system, and wherein the transition from step (d) to step (e), the transition from step (e) to step (f), and/or the transition from step (f) to step (g) occurs without opening the system.

[00196] In some embodiments, the rapid second expansion is performed by culturing the third or fourth population of TILs in the second cell culture medium for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3-6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00197] In some embodiments, the step of gene-editing at least a portion of the second or third population of TILs comprises performing a sterile electroporation step or a SQZ microfluidic

membrane disruption step on the second or third population of TILs, wherein the sterile electroporation step or the SQZ microfluidic membrane disruption step mediates the transfer of at least two gene editors.

[00198] In some embodiments, the electroporation step or the SQZ microfluidic membrane disruption step consists of a single event that mediates the transfer of the at least two gene editors.

[00199] In some embodiments, in the electroporation step or the SQZ microfluidic membrane disruption step each of the at least two gene editors is transferred individually by an event independently of the transfer of any other gene editor.

[00200] In some embodiments, the electroporation step further comprises a rest period after each event.

[00201] In some embodiments, the electroporation step or the SQZ microfluidic membrane disruption step comprises a first event that mediates the transfer of a first gene editor for modulating expression of a first protein, a first rest period, a second event that mediates the transfer of a second gene editor for modulating expression of a second protein, and a second rest period, wherein the first and second rest periods are the same or different.

[00202] In some embodiments, the first and second rest periods comprise incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

[00203] In some embodiments, the first and second rest periods comprise incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

[00204] In some embodiments, the first and second rest periods are independently about 10 hours to 5 days.

[00205] In some embodiments, the first and second rest periods are independently about 10 hours to 3 days.

[00206] In some embodiments, the first rest period is about 1 to 3 days.

[00207] In some embodiments, the first rest period is about 3 days.

[00208] In some embodiments, the second rest period is about 10 hours to 1 day.

[00209] In some embodiments, the second rest period is about 12 hours to 24 hours.

[00210] In some embodiments, the second rest period is about 15 hours to about 18 hours.

[00211] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

[00212] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

[00213] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

[00214] In some embodiments, the first rest period is about 3 days and the second rest period is about 10 to 16 hours.

[00215] In some embodiments, the at least two gene editors comprise a first gene editor comprising a first TALE nuclease system for modulating expression of a first protein and a second gene editor comprising a second TALE nuclease system for modulating expression of a second protein.

[00216] In some embodiments, the electroporation step or the SQZ microfluidic membrane disruption step comprises a first event that mediates the transfer of the first TALE nuclease system, a first rest period, a second event that mediates the transfer of the second TALE nuclease system, and a second rest period, wherein the first and second rest periods are the same or different.

[00217] In some embodiments, the first and second rest periods comprise incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

[00218] In some embodiments, the first and second rest periods comprise incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

[00219] In some embodiments, the first and second rest periods are independently about 10 hours to 5 days.

[00220] In some embodiments, the first and second rest periods are independently about 10 hours to 3 days.

[00221] In some embodiments, the first rest period is about 1 to 3 days.

[00222] In some embodiments, the first rest period is about 3 days.

[00223] In some embodiments, the second rest period is about 10 hours to 1 day.

[00224] In some embodiments, the second rest period is about 12 hours to 24 hours.

[00225] In some embodiments, the second rest period is about 15 hours to about 18 hours.

[00226] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

[00227] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

[00228] In some embodiments, the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

[00229] In some embodiments, the first rest period is about 3 days and the second rest period is about 10 to 16 hours.

[00230] In some embodiments, the step of gene-editing at least a portion of the second or third population of TILs comprises performing a sterile electroporation step or a SQZ microfluidic membrane disruption step on the second or third population of TILs, wherein the sterile electroporation step or the SQZ microfluidic membrane disruption step mediates the transfer of at least one gene editor.

[00231] In some embodiments, the gene editor is a TALE nuclease system for modulating the expression of at least one protein.

[00232] In some embodiments, the TALE nuclease system modulates expression of PD-1, CTLA-4, TIGIT, CBL-B and/or LAG-3.

[00233] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CTLA-4.

[00234] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and LAG-3.

[00235] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CISH.

[00236] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CBL-B.

[00237] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and TIGIT.

[00238] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and LAG-3.

[00239] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and CISH.

[00240] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and CBL-B.

[00241] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CISH and CBL-B.

[00242] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CISH and TIGIT.

[00243] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of PD-1.

[00244] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4.

[00245] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of LAG-3.

[00246] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CISH.

[00247] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of CBL-B.

[00248] In some embodiments, the gene editor comprises a TALE nuclease system that modulates expression of TIGIT.

[00249] In some embodiments, the method further comprises the step of resting the third or fourth population of TILs after the gene-editing step and before the step of culturing the third or fourth population of TILs.

[00250] In some embodiments, the resting step comprises incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

[00251] In some embodiments, the method further comprises the step of resting the third or fourth population of TILs for about one day after the gene-editing step and before the step of culturing the third or fourth population of TILs.

[00252] The method of any of claims 352-369, wherein the method further comprises the step of resting the third or fourth population of TILs for about 12 hours to 24 hours after the gene-editing step and before the step of culturing the third or fourth population of TILs.

[00253] In some embodiments, the step of resting the third or fourth population of TILs comprises resting the third or fourth population of TILs for about 15 hours to 18 hours.

[00254] In some embodiments, the step of resting the third or fourth population of TILs comprises resting the third or fourth population of TILs for about 15 hours.

[00255] In some embodiments, the step of resting the third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

[00256] In some embodiments, the step of resting the third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

[00257] In some embodiments, the step of resting third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

[00258] In some embodiments, the step of resting the third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

[00259] In some embodiments, the first protein and the second protein are independently selected from the group consisting of PD-1, CTLA-4, LAG-3, CISH, TIGIT and CBL-B, with the proviso that the first protein and the second protein are different.

[00260] In some embodiments, the first protein and the second protein are selected from the group consisting of PD-1 and CTLA-4.

[00261] In some embodiments, the first protein and the second protein are selected from the group consisting of PD-1 and LAG-3.

[00262] In some embodiments, the first protein and the second protein are selected from the group consisting of PD-1 and CISH.

[00263] In some embodiments, the first protein and the second protein are selected from the group consisting of PD-1 and CBL-B.

[00264] In some embodiments, the first protein and the second protein are selected from the group consisting of PD-1 and TIGIT.

[00265] In some embodiments, the first protein and the second protein are selected from the group consisting of CTLA-4 and LAG-3.

[00266] In some embodiments, the first protein and the second protein are selected from the group consisting of CTLA-4 and CISH.

[00267] In some embodiments, the first protein and the second protein are selected from the group consisting of CTLA-4 and CBL-B.

[00268] In some embodiments, the first protein and the second protein are selected from the group consisting of LAG-3 and CISH.

[00269] In some embodiments, the first protein and the second protein are selected from the group consisting of LAG-3 and CBL-B.

[00270] In some embodiments, the first protein and the second protein are selected from the group consisting of CISH and CBL-B.

[00271] In some embodiments, the first protein is PD-1 and the second protein is CTLA-4.

[00272] In some embodiments, the first protein is CTLA-4 and the second protein is PD-1.

[00273] In some embodiments, the first protein is PD-1 and the second protein is LAG-3.

[00274] In some embodiments, the first protein is LAG-3 and the second protein is PD-1.

[00275] In some embodiments, the first protein is PD-1 and the second protein is CISH.

[00276] In some embodiments, the first protein is CISH and the second protein is PD-1.

[00277] In some embodiments, the first protein is PD-1 and the second protein is CBL-B.

[00278] In some embodiments, the first protein is CBL-B and the second protein is PD-1.

[00279] In some embodiments, the first protein is PD-1 and the second protein is TIGIT.

[00280] In some embodiments, the first protein is TIGIT and the second protein is PD-1.

[00281] In some embodiments, the first protein is CTLA-4 and the second protein is LAG-3.

[00282] In some embodiments, the first protein is LAG-3 and the second protein is CTLA-4.

[00283] In some embodiments, the first protein is CTLA-4 and the second protein is CISH.

[00284] In some embodiments, the first protein is CISH and the second protein is CTLA-4.

[00285] In some embodiments, the first protein is CTLA-4 and the second protein is CBL-B.

[00286] In some embodiments, the first protein is CBL-B and the second protein is CTLA-4.

[00287] In some embodiments, the first protein is LAG-3 and the second protein is CISH.

[00288] In some embodiments, the first protein is CISH and the second protein is LAG-3.

[00289] In some embodiments, the first protein is LAG-3 and the second protein is CBL-B.

[00290] In some embodiments, the first protein is CBL-B and the second protein is LAG-3.

[00291] In some embodiments, the first protein is CISH and the second protein is CBL-B.

[00292] In some embodiments, the first protein is CBL-B and the second protein is CISH.

[00293] In some embodiments, the first protein or the second protein is PD-1.

[00294] In some embodiments, the first protein or the second protein is CTLA-4.

[00295] In some embodiments, the first protein or the second protein is LAG-3.

[00296] In some embodiments, the first protein or the second protein is CISH.

[00297] In some embodiments, the first protein or the second protein is CBL-B.

[00298] In some embodiments, the first protein or the second protein is TIGIT.

[00299] In some embodiments, the first gene editor downregulates expression of the first protein and the second gene editor downregulates expression of the second protein.

[00300] In some embodiments, the expanded number of TILs comprises a therapeutic population of TILs.

[00301] In some embodiments, the antigen presenting cells (APCs) are PBMCs.

[00302] In some embodiments, the PBMCs are irradiated and allogeneic.

[00303] In some embodiments, the antigen-presenting cells are artificial antigen-presenting cells.

[00304] In some embodiments, the IL-2 concentration is about 10,000 IU/mL to about 5,000 IU/mL.

[00305] In some embodiments, the first cell culture medium and/or the second cell culture medium further comprises a 4-1BB agonist and/or an OX40 agonist.

[00306] In some embodiments, the patient is naïve to an ICI treatment, an anti-VEGF treatment, a chemotherapeutic treatment, or combinations thereof.

[00307] In some embodiments, the patient is naïve to any cancer treatment.

[00308] In some embodiments, the patient receives a first-line ICI treatment and/or standard treatment.

[00309] In some embodiments, the patient receives a second-line ICI treatment and/or standard treatment.

[00310] In some embodiments, step of thawing and the subsequent steps are performed after the patient receives the cancer treatment or resumes the maintenance therapy and exhibits progressive disease.

[00311] In some embodiments, the patient is in a washout period at initiation of step (a).

[00312] In some embodiments, the present disclosures provide a method of treating a cancer patient by administering a population of tumor infiltrating lymphocytes (TILs) to the cancer patient in need thereof, wherein the cancer patient has received at least one prior therapy and has exhibited cancer progression on or after the at least one prior therapy, wherein obtaining the population of the TILs comprises multilesional sampling, wherein the population of TILs was made from a tumor sample harvested before the cancer patient receives the at least one prior therapy; and wherein the population of TILs is administered to the subject or patient after the cancer patient has exhibited cancer progression on or after the at least one prior therapy.

[00313] In some embodiments, the present disclosures provide a method of treating a cancer patient by administering a population of tumor infiltrating lymphocytes (TILs) to the cancer patient in need thereof, wherein the cancer patient has received at least one prior therapy and has exhibited cancer progression on or after the at least one prior therapy, wherein obtaining the population of the TILs comprises multilesional sampling, wherein the population of TILs was made before the cancer patient receives the at least one prior therapy and wherein the population of TILs is administered to the subject or patient after the cancer patient has exhibited cancer progression on or after the at least one prior therapy.

[00314] In some embodiments, at the time of harvesting the tumor sample, the cancer patient is naïve to any cancer treatment.

[00315] In some embodiments, at the time of harvesting the tumor sample, the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

[00316] In some embodiments, at the time of harvesting the tumor sample, the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after cryopreserving.

[00317] In some embodiments, at the time of harvesting the tumor sample, the patient is in a washout period at initiation of step of cryopreserving.

[00318] In some embodiments, the patient receives or is going to receive a first-line ICI treatment and/or standard treatment.

[00319] In some embodiments, the patient receives or is going to receive a second-line ICI treatment and/or standard treatment.

[00320] In some embodiments, the method further comprising administering an ICI to the cancer patient.

[00321] In some embodiments, the ICI is an inhibitor of a gene selected from the group consisting of PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00322] The method of any one of Claims 1 to 76, further comprising the step of treating the patient with a non-myeloablative lymphodepletion regimen prior to administering the population of TILs to the patient.

[00323] The method of claim 77, wherein the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m2/day for two days followed by administration of fludarabine at a dose of 25 mg/m2/day for five days.

[00324] The method of Claim 77, wherein the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m2/day and

fludarabine at a dose of 25 mg/m2/day for two days followed by administration of fludarabine at a dose of 25 mg/m2/day for three days.

[00325] The method of Claim 79 to 79, wherein the cyclophosphamide is administered with mesna.

[00326] The method of any one of Claims 1 to 80, further comprising the step of treating the patient with an IL-2 regimen starting on the day after administration of the population of TILs to the patient.

[00327] The method of any one of Claims 1 to 80, further comprising the step of treating the patient with an IL-2 regimen starting on the same day as administration of the population of TILs to the patient.

[00328] The method of any one of Claims 1 to 82, wherein the IL-2 regimen is a high-dose IL-2 regimen comprising 600,000 or 720,000 IU/kg of aldesleukin, or a biosimilar or variant thereof, administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

[00329] An expanded number of tumor infiltrating lymphocytes (TILs) or a therapeutic population of TILs manufactured by the method of any of claims 1-291.

[00330] A pharmaceutical composition comprising the expanded number of TILs or therapeutic population of TILs provided herein and a pharmaceutically acceptable carrier.

[00331] A population of TILs manufactured using the method disclosed herein.

[00332] A pharmaceutical composition comprising the population of TILs disclosed herein.

[00333] The pharmaceutical composition disclosed herein, further comprising an ICI.

[00334] The pharmaceutical composition disclosed herein, wherein the ICI is an inhibitor of a gene selected from the group consisting of PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00335] In some embodiments, the present disclosures provide a method of treating a cancer patient by administering the population of TILs disclosed herein or the pharmaceutical composition disclosed herein to the cancer patient, wherein the cancer patient has received at least one prior therapy, and the cancer patient exhibits cancer progression on or after the at least one prior therapy.

BRIEF DESCRIPTION OF THE DRAWINGS

[00336] Figure 1: Exemplary Gen 2 (Process 2A) type chart providing an overview of Steps A through F.

[00337] Figures 2A-2C: Exemplary process flow chart of Gen 2 (Process 2A) type process.

[00338] Figure 3: Shows a diagram of an embodiment of a cryopreserved TIL exemplary manufacturing process (~22 days).

[00339] Figure 4: Shows a diagram of an embodiment of Gen 2, a 22-day process for TIL manufacturing.

[00340] Figure 5: Comparison table of Steps A through F from exemplary embodiments of process 1C and Gen 2.

[00341] Figure 6: Detailed comparison of an embodiment of process 1C and an embodiment of Gen 2.

[00342] Figure 7: Exemplary Gen 3 type process for NSCLC tumors.

[00343] Figure 8A-8D: A) Shows a comparison between the 2A process (approximately 22-day process) and an embodiment of the Gen 3 process for TIL manufacturing (approximately 14-days to 16-days process). **B)** Exemplary Process Gen 3 chart providing an overview of Steps A through F (approximately 14-days to 16-days process). **C)** Chart providing three exemplary Gen 3 processes with an overview of Steps A through F (approximately 14-days to 16-days process) for each of the three process variations. **D)** Exemplary Modified Gen 2-like process providing an overview of Steps A through F (approximately 22-days process).

[00344] Figure 9: Provides an experimental flow chart for comparability between Gen 2 (Gen 2) versus Gen 3.

[00345] Figure 10: Shows a comparison between various Gen 2 (2A process) and the Gen 3.1 process embodiment.

[00346] Figure 11: Table describing various features of embodiments of the Gen 2, Gen 2.1 and Gen 3.0 process.

[00347] Figure 12: Overview of the media conditions for an embodiment of the Gen 3 process, referred to as Gen 3.1.

[00348] Figure 13: Table describing various features of embodiments of the Gen 2, Gen 2.1 and Gen 3.0 process.

[00349] Figure 14: Table comparing various features of embodiments of the Gen 2 and Gen 3.0 processes.

[00350] Figure 15: Table providing media uses in the various embodiments of the described expansion processes.

[00351] Figure 16: Schematic of an exemplary embodiment of the Gen 3 process (a 16-day process).

[00352] Figure 17: Schematic of an exemplary embodiment of a method for expanding T cells from hematopoietic malignancies using Gen 3 expansion platform.

[00353] Figure 18: Provides the structures I-A and I-B, the cylinders refer to individual polypeptide binding domains. Structures I-A and I-B comprise three linearly-linked TNFRSF binding domains derived from *e.g.*, 4-1BBL or an antibody that binds 4-1BB, which fold to form a trivalent protein, which is then linked to a second trivalent protein through IgG1-Fc (including CH3 and CH2 domains) is then used to link two of the trivalent proteins together through disulfide bonds (small elongated ovals), stabilizing the structure and providing an agonists capable of bringing together the intracellular signaling domains of the six receptors and signaling proteins to form a signaling complex. The TNFRSF binding domains denoted as cylinders may be scFv domains comprising, *e.g.*, a VH and a VL chain connected by a linker that may comprise hydrophilic residues and Gly and Ser sequences for flexibility, as well as Glu and Lys for solubility.

[00354] Figure 19: Schematic of an exemplary embodiment of the Gen 3 process (a 16-day process).

[00355] Figure 20: Provides a process overview for an exemplary embodiment of the Gen 3.1 process (a 16 day process).

[00356] Figure 21: Schematic of an exemplary embodiment of the Gen 3.1 Test process (a 16-17 day process).

[00357] Figure 22: Schematic of an exemplary embodiment of the Gen 3 process (a 16-day process).

[00358] Figure 23A-23B: Comparison table for exemplary Gen 2 and exemplary Gen 3 processes.

[00359] Figure 24: Schematic of an exemplary embodiment of the Gen 3 process (a 16/17 day process) preparation timeline.

[00360] Figure 25: Schematic of an exemplary embodiment of the Gen 3 process (a 14-16 day process).

[00361] Figure 26A-26B: Schematic of an exemplary embodiment of the Gen 3 process (a 16 day process).

[00362] Figure 27: Schematic of an exemplary embodiment of the Gen 3 process (a 16 day process).

[00363] Figure 28: Comparison of Gen 2, Gen 2.1 and an embodiment of the Gen 3 process (a 16 day process).

[00364] Figure 29: Comparison of Gen 2, Gen 2.1 and an embodiment of the Gen 3 process (a 16 day process).

[00365] Figure 30: Gen 3 embodiment components.

[00366] Figure 31: Gen 3 embodiment flow chart comparison (Gen 3.0, Gen 3.1 control, Gen 3.1 Test).

[00367] Figure 32: Shown are the components of an exemplary embodiment of the Gen 3 process (a 16-17 day process).

[00368] Figure 33: Acceptance criteria table.

[00369] Figure 34: Diagram of Study Design related to study described in Example 19.

[00370] Figure 35: Schematic of TIL-based immunotherapy manufacturing process related to the study described in Example 19. Abbreviations: CMO = contract manufacturing organization; GMP = Good Manufacturing Practices; IL-2 = interleukin-2; OKT3 = monoclonal antibody to CD3; TIL = tumor infiltrating lymphocytes.

[00371] Figure 36: Study Flowchart (all four cohorts).

[00372] Figure 37: Patient journey and central Gen 2 GMP manufacturing.

[00373] Figure 38: Cohort 3B patient treatment schema.

[00374] Figure 39: Patient disposition.

[00375] Figure 40: Adverse events over time (FAS).

[00376] Figure 41: Best percentage change from baseline in target lesion sum of diameters (efficacy-evaluable set).

[00377] **Figure 42:** Time to first response, duration of response, and time on efficacy assessment for confirmed responders who achieved PR or better.

[00378] **Figure 43:** Percentage change from baseline in target lesion sum of diameters (FAS).

[00379] **Figure 44:** TIL manufacturing and patient journey.

[00380] **Figure 45:** Study design and endpoints.

[00381] **Figure 46:** Treatment schema.

[00382] **Figure 47:** Treatment schema for patients with post- and pre-progression tumor harvest.

[00383] **Figure 48A-48D:** Schematics of exemplary embodiments of the KO TIL TALEN process.

[00384] **Figure 49:** Experimental flow diagram of full-scale PD-1 KO TIL TALEN process.

[00385] **Figure 50:** Experimental flow diagram of full-scale PD-1 KO TIL TALEN process.

[00386] **Figure 51A-51J:** Exemplary membrane anchored immunomodulatory fusion proteins that can be included in the TILs described herein.

[00387] **Figure 52A-52D:** Exemplary membrane anchored immunomodulatory fusion proteins that can be included in the TILs described herein.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

[00388] SEQ ID NO:1 is the amino acid sequence of the heavy chain of muromonab.

[00389] SEQ ID NO:2 is the amino acid sequence of the light chain of muromonab.

[00390] SEQ ID NO:3 is the amino acid sequence of a recombinant human IL-2 protein.

[00391] SEQ ID NO:4 is the amino acid sequence of aldesleukin.

[00392] SEQ ID NO:5 is an IL-2 form.

[00393] SEQ ID NO:6 is the amino acid sequence of nemvaleukin alfa.

[00394] SEQ ID NO:7 is an IL-2 form.

[00395] SEQ ID NO:8 is a mucin domain polypeptide.

[00396] SEQ ID NO:9 is the amino acid sequence of a recombinant human IL-4 protein.

[00397] SEQ ID NO:10 is the amino acid sequence of a recombinant human IL-7 protein.

[00398] SEQ ID NO:11 is the amino acid sequence of a recombinant human IL-15 protein.

[00399] SEQ ID NO:12 is the amino acid sequence of a recombinant human IL-21 protein.

[00400] SEQ ID NO:13 is an IL-2 sequence.

[00401] SEQ ID NO:14 is an IL-2 mutein sequence.

[00402] SEQ ID NO:15 is an IL-2 mutein sequence.

[00403] SEQ ID NO:16 is the HCDR1_IL-2 for IgG.IL2R67A.H1.

[00404] SEQ ID NO:17 is the HCDR2 for IgG.IL2R67A.H1.

[00405] SEQ ID NO:18 is the HCDR3 for IgG.IL2R67A.H1.

[00406] SEQ ID NO:19 is the HCDR1_IL-2 kabat for IgG.IL2R67A.H1.

[00407] SEQ ID NO:20 is the HCDR2 kabat for IgG.IL2R67A.H1.

[00408] SEQ ID NO:21 is the HCDR3 kabat for IgG.IL2R67A.H1.

[00409] SEQ ID NO:22 is the HCDR1_IL-2 clothia for IgG.IL2R67A.H1.

[00410] SEQ ID NO:23 is the HCDR2 clothia for IgG.IL2R67A.H1.

[00411] SEQ ID NO:24 is the HCDR3 clothia for IgG.IL2R67A.H1.

[00412] SEQ ID NO:25 is the HCDR1_IL-2 IMGT for IgG.IL2R67A.H1.

[00413] SEQ ID NO:26 is the HCDR2 IMGT for IgG.IL2R67A.H1.

[00414] SEQ ID NO:27 is the HCDR3 IMGT for IgG.IL2R67A.H1.

[00415] SEQ ID NO:28 is the VH chain for IgG.IL2R67A.H1.

[00416] SEQ ID NO:29 is the heavy chain for IgG.IL2R67A.H1.

[00417] SEQ ID NO:30 is the LCDR1 kabat for IgG.IL2R67A.H1.

[00418] SEQ ID NO:31 is the LCDR2 kabat for IgG.IL2R67A.H1.

[00419] SEQ ID NO:32 is the LCDR3 kabat for IgG.IL2R67A.H1.

[00420] SEQ ID NO:33 is the LCDR1 chothia for IgG.IL2R67A.H1.

[00421] SEQ ID NO:34 is the LCDR2 chothia for IgG.IL2R67A.H1.

[00422] SEQ ID NO:35 is the LCDR3 chothia for IgG.IL2R67A.H1.

[00423] SEQ ID NO:36 is a VL chain.

[00424] SEQ ID NO:37 is a light chain.

[00425] SEQ ID NO:38 is a light chain.

[00426] SEQ ID NO:39 is a light chain.

[00427] SEQ ID NO:40 is the amino acid sequence of human 4-1BB.

[00428] SEQ ID NO:41 is the amino acid sequence of murine 4-1BB.

[00429] SEQ ID NO:42 is the heavy chain for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00430] SEQ ID NO:43 is the light chain for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00431] SEQ ID NO:44 is the heavy chain variable region (V_H) for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00432] SEQ ID NO:45 is the light chain variable region (V_L) for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00433] SEQ ID NO:46 is the heavy chain CDR1 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00434] SEQ ID NO:47 is the heavy chain CDR2 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00435] SEQ ID NO:48 is the heavy chain CDR3 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00436] SEQ ID NO:49 is the light chain CDR1 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00437] SEQ ID NO:50 is the light chain CDR2 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00438] SEQ ID NO:51 is the light chain CDR3 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[00439] SEQ ID NO:52 is the heavy chain for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00440] SEQ ID NO:53 is the light chain for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00441] SEQ ID NO:54 is the heavy chain variable region (VH) for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00442] SEQ ID NO:55 is the light chain variable region (VL) for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00443] SEQ ID NO:56 is the heavy chain CDR1 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00444] SEQ ID NO:57 is the heavy chain CDR2 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00445] SEQ ID NO:58 is the heavy chain CDR3 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00446] SEQ ID NO:59 is the light chain CDR1 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00447] SEQ ID NO:60 is the light chain CDR2 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00448] SEQ ID NO:61 is the light chain CDR3 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[00449] SEQ ID NO:62 is an Fc domain for a TNFRSF agonist fusion protein.

[00450] SEQ ID NO:63 is a linker for a TNFRSF agonist fusion protein.

[00451] SEQ ID NO:64 is a linker for a TNFRSF agonist fusion protein.

[00452] SEQ ID NO:65 is a linker for a TNFRSF agonist fusion protein.

[00453] SEQ ID NO:66 is a linker for a TNFRSF agonist fusion protein.

[00454] SEQ ID NO:67 is a linker for a TNFRSF agonist fusion protein.

[00455] SEQ ID NO:68 is a linker for a TNFRSF agonist fusion protein.

[00456] SEQ ID NO:69 is a linker for a TNFRSF agonist fusion protein.

[00457] SEQ ID NO:70 is a linker for a TNFRSF agonist fusion protein.

[00458] SEQ ID NO:71 is a linker for a TNFRSF agonist fusion protein.

[00459] SEQ ID NO:72 is a linker for a TNFRSF agonist fusion protein.

[00460] SEQ ID NO:73 is an Fc domain for a TNFRSF agonist fusion protein.

[00461] SEQ ID NO:74 is a linker for a TNFRSF agonist fusion protein.

[00462] SEQ ID NO:75 is a linker for a TNFRSF agonist fusion protein.

[00463] SEQ ID NO:76 is a linker for a TNFRSF agonist fusion protein.

[00464] SEQ ID NO:77 is a 4-1BB ligand (4-1BBL) amino acid sequence.

[00465] SEQ ID NO:78 is a soluble portion of 4-1BBL polypeptide.

[00466] SEQ ID NO:79 is a heavy chain variable region (V_H) for the 4-1BB agonist antibody 4B4-1-1 version 1.

[00467] SEQ ID NO:80 is a light chain variable region (V_L) for the 4-1BB agonist antibody 4B4-1-1 version 1.

[00468] SEQ ID NO:81 is a heavy chain variable region (VH) for the 4-1BB agonist antibody 4B4-1-1 version 2.

[00469] SEQ ID NO:82 is a light chain variable region (V_L) for the 4-1BB agonist antibody 4B4-1-1 version 2.

[00470] SEQ ID NO:83 is a heavy chain variable region (V_H) for the 4-1BB agonist antibody H39E3-2.

[00471] SEQ ID NO:84 is a light chain variable region (V_L) for the 4-1BB agonist antibody H39E3-2.

[00472] SEQ ID NO:85 is the amino acid sequence of human OX40.

[00473] SEQ ID NO:86 is the amino acid sequence of murine OX40.

[00474] SEQ ID NO:87 is the heavy chain for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00475] SEQ ID NO:88 is the light chain for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00476] SEQ ID NO:89 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00477] SEQ ID NO:90 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00478] SEQ ID NO:91 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00479] SEQ ID NO:92 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00480] SEQ ID NO:93 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00481] SEQ ID NO:94 is the light chain CDR1 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00482] SEQ ID NO:95 is the light chain CDR2 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00483] SEQ ID NO:96 is the light chain CDR3 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00484] SEQ ID NO:97 is the heavy chain for the OX40 agonist monoclonal antibody 11D4.

[00485] SEQ ID NO:98 is the light chain for the OX40 agonist monoclonal antibody 11D4.

[00486] SEQ ID NO:99 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 11D4.

[00487] SEQ ID NO:100 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 11D4.

[00488] SEQ ID NO:101 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody 11D4.

[00489] SEQ ID NO:102 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody 11D4.

[00490] SEQ ID NO:103 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody 11D4.

[00491] SEQ ID NO:104 is the light chain CDR1 for the OX40 agonist monoclonal antibody 11D4.

[00492] SEQ ID NO:105 is the light chain CDR2 for the OX40 agonist monoclonal antibody 11D4.

[00493] SEQ ID NO:106 is the light chain CDR3 for the OX40 agonist monoclonal antibody 11D4.

[00494] SEQ ID NO:107 is the heavy chain for the OX40 agonist monoclonal antibody 18D8.

[00495] SEQ ID NO:108 is the light chain for the OX40 agonist monoclonal antibody 18D8.

[00496] SEQ ID NO:109 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 18D8.

[00497] SEQ ID NO:110 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 18D8.

[00498] SEQ ID NO:111 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody 18D8.

[00499] SEQ ID NO:112 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody 18D8.

[00500] SEQ ID NO:113 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody 18D8.

[00501] SEQ ID NO:114 is the light chain CDR1 for the OX40 agonist monoclonal antibody 18D8.

[00502] SEQ ID NO:115 is the light chain CDR2 for the OX40 agonist monoclonal antibody 18D8.

[00503] SEQ ID NO:116 is the light chain CDR3 for the OX40 agonist monoclonal antibody 18D8.

[00504] SEQ ID NO:117 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody Hu119-122.

[00505] SEQ ID NO:118 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody Hu119-122.

[00506] SEQ ID NO:119 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody Hu119-122.

[00507] SEQ ID NO:120 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody Hu119-122.

[00508] SEQ ID NO:121 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody Hu119-122.

[00509] SEQ ID NO:122 is the light chain CDR1 for the OX40 agonist monoclonal antibody Hu119-122.

[00510] SEQ ID NO:123 is the light chain CDR2 for the OX40 agonist monoclonal antibody Hu119-122.

[00511] SEQ ID NO:124 is the light chain CDR3 for the OX40 agonist monoclonal antibody Hu119-122.

[00512] SEQ ID NO:125 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody Hu106-222.

[00513] SEQ ID NO:126 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody Hu106-222.

[00514] SEQ ID NO:127 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody Hu106-222.

[00515] SEQ ID NO:128 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody Hu106-222.

[00516] SEQ ID NO:129 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody Hu106-222.

[00517] SEQ ID NO:130 is the light chain CDR1 for the OX40 agonist monoclonal antibody Hu106-222.

[00518] SEQ ID NO:131 is the light chain CDR2 for the OX40 agonist monoclonal antibody Hu106-222.

[00519] SEQ ID NO:132 is the light chain CDR3 for the OX40 agonist monoclonal antibody Hu106-222.

[00520] SEQ ID NO:133 is an OX40 ligand (OX40L) amino acid sequence.

[00521] SEQ ID NO:134 is a soluble portion of OX40L polypeptide.

[00522] SEQ ID NO:135 is an alternative soluble portion of OX40L polypeptide.

[00523] SEQ ID NO:136 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 008.

[00524] SEQ ID NO:137 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 008.

[00525] SEQ ID NO:138 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 011.

[00526] SEQ ID NO:139 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 011.

[00527] SEQ ID NO:140 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 021.

[00528] SEQ ID NO:141 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 021.

[00529] SEQ ID NO:142 is the heavy chain variable region (V_H) for the OX40 agonist monoclonal antibody 023.

[00530] SEQ ID NO:143 is the light chain variable region (V_L) for the OX40 agonist monoclonal antibody 023.

[00531] SEQ ID NO:144 is the heavy chain variable region (V_H) for an OX40 agonist monoclonal antibody.

[00532] SEQ ID NO:145 is the light chain variable region (V_L) for an OX40 agonist monoclonal antibody.

[00533] SEQ ID NO:146 is the heavy chain variable region (V_H) for an OX40 agonist monoclonal antibody.

[00534] SEQ ID NO:147 is the light chain variable region (V_L) for an OX40 agonist monoclonal antibody.

[00535] SEQ ID NO:148 is the heavy chain variable region (V_H) for a humanized OX40 agonist monoclonal antibody.

[00536] SEQ ID NO:149 is the heavy chain variable region (V_H) for a humanized OX40 agonist monoclonal antibody.

[00537] SEQ ID NO:150 is the light chain variable region (V_L) for a humanized OX40 agonist monoclonal antibody.

[00538] SEQ ID NO:151 is the light chain variable region (V_L) for a humanized OX40 agonist monoclonal antibody.

[00539] SEQ ID NO:152 is the heavy chain variable region (V_H) for a humanized OX40 agonist monoclonal antibody.

[00540] SEQ ID NO:153 is the heavy chain variable region (V_H) for a humanized OX40 agonist monoclonal antibody.

[00541] SEQ ID NO:154 is the light chain variable region (V_L) for a humanized OX40 agonist monoclonal antibody.

[00542] SEQ ID NO:155 is the light chain variable region (V_L) for a humanized OX40 agonist monoclonal antibody.

[00543] SEQ ID NO:156 is the heavy chain variable region (V_H) for an OX40 agonist monoclonal antibody.

[00544] SEQ ID NO:157 is the light chain variable region (V_L) for an OX40 agonist monoclonal antibody.

[00545] SEQ ID NO:158 is the heavy chain amino acid sequence of the PD-1 inhibitor nivolumab.

[00546] SEQ ID NO:159 is the light chain amino acid sequence of the PD-1 inhibitor nivolumab.

[00547] SEQ ID NO:160 is the heavy chain variable region (V_H) amino acid sequence of the PD-1 inhibitor nivolumab.

[00548] SEQ ID NO:161 is the light chain variable region (V_L) amino acid sequence of the PD-1 inhibitor nivolumab.

[00549] SEQ ID NO:162 is the heavy chain CDR1 amino acid sequence of the PD-1 inhibitor nivolumab.

[00550] SEQ ID NO:163 is the heavy chain CDR2 amino acid sequence of the PD-1 inhibitor nivolumab.

[00551] SEQ ID NO:164 is the heavy chain CDR3 amino acid sequence of the PD-1 inhibitor nivolumab.

[00552] SEQ ID NO:165 is the light chain CDR1 amino acid sequence of the PD-1 inhibitor nivolumab.

[00553] SEQ ID NO:166 is the light chain CDR2 amino acid sequence of the PD-1 inhibitor nivolumab.

[00554] SEQ ID NO:167 is the light chain CDR3 amino acid sequence of the PD-1 inhibitor nivolumab.

[00555] SEQ ID NO:168 is the heavy chain amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00556] SEQ ID NO:169 is the light chain amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00557] SEQ ID NO:170 is the heavy chain variable region (V_H) amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00558] SEQ ID NO:171 is the light chain variable region (V_L) amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00559] SEQ ID NO:172 is the heavy chain CDR1 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00560] SEQ ID NO:173 is the heavy chain CDR2 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00561] SEQ ID NO:174 is the heavy chain CDR3 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00562] SEQ ID NO:175 is the light chain CDR1 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00563] SEQ ID NO:176 is the light chain CDR2 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00564] SEQ ID NO:177 is the light chain CDR3 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00565] SEQ ID NO:178 is the heavy chain amino acid sequence of the PD-L1 inhibitor durvalumab.

[00566] SEQ ID NO:179 is the light chain amino acid sequence of the PD-L1 inhibitor durvalumab.

[00567] SEQ ID NO:180 is the heavy chain variable region (V_H) amino acid sequence of the PD-L1 inhibitor durvalumab.

[00568] SEQ ID NO:181 is the light chain variable region (V_L) amino acid sequence of the PD-L1 inhibitor durvalumab.

[00569] SEQ ID NO:182 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00570] SEQ ID NO:183 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00571] SEQ ID NO:184 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00572] SEQ ID NO:185 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00573] SEQ ID NO:186 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00574] SEQ ID NO:187 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00575] SEQ ID NO:188 is the heavy chain amino acid sequence of the PD-L1 inhibitor avelumab.

[00576] SEQ ID NO:189 is the light chain amino acid sequence of the PD-L1 inhibitor avelumab.

[00577] SEQ ID NO:190 is the heavy chain variable region (V_H) amino acid sequence of the PD-L1 inhibitor avelumab.

[00578] SEQ ID NO:191 is the light chain variable region (V_L) amino acid sequence of the PD-L1 inhibitor avelumab.

[00579] SEQ ID NO:192 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor avelumab.

[00580] SEQ ID NO:193 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor avelumab.

[00581] SEQ ID NO:194 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor avelumab.

[00582] SEQ ID NO:195 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor avelumab.

[00583] SEQ ID NO:196 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor avelumab.

[00584] SEQ ID NO:197 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor avelumab.

[00585] SEQ ID NO:198 is the heavy chain amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00586] SEQ ID NO:199 is the light chain amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00587] SEQ ID NO:200 is the heavy chain variable region (V_H) amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00588] SEQ ID NO:201 is the light chain variable region (V_L) amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00589] SEQ ID NO:202 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00590] SEQ ID NO:203 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00591] SEQ ID NO:204 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00592] SEQ ID NO:205 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00593] SEQ ID NO:206 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00594] SEQ ID NO:207 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00595] SEQ ID NO:208 is the heavy chain amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00596] SEQ ID NO:209 is the light chain amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00597] SEQ ID NO:210 is the heavy chain variable region (V_H) amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00598] SEQ ID NO:211 is the light chain variable region (V_L) amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00599] SEQ ID NO:212 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00600] SEQ ID NO:213 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00601] SEQ ID NO:214 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00602] SEQ ID NO:215 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00603] SEQ ID NO:216 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00604] SEQ ID NO:217 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00605] SEQ ID NO:218 is the heavy chain amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00606] SEQ ID NO:219 is the light chain amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00607] SEQ ID NO:220 is the heavy chain variable region (V_H) amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00608] SEQ ID NO:221 is the light chain variable region (V_L) amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00609] SEQ ID NO:222 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00610] SEQ ID NO:223 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00611] SEQ ID NO:224 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00612] SEQ ID NO:225 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00613] SEQ ID NO:226 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00614] SEQ ID NO:227 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00615] SEQ ID NO:228 is the heavy chain amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00616] SEQ ID NO:229 is the light chain amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00617] SEQ ID NO:230 is the heavy chain variable region (V_H) amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00618] SEQ ID NO:231 is the light chain variable region (V_L) amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00619] SEQ ID NO:232 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00620] SEQ ID NO:233 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00621] SEQ ID NO:234 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00622] SEQ ID NO:235 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00623] SEQ ID NO:236 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00624] SEQ ID NO:237 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00625] SEQ ID NO:238 is a CD8a transmembrane domain.

[00626] SEQ ID NO:239 is a B7-1 transmembrane-intracellular domain

[00627] SEQ ID NOs:240-245 are exemplary glycine-serine linkers that are useful in the immunomodulatory fusion proteins described herein.

[00628] SEQ ID NO:246 is an exemplary linker that is useful in the immunomodulatory fusion proteins described herein.

[00629] SEQ ID NO:247 is a 2A peptide C-terminus sequence.

[00630] SEQ ID NO:248 is a porcine teschovirus-1 2A peptide.

[00631] SEQ ID NO:249 is an equine rhinitis A virus 2A peptide.

[00632] SEQ ID NO:250 is a foot-and-mouth disease virus 2A peptide.

[00633] SEQ ID NO:251 is an exemplary furin-cleavable 2A peptide.

[00634] SEQ ID NOs:252 and 253 are human IgE signal peptide sequences.

[00635] SEQ ID NO:254 is a human IL-2 signal peptide sequence.

[00636] SEQ ID NO:255 is a 6X NFAT IL-2 minimal promoter.

[00637] SEQ ID NO:256 is an NFAT responsive element.

[00638] SEQ ID NO:257 is a human IL-2 promoter sequence.

[00639] SEQ ID NO:258 is human IL-15 (N72D mutant).

[00640] SEQ ID NO:259 is human IL-15R-alpha-Su/Fc domain.

[00641] SEQ ID NO:260 is human IL-15R-alpha-Su (65aa truncated extracellular domain).

[00642] SEQ ID NO:261 is human IL-15 isoform 2.

[00643] SEQ ID NO:262 is human IL-15 isoform 1.

[00644] SEQ ID NO:263 is human IL-15 (without signal peptide).

[00645] SEQ ID NO:264 is human IL-15R-alpha (85 aa truncated extracellular domain).

[00646] SEQ ID NO:265 is human IL-15R-alpha (182aa truncated extracellular domain).

[00647] SEQ ID NO:266 is human IL-15R-alpha.

[00648] SEQ ID NO:267 is human IL-12 p35 subunit.

[00649] SEQ ID NO:268 is human IL-12 p40 subunit.

[00650] SEQ ID NO:269 is human IL-18

[00651] SEQ ID NO:270is a human IL-18 variant

[00652] SEQ ID NO:271 is human IL-21.

[00653] SEQ ID NO: 272 is human IL-2

[00654] SEQ ID NO:273 is human CD40L

[00655] SEQ ID NO:274 is agonistic anti-human CD40 VH (Sotigalimab)

[00656] SEQ ID NO:275 is agonistic anti-human CD40 VL (Sotigalimab)

[00657] SEQ ID NO:276 is agonistic anti-human CD40 scFv (Sotigalimab)

[00658] SEQ ID NO:277 is agonistic anti-human CD40 VH (Dacetuzumab)

[00659] SEQ ID NO:278 is agonistic anti-human CD40 VL (Dacetuzumab)

[00660] SEQ ID NO:279 is agonistic anti-human CD40 scFv (Dacetuzumab)

[00661] SEQ ID NO:280 is agonistic anti-human CD40 VH (Lucatutuzumab)

[00662] SEQ ID NO:281 is agonistic anti-human CD40 VL (Lucatutuzumab)

[00663] SEQ ID NO:282 is agonistic anti-human CD40 scFv (Lucatutuzumab)

[00664] SEQ ID NO:283 is agonistic anti-human CD40 VH (Selicrelumab)

[00665] SEQ ID NO:284 is agonistic anti-human CD40 VL (Selicrelumab)

[00666] SEQ ID NO:285 is agonistic anti-human CD40 scFv (Selicrelumab)

[00667] SEQ ID NO:286 is a target PD-1 sequence.

[00668] SEQ ID NO:287 is a target PD-1 sequence.

[00669] SEQ ID NO:288 is a repeat PD-1 left repeat sequence.

[00670] SEQ ID NO:289 is a repeat PD-1 right repeat sequence.

[00671] SEQ ID NO:290 is a repeat PD-1 left repeat sequence.

[00672] SEQ ID NO:291 is a repeat PD-1 right repeat sequence.

[00673] SEQ ID NO:292 is a PD-1 left TALEN nuclease sequence.

[00674] SEQ ID NO:293 is a PD-1 right TALEN nuclease sequence.

[00675] SEQ ID NO:294 is a PD-1 left TALEN nuclease sequence.

[00676] SEQ ID NO:295 is a PD-1 right TALEN nuclease sequence.

[00677] SEQ ID NO:296 is a nucleic acid sequence that encodes for the tethered IL-15 of SEQ ID NO:328

[00678] SEQ ID NO:297 is a nucleic acid sequence that encodes for the tethered IL-21 fusion protein of SEQ ID NO: 331.

[00679] SEQ ID NO:298 is a nucleic acid sequence that encodes for the tethered IL-15 fusion protein of SEQ ID NO:328 and tether IL-21 fusion protein of SEQ ID NO:331.

[00680] SEQ ID NO:299 is a nucleic acid sequence that encodes for the tethered IL-12 fusion protein of SEQ ID NO:303. The nucleic acid sequence includes an NFAT promoter.

[00681] SEQ ID NO:300 is a nucleic acid sequence that encodes for the tethered IL-15 fusion protein of SEQ ID NO:328. The nucleic acid sequence includes an NFAT promoter.

[00682] SEQ ID NO:301 is a nucleic acid sequence that encodes for the tethered IL-21 fusion protein of SEQ ID NO:331. The nucleic acid sequence includes an NFAT promoter.

[00683] SEQ ID NO:302 is a nucleic acid sequence that encodes for the tethered IL-15 fusion protein of SEQ ID NO:328 and tether IL-21 fusion protein of SEQ ID NO:331. The nucleic acid sequence includes an NFAT promoter.

[00684] SEQ ID NO:303 is the amino acid sequence of an exemplary tethered IL-12 (tethered IL-12-Lr1-Ar2).

[00685] SEQ ID NO:304 is a nucleic acid sequence that encodes for the tethered IL-12 of SEQ ID NO:303.

[00686] SEQ ID NO:305 is the amino acid sequence of an exemplary tethered IL-18 (tethered IL-18-Lr1-Ar2).

[00687] SEQ ID NO:306 is a nucleic acid sequence that encodes for the tethered IL-18 of SEQ ID NO:305.

[00688] SEQ ID NO:307 is the amino acid sequence of an exemplary tethered variant IL-18 (tethered DR-IL-18 (6-27 variant)-Lr1-Ar2).

[00689] SEQ ID NO:308 is a nucleic acid sequence that encodes for the tethered variant IL-18 of SEQ ID NO:307.

[00690] SEQ ID NO:309 is the amino acid sequence of an exemplary tethered IL-12/IL-15.

[00691] SEQ ID NO:310 is a nucleic acid sequence that encodes for the tethered IL-12/IL-15 of SEQ ID NO:309.

[00692] SEQ ID NO:311 is the amino acid sequence of an exemplary tethered IL-18/IL-15.

[00693] SEQ ID NO:312 is a nucleic acid sequence that encodes for the tethered IL-18/IL-15 of SEQ ID NO:311.

[00694] SEQ ID NO:313 is the amino acid sequence of an exemplary tethered anti-CD40scFV (APX005M).

[00695] SEQ ID NO:314 is a nucleic acid sequence that encodes for the tethered anti-CD40scFV (APX005M) of SEQ ID NO:313.

[00696] SEQ ID NO:315 is the amino acid sequence of an exemplary tethered anti-CD40scFV (Dacetuzumab).

[00697] SEQ ID NO:316 is a nucleic acid sequence that encodes for the tethered anti-CD40scFV (Dacetuzumab) of SEQ ID NO:315.

[00698] SEQ ID NO:317 is the amino acid sequence of an exemplary tethered anti-CD40scFV (Lucatutuzumab).

[00699] SEQ ID NO:318 is a nucleic acid sequence that encodes for the tethered anti-CD40scFV (Lucatutuzumab) of SEQ ID NO:317.

[00700] SEQ ID NO:319 is the amino acid sequence of an exemplary tethered anti-CD40scFV (Selicrelumab).

[00701] SEQ ID NO:320 is a nucleic acid sequence that encodes for the tethered anti-CD40scFV (Selicrelumab) of SEQ ID NO:319.

[00702] SEQ ID NO:321 is a nucleic acid sequence that encodes for the CD40L of SEQ ID NO:273.

[00703] SEQ ID NO:322 is the amino acid sequence an exemplary tethered CD40L/IL-15.

[00704] SEQ ID NO:323 is a nucleic acid sequence that encodes for the tethered CD40L/IL-15 of SEQ ID NO:311.

[00705] SEQ ID NO:324 is the amino acid sequence of an exemplary tethered IL-2.

[00706] SEQ ID NO:325 is a nucleic acid sequence that encodes for the tethered IL-2 of SEQ ID NO:313.

[00707] SEQ ID NO:326 is the amino acid sequence of an exemplary tethered IL-12.

[00708] SEQ ID NO:327 is a nucleic acid sequence that encodes for the tethered IL-12 of SEQ ID NO:315.

[00709] SEQ ID NO:328 is the amino acid sequence of an exemplary tethered IL-15.

[00710] SEQ ID NO:329 is a nucleic acid sequence that encodes for the tethered IL-15 of SEQ ID NO:317.

[00711] SEQ ID NO:330 is a nucleic acid sequence that encodes for GFP.

[00712] SEQ ID NO:331 is the amino acid sequence of an exemplary tethered IL-21.

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

[00713] Adoptive cell therapy utilizing TILs cultured *ex vivo* by the Rapid Expansion Protocol (REP) has produced successful adoptive cell therapy following host immunosuppression in patients with cancer such as melanoma. Current infusion acceptance parameters rely on readouts of the composition of TILs (*e.g.*, CD28, CD8, or CD4 positivity) and on the numerical folds of expansion and viability of the REP product.

[00714] Current REP protocols give little insight into the health of the TIL that will be infused into the patient. T cells undergo a profound metabolic shift during the course of their maturation from naïve to effector T cells (see Chang, *et al.*, *Nat. Immunol.* **2016,** *17,* 364, hereby expressly incorporated in its entirety, and in particular for the discussion and markers of anaerobic and aerobic metabolism). For example, naïve T cells rely on mitochondrial respiration to produce ATP, while mature, healthy effector T cells such as TIL are highly glycolytic, relying on aerobic glycolysis to provide the bioenergetics substrates they require for proliferation, migration, activation, and anti-tumor efficacy.

[00715] Current TIL manufacturing and treatment processes are limited by length, cost, sterility concerns, and other factors described herein such that the potential to treat patients which are refractory to anti-PD1 and as such have been severely limited. There is an urgent need to provide TIL manufacturing processes and therapies based on such processes that are appropriate for use in treating patients for whom very few or no viable treatment options remain. The present invention meets this need by providing a shortened manufacturing process for use in generating TILs which can then be employed in the treatment of non-small cell lung carcinoma (NSCLC) patients whom are refractory to anti-PD-1 treatment.

II. Definitions

[00716] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which this invention belongs. All patents and publications referred to herein are incorporated by reference in their entireties.

[00717] The terms "co-administration," "co-administering," "administered in combination with," "administering in combination with," "simultaneous," and "concurrent," as used herein, encompass administration of two or more active pharmaceutical ingredients (in a preferred embodiment of the present invention, for example, a plurality of TILs) to a subject so that both active pharmaceutical ingredients and/or their metabolites are present in the subject at the same time. Co-administration includes simultaneous administration in separate compositions, administration at different times in separate compositions, or administration in a composition in which two or more active pharmaceutical ingredients are present. Simultaneous administration in separate compositions and administration in a composition in which both agents are present are preferred.

[00718] The term "*in vivo*" refers to an event that takes place in a subject's body.

[00719] The term "*in vitro*" refers to an event that takes places outside of a subject's body. In vitro assays encompass cell-based assays in which cells alive or dead are employed and may also encompass a cell-free assay in which no intact cells are employed.

[00720] The term "*ex vivo*" refers to an event which involves treating or performing a procedure on a cell, tissue and/or organ which has been removed from a subject's body. Aptly, the cell, tissue and/or organ may be returned to the subject's body in a method of surgery or treatment.

[00721] The term "rapid expansion" means an increase in the number of antigen-specific TILs of at least about 3-fold (or 4-, 5-, 6-, 7-, 8-, or 9-fold) over a period of a week, more preferably at least about 10-fold (or 20-, 30-, 40-, 50-, 60-, 70-, 80-, or 90-fold) over a period of a week, or most preferably at least about 100-fold over a period of a week. A number of rapid expansion protocols are described herein.

[00722] By "tumor infiltrating lymphocytes" or "TILs" herein is meant a population of cells originally obtained as white blood cells that have left the bloodstream of a subject and migrated into a tumor. TILs include, but are not limited to, $CD8^+$ cytotoxic T cells (lymphocytes), Th1 and Th17 $CD4^+$ T cells, natural killer cells, dendritic cells and M1 macrophages. TILs include both primary and secondary TILs. "Primary TILs" are those that are obtained from patient tissue samples as outlined herein (sometimes referred to as "freshly harvested"), and "secondary TILs" are any TIL cell populations that have been expanded or proliferated as discussed herein, including, but not limited to

bulk TILs and expanded TILs ("REP TILs" or "post-REP TILs"). TIL cell populations can include genetically modified TILs.

[00723] By "population of cells" (including TILs) herein is meant a number of cells that share common traits. In general, populations generally range from 1 X 10^6 to 1 X 10^{10} in number, with different TIL populations comprising different numbers. For example, initial growth of primary TILs in the presence of IL-2 results in a population of bulk TILs of roughly 1×10^8 cells. REP expansion is generally done to provide populations of 1.5×10^9 to 1.5×10^{10} cells for infusion.

[00724] By "cryopreserved TILs" herein is meant that TILs, either primary, bulk, or expanded (REP TILs), are treated and stored in the range of about -150°C to -60°C. General methods for cryopreservation are also described elsewhere herein, including in the Examples. For clarity, "cryopreserved TILs" are distinguishable from frozen tissue samples which may be used as a source of primary TILs.

[00725] By "thawed cryopreserved TILs" herein is meant a population of TILs that was previously cryopreserved and then treated to return to room temperature or higher, including but not limited to cell culture temperatures or temperatures wherein TILs may be administered to a patient.

[00726] TILs can generally be defined either biochemically, using cell surface markers, or functionally, by their ability to infiltrate tumors and effect treatment. TILs can be generally categorized by expressing one or more of the following biomarkers: CD4, CD8, TCR αβ, CD27, CD28, CD56, CCR7, CD45Ra, CD95, PD-1, and CD25. Additionally and alternatively, TILs can be functionally defined by their ability to infiltrate solid tumors upon reintroduction into a patient.

[00727] The term "cryopreservation media" or "cryopreservation medium" refers to any medium that can be used for cryopreservation of cells. Such media can include media comprising 7% to 10% DMSO. Exemplary media include CryoStor CS10, Hyperthermasol, as well as combinations thereof. The term "CS10" refers to a cryopreservation medium which is obtained from Stemcell Technologies or from Biolife Solutions. The CS10 medium may be referred to by the trade name "CryoStor® CS10". The CS10 medium is a serum-free, animal component-free medium which comprises DMSO.

[00728] The term "central memory T cell" refers to a subset of T cells that in the human are CD45R0+ and constitutively express CCR7 ($CCR7^{hi}$) and CD62L ($CD62^{hi}$). The surface phenotype of central memory T cells also includes TCR, CD3, CD127 (IL-7R), and IL-15R. Transcription factors for central memory T cells include BCL-6, BCL-6B, MBD2, and BMI1. Central memory T cells primarily secret IL-2 and CD40L as effector molecules after TCR triggering. Central memory T cells are predominant in the CD4 compartment in blood, and in the human are proportionally enriched in lymph nodes and tonsils.

[00729] The term "effector memory T cell" refers to a subset of human or mammalian T cells that, like central memory T cells, are CD45R0+, but have lost the constitutive expression of CCR7 ($CCR7^{lo}$) and are heterogeneous or low for CD62L expression ($CD62L^{lo}$). The surface phenotype of central memory T cells also includes TCR, CD3, CD127 (IL-7R), and IL-15R. Transcription factors for central memory T cells include BLIMP1. Effector memory T cells rapidly secret high levels of inflammatory cytokines following antigenic stimulation, including interferon-γ, IL-4, and IL-5. Effector memory T cells are predominant in the CD8 compartment in blood, and in the human are proportionally enriched in the lung, liver, and gut. CD8+ effector memory T cells carry large amounts of perforin.

[00730] The term "closed system" refers to a system that is closed to the outside environment. Any closed system appropriate for cell culture methods can be employed with the methods of the present invention. Closed systems include, for example, but are not limited to closed G-containers. Once a tumor segment is added to the closed system, the system is no opened to the outside environment until the TILs are ready to be administered to the patient.

[00731] The terms "fragmenting," "fragment," and "fragmented," as used herein to describe processes for disrupting a tumor, includes mechanical fragmentation methods such as crushing, slicing, dividing, and morcellating tumor tissue as well as any other method for disrupting the physical structure of tumor tissue.

[00732] The terms "peripheral blood mononuclear cells" and "PBMCs" refers to a peripheral blood cell having a round nucleus, including lymphocytes (T cells, B cells, NK cells) and monocytes. When used as an antigen presenting cell (PBMCs are a type of antigen-presenting cell), the peripheral blood mononuclear cells are preferably irradiated allogeneic peripheral blood mononuclear cells.

[00733] The terms "peripheral blood lymphocytes" and "PBLs" refer to T cells expanded from peripheral blood. In some embodiments, PBLs are separated from whole blood or apheresis product from a donor. In some embodiments, PBLs are separated from whole blood or apheresis product from a donor by positive or negative selection of a T cell phenotype, such as the T cell phenotype of CD3+ CD45+.

[00734] The term "anti-CD3 antibody" refers to an antibody or variant thereof, *e.g.*, a monoclonal antibody and including human, humanized, chimeric or murine antibodies which are directed against the CD3 receptor in the T cell antigen receptor of mature T cells. Anti-CD3 antibodies include OKT-3, also known as muromonab. Anti-CD3 antibodies also include the UHCT1 clone, also known as T3 and CD3ε. Other anti-CD3 antibodies include, for example, otelixizumab, teplizumab, and visilizumab.

[00735] The term "OKT-3" (also referred to herein as "OKT3") refers to a monoclonal antibody or biosimilar or variant thereof, including human, humanized, chimeric, or murine antibodies, directed against the CD3 receptor in the T cell antigen receptor of mature T cells, and includes commercially-available forms such as OKT-3 (30 ng/mL, MACS GMP CD3 pure, Miltenyi Biotech, Inc., San Diego, CA, USA) and muromonab or variants, conservative amino acid substitutions, glycoforms, or biosimilars thereof. The amino acid sequences of the heavy and light chains of muromonab are given in Table 1 (SEQ ID NO:1 and SEQ ID NO:2). A hybridoma capable of producing OKT-3 is deposited with the American Type Culture Collection and assigned the ATCC accession number CRL 8001. A hybridoma capable of producing OKT-3 is also deposited with European Collection of Authenticated Cell Cultures (ECACC) and assigned Catalogue No. 86022706.

TABLE 1. Amino acid sequences of muromonab (exemplary OKT-3 antibody).

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:1 muromonab heavy chain	QVQLQQSGAE LARPGASVKM SCKASGYTFT RYTMHWVKQR PGQGLEWIGY INPSRGYTNY NQKFKDKATL TTDKSSSTAY MQLSSLTSED SAVYYCARYY DDHYCLDYWG QGTTLTVSSA KTTAPSVYPL APVCGGTTGS SVTLGCLVKG YFPEPVTLTW NSGSLSSGVH TFPAVLQSDL YTLSSSVTVT SSTWPSQSIT CNVAHPASST KVDKKIEPRP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK	60 120 180 240 300 360 420 450
SEQ ID NO:2 muromonab light chain	QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMNWYQQKSG TSPKRWIYDT SKLASGVPAH FRGSGSGTSY SLTISGMEAE DAATYYCQQW SSNPFTFGSG TKLEINRADT APTVSIFPPS SEQLTSGGAS VVCFLNNFYP KDINVKWKID GSERQNGVLN SWTDQDSKDS TYSMSSTLTL TKDEYERHNS YTCEATHKTS TSPIVKSFNR NEC	60 120 180 213

[00736] The term "IL-2" (also referred to herein as "IL2") refers to the T cell growth factor known as interleukin-2, and includes all forms of IL-2 including human and mammalian forms, conservative amino acid substitutions, glycoforms, biosimilars, and variants thereof. IL-2 is described, *e.g.*, in Nelson, *J. Immunol.* **2004,** *172,* 3983-88 and Malek, *Annu. Rev. Immunol.* **2008,** *26,* 453-79, the disclosures of which are incorporated by reference herein. The amino acid sequence of recombinant human IL-2 suitable for use in the invention is given in Table 2 (SEQ ID NO:3). For example, the term IL-2 encompasses human, recombinant forms of IL-2 such as aldesleukin (PROLEUKIN, available commercially from multiple suppliers in 22 million IU per single use vials), as well as the form of recombinant IL-2 commercially supplied by CellGenix, Inc., Portsmouth, NH, USA (CELLGRO GMP) or ProSpec-Tany TechnoGene Ltd., East Brunswick, NJ, USA (Cat. No. CYT-209-b) and other commercial equivalents from other vendors. Aldesleukin (des-alanyl-1, serine-125 human IL-2) is a nonglycosylated human recombinant form of IL-2 with a molecular weight of approximately 15 kDa. The amino acid sequence of aldesleukin suitable for use in the invention is given in Table 2 (SEQ ID NO:4). The term IL-2 also encompasses pegylated forms of IL-2, as described herein, including the pegylated IL2 prodrug bempegaldesleukin (NKTR-214, pegylated human recombinant IL-2 as in SEQ ID NO:4 in which an average of 6 lysine residues are N^6

substituted with [(2,7-bis{[methylpoly(oxyethylene)]carbamoyl}-9H-fluoren-9-yl)methoxy]carbonyl), which is available from Nektar Therapeutics, South San Francisco, CA, USA, or which may be prepared by methods known in the art, such as the methods described in Example 19 of International Patent Application Publication No. WO 2018/132496 A1 or the method described in Example 1 of U.S. Patent Application Publication No. US 2019/0275133 A1, the disclosures of which are incorporated by reference herein. Bempegaldesleukin (NKTR-214) and other pegylated IL-2 molecules suitable for use in the invention is described in U.S. Patent Application Publication No. US 2014/0328791 A1 and International Patent Application Publication No. WO 2012/065086 Al, the disclosures of which are incorporated by reference herein. Alternative forms of conjugated IL-2 suitable for use in the invention are described in U.S. Patent Nos. 4,766,106, 5,206,344, 5,089,261 and 4,902,502, the disclosures of which are incorporated by reference herein. Formulations of IL-2 suitable for use in the invention are described in U.S. Patent No. 6,706,289, the disclosure of which is incorporated by reference herein.

[00737] In some embodiments, an IL-2 form suitable for use in the present invention is THOR-707, available from Synthorx, Inc. The preparation and properties of THOR-707 and additional alternative forms of IL-2 suitable for use in the invention are described in U.S. Patent Application Publication Nos. US 2020/0181220 A1 and US 2020/0330601 A1, the disclosures of which are incorporated by reference herein. In some embodiments, and IL-2 form suitable for use in the invention is an interleukin 2 (IL-2) conjugate comprising: an isolated and purified IL-2 polypeptide; and a conjugating moiety that binds to the isolated and purified IL-2 polypeptide at an amino acid position selected from K35, T37, R38, T41, F42, K43, F44, Y45, E61, E62, E68, K64, P65, V69, L72, and Y107, wherein the numbering of the amino acid residues corresponds to SEQ ID NO:5. In some embodiments, the amino acid position is selected from T37, R38, T41, F42, F44, Y45, E61, E62, E68, K64, P65, V69, L72, and Y107. In some embodiments, the amino acid position is selected from T37, R38, T41, F42, F44, Y45, E61, E62, E68, P65, V69, L72, and Y107. In some embodiments, the amino acid position is selected from T37, T41, F42, F44, Y45, P65, V69, L72, and Y107. In some embodiments, the amino acid position is selected from R38 and K64. In some embodiments, the amino acid position is selected from E61, E62, and E68. In some embodiments, the amino acid position is at E62. In some embodiments, the amino acid residue selected from K35, T37, R38, T41, F42, K43, F44, Y45, E61, E62, E68, K64, P65, V69, L72, and Y107 is further mutated to lysine, cysteine, or histidine. In some embodiments, the amino acid residue is mutated to cysteine. In some embodiments, the amino acid residue is mutated to lysine. In some embodiments, the amino acid residue selected from K35, T37, R38, T41, F42, K43, F44, Y45, E61, E62, E68, K64, P65, V69, L72, and Y107 is further mutated to an unnatural amino acid. In some embodiments, the unnatural amino acid comprises N6-azidoethoxy-L-lysine (AzK), N6-propargylethoxy-L-lysine (PraK), BCN-L-lysine, norbornene lysine, TCO-lysine, methyltetrazine lysine, allyloxycarbonyllysine, 2-amino-8-

oxononanoic acid, 2-amino-8-oxooctanoic acid, p-acetyl-L-phenylalanine, p-azidomethyl-L-phenylalanine (pAMF), p-iodo-L-phenylalanine, m-acetylphenylalanine, 2-amino-8-oxononanoic acid, p-propargyloxyphenylalanine, p-propargyl-phenylalanine, 3-methyl-phenylalanine, L-Dopa, fluorinated phenylalanine, isopropyl-L-phenylalanine, p-azido-L-phenylalanine, p-acyl-L-phenylalanine, p-benzoyl-L-phenylalanine, p-bromophenylalanine, p-amino-L-phenylalanine, isopropyl-L-phenylalanine, O-allyltyrosine, O-methyl-L-tyrosine, O-4-allyl-L-tyrosine, 4-propyl-L-tyrosine, phosphonotyrosine, tri-O-acetyl-GlcNAcp-serine, L-phosphoserine, phosphonoserine, L-3-(2-naphthyl)alanine, 2-amino-3-((2-((3-(benzyloxy)-3-oxopropyl)amino)ethyl)selanyl)propanoic acid, 2-amino-3-(phenylselanyl)propanoic, or selenocysteine. In some embodiments, the IL-2 conjugate has a decreased affinity to IL-2 receptor α (IL-2Rα) subunit relative to a wild-type IL-2 polypeptide. In some embodiments, the decreased affinity is about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or greater than 99% decrease in binding affinity to IL-2Rα relative to a wild-type IL-2 polypeptide. In some embodiments, the decreased affinity is about 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 30-fold, 50-fold, 100-fold, 200-fold, 300-fold, 500-fold, 1000-fold, or more relative to a wild-type IL-2 polypeptide. In some embodiments, the conjugating moiety impairs or blocks the binding of IL-2 with IL-2Rα. In some embodiments, the conjugating moiety comprises a water-soluble polymer. In some embodiments, the additional conjugating moiety comprises a water-soluble polymer. In some embodiments, each of the water-soluble polymers independently comprises polyethylene glycol (PEG), poly(propylene glycol) (PPG), copolymers of ethylene glycol and propylene glycol, poly(oxyethylated polyol), poly(olefinic alcohol), poly(vinylpyrrolidone), poly(hydroxyalkylmethacrylamide), poly(hydroxyalkylmethacrylate), poly(saccharides), poly(α-hydroxy acid), poly(vinyl alcohol), polyphosphazene, polyoxazolines (POZ), poly(N-acryloylmorpholine), or a combination thereof. In some embodiments, each of the water-soluble polymers independently comprises PEG. In some embodiments, the PEG is a linear PEG or a branched PEG. In some embodiments, each of the water-soluble polymers independently comprises a polysaccharide. In some embodiments, the polysaccharide comprises dextran, polysialic acid (PSA), hyaluronic acid (HA), amylose, heparin, heparan sulfate (HS), dextrin, or hydroxyethyl-starch (HES). In some embodiments, each of the water-soluble polymers independently comprises a glycan. In some embodiments, each of the water-soluble polymers independently comprises polyamine. In some embodiments, the conjugating moiety comprises a protein. In some embodiments, the additional conjugating moiety comprises a protein. In some embodiments, each of the proteins independently comprises an albumin, a transferrin, or a transthyretin. In some embodiments, each of the proteins independently comprises an Fc portion. In some embodiments, each of the proteins independently comprises an Fc portion of IgG. In some embodiments, the conjugating moiety comprises a polypeptide. In some embodiments, the additional conjugating moiety comprises a polypeptide. In some embodiments, each of the polypeptides independently comprises a XTEN

peptide, a glycine-rich homoamino acid polymer (HAP), a PAS polypeptide, an elastin-like polypeptide (ELP), a CTP peptide, or a gelatin-like protein (GLK) polymer. In some embodiments, the isolated and purified IL-2 polypeptide is modified by glutamylation. In some embodiments, the conjugating moiety is directly bound to the isolated and purified IL-2 polypeptide. In some embodiments, the conjugating moiety is indirectly bound to the isolated and purified IL-2 polypeptide through a linker. In some embodiments, the linker comprises a homobifunctional linker. In some embodiments, the homobifunctional linker comprises Lomant's reagent dithiobis (succinimidylpropionate) DSP, 3′3′-dithiobis(sulfosuccinimidyl proprionate) (DTSSP), disuccinimidyl suberate (DSS), bis(sulfosuccinimidyl)suberate (BS), disuccinimidyl tartrate (DST), disulfosuccinimidyl tartrate (sulfo DST), ethylene glycobis(succinimidylsuccinate) (EGS), disuccinimidyl glutarate (DSG), N,N′-disuccinimidyl carbonate (DSC), dimethyl adipimidate (DMA), dimethyl pimelimidate (DMP), dimethyl suberimidate (DMS), dimethyl-3,3′-dithiobispropionimidate (DTBP), 1,4-di-(3′-(2′-pyridyldithio)propionamido)butane (DPDPB), bismaleimidohexane (BMH), aryl halide-containing compound (DFDNB), such as e.g. 1,5-difluoro-2,4-dinitrobenzene or 1,3-difluoro-4,6-dinitrobenzene, 4,4′-difluoro-3,3′-dinitrophenylsulfone (DFDNPS), bis-[β-(4-azidosalicylamido)ethyl]disulfide (BASED), formaldehyde, glutaraldehyde, 1,4-butanediol diglycidyl ether, adipic acid dihydrazide, carbohydrazide, o-toluidine, 3,3′-dimethylbenzidine, benzidine, α,α′-p-diaminodiphenyl, diiodo-p-xylene sulfonic acid, N,N′-ethylene-bis(iodoacetamide), or N,N′-hexamethylene-bis(iodoacetamide). In some embodiments, the linker comprises a heterobifunctional linker. In some embodiments, the heterobifunctional linker comprises N-succinimidyl 3-(2-pyridyldithio)propionate (sPDP), long-chain N-succinimidyl 3-(2-pyridyldithio)propionate (LC-sPDP), water-soluble-long-chain N-succinimidyl 3-(2-pyridyldithio) propionate (sulfo-LC-sPDP), succinimidyloxycarbonyl-α-methyl-α-(2-pyridyldithio)toluene (sMPT), sulfosuccinimidyl-6-[α-methyl-α-(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-sMPT), succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sMCC), sulfosuccinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-sMCC), m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBs), m-maleimidobenzoyl-N-hydroxysulfosuccinimide ester (sulfo-MBs), N-succinimidyl(4-iodoacteyl)aminobenzoate (sIAB), sulfosuccinimidyl(4-iodoacteyl)aminobenzoate (sulfo-sIAB), succinimidyl-4-(p-maleimidophenyl)butyrate (sMPB), sulfosuccinimidyl-4-(p-maleimidophenyl)butyrate (sulfo-sMPB), N-(γ-maleimidobutyryloxy)succinimide ester (GMBs), N-(γ-maleimidobutyryloxy) sulfosuccinimide ester (sulfo-GMBs), succinimidyl 6-((iodoacetyl)amino)hexanoate (sIAX), succinimidyl 6-[6-(((iodoacetyl)amino)hexanoyl)amino]hexanoate (sIAXX), succinimidyl 4-(((iodoacetyl)amino)methyl)cyclohexane-1-carboxylate (sIAC), succinimidyl 6-(((((4-iodoacetyl)amino)methyl)cyclohexane-1-carbonyl)amino) hexanoate (sIACX), p-nitrophenyl iodoacetate (NPIA), carbonyl-reactive and sulfhydryl-reactive cross-linkers such as 4-(4-N-

maleimidophenyl)butyric acid hydrazide (MPBH), 4-(N-maleimidomethyl)cyclohexane-1-carboxyl-hydrazide-8 (M2C2H), 3-(2-pyridyldithio)propionyl hydrazide (PDPH), N-hydroxysuccinimidyl-4-azidosalicylic acid (NHs-AsA), N-hydroxysulfosuccinimidyl-4-azidosalicylic acid (sulfo-NHs-AsA), sulfosuccinimidyl-(4-azidosalicylamido)hexanoate (sulfo-NHs-LC-AsA), sulfosuccinimidyl-2-(p-azidosalicylamido)ethyl-1,3′-dithiopropionate (sAsD), N-hydroxysuccinimidyl-4-azidobenzoate (HsAB), N-hydroxysulfosuccinimidyl-4-azidobenzoate (sulfo-HsAB), N-succinimidyl-6-(4′-azido-2′-nitrophenyl amino)hexanoate (sANPAH), sulfosuccinimidyl-6-(4′-azido-2′-nitrophenylamino)hexanoate (sulfo-sANPAH), N-5-azido-2-nitrobenzoyloxysuccinimide (ANB-NOs), sulfosuccinimidyl-2-(m-azido-o-nitrobenzamido)-ethyl-1,3′-dithiopropionate (sAND), N-succinimidyl-4(4-azidophenyl)1,3′-dithiopropionate (sADP), N-sulfosuccinimidyl(4-azidophenyl)-1,3′-dithiopropionate (sulfo-sADP), sulfosuccinimidyl 4-(ρ-azidophenyl)butyrate (sulfo-sAPB), sulfosuccinimidyl 2-(7-azido-4-methylcoumarin-3-acetamide)ethyl-1,3′-dithiopropionate (sAED), sulfosuccinimidyl 7-azido-4-methylcoumain-3-acetate (sulfo-sAMCA), p-nitrophenyl diazopyruvate (pNPDP), p-nitrophenyl-2-diazo-3,3,3-trifluoropropionate (PNP-DTP), 1-(ρ-azidosalicylamido)-4-(iodoacetamido)butane (AsIB), N-[4-(ρ-azidosalicylamido)butyl]-3′-(2′-pyridyldithio) propionamide (APDP), benzophenone-4-iodoacetamide, p-azidobenzoyl hydrazide (ABH), 4-(ρ-azidosalicylamido)butylamine (AsBA), or p-azidophenyl glyoxal (APG). In some embodiments, the linker comprises a cleavable linker, optionally comprising a dipeptide linker. In some embodiments, the dipeptide linker comprises Val-Cit, Phe-Lys, Val-Ala, or Val-Lys. In some embodiments, the linker comprises a non-cleavable linker. In some embodiments, the linker comprises a maleimide group, optionally comprising maleimidocaproyl (mc), succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sMCC), or sulfosuccinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-sMCC). In some embodiments, the linker further comprises a spacer. In some embodiments, the spacer comprises p-aminobenzyl alcohol (PAB), p-aminobenzyoxycarbonyl (PABC), a derivative, or an analog thereof. In some embodiments, the conjugating moiety is capable of extending the serum half-life of the IL-2 conjugate. In some embodiments, the additional conjugating moiety is capable of extending the serum half-life of the IL-2 conjugate. In some embodiments, the IL-2 form suitable for use in the invention is a fragment of any of the IL-2 forms described herein. In some embodiments, the IL-2 form suitable for use in the invention is pegylated as disclosed in U.S. Patent Application Publication No. US 2020/0181220 A1 and U.S. Patent Application Publication No. US 2020/0330601 A1. In some embodiments, the IL-2 form suitable for use in the invention is an IL-2 conjugate comprising: an IL-2 polypeptide comprising an N6-azidoethoxy-L-lysine (AzK) covalently attached to a conjugating moiety comprising a polyethylene glycol (PEG), wherein: the IL-2 polypeptide comprises an amino acid sequence having at least 80% sequence identity to SEQ ID NO:5; and the AzK substitutes for an amino acid at position K35, F42, F44, K43, E62, P65, R38, T41, E68, Y45, V69, or L72 in reference

to the amino acid positions within SEQ ID NO:5. In some embodiments, the IL-2 polypeptide comprises an N-terminal deletion of one residue relative to SEQ ID NO:5. In some embodiments, the IL-2 form suitable for use in the invention lacks IL-2R alpha chain engagement but retains normal binding to the intermediate affinity IL-2R beta-gamma signaling complex. In some embodiments, the IL-2 form suitable for use in the invention is an IL-2 conjugate comprising: an IL-2 polypeptide comprising an N6-azidoethoxy-L-lysine (AzK) covalently attached to a conjugating moiety comprising a polyethylene glycol (PEG), wherein: the IL-2 polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO:5; and the AzK substitutes for an amino acid at position K35, F42, F44, K43, E62, P65, R38, T41, E68, Y45, V69, or L72 in reference to the amino acid positions within SEQ ID NO:5. In some embodiments, the IL-2 form suitable for use in the invention is an IL-2 conjugate comprising: an IL-2 polypeptide comprising an N6-azidoethoxy-L-lysine (AzK) covalently attached to a conjugating moiety comprising a polyethylene glycol (PEG), wherein: the IL-2 polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO:5; and the AzK substitutes for an amino acid at position K35, F42, F44, K43, E62, P65, R38, T41, E68, Y45, V69, or L72 in reference to the amino acid positions within SEQ ID NO:5. In some embodiments, the IL-2 form suitable for use in the invention is an IL-2 conjugate comprising: an IL-2 polypeptide comprising an N6-azidoethoxy-L-lysine (AzK) covalently attached to a conjugating moiety comprising a polyethylene glycol (PEG), wherein: the IL-2 polypeptide comprises an amino acid sequence having at least 98% sequence identity to SEQ ID NO:5; and the AzK substitutes for an amino acid at position K35, F42, F44, K43, E62, P65, R38, T41, E68, Y45, V69, or L72 in reference to the amino acid positions within SEQ ID NO:5.

[00738] In some embodiments, an IL-2 form suitable for use in the invention is nemvaleukin alfa, also known as ALKS-4230 (SEQ ID NO:6), which is available from Alkermes, Inc. Nemvaleukin alfa is also known as human interleukin 2 fragment (1-59), variant (Cys^{125}>Ser^{51}), fused via peptidyl linker ($^{60}GG^{61}$) to human interleukin 2 fragment (62-132), fused via peptidyl linker ($^{133}GSGGGS^{138}$) to human interleukin 2 receptor α-chain fragment (139-303), produced in Chinese hamster ovary (CHO) cells, glycosylated; human interleukin 2 (IL-2) (75-133)-peptide [Cys^{125}(51)>Ser]-mutant (1-59), fused via a G_2 peptide linker (60-61) to human interleukin 2 (IL-2) (4-74)-peptide (62-132) and via a GSG_3S peptide linker (133-138) to human interleukin 2 receptor α-chain (IL2R subunit alpha, IL2Rα, IL2RA) (1-165)-peptide (139-303), produced in Chinese hamster ovary (CHO) cells, glycoform alfa. The amino acid sequence of nemvaleukin alfa is given in SEQ ID NO:6. In some embodiments, nemvaleukin alfa exhibits the following post-translational modifications: disulfide bridges at positions: 31-116, 141-285, 184-242, 269-301, 166-197 or 166-199, 168-199 or 168-197 (using the numbering in SEQ ID NO:6), and glycosylation sites at positions: N187, N206, T212 using the numbering in SEQ ID NO:6. The preparation and properties of nemvaleukin alfa, as well as additional alternative forms of IL-2 suitable for use in the invention, is

described in U.S. Patent Application Publication No. US 2021/0038684 A1 and U.S. Patent No. 10,183,979, the disclosures of which are incorporated by reference herein. In some embodiments, an IL-2 form suitable for use in the invention is a protein having at least 80%, at least 90%, at least 95%, or at least 90% sequence identity to SEQ ID NO:6. In some embodiments, an IL-2 form suitable for use in the invention has the amino acid sequence given in SEQ ID NO:6 or conservative amino acid substitutions thereof. In some embodiments, an IL-2 form suitable for use in the invention is a fusion protein comprising amino acids 24-452 of SEQ ID NO:7, or variants, fragments, or derivatives thereof. In some embodiments, an IL-2 form suitable for use in the invention is a fusion protein comprising an amino acid sequence having at least 80%, at least 90%, at least 95%, or at least 90% sequence identity to amino acids 24-452 of SEQ ID NO:7, or variants, fragments, or derivatives thereof. Other IL-2 forms suitable for use in the present invention are described in U.S. Patent No. 10,183,979, the disclosures of which are incorporated by reference herein. Optionally, in some embodiments, an IL-2 form suitable for use in the invention is a fusion protein comprising a first fusion partner that is linked to a second fusion partner by a mucin domain polypeptide linker, wherein the first fusion partner is IL-1Rα or a protein having at least 98% amino acid sequence identity to IL-1Rα and having the receptor antagonist activity of IL-Rα, and wherein the second fusion partner comprises all or a portion of an immunoglobulin comprising an Fc region, wherein the mucin domain polypeptide linker comprises SEQ ID NO:8 or an amino acid sequence having at least 90% sequence identity to SEQ ID NO:8 and wherein the half-life of the fusion protein is improved as compared to a fusion of the first fusion partner to the second fusion partner in the absence of the mucin domain polypeptide linker.

TABLE 2. Amino acid sequences of interleukins.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:3 recombinant human IL-2 (rhIL-2)	MAPTSSSTKK TQLQLEHLLL DLQMILNGIN NYKNPKLTRM LTFKFYMPKK ATELKHLQCL EEELKPLEEV LNLAQSKNFH LRPRDLISNI NVIVLELKGS ETTFMCEYAD ETATIVEFLN RWITFCQSII STLT	60 120 134
SEQ ID NO:4 Aldesleukin	PTSSSTKKTQ LQLEHLLLDL QMILNGINNY KNPKLTRMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFSQSIIST LT	60 120 132
SEQ ID NO:5 IL-2 form	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT	60 120 133
SEQ ID NO:6 Nemvaleukin alfa	SKNFHLRPRD LISNINVIVL ELKGSETTFM CEYADETATI VEFLNRWITF SQSIISTLTG GSSSTKKTQL QLEHLLLDLQ MILNGINNYK NPKLTRMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQGSGGGSEL CDDDPPEIPH ATFKAMAYKE GTMLNCECKR GFRRIKSGSL YMLCTGNSSH SSWDNQCQCT SSATRNTTKQ VTPQPEEQKE RKTTEMQSPM QPVDQASLPG HCREPPPWEN EATERIYHFV VGQMVYYQCV QGYRALHRGP AESVCKMTHG KTRWTQPQLI CTG	60 120 180 240 300 303
SEQ ID NO:7 IL-2 form	MDAMKRGLCC VLLLCGAVFV SARRPSGRKS SKMQAFRIWD VNQKTFYLRN NQLVAGYLQG PNVNLEEKID VVPIEPHALF LGIHGGKMCL SCVKSGDETR LQLEAVNITD LSENRKQDKR FAFIRSDSGP TTSFESAACP GWFLCTAMEA DQPVSLTNMP DEGVMVTKFY FQEDESGSGG ASSESSASSD GPHPVITESR ASSESSASSD GPHPVITESR EPKSSDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	60 120 180 240 300 360 420

	RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK	452
SEQ ID NO:8 mucin domain polypeptide	SESSASSDGP HPVITP	16
SEQ ID NO:9 recombinant human IL-4 (rhIL-4)	MHKCDITLQE IIKTLNSLTE QKTLCTELTV TDIFAASKNT TEKETFCRAA TVLRQFYSHH EKDTRCLGAT AQQFHRHKQL IRFLKRLDRN LWGLAGLNSC PVKEANQSTL ENFLERLKTI MREKYSKCSS	60 120 130
SEQ ID NO:10 recombinant human IL-7 (rhIL-7)	MDCDIEGKDG KQYESVLMVS IDQLLDSMKE IGSNCLNNEF NFFKRHICDA NKEGMFLFRA ARKLRQFLKM NSTGDFDLHL LKVSEGTTIL LNCTGQVKGR KPAALGEAQP TKSLEENKSL KEQKKLNDLC FLKRLLQEIK TCWNKILMGT KEH	60 120 153
SEQ ID NO:11 recombinant human IL-15 (rhIL-15)	MNWVNVISDL KKIEDLIQSM HIDATLYTES DVHPSCKVTA MKCFLLELQV ISLESGDASI HDTVENLIIL ANNSLSSNGN VTESGCKECE ELEEKNIKEF LQSFVHIVQM FINTS	60 115
SEQ ID NO:12 recombinant human IL-21 (rhIL-21)	MQDRHMIRMR QLIDIVDQLK NYVNDLVPEF LPAPEDVETN CEWSAFSCFQ KAQLKSANTG NNERIINVSI KKLKRKPPST NAGRRQKHRL TCPSCDSYEK KPPKEFLERF KSLLQKMIHQ HLSSRTHGSE DS	60 120 132

[00739] In some embodiments, an IL-2 form suitable for use in the invention includes a antibody cytokine engrafted protein comprises a heavy chain variable region (V_H), comprising complementarity determining regions HCDR1, HCDR2, HCDR3; a light chain variable region (V_L), comprising LCDR1, LCDR2, LCDR3; and an IL-2 molecule or a fragment thereof engrafted into a CDR of the V_H or the V_L, wherein the antibody cytokine engrafted protein preferentially expands T effector cells over regulatory T cells. Insome embodiments, the antibody cytokine engrafted protein comprises a heavy chain variable region (V_H), comprising complementarity determining regions HCDR1, HCDR2, HCDR3; a light chain variable region (V_L), comprising LCDR1, LCDR2, LCDR3; and an IL-2 molecule or a fragment thereof engrafted into a CDR of the V_H or the V_L, wherein the IL-2 molecule is a mutein, and wherein the antibody cytokine engrafted protein preferentially expands T effector cells over regulatory T cells. In some embodiments, the IL-2 regimen comprises administration of an antibody described in U.S. Patent Application Publication No. US 2020/0270334 A1, the disclosures of which are incorporated by reference herein. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain variable region (VH), comprising complementarity determining regions HCDR1, HCDR2, HCDR3; a light chain variable region (VL), comprising LCDR1, LCDR2, LCDR3; and an IL-2 molecule or a fragment thereof engrafted into a CDR of the V_H or the V_L, wherein the IL-2 molecule is a mutein, wherein the antibody cytokine engrafted protein preferentially expands T effector cells over regulatory T cells, and wherein the antibody further comprises an IgG class heavy chain and an IgG class light chain selected from the group consisting of: a IgG class light chain comprising SEQ ID NO:39 and a IgG class heavy chain comprising SEQ ID NO:38; a IgG class light chain comprising SEQ ID NO:37 and a IgG class heavy chain comprising SEQ ID NO:29; a IgG class light chain comprising SEQ ID NO:39 and a IgG class heavy chain comprising SEQ ID NO:29; and a IgG class light chain comprising SEQ ID NO:37 and a IgG class heavy chain comprising SEQ ID NO:38.

[00740] In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into HCDR1 of the V_H, wherein the IL-2 molecule is a mutein. In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into HCDR2 of the V_H, wherein the IL-2 molecule is a mutein. In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into HCDR3 of the V_H, wherein the IL-2 molecule is a mutein. In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into LCDR1 of the V_L, wherein the IL-2 molecule is a mutein. In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into LCDR2 of the V_L, wherein the IL-2 molecule is a mutein. In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into LCDR3 of the VL, wherein the IL-2 molecule is a mutein.

[00741] The insertion of the IL-2 molecule can be at or near the N-terminal region of the CDR, in the middle region of the CDR or at or near the C-terminal region of the CDR. In some embodiments, the antibody cytokine engrafted protein comprises an IL-2 molecule incorporated into a CDR, wherein the IL2 sequence does not frameshift the CDR sequence. In some embodiments, the antibody cytokine engrafted protein comprises an IL-2 molecule incorporated into a CDR, wherein the IL-2 sequence replaces all or part of a CDR sequence. The replacement by the IL-2 molecule can be the N-terminal region of the CDR, in the middle region of the CDR or at or near the C-terminal region the CDR. A replacement by the IL-2 molecule can be as few as one or two amino acids of a CDR sequence, or the entire CDR sequences.

[00742] In some embodiments, an IL-2 molecule is engrafted directly into a CDR without a peptide linker, with no additional amino acids between the CDR sequence and the IL-2 sequence. In some embodiments, an IL-2 molecule is engrafted indirectly into a CDR with a peptide linker, with one or more additional amino acids between the CDR sequence and the IL-2 sequence.

[00743] In some embodiments, the IL-2 molecule described herein is an IL-2 mutein. In some instances, the IL-2 mutein comprising an R67A substitution. In some embodiments, the IL-2 mutein comprises the amino acid sequence SEQ ID NO:14 or SEQ ID NO:15. In some embodiments, the IL-2 mutein comprises an amino acid sequence in Table 1 in U.S. Patent Application Publication No. US 2020/0270334 A1, the disclosure of which is incorporated by reference herein.

[00744] In some embodiments, the antibody cytokine engrafted protein comprises an HCDR1 selected from the group consisting of SEQ ID NO:16, SEQ ID NO:19, SEQ ID NO:22 and SEQ ID NO:25. In some embodiments, the antibody cytokine engrafted protein comprises an HCDR1 selected from the group consisting of SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:13 and SEQ ID NO:16. In some embodiments, the antibody cytokine engrafted protein comprises an HCDR1 selected from the group consisting of HCDR2 selected from the group consisting of SEQ ID NO:17, SEQ ID NO:20, SEQ ID NO:23, and SEQ ID NO:26. In some embodiments, the antibody cytokine engrafted protein

comprises an HCDR3 selected from the group consisting of SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:24, and SEQ ID NO:27. In some embodiments, the antibody cytokine engrafted protein comprises a V_H region comprising the amino acid sequence of SEQ ID NO:28. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO:29. In some embodiments, the antibody cytokine engrafted protein comprises a V_L region comprising the amino acid sequence of SEQ ID NO:36. In some embodiments, the antibody cytokine engrafted protein comprises a light chain comprising the amino acid sequence of SEQ ID NO:37. In some embodiments, the antibody cytokine engrafted protein comprises a V_H region comprising the amino acid sequence of SEQ ID NO:28 and a V_L region comprising the amino acid sequence of SEQ ID NO:36. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain region comprising the amino acid sequence of SEQ ID NO:29 and a light chain region comprising the amino acid sequence of SEQ ID NO:37. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain region comprising the amino acid sequence of SEQ ID NO:29 and a light chain region comprising the amino acid sequence of SEQ ID NO:39. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain region comprising the amino acid sequence of SEQ ID NO:38 and a light chain region comprising the amino acid sequence of SEQ ID NO:37. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain region comprising the amino acid sequence of SEQ ID NO:38 and a light chain region comprising the amino acid sequence of SEQ ID NO:39. In some embodiments, the antibody cytokine engrafted protein comprises IgG.IL2F71A.H1 or IgG.IL2R67A.H1 of U.S. Patent Application Publication No. 2020/0270334 A1, or variants, derivatives, or fragments thereof, or conservative amino acid substitutions thereof, or proteins with at least 80%, at least 90%, at least 95%, or at least 98% sequence identity thereto. In some embodiments, the antibody components of the antibody cytokine engrafted protein described herein comprise immunoglobulin sequences, framework sequences, or CDR sequences of palivizumab. In some embodiments, the antibody cytokine engrafted protein described herein has a longer serum half-life that a wild-type IL-2 molecule such as, but not limited to, aldesleukin or a comparable molecule. In some embodiments, the antibody cytokine engrafted protein described herein has a sequence as set forth in Table 3.

TABLE 3: Sequences of exemplary palivizumab antibody-IL-2 engrafted proteins

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:13 IL-2	MYRMQLLSCI ALSLALVTNS APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 153	60 120
SEQ ID NO:14 IL-2 mutein	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 133	60 120
SEQ ID NO:15 IL-2 mutein	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 133	60 120
SEQ ID NO:16 HCDR1_IL-2	GFSLAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TAMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE	60 120

	FLNRWITFCQ SIISTLTSTS GMSVG 145	
SEQ ID NO:17 HCDR2	DIWWDDKKDY NPSLKS 16	
SEQ ID NO:18 HCDR3	SMITNWYFDV 10	
SEQ ID NO:19 HCDR1_IL-2 kabat	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLTSTSGMSV G 141	60 120
SEQ ID NO:20 HCDR2 kabat	DIWWDDKKDY NPSLKS 16	
SEQ ID NO:21 HCDR3 kabat	SMITNWYFDV 10	
SEQ ID NO:22 HCDR1_IL-2 clothia	GFSLAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TAMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLTSTS GM 142	60 120
SEQ ID NO:23 HCDR2 clothia	WWDDK	5
SEQ ID NO:24 HCDR3 clothia	SMITNWYFDV 10	
SEQ ID NO:25 HCDR1_IL-2 IMGT	GFSLAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TAMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLTSTS GMS 143	60 120
SEQ ID NO:26 HCDR2 IMGT	IWWDDKK	7
SEQ ID NO:27 HCDR3 IMGT	ARSMITNWYF DV 12	
SEQ ID NO:28 V_H	QVTLRESGPA LVKPTQTLTL TCTFSGFSLA PTSSSTKKTQ LQLEHLLLDL QMILNGINNY KNPKLTAMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LTSTSGMSVG WIRQPPGKAL EWLADIWWDD KKDYNPSLKS RLTISKDTSK NQVVLKVTNM DPADTATYYC ARSMITNWYF DVWGAGTTVT VSS 253	60 120 180 240
SEQ ID NO:29 Heavy chain	QMILNGINNY KNPKLTAMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LTSTSGMSVG WIRQPPGKAL EWLADIWWDD KKDYNPSLKS RLTISKDTSK NQVVLKVTNM DPADTATYYC ARSMITNWYF DVWGAGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV AVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALAAPIEK TISKAKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK 533	60 120 180 240 300 360 420 480 533
SEQ ID NO:30 LCDR1 kabat	KAQLSVGYMH 10	
SEQ ID NO:31 LCDR2 kabat	DTSKLAS	7
SEQ ID NO:32 LCDR3 kabat	FQGSGYPFT 9	
SEQ ID NO:33 LCDR1 chothia	QLSVGY	6
SEQ ID NO:34 LCDR2 chothia	DTS	3
SEQ ID NO:35 LCDR3 chothia	GSGYPF	6
SEQ ID NO:36 V_L	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIK 106	60
SEQ ID NO:37 Light chain	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC	60 120 180 213
SEQ ID NO:38 Light chain	QVTLRESGPA LVKPTQTLTL TCTFSGFSLA PTSSSTKKTQ LQLEHLLLDL QMILNGINNY KNPKLTRMLT AKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LTSTSGMSVG WIRQPPGKAL EWLADIWWDD KKDYNPSLKS RLTISKDTSK NQVVLKVTNM DPADTATYYC ARSMITNWYF DVWGAGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV AVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALAAPIEK TISKAKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK 583	60 120 180 240 300 360 420 480 540 583
SEQ ID NO:39	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR	60

Light chain	FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIKRTVA APSVFIFPPS	120
	DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL	180
	SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC	213

[00745] The term "IL-4" (also referred to herein as "IL4") refers to the cytokine known as interleukin 4, which is produced by Th2 T cells and by eosinophils, basophils, and mast cells. IL-4 regulates the differentiation of naïve helper T cells (Th0 cells) to Th2 T cells. Steinke and Borish, *Respir. Res.* **2001,** *2,* 66-70. Upon activation by IL-4, Th2 T cells subsequently produce additional IL-4 in a positive feedback loop. IL-4 also stimulates B cell proliferation and class II MHC expression, and induces class switching to IgE and IgG_1 expression from B cells. Recombinant human IL-4 suitable for use in the invention is commercially available from multiple suppliers, including ProSpec-Tany TechnoGene Ltd., East Brunswick, NJ, USA (Cat. No. CYT-211) and ThermoFisher Scientific, Inc., Waltham, MA, USA (human IL-15 recombinant protein, Cat. No. Gibco CTP0043). The amino acid sequence of recombinant human IL-4 suitable for use in the invention is given in Table 2 (SEQ ID NO:9).

[00746] The term "IL-7" (also referred to herein as "IL7") refers to a glycosylated tissue-derived cytokine known as interleukin 7, which may be obtained from stromal and epithelial cells, as well as from dendritic cells. Fry and Mackall, *Blood* **2002,** *99,* 3892-904. IL-7 can stimulate the development of T cells. IL-7 binds to the IL-7 receptor, a heterodimer consisting of IL-7 receptor alpha and common gamma chain receptor, which in a series of signals important for T cell development within the thymus and survival within the periphery. Recombinant human IL-7 suitable for use in the invention is commercially available from multiple suppliers, including ProSpec-Tany TechnoGene Ltd., East Brunswick, NJ, USA (Cat. No. CYT-254) and ThermoFisher Scientific, Inc., Waltham, MA, USA (human IL-15 recombinant protein, Cat. No. Gibco PHC0071). The amino acid sequence of recombinant human IL-7 suitable for use in the invention is given in Table 2 (SEQ ID NO:10).

[00747] The term "IL-15" (also referred to herein as "IL15") refers to the T cell growth factor known as interleukin-15, and includes all forms of IL-2 including human and mammalian forms, conservative amino acid substitutions, glycoforms, biosimilars, and variants thereof. IL-15 is described, *e.g.*, in Fehniger and Caligiuri, *Blood* **2001,** *97,* 14-32, the disclosure of which is incorporated by reference herein. IL-15 shares β and γ signaling receptor subunits with IL-2. Recombinant human IL-15 is a single, non-glycosylated polypeptide chain containing 114 amino acids (and an N-terminal methionine) with a molecular mass of 12.8 kDa. Recombinant human IL-15 is commercially available from multiple suppliers, including ProSpec-Tany TechnoGene Ltd., East Brunswick, NJ, USA (Cat. No. CYT-230-b) and ThermoFisher Scientific, Inc., Waltham, MA, USA (human IL-15 recombinant protein, Cat. No. 34-8159-82). The amino acid sequence of recombinant human IL-15 suitable for use in the invention is given in Table 2 (SEQ ID NO:11).

[00748] The term "IL-21" (also referred to herein as "IL21") refers to the pleiotropic cytokine protein known as interleukin-21, and includes all forms of IL-21 including human and mammalian forms, conservative amino acid substitutions, glycoforms, biosimilars, and variants thereof. IL-21 is described, *e.g.*, in Spolski and Leonard, *Nat. Rev. Drug. Disc.* **2014,** *13,* 379-95, the disclosure of which is incorporated by reference herein. IL-21 is primarily produced by natural killer T cells and activated human $CD4^+$ T cells. Recombinant human IL-21 is a single, non-glycosylated polypeptide chain containing 132 amino acids with a molecular mass of 15.4 kDa. Recombinant human IL-21 is commercially available from multiple suppliers, including ProSpec-Tany TechnoGene Ltd., East Brunswick, NJ, USA (Cat. No. CYT-408-b) and ThermoFisher Scientific, Inc., Waltham, MA, USA (human IL-21 recombinant protein, Cat. No. 14-8219-80). The amino acid sequence of recombinant human IL-21 suitable for use in the invention is given in Table 2 (SEQ ID NO:12).

[00749] When "an anti-tumor effective amount", "a tumor-inhibiting effective amount", or "therapeutic amount" is indicated, the precise amount of the compositions of the present invention to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical composition comprising the tumor infiltrating lymphocytes (*e.g.,* secondary TILs or genetically modified cytotoxic lymphocytes) described herein may be administered at a dosage of 10^4 to 10^{11} cells/kg body weight (*e.g.*, 10^5 to 10^6, 10^5 to 10^{10}, 10^5 to 10^{11}, 10^6 to 10^{10}, 10^6 to 10^{11},10^7 to 10^{11}, 10^7 to 10^{10}, 10^8 to 10^{11}, 10^8 to 10^{10}, 10^9 to 10^{11}, or 10^9 to 10^{10} cells/kg body weight), including all integer values within those ranges. TILs (including in some cases, genetically modified cytotoxic lymphocytes) compositions may also be administered multiple times at these dosages. The TILs (inlcuding in some cases, genetically) can be administered by using infusion techniques that are commonly known in immunotherapy (*see, e.g.*, Rosenberg et al., *New Eng. J. of Med. 1988,* 319: 1676). The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly.

[00750] The term "hematological malignancy", "hematologic malignancy" or terms of correlative meaning refer to mammalian cancers and tumors of the hematopoietic and lymphoid tissues, including but not limited to tissues of the blood, bone marrow, lymph nodes, and lymphatic system. Hematological malignancies are also referred to as "liquid tumors." Hematological malignancies include, but are not limited to, acute lymphoblastic leukemia (ALL), chronic lymphocytic lymphoma (CLL), small lymphocytic lymphoma (SLL), acute myelogenous leukemia (AML), chronic myelogenous leukemia (CML), multiple myeloma, acute monocytic leukemia (AMoL), Hodgkin's lymphoma, and non-Hodgkin's lymphomas. The term "B cell hematological malignancy" refers to hematological malignancies that affect B cells.

[00751] The term "liquid tumor" refers to an abnormal mass of cells that is fluid in nature. Liquid tumor cancers include, but are not limited to, leukemias, myelomas, and lymphomas, as well as other hematological malignancies. TILs obtained from liquid tumors may also be referred to herein as marrow infiltrating lymphocytes (MILs). TILs obtained from liquid tumors, including liquid tumors circulating in peripheral blood, may also be referred to herein as PBLs. The terms MIL, TIL, and PBL are used interchangeably herein and differ only based on the tissue type from which the cells are derived.

[00752] The term "microenvironment," as used herein, may refer to the solid or hematological tumor microenvironment as a whole or to an individual subset of cells within the microenvironment. The tumor microenvironment, as used herein, refers to a complex mixture of "cells, soluble factors, signaling molecules, extracellular matrices, and mechanical cues that promote neoplastic transformation, support tumor growth and invasion, protect the tumor from host immunity, foster therapeutic resistance, and provide niches for dominant metastases to thrive," as described in Swartz, *et al., Cancer Res.,* **2012,** *72,* 2473. Although tumors express antigens that should be recognized by T cells, tumor clearance by the immune system is rare because of immune suppression by the microenvironment.

[00753] In some embodiments, the invention includes a method of treating a cancer with a population of TILs, wherein a patient is pre-treated with non-myeloablative chemotherapy prior to an infusion of TILs according to the invention. In some embodiments, the population of TILs may be provided wherein a patient is pre-treated with nonmyeloablative chemotherapy prior to an infusion of TILs according to the present invention. In some embodiments, the non-myeloablative chemotherapy is cyclophosphamide 60 mg/kg/d for 2 days (days 27 and 26 prior to TIL infusion) and fludarabine 25 mg/m2/d for 5 days (days 27 to 23 prior to TIL infusion). In some embodiments, after non-myeloablative chemotherapy and TIL infusion (at day 0) according to the invention, the patient receives an intravenous infusion of IL-2 intravenously at 720,000 IU/kg every 8 hours to physiologic tolerance.

[00754] Experimental findings indicate that lymphodepletion prior to adoptive transfer of tumor-specific T lymphocytes plays a key role in enhancing treatment efficacy by eliminating regulatory T cells and competing elements of the immune system ("cytokine sinks"). Accordingly, some embodiments of the invention utilize a lymphodepletion step (sometimes also referred to as "immunosuppressive conditioning") on the patient prior to the introduction of the TILs of the invention.

[00755] The term "effective amount" or "therapeutically effective amount" refers to that amount of a compound or combination of compounds as described herein that is sufficient to effect the intended application including, but not limited to, disease treatment. A therapeutically effective amount may

vary depending upon the intended application (in vitro or in vivo), or the subject and disease condition being treated (*e.g.*, the weight, age and gender of the subject), the severity of the disease condition, or the manner of administration. The term also applies to a dose that will induce a particular response in target cells (*e.g.*, the reduction of platelet adhesion and/or cell migration). The specific dose will vary depending on the particular compounds chosen, the dosing regimen to be followed, whether the compound is administered in combination with other compounds, timing of administration, the tissue to which it is administered, and the physical delivery system in which the compound is carried.

[00756] The terms "treatment", "treating", "treat", and the like, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment", as used herein, covers any treatment of a disease in a mammal, particularly in a human, and includes: (a) preventing the disease from occurring in a subject which may be predisposed to the disease but has not yet been diagnosed as having it; (b) inhibiting the disease, i.e., arresting its development or progression; and (c) relieving the disease, i.e., causing regression of the disease and/or relieving one or more disease symptoms. "Treatment" is also meant to encompass delivery of an agent in order to provide for a pharmacologic effect, even in the absence of a disease or condition. For example, "treatment" encompasses delivery of a composition that can elicit an immune response or confer immunity in the absence of a disease condition, *e.g.*, in the case of a vaccine.

[00757] As used herein, the term "immune checkpoint inhibitor (ICI)" has its general meaning in the art and refers to any compound inhibiting the function of an immune inhibitory checkpoint protein. As used herein the term "immune checkpoint protein" has its general meaning in the art and refers to a molecule that is expressed by T cells in that either turn up a signal (stimulatory checkpoint molecules) or turn down a signal (inhibitory checkpoint molecules). Immune checkpoint molecules are recognized in the art to constitute immune checkpoint pathways similar to the CTLA-4 and PD-l dependent pathways (see e.g., Pardoll, 2012. Nature Rev Cancer 12:252-264; Mellman et ah, 2011. Nature 480:480- 489). Examples of inhibitory checkpoint molecules include A2AR, B7-H3, B7-H4, CD277, IDO, KIR, VISTA, PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR. For example, immune checkpoint genes that may be silenced or inhibited in TILs of the present invention may be selected from the group comprising PD-1, CTLA-4, LAG-3, TIM-3, Cish, CBL-B, TIGIT,

TET2, TGFβ, and PKA. BAFF (BR3) is described in Bloom, *et al.*, *J. Immunother.*, **2018,** in press. According to another example, immune checkpoint genes that may be silenced or inhibited in TILs of the present invention may be selected from the group comprising PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof.

[00758] Inhibition includes reduction of function and full blockade. Preferred immune checkpoint inhibitors are antibodies that specifically recognize immune checkpoint proteins. A number of immune checkpoint inhibitors are known and in analogy of these known immune checkpoint protein inhibitors, alternative immune checkpoint inhibitors may be developed in the (near) future. The immune checkpoint inhibitors include peptides, antibodies, nucleic acid molecules and small molecules.

[00759] The term "heterologous" when used with reference to portions of a nucleic acid or protein indicates that the nucleic acid or protein comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one source and a coding region from another source, or coding regions from different sources. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

[00760] The terms "sequence identity," "percent identity," and "sequence percent identity" (or synonyms thereof, *e.g.*, "99% identical") in the context of two or more nucleic acids or polypeptides, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned (introducing gaps, if necessary) for maximum correspondence, not considering any conservative amino acid substitutions as part of the sequence identity. The percent identity can be measured using sequence comparison software or algorithms or by visual inspection. Various algorithms and software are known in the art that can be used to obtain alignments of amino acid or nucleotide sequences. Suitable programs to determine percent sequence identity include for example the BLAST suite of programs available from the U.S. Government's National Center for Biotechnology Information BLAST web site. Comparisons between two sequences can be carried using either the BLASTN or BLASTP algorithm. BLASTN is used to compare nucleic acid sequences, while BLASTP is used to compare amino acid sequences. ALIGN, ALIGN-2 (Genentech, South San Francisco, California) or MegAlign, available from DNASTAR, are additional publicly available software programs that can be used to align sequences. One skilled in the art can determine appropriate parameters for maximal alignment by particular alignment software. In certain embodiments, the default parameters of the alignment software are used.

[00761] As used herein, the term "variant" encompasses but is not limited to antibodies or fusion proteins which comprise an amino acid sequence which differs from the amino acid sequence of a reference antibody by way of one or more substitutions, deletions and/or additions at certain positions within or adjacent to the amino acid sequence of the reference antibody. The variant may comprise one or more conservative substitutions in its amino acid sequence as compared to the amino acid sequence of a reference antibody. Conservative substitutions may involve, *e.g.*, the substitution of similarly charged or uncharged amino acids. The variant retains the ability to specifically bind to the antigen of the reference antibody. The term variant also includes pegylated antibodies or proteins.

[00762] By "tumor infiltrating lymphocytes" or "TILs" herein is meant a population of cells originally obtained as white blood cells that have left the bloodstream of a subject and migrated into a tumor. TILs include, but are not limited to, $CD8^+$ cytotoxic T cells (lymphocytes), Th1 and Th17 $CD4^+$ T cells, natural killer cells, dendritic cells and M1 macrophages. TILs include both primary and secondary TILs. "Primary TILs" are those that are obtained from patient tissue samples as outlined herein (sometimes referred to as "freshly harvested"), and "secondary TILs" are any TIL cell populations that have been expanded or proliferated as discussed herein, including, but not limited to bulk TILs, expanded TILs ("REP TILs") as well as "reREP TILs" as discussed herein. reREP TILs can include for example second expansion TILs or second additional expansion TILs (such as, for example, those described in Step D of Figure 8, including TILs referred to as reREP TILs).

[00763] TILs can generally be defined either biochemically, using cell surface markers, or functionally, by their ability to infiltrate tumors and effect treatment. TILs can be generally categorized by expressing one or more of the following biomarkers: CD4, CD8, TCR αβ, CD27, CD28, CD56, CCR7, CD45Ra, CD95, PD-1, and CD25. Additionally, and alternatively, TILs can be functionally defined by their ability to infiltrate solid tumors upon reintroduction into a patient. TILs may further be characterized by potency – for example, TILs may be considered potent if, for example, interferon (IFN) release is greater than about 50 pg/mL, greater than about 100 pg/mL, greater than about 150 pg/mL, or greater than about 200 pg/mL. TILs may be considered potent if, for example, interferon (IFNγ) release is greater than about 50 pg/mL, greater than about 100 pg/mL, greater than about 150 pg/mL, or greater than about 200 pg/mL, greater than about 300 pg/mL, greater than about 400 pg/mL, greater than about 500 pg/mL, greater than about 600 pg/mL, greater than about 700 pg/mL, greater than about 800 pg/mL, greater than about 900 pg/mL, greater than about 1000 pg/mL.

[00764] The term "deoxyribonucleotide" encompasses natural and synthetic, unmodified and modified deoxyribonucleotides. Modifications include changes to the sugar moiety, to the base moiety and/or to the linkages between deoxyribonucleotide in the oligonucleotide.

[00765] The term "RNA" defines a molecule comprising at least one ribonucleotide residue. The term "ribonucleotide" defines a nucleotide with a hydroxyl group at the 2' position of a b-D-ribofuranose moiety. The term RNA includes double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Nucleotides of the RNA molecules described herein may also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

[00766] The terms "pharmaceutically acceptable carrier" or "pharmaceutically acceptable excipient" are intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and inert ingredients. The use of such pharmaceutically acceptable carriers or pharmaceutically acceptable excipients for active pharmaceutical ingredients is well known in the art. Except insofar as any conventional pharmaceutically acceptable carrier or pharmaceutically acceptable excipient is incompatible with the active pharmaceutical ingredient, its use in therapeutic compositions of the invention is contemplated. Additional active pharmaceutical ingredients, such as other drugs, can also be incorporated into the described compositions and methods.

[00767] The terms "about" and "approximately" mean within a statistically meaningful range of a value. Such a range can be within an order of magnitude, preferably within 50%, more preferably within 20%, more preferably still within 10%, and even more preferably within 5% of a given value or range. The allowable variation encompassed by the terms "about" or "approximately" depends on the particular system under study, and can be readily appreciated by one of ordinary skill in the art. Moreover, as used herein, the terms "about" and "approximately" mean that dimensions, sizes, formulations, parameters, shapes and other quantities and characteristics are not and need not be exact, but may be approximate and/or larger or smaller, as desired, reflecting tolerances, conversion factors, rounding off, measurement error and the like, and other factors known to those of skill in the art. In general, a dimension, size, formulation, parameter, shape or other quantity or characteristic is "about" or "approximate" whether or not expressly stated to be such. It is noted that embodiments of very different sizes, shapes and dimensions may employ the described arrangements.

[00768] The transitional terms "comprising," "consisting essentially of," and "consisting of," when used in the appended claims, in original and amended form, define the claim scope with respect to what unrecited additional claim elements or steps, if any, are excluded from the scope of the claim(s). The term "comprising" is intended to be inclusive or open-ended and does not exclude any additional, unrecited element, method, step or material. The term "consisting of" excludes any element, step or

material other than those specified in the claim and, in the latter instance, impurities ordinary associated with the specified material(s). The term "consisting essentially of" limits the scope of a claim to the specified elements, steps or material(s) and those that do not materially affect the basic and novel characteristic(s) of the claimed invention. All compositions, methods, and kits described herein that embody the present invention can, in alternate embodiments, be more specifically defined by any of the transitional terms "comprising," "consisting essentially of," and "consisting of."

[00769] The terms "antibody" and its plural form "antibodies" refer to whole immunoglobulins and any antigen-binding fragment ("antigen-binding portion") or single chains thereof. An "antibody" further refers to a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen-binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as V_H) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as V_L) and a light chain constant region. The light chain constant region is comprised of one domain, C_L. The V_H and V_L regions of an antibody may be further subdivided into regions of hypervariability, which are referred to as complementarity determining regions (CDR) or hypervariable regions (HVR), and which can be interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen epitope or epitopes. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (Clq) of the classical complement system.

[00770] The term "antigen" refers to a substance that induces an immune response. In some embodiments, an antigen is a molecule capable of being bound by an antibody or a TCR if presented by major histocompatibility complex (MHC) molecules. The term "antigen", as used herein, also encompasses T cell epitopes. An antigen is additionally capable of being recognized by the immune system. In some embodiments, an antigen is capable of inducing a humoral immune response or a cellular immune response leading to the activation of B lymphocytes and/or T lymphocytes. In some cases, this may require that the antigen contains or is linked to a Th cell epitope. An antigen can also have one or more epitopes (*e.g.*, B- and T-epitopes). In some embodiments, an antigen will preferably react, typically in a highly specific and selective manner, with its corresponding antibody or TCR and not with the multitude of other antibodies or TCRs which may be induced by other antigens.

[00771] The terms "monoclonal antibody," "mAb," "monoclonal antibody composition," or their plural forms refer to a preparation of antibody molecules of single molecular composition. A

monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope. Monoclonal antibodies specific to certain receptors can be made using knowledge and skill in the art of injecting test subjects with suitable antigen and then isolating hybridomas expressing antibodies having the desired sequence or functional characteristics. DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Recombinant production of antibodies will be described in more detail below.

[00772] The terms "antigen-binding portion" or "antigen-binding fragment" of an antibody (or simply "antibody portion" or "fragment"), as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and CH1 domains; (ii) a F(ab')2 fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and CH1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a domain antibody (dAb) fragment (Ward, *et al., Nature,* **1989,** *341,* 544-546), which may consist of a V_H or a V_L domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules known as single chain Fv (scFv); see, *e.g.*, Bird, *et al.*, *Science* **1988,** *242,* 423-426; and Huston, *et al.*, *Proc. Natl. Acad. Sci. USA* **1988,** *85,* 5879-5883). Such scFv antibodies are also intended to be encompassed within the terms "antigen-binding portion" or "antigen-binding fragment" of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies. In some embodiments, a scFv protein domain comprises a V_H portion and a V_L portion. A scFv molecule is denoted as either V_L-L-V_H if the V_L domain is the N-terminal part of the scFv molecule, or as V_H-L-V_L if the V_H domain is the N-terminal part of the scFv molecule. Methods for making scFv molecules and designing suitable peptide linkers are described in U.S. Pat. No. 4,704,692, U.S. Pat. No. 4,946,778, R. Raag and M. Whitlow, "Single Chain Fvs." FASEB Vol 9:73-80 (1995) and R. E. Bird and B. W. Walker, Single Chain Antibody Variable

Regions, TIBTECH, Vol 9: 132-137 (1991), the disclosures of which are incorporated by reference herein.

[00773] The term "human antibody," as used herein, is intended to include antibodies having variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). The term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[00774] The term "human monoclonal antibody" refers to antibodies displaying a single binding specificity which have variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. In some embodiments, the human monoclonal antibodies are produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, *e.g.*, a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell.

[00775] The term "recombinant human antibody", as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (such as a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom (described further below), (b) antibodies isolated from a host cell transformed to express the human antibody, *e.g.*, from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable regions in which the framework and CDR regions are derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies can be subjected to *in vitro* mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire *in vivo*.

[00776] As used herein, "isotype" refers to the antibody class (*e.g.*, IgM or IgG1) that is encoded by the heavy chain constant region genes.

[00777] The phrases "an antibody recognizing an antigen" and "an antibody specific for an antigen" are used interchangeably herein with the term "an antibody which binds specifically to an antigen."

[00778] The term "human antibody derivatives" refers to any modified form of the human antibody, including a conjugate of the antibody and another active pharmaceutical ingredient or antibody. The terms "conjugate," "antibody-drug conjugate", "ADC," or "immunoconjugate" refers to an antibody, or a fragment thereof, conjugated to another therapeutic moiety, which can be conjugated to antibodies described herein using methods available in the art.

[00779] The terms "humanized antibody," "humanized antibodies," and "humanized" are intended to refer to antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences. Additional framework region modifications may be made within the human framework sequences. Humanized forms of non-human (for example, murine) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. 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 15 hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or nonhuman primate having the desired specificity, affinity, and capacity. In some instances, Fv 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 FR regions 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* **1986,** *321,* 522-525; Riechmann, *et al.*, *Nature* **1988,** *332,* 323-329; and Presta, *Curr. Op. Struct. Biol.* **1992,** *2,* 593-596. The antibodies described herein may also be modified to employ any Fc variant which is known to impart an improvement (*e.g.*, reduction) in effector function and/or FcR binding. The Fc variants may include, for example, any one of the amino acid substitutions disclosed in International Patent Application Publication Nos. WO 1988/07089 A1, WO 1996/14339 A1, WO 1998/05787 A1, WO 1998/23289 A1, WO 1999/51642 A1, WO 99/58572 A1, WO 2000/09560 A2, WO 2000/32767 A1, WO 2000/42072 A2, WO 2002/44215 A2, WO 2002/060919 A2, WO 2003/074569 A2, WO 2004/016750 A2, WO 2004/029207 A2, WO 2004/035752 A2, WO 2004/063351 A2, WO 2004/074455 A2, WO 2004/099249 A2, WO 2005/040217 A2, WO 2005/070963 A1, WO 2005/077981 A2, WO 2005/092925 A2, WO 2005/123780 A2, WO 2006/019447 A1, WO

2006/047350 A2, and WO 2006/085967 A2; and U.S. Patent Nos. 5,648,260; 5,739,277; 5,834,250; 5,869,046; 6,096,871; 6,121,022; 6,194,551; 6,242,195; 6,277,375; 6,528,624; 6,538,124; 6,737,056; 6,821,505; 6,998,253; and 7,083,784; the disclosures of which are incorporated by reference herein.

[00780] The term "chimeric antibody" is intended to refer to antibodies in which the variable region sequences are derived from one species and the constant region sequences are derived from another species, such as an antibody in which the variable region sequences are derived from a mouse antibody and the constant region sequences are derived from a human antibody.

[00781] A "diabody" is a small antibody fragment with two antigen-binding sites. The fragments comprises a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H-V_L or V_L-V_H). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, *e.g.*, European Patent No. EP 404,097, International Patent Publication No. WO 93/11161; and Bolliger, *et al.*, *Proc. Natl. Acad. Sci. USA* **1993,** *90,* 6444-6448.

[00782] The term "glycosylation" refers to a modified derivative of an antibody. An aglycoslated antibody lacks glycosylation. Glycosylation can be altered to, for example, increase the affinity of the antibody for antigen. Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site. Aglycosylation may increase the affinity of the antibody for antigen, as described in U.S. Patent Nos. 5,714,350 and 6,350,861. Additionally or alternatively, an antibody can be made that has an altered type of glycosylation, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to increase the ability of antibodies. Such carbohydrate modifications can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies of the invention to thereby produce an antibody with altered glycosylation. For example, the cell lines Ms704, Ms705, and Ms709 lack the fucosyltransferase gene, FUT8 (alpha (1,6) fucosyltransferase), such that antibodies expressed in the Ms704, Ms705, and Ms709 cell lines lack fucose on their carbohydrates. The Ms704, Ms705, and Ms709 FUT8−/− cell lines were created by the targeted disruption of the FUT8 gene in CHO/DG44 cells using two replacement vectors (see *e.g.* U.S. Patent Publication No. 2004/0110704 or Yamane-Ohnuki, *et al.*, *Biotechnol. Bioeng.*, **2004,** *87,* 614-622). As another example, European Patent No. EP 1,176,195 describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase,

such that antibodies expressed in such a cell line exhibit hypofucosylation by reducing or eliminating the alpha 1,6 bond-related enzyme, and also describes cell lines which have a low enzyme activity for adding fucose to the N-acetylglucosamine that binds to the Fc region of the antibody or does not have the enzyme activity, for example the rat myeloma cell line YB2/0 (ATCC CRL 1662). International Patent Publication WO 03/035835 describes a variant CHO cell line, Lec 13 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields, *et al., J. Biol. Chem.* **2002,** *277,* 26733-26740. International Patent Publication WO 99/54342 describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (*e.g.*, beta(1,4)-N-acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies (see also Umana, *et al.*, *Nat. Biotech.* **1999,** *17,* 176-180). Alternatively, the fucose residues of the antibody may be cleaved off using a fucosidase enzyme. For example, the fucosidase alpha-L-fucosidase removes fucosyl residues from antibodies as described in Tarentino, *et al.*, *Biochem.* **1975,** *14,* 5516-5523.

[00783] "Pegylation" refers to a modified antibody, or a fragment thereof, that typically is reacted with polyethylene glycol (PEG), such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. Pegylation may, for example, increase the biological (*e.g.*, serum) half life of the antibody. Preferably, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C_1-C_{10})alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. The antibody to be pegylated may be an aglycosylated antibody. Methods for pegylation are known in the art and can be applied to the antibodies of the invention, as described for example in European Patent Nos. EP 0154316 and EP 0401384 and U.S. Patent No. 5,824,778, the disclosures of each of which are incorporated by reference herein.

[00784] The term "biosimilar" means a biological product, including a monoclonal antibody or protein, that is highly similar to a U.S. licensed reference biological product notwithstanding minor differences in clinically inactive components, and for which there are no clinically meaningful differences between the biological product and the reference product in terms of the safety, purity, and potency of the product. Furthermore, a similar biological or "biosimilar" medicine is a biological medicine that is similar to another biological medicine that has already been authorized for use by the European Medicines Agency. The term "biosimilar" is also used synonymously by other national and regional regulatory agencies. Biological products or biological medicines are medicines that are made by or derived from a biological source, such as a bacterium or yeast. They can consist of relatively

small molecules such as human insulin or erythropoietin, or complex molecules such as monoclonal antibodies. For example, if the reference IL-2 protein is aldesleukin (PROLEUKIN), a protein approved by drug regulatory authorities with reference to aldesleukin is a "biosimilar to" aldesleukin or is a "biosimilar thereof" of aldesleukin. In Europe, a similar biological or "biosimilar" medicine is a biological medicine that is similar to another biological medicine that has already been authorized for use by the European Medicines Agency (EMA). The relevant legal basis for similar biological applications in Europe is Article 6 of Regulation (EC) No 726/2004 and Article 10(4) of Directive 2001/83/EC, as amended and therefore in Europe, the biosimilar may be authorized, approved for authorization or subject of an application for authorization under Article 6 of Regulation (EC) No 726/2004 and Article 10(4) of Directive 2001/83/EC. The already authorized original biological medicinal product may be referred to as a "reference medicinal product" in Europe. Some of the requirements for a product to be considered a biosimilar are outlined in the CHMP Guideline on Similar Biological Medicinal Products. In addition, product specific guidelines, including guidelines relating to monoclonal antibody biosimilars, are provided on a product-by-product basis by the EMA and published on its website. A biosimilar as described herein may be similar to the reference medicinal product by way of quality characteristics, biological activity, mechanism of action, safety profiles and/or efficacy. In addition, the biosimilar may be used or be intended for use to treat the same conditions as the reference medicinal product. Thus, a biosimilar as described herein may be deemed to have similar or highly similar quality characteristics to a reference medicinal product. Alternatively, or in addition, a biosimilar as described herein may be deemed to have similar or highly similar biological activity to a reference medicinal product. Alternatively, or in addition, a biosimilar as described herein may be deemed to have a similar or highly similar safety profile to a reference medicinal product. Alternatively, or in addition, a biosimilar as described herein may be deemed to have similar or highly similar efficacy to a reference medicinal product. As described herein, a biosimilar in Europe is compared to a reference medicinal product which has been authorized by the EMA. However, in some instances, the biosimilar may be compared to a biological medicinal product which has been authorized outside the European Economic Area (a non-EEA authorized "comparator") in certain studies. Such studies include for example certain clinical and in vivo non-clinical studies. As used herein, the term "biosimilar" also relates to a biological medicinal product which has been or may be compared to a non-EEA authorized comparator. Certain biosimilars are proteins such as antibodies, antibody fragments (for example, antigen binding portions) and fusion proteins. A protein biosimilar may have an amino acid sequence that has minor modifications in the amino acid structure (including for example deletions, additions, and/or substitutions of amino acids) which do not significantly affect the function of the polypeptide. The biosimilar may comprise an amino acid sequence having a sequence identity of 97% or greater to the amino acid sequence of its reference medicinal product, *e.g.*, 97%, 98%, 99% or 100%. The biosimilar may comprise one or

more post-translational modifications, for example, although not limited to, glycosylation, oxidation, deamidation, and/or truncation which is/are different to the post-translational modifications of the reference medicinal product, provided that the differences do not result in a change in safety and/or efficacy of the medicinal product. The biosimilar may have an identical or different glycosylation pattern to the reference medicinal product. Particularly, although not exclusively, the biosimilar may have a different glycosylation pattern if the differences address or are intended to address safety concerns associated with the reference medicinal product. Additionally, the biosimilar may deviate from the reference medicinal product in for example its strength, pharmaceutical form, formulation, excipients and/or presentation, providing safety and efficacy of the medicinal product is not compromised. The biosimilar may comprise differences in for example pharmacokinetic (PK) and/or pharmacodynamic (PD) profiles as compared to the reference medicinal product but is still deemed sufficiently similar to the reference medicinal product as to be authorized or considered suitable for authorization. In certain circumstances, the biosimilar exhibits different binding characteristics as compared to the reference medicinal product, wherein the different binding characteristics are considered by a Regulatory Authority such as the EMA not to be a barrier for authorization as a similar biological product. The term "biosimilar" is also used synonymously by other national and regional regulatory agencies.

III. Making a cryopreserved TIL preparation from tumor harvest

[00785] Some emboidments of the present invention provided herein are directed to methods of making a cryopreserved TIL preparation from a tumor sample harvested from a cancer patient before the patient receives immune-check point inhibitor (ICI) and/or standard of care treatment.

[00786] In some embodiments, the patient receives ICI treatment (such as anti-immune checkpoint antibodies as described herein) after the tumor harvest and cryopreservation.

[00787] In some embodiments, the patient receives standard of care treatment for cancer after the tumor harvest and cryopreservation. Several of the methods of treatment described herein comprise the administration of a standard of care treatment to a patient. As used herein, a "standard of care treatment" is a treatment process, including a drug or combination of drugs, radiation therapy, surgery or other medical intervention that is recognized by medical practitioners as appropriate, accepted, and/or widely used for a certain type of patient, disease or clinical circumstance. Standard of care treatments for treating different types of cancer are well known by persons of skill in the art. For example, the National Comprehensive Cancer Network (NCCN), an alliance of 21 major cancer centers in the USA, publishes the NCCN Clinical Practice Guidelines in Oncology (NCCN GUIDELINES®) that provide detailed up-to-date information on the standard-of-care treatments for a

wide variety of cancers (see NCCN GUIDELINES®, 2013). In some embodiments, the standard of care treatment is chemotherapy, radiation therapy, surgery, targeted therapy, or any combinations thereof.

[00788] In some embodiments, the cryopreserved tumor harvest from the patient or subject is used to make a population of TILs subsequent to the patient is treated with an ICI and/or standard of care treatment and shows progression of the cancer. In some embodiments, after the cryopreserving of the tumor harvest, the patient or subject receives immune-check point inhibitor (ICI) and/or standard of care treatment and is monitored for progression of the cancer. In some embodiments, the progression of the cancer is indicative of the need of an autologous TIL therapy.

[00789] In other embodiments, the cryopreserving of the tumor harvest from the patient or subject is completed prior to the progression of the cancer.

[00790] In some embodiments, the methods disclosed herein provide a pharmacoeconomic advantage in the form of avoiding the cost of TIL production in the event that the paetint does not develop progressive sdisease or is otherwise indicated for TIL therapy in the future.

[00791] The method of any one of claims 1 to 14, wherein the patient exhibits progressive disease at least about 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 month, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 25 months, 26 months, 27 months, 28 months, 29 months, 30 months, 31 months, 32 months, 33 months, 34 months, 35 months, 36 months, after the step of cryopreserving.

[00792] In some embodiments, the cryopreserved TIL preparation can be made from a tumor sample comprising a population of TILs that is obtained and/or received from the patient or subject. A patient tumor sample may be obtained using methods known in the art, generally via surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells. In some embodiments, multilesional sampling is used. In some embodiments, surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells includes multilesional sampling (i.e., obtaining samples from one or more tumor sites and/or locations in the patient, as well as one or more tumors in the same location or in close proximity). In general, the tumor sample may be from any solid tumor, including primary tumors, invasive tumors or metastatic tumors. The tumor sample may also be a liquid tumor, such as a tumor obtained from a hematological malignancy. The solid tumor may be of lung tissue. In some embodiments, useful TILs are obtained from non-small cell lung carcinoma (NSCLC). The solid tumor may be of skin tissue. In some embodiments, useful TILs are obtained from a melanoma.

[00793] Once obtained, the tumor sample is generally fragmented using sharp dissection into small pieces of between 1 to about 8 mm^3, with from about 2-3 mm^3 being particularly useful. In some embodiments, the TILs are cultured from these fragments using enzymatic tumor digests. Such tumor digests may be produced by incubation in enzymatic media (e.g., Roswell Park Memorial Institute (RPMI) 1640 buffer, 2 mM glutamate, 10 mcg/mL gentamicine, 30 units/mL of DNase and 1.0 mg/mL of collagenase) followed by mechanical dissociation (e.g., using a tissue dissociator). Tumor digests may be produced by placing the tumor in enzymatic media and mechanically dissociating the tumor for approximately 1 minute, followed by incubation for 30 minutes at 37 °C in 5% CO2, followed by repeated cycles of mechanical dissociation and incubation under the foregoing conditions until only small tissue pieces are present. At the end of this process, if the cell suspension contains a large number of red blood cells or dead cells, a density gradient separation using FICOLL branched hydrophilic polysaccharide may be performed to remove these cells. Alternative methods known in the art may be used, such as those described in U.S. Patent Application Publication No. 2012/0244133 A1, the disclosure of which is incorporated by reference herein. Any of the foregoing methods may be used in any of the embodiments described herein for methods of expanding TILs or methods treating a cancer.

[00794] In some embodiments, the cryopreserved TIL preparation is stored for future use. In some embodiments, the cryopreservation of the tumor harvest is completed pre-progression. In some embodiments, after the making of the cryopreserved TIL preparation, the patient is monitored for exhibitions of progressive disease on or after ICI and/or standard of care treatment. In some embodiments, the patient exhibits progressive cancer on or after ICI and/or standard of care treatment and is indicated for autologous TIL therapy. In some embodiments, after progression, the cryopreserved TIL preparation is thawed and expanded according to expansion methods described in the sections below.

[00795] In some embodiments, the patient is a NSCLC cancer patient. In some embodiments, the patient is suffering from, suffered from, or is prone to NSCLC. In some embodiments, the patient has metastatic NSCLC. In some embodiments, the patient has metastatic stage IV NSCLC.

[00796] In some emboidments, the subject or patient has at least one of:

i. a predetermined tumor proportion score (TPS) of PD-L1 of < 1%,

ii. a TPS score of PD-L1 of 1%-49%, or

iii. a predetermined absence of one or more driver mutations.

[00797] In some embodiments, the NSCLC patient is without one or more actionable driver mutations. In some embodiments, the actionable driver mutations disclosed herein include but are not

limited to an EGFR mutation, an EGFR insertion, EGFR exon20, a KRAS mutation, a BRAF-mutation, a BRAF V600E mutation, a BRAF V600K mutation, a BRAF V600 mutation, an ALK mutation, a c-ROS mutation (ROS1-mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation, a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation. In some embodiments, the NSCLC exhibits a TPS of < 1% and has a predetermined absence of one or more driver mutations.

[00798] In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is naïve to all cancer treatment. In some embodiments, the patient is naïve to targeted therapies. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is naïve to ICI treatment. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is naïve to anti-VEGF (e.g. avastin/bevacizumab) treatment. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is naïve to chemotherapy treatment. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is naïve to a combination of two or more of the foregoing treatments.

[00799] In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is on maintenance therapy. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient's maintenance therapy is interrupted. In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is in a washout period following the interruption of their maintenance therapy, followed by the resumption of the maintenance therapy or a different therapy. In some embodiments, the maintenance therapy will resume after a tumor sample is harvested from the patient. In some embodiments, the cancer (such as NSCLC) processes on or after the maintenance therapy.

[00800] In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is going to receive first-line (1L) ICI and/or standard therapy for cancer.

[00801] In some embodiments, at the time the cryopreserved TIL preparation is made, the patient is going to receive second-line (2L) ICI and/or standard therapy for cancer.

[00802] In some embodiments, the harvested tumor sample of the patient is cryopreserved using flash-freezing methods or controlled rate freezing. Exemplary flash-freezing methods and controlled

rate freezing methods can be found in International Patent Publication No. WO/2020/061429, which is incorporated herein by reference in its entirety for all purposes.

[00803] In some embodiments, the flash-freezing methods of the present invention comprise:

(i) fragmenting the tumor tissue;

(ii) incubating the fragments in a cryopreservation medium; and,

(iii) freezing the fragments wherein the freezing is flash freezing using the vapor phase of liquid nitrogen.

[00804] In an embodiment, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to about 6 mm. In a preferred embodiment, the approximately spherical fragments have a diameter of about 6 mm. In an embodiment, the approximately spherical fragments have a diameter of about 3 mm.

[00805] In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 1.5 mm and a longest edge length of about 6 mm. In an embodiment, the tumor tissue is fragmented into generally cubical fragments having edge lengths of between about 1.5 mm and 6 mm. In an embodiment, the generally cubical fragments have edge lengths of about 6 mm. In an embodiment, the generally cubical fragments have edge lengths of about 3 mm.

[00806] In some embodiments, the tissue sample is trimmed to separate non-tumor tissue from tumor tissue.

[00807] In some embodiments, the tumor tissue is from a dissected tumor. In an embodiment, the tumor tissue is from a tumor biopsy. In some embodiments the tumor tissue is from an incisional biopsy. In some embodiments the tumor tissue is from an excisional biopsy. In some embodiments the tumor tissues may be from one or more core needle biopsies.

[00808] In some embodiments, the fresh tumor tissue is trimmed into fragments with a cross section of about 1.5 mm × 1.5 mm, about 2 mm × 2 mm, about 2.5 mm × 2.5 mm, about 3 mm × 3 mm, about 3.5 mm × 3.5 mm, about 4 mm × 4 mm, about 4.5 mm × 4.5 mm, about 5 mm × 5 mm, about 5.5 mm × about 5.5 mm, or about 6 mm × about 6 mm.

[00809] In an embodiment, the tumor tissue is less than twelve hours old. In an embodiment, the tumor tissue is less than eight hours old. In an embodiment, the tumor tissue is less than three, less than two, or less than one-hour old.

[00810] Any suitable cryopreservation medium known to those skilled in the art in view of the present disclosure can be used in the methods described herein. Examples of suitable cryopreservation mediums include, but are not limited to, CryoStor® CS10, HypoThermosol®, or a combination thereof. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO to about 15% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 3% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 4% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 5% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 6% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 7% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 8% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 9% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 10% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 11% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 12% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 13% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 14% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 15% v/v DMSO. In some embodiments, the cryopreservation medium comprises at least one antimicrobial agent. Any suitable antimicrobial agent known to those skilled in the art in view of the present disclosure can be used in the methods described herein. In some embodiments, the cryopreservation medium comprises gentamicin. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 50 µg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 40 µg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 30 µg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 20 µg/mL.

[00811] In some embodiments, the tumor fragments are incubated in cryopreservation medium for about 20 minutes to about 70 minutes. In some embodiments, the tumor fragments are incubated in cryopreservation medium for about 30 minutes to about 60 minutes. In some embodiments the incubation is at least 10 minutes; at least 20 minutes; at least 25 minutes; at least 30 minutes; at least 35 minutes; at least 40 minutes; at least 45 minutes; at least 50 minutes; at least 55 minutes; at least 60 minutes; or at least 70 minutes. In some embodiments the incubation is about 10 minutes; about 20 minutes; about 25 minutes; about 30 minutes; about 35 minutes; about 40 minutes; about 45 minutes; about 50 minutes; about 55 minutes; about 60 minutes; or about 70 minutes. In some embodiments the incubation is less than 10 minutes; less than 20 minutes; less than 25 minutes; less than 30

minutes; less than 35 minutes; less than 40 minutes; less than 45 minutes; less than 50 minutes; less than 55 minutes; less than 60 minutes; or less than 70 minutes. In some embodiments the incubation time is proportional to tumor fragment density. In some embodiments the incubation time is proportional to tumor fragment surface to volume ratio.

[00812] In some embodiments, the tumor fragments are incubated in a cryopreservation medium at a temperature from about 2°C to about 8°C.

[00813] In some embodiments, the tumor tissue is washed in a physiologically buffered isotonic saline solution. In some embodiments, the washing comprises three serial washes of at least three minutes each, with the physiologically buffered isotonic saline solution replaced after each serial wash. In some embodiments, the physiologically buffered isotonic saline solution comprises Hank's Balance Salt Solution (HBSS). In some embodiments, the physiologically buffered isotonic saline solution comprises tris-buffered saline (TBS). In some embodiments, the physiologically buffered isotonic saline solution comprises phosphate buffered saline (PBS). In some embodiments, the physiologically buffered isotonic saline solution comprises Dulbecco's phosphate-buffered saline (DPBS). In some embodiments, the physiologically buffered isotonic saline solution in one serial wash may be a different physiologically buffered isotonic saline solution than used in one or more of the other serial washes.

[00814] In an embodiment, the freezing takes place at a temperature in the range from about -125°C to about -196°C. In an embodiment, the freezing takes place at a temperature in the range of about -140°C to about -185°C. In an embodiment, the freezing takes place at a temperature in the range of about -140°C to about -175°C. In an embodiment, the freezing takes place at a temperature of about -145°C. In some embodiments, the freezing takes place in the vapor phase of liquid nitrogen.

[00815] A problem well-known in the art is to cryopreserve cells or tissues without damaging them during the freezing process. Without being bound by theory, one source of damage during freezing is intracellular ice nucleation resulting in cellular rupture. Muldrew and McGann outline a quantitative theory for this well-known and widely recognized difficulty with cellular and, in particular, whole tissue cryopreservation in "The osmotic rupture hypothesis of intracellular freezing injury", *Biophysical Journal*, **66**:532-41 (1994). Acker and McGann further develop the fundamental mechanisms of intracellular ice formation and cellular damage in a later article, "Membrane damage occurs during the formation of intracellular ice," *Cryo Letter*, **22**:241-54 (2001).

[00816] Damage during freezing is detected wherein upon thawing, the tissues have substantially lost their physiological structures or the cells comprising the tissue have substantially lost their viability. Viability may be determined by the fraction of cells introduced into a culture medium compared to the number of such cells that grow or show markers of normal cellular function.

Numerous methods are known in the art to identify the fraction of viable cells, for example, and without limitation, dye exclusion tests, such as trypan blue exclusion. *See*, for example, Strober, *Curr. Protoc. Immunol.*, **2001**, Appendix 3B, available at https://dx.doi.org/10.1002/0471142735.ima03bs21. Without limitation, viability may also be determined by metabolic activity assays, such as the MTT assay, wherein MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, is metabolized by cellular enzymes into formazan. This enzymatic reaction converts the yellow MTT into purple formazan. *See*, for example, Berridge *et al.*, Tetrazolium dyes as tools in cell biology: new insights into their cellular reduction. *Biotechnology Annual Review*, **11**: 127-152 (2005); Mosmann, "Rapid colorimetric assay for cellular growth and survival: application to proliferation and cytotoxicity assays," *J. Immunol. Methods* **65** (1–2): 55–63 (1983).

[00817] Without being bound by theory, slow cooling is hypothesized to produce innocuous intracellular ice, *see* Acker and McGann, "Protective effect of intracellular ice during freezing?" *Cryobiology*, **46**(2): 197-202 (2003). A conventional approach to achieve freezing without excessive cellular damage or to achieve freezing without significantly reducing cellular viability has been to employ slow freezing rates. Watson *et al.*, U.S. Patent 5,891,617, emphasize this approach, for example claim one, step (c), teaches a very slow rate of cooling: "about -0.3° C. per minute or less." Similarly, Comhaire *et al.*, U.S. Patent 9,938,495, teach "high cell viability after thawing were obtained by slow freezing using a DMSO-free cryopreservation medium" for stem cells.

[00818] Based on these exemplary teachings, the methods and products of the present disclosure are surprising and unexpected. Further the present disclosure, including the examples and the data therein, demonstrate a technical solution to the problem of rapidly and efficiently cryoprotecting tumor tissues, tumor fragments, or tumor specimens, for the use in the manufacture of tumor infiltrating lymphocytes for therapeutic use.

[00819] In some embodiments, the method of cryopreserving tumor tissue for the manufacture of tumor infiltrating lymphocytes (TILs), further comprises a step (iv) storing the frozen fragments at a temperature below at least -130°C. In some embodiments, the frozen fragments are stored in the vapor phase of liquid nitrogen. In some embodiments, the frozen fragments are stored submerged in liquid nitrogen. In some embodiments, the cryopreserved fragments are stored for later manufacture of TILs for autologous therapeutic use.

[00820] In some embodiments, the disclosures provide herein methods for cryopreserving tumor tissue using controlled-rate freezing/slow-freezing methods.

[00821] In some embodiments, the present invention provides a method for cryopreserving tumor tissue, and a cryopreserved tumor tissue prepared by a process comprising the steps of:

(i) adding cryopreservation medium to a closable vessel;

(ii) pre-cooling the closable vessel in a controlled-rate freezing device;

(iii) fragmenting tumor tissue to obtain tumor fragments;

(iv) placing the tumor fragments in the closable vessel comprising cryopreservation medium and closing the vessel;

(v) optionally incubating the closed vessel comprising the tumor fragments and cryopreservation medium;

(vi) slow-freezing the vessel in a controlled-rate freezing device; and

(vii) transferring the vessel to a liquid nitrogen freezer.

[00822] In some embodiments, the present invention provides a method for cryopreserving tumor tissue, and a cryopreserved tumor tissue prepared by a process comprising the steps of:

(i) placing in a pre-cooled closable vessel comprising cryopreservation medium tumor fragments obtained from fragmenting tumor tissue and closing the vessel;

(ii) optionally incubating the closed vessel comprising the tumor fragments and cryopreservation medium;

(iii) slow-freezing the vessel in a controlled-rate freezing device; and

(iv) transferring the vessel to a liquid nitrogen freezer.

[00823] In some embodiments, the present invention provides a method for cryopreserving tumor tissue, and a cryopreserved tumor tissue prepared by a process comprising the steps of:

(i) placing in a pre-cooled closable vessel comprising cryopreservation medium a tumor digest obtained from digesting in an enzymatic media tumor tissue or tumor fragments produced from fragmenting tumor tissue and closing the vessel;

(ii) optionally incubating the closed vessel comprising the tumor digest and cryopreservation medium;

(iii) slow-freezing the vessel in a controlled-rate freezing device; and

(iv) transferring the vessel to a liquid nitrogen freezer.

[00824] In some embodiments, the present invention provides a method for cryopreserving tumor tissue, and a cryopreserved tumor tissue prepared by a process comprising the steps of:

(i) adding cryopreservation medium to a closable vessel;

(ii) pre-cooling the closable vessel in a controlled-rate freezing device;

(iii) digesting tumor tissue in an enzymatic media to obtain a tumor digest;

(iv) placing the tumor digest in the cryopreservation medium in the closable vessel and closing the vessel;

(v) optionally incubating the closed vessel comprising the tumor digest and cryopreservation medium;

(vi) slow-freezing the vessel in a controlled-rate freezing device; and

(vii) transferring the vessel to a liquid nitrogen freezer.

[00825] Any suitable cryopreservation medium known to those skilled in the art in view of the present disclosure can be used in the methods described herein. Examples of suitable cryopreservation mediums include, but are not limited to, CryoStor® CS10, HypoThermosol®, or a combination thereof. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO to about 15% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 2% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 3% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 4% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 5% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 6% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 7% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 8% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 9% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 10% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 11% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 12% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 13% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 14% v/v DMSO. In some embodiments, the cryopreservation medium comprises about 15% v/v DMSO. In some embodiments, the cryopreservation medium comprises at least one antimicrobial agent. Any suitable antimicrobial agent known to those skilled in the art in view of the present disclosure can be used in the methods described herein. In some embodiments, the cryopreservation medium comprises gentamicin. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 50 µg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration

of at least 40 μg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 30 μg/mL. In some embodiments, the cryopreservation medium comprises gentamicin at a concentration of at least 20 μg/mL.

[00826] Any suitable closable vessel known to those skilled in the art in view of the present disclosure can be used in the methods described herein. Examples of suitable closable vessels include, but are not limited to, capped microcentrifuge tubes, lidded microcentrifuge tubes, and cryogenic specimen storage vials, including, but not limited to, cryovials. The term "cryogenic specimen storage vial" is meant to include the terms cryovial, cryo-container, cryogenic tube, and the like, including any and all closed, sealed, or re-closable containers (e.g., with screw caps or frictionally sealing snap caps) in which the container can be safely and securely stored at cryogenic temperatures (meaning at -80C or below, and optionally submerged in liquid nitrogen or suspended in the vapor phase above liquid nitrogen at a temperature of approximately -196C). Capped or lidded microcentrifuge tubes and cryovials commonly fabricated from polyethylene or polypropylene are often used as cryogenic specimen storage vials.

[00827] In some embodiments, the closable vessel is filled from about 50% to about 85% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 50% to about 85% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 50% to about 75% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 50% to about 65% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 50% to about 55% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 60% to about 85% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 60% to about 75% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 60% to about 65% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 70% to about 85% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 70% to about 75% volume with cryopreservation medium. In some embodiments, the closable vessel is filled from about 80% to about 85% volume with cryopreservation medium.

[00828] In some embodiments, the pre-cooling step comprises placing the closable vessel in a controlled-rate freezing device that is at a temperature of about -80C to about 8C for a period of at least about 5 minutes to about 8 hours. In some embodiments, the pre-cooling step comprises placing the closable vessel in a controlled-rate freezing device that is at a temperature of about -80C, about -79C, about -78C, about -77C, about -76C, about -75C, about -70C, about -65C, about -60C, about -55C, about -50C, about -45C, about -40C, about -35C, about -30C, about -25C, about -20C, about -15C, about -10C, about -5C, about 0C, about 1C, about 2C, about 3C, about 4C, about 5C, about 6C,

about 7C, about 8C, or any temperature in between, for a period of at least about 5 minutes, at least about 10 minutes, at least about 15 minutes, at least about 20 minutes, at least about 25 minutes, at least about 30 minutes, at least about 35 minutes, at least about 40 minutes, at least about 45 minutes, at least about 50 minutes, at least about 55 minutes, at least about 1 hour, at least about 1.5 hours, at least about 2 hours, at least about 3 hours, at least about 4 hours, at least about 5 hours, at least about 6 hours, at least about 7 hours, at least about 8 hours, or more.

[00829] In some embodiments, closed vessels comprising tumor fragments and cryopreservation medium are incubated at a temperature of about 2-8C for a period of about 30 to 60 minutes before slow-freezing the vessels in the controlled-rate freezing device. In some embodiments, vessels comprising tumor fragments and cryopreservation medium are incubated at a temperature of about 2C, about 3C, about 4C, about 5C, about 6C, about 7C, about 8C, or any temperature in between, for a period of about 5 minutes, about 10 minutes, about 15 minutes, about 20 minutes, about 25 minutes, about 30 minutes, about 35 minutes, about 40 minutes, about 45 minutes, about 50 minutes, about 55 minutes, about 60 minutes, or more, before slow-freezing the vessels in the controlled-rate freezing device.

[00830] Any suitable controlled-rate freezing device known to those skilled in the art in view of the present disclosure can be used in the methods described herein. Examples of suitable controlled-rate freezing devices include, but are not limited to, a Corning CoolCell™ device or a Nalgene Mr. Frosty™ device. In some embodiments, the controlled-rate freezing device is an IPA-free controlled rate freezing device that cools at a rate of about -0.1C/min to about -10C/min. In some embodiments, the controlled-rate freezing device is an IPA-free controlled rate freezing device that cools at a rate of about -0.1C/min to about -10C/min, about -0.2C/min to about -5C/min, about -0.5C/min to about -2.5C/min, about -1C/min to about -2C/min. In some embodiments, the controlled-rate freezing device is an IPA-free controlled rate freezing device that cools at a rate of about -1° C/min.

[00831] In some embodiments, all of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some embodiments, 90% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some embodiments, 80% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some embodiments, 70% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some embodiments, 60% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some embodiments, 50% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium. In some

embodiments, 40% or more of the positions of the controlled-rate freezing device are filled with closable vessels containing cryopreservation medium.

[00832] The term, "slow freezing method" as used herein refers to a process in which a sample is cooled at a controlled rate in a cooling environment before final cryopreservation in liquid nitrogen or the like. In some embodiments, the cooling rate is about -0.1C/min to about -10C/min, about -0.2C/min to about -5C/min, about -0.5C/min to about -2.5C/min, about -1C/min to about -2C/min. In some embodiments, the cooling rate is about -1C/min. In some embodiments, the cooling environment is a -80C freezer set between about -90C and about -70C, such as about -90C, about -89C, about -88C, about -87C, about -86C, about -85C, about -84C, about -83C, about -82C, about -81C, about -80C, about -79C, about -78C, about -77C, about -76C, about -75C, about -74C, about -73C, about -72C, about -72C, about -71C, or any temperature between, or dry ice.

[00833] In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -70°C to about -90°C. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -75°C to about -85°C. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -78°C to about -80°C. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device with dry ice. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device in a -80°C freezer. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device in dry ice.

[00834] In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -80°C, for about 3-5 hours. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -80°C, for about 3 hours. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -80°C, for about 4 hours. In some embodiments, the slow-freezing comprises incubating the controlled-rate freezing device at a temperature of about -80°C, for about 5 hours.

[00835] In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 80%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 75%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 70%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 65%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 60%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 55%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least

about 50%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 45%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 40%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 35%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 30%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 25%. In some embodiments, after recovery from freezing, the cells have a post-thaw viability of at least about 20%. Any suitable methods to measure or determine post-thaw viability known in the art in view of the present disclosure can be used in the methods described herein.

[00836] In some embodiments, tumor digests are generated by incubating the tumor in enzyme media, for example but not limited to RPMI 1640, 2mM GlutaMAX, 10 mg/mL gentamicin, 30 U/mL DNase, and 1.0 mg/mL collagenase, followed by mechanical dissociation (GentleMACS, Miltenyi Biotec, Auburn, CA). In some embodiments, the tumor is placed in a tumor dissociating enzyme mixture including one or more dissociating (digesting) enzymes such as, but not limited to, collagenase (including any blend or type of collagenase), Accutase™, Accumax™, hyaluronidase, neutral protease (dispase), chymotrypsin, chymopapain, trypsin, caseinase, elastase, papain, protease type XIV (pronase), deoxyribonuclease I (DNase), trypsin inhibitor, any other dissociating or proteolytic enzyme, and any combination thereof. In other embodiments, the tumor is placed in a tumor dissociating enzyme mixture including collagenase (including any blend or type of collagenase), neutral protease (dispase) and deoxyribonuclease I (DNase).

IV. Gene-Editing Processes

A. Overview: TIL Expansion + Gene-Editing

[001] In some embodiments of the present invention is directed to methods for expanding TIL populations, the methods comprise one or more steps of gene-editing at least a portion of the TILs in order to enhance their therapeutic effect. As used herein, "gene-editing," "gene editing," and "genome editing" refer to a type of genetic modification in which DNA is permanently modified in the genome of a cell, *e.g.*, DNA is inserted, deleted, modified or replaced within the cell's genome. In some embodiments, gene-editing causes the expression of a DNA sequence to be silenced (sometimes referred to as a gene knockout) or inhibited/reduced (sometimes referred to as a gene knockdown). In other embodiments, gene-editing causes the expression of a DNA sequence to be enhanced (*e.g.*, by causing over-expression). In accordance with embodiments of the present invention, gene-editing technology is used to enhance the effectiveness of a therapeutic population of TILs. Exemplary gene-editing processes/methods of the present invention, as well as gene-edited TIL products can also be found in International Patent Application No. PCT/US22/14425, U.S. Provisional Application Nos.

63/304,498 and 63/242,373, all of which are incorporated herein by reference in their entireties for all related purposes.

[002] A method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, an exemplary TIL expansion method known as process 2A is described below), wherein the method further comprises gene-editing at least a portion of the TILs. According to additional embodiments, a method for expanding TILs into a therapeutic population of TILs is carried out in accordance with any embodiment of the methods described in U.S. Pat. No. 10,517,894, U.S. Patent Application Publication No. 2020/0121719 A1, or U.S. Pat. No. 10,894,063, which are incorporated by reference herein in their entireties, wherein the method further comprises gene-editing at least a portion of the TILs. Thus, some embodiments of the present invention provides a therapeutic population of TILs that has been expanded in accordance with any embodiment described herein, wherein at least a portion of the therapeutic population has been gene-edited, *e.g.,* at least a portion of the therapeutic population of TILs that is transferred to the infusion bag is permanently gene-edited.

[003] In some embodiments of the present invention directed to methods for expanding TIL populations, the methods comprise one or more steps of introducing into at least a portion of the TILs nucleic acids, e.g., mRNAs, for transient expression of an immunomodulatory protein, e.g., an immunomodulatory fusion protein comprising an immunomodulatory protein fused to a membrane anchor, in order to produce modified TILs with (i) reduced dependence on cytokines in when expanded in culture and/or (ii) an enhanced therapeutic effect. As used herein, "transient gene-editing", "transient gene editing", "transient phenotypic alteration," "transient phenotypic modification", "temporary phenotypic alteration," "temporary phenotypic modification", "transient cellular change", "transient cellular modification", "temporary cellular alteration", "temporary cellular modification", "transient expression", "transient alteration of expression", "transient alteration of protein expression", "transient modification", "transitory phenotypic alteration", "non-permanent phenotypic alteration", "transiently modified", "temporarily modified", "non-permanently modified", "transiently altered", "temporarily altered", grammatical variations of any of the foregoing, and any expressions of similar meaning, refer to a type of cellular modification or phenotypic change in which nucleic acid (e.g., mRNA) is introduced into a cell, such as transfer of nucleic acid into a cell by electroporation, calcium phosphate transfection, viral transduction, etc., and expressed in the cell (e.g., expression of an immunomodulatory protein, such as an immunomodulatory fusion protein comprising an immunomodulatory protein fused to a membrane anchor) in order to effect a transient or non-permanent phenotypic change in the cell, such as the transient display of membrane-anchored immunomodulatory fusion protein on the cell surface. In accordance with embodiments of the present invention, transient phenotypic alteration technology is used to reduce dependence on

cytokines in the expansion of TILs in culture and/or enhance the effectiveness of a therapeutic population of TILs.

[004] In some embodiments, a microfluidic platform is used for intracellular delivery of nucleic acids encoding the immunomodulatory fusion proteins provided herein. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. The SQZ platform is capable of delivering nucleic acids and proteins, to a variety of primary human cells, including T cells (Sharei *et al.* PNAS 2013, as well as Sharei et al. PLOS ONE 2015 and Greisbeck et al. J. Immunology vol. 195, 2015). In the SQZ platform, the cell membranes of the cells for modification (e.g., TILs) are temporarily disrupted by microfluidic constriction, thereby allowing the delivery of nucleic acids encoding the immunomodulatory fusion proteins into the cells. Such methods as described in International Patent Application Publication Nos. WO 2013/059343A1, WO 2017/008063A1, or WO 2017/123663A1, or U.S. Patent Application Publication Nos. US 2014/0287509A1, US 2018/0201889A1, or US 2018/0245089A1 (incorporated herein by reference in their entirties) can be employed with the present invention for delivering nucleic acids encoding the subject immunomodulatory fusion proteins to a population of TILs. In some embodiments, the delivered nucleic acid allows for transient protein expression of the immunomodulatory fusion proteins in the modified TILs. In some embodiments, the SQZ platform is used for stable incorporation of the delivered nucleic acid encoding the immunomodulatory fusion protein into the TIL cell genome. Additional exemplary disclosures for the SQZ platform and its use can be found in International Patent Application Publication No. WO/2019/136456, which is incorporated herein by reference in its entirety for all purposes.

B. Timing of Gene-Editing / Transient Phenotypic Alteration During TIL Expansion

[005] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3 (*e.g.*, OKT-3 may be present in the culture medium beginning on the start date of the expansion process), to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (b) to step (c) occurs without opening the system;

(d) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) harvesting the therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system;

(f) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(g) at any time during the method prior to the transfer to the infusion bag in step (f), gene-editing at least a portion of the TIL cells to express an immunomodulatory composition comprising an immunomodulatory agent (e.g., a membrane anchored immunomodulatory fusion protein described herein) on the surface of the TIL cells. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[006] As stated in step (g) of the embodiments described above, the gene-editing process may be carried out at any time during the TIL expansion method prior to the transfer to the infusion bag in step (f), which means that the gene editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(f) outlined in the method above, or before or after any of steps (a)-(e) outlined in the method above. According to certain embodiments, TILs are collected during the expansion method (*e.g.*, the expansion method is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the expansion method (*e.g.*, back into the culture medium) to continue the expansion process, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited. In some embodiments, the gene-editing process may be carried out before expansion by activating TILs, performing a gene-editing step on the activated TILs, and expanding the gene-edited TILs according to the processes described herein. In some embodiments, nucleic acids for gene editing are delivered

to the TILs using a microfluidic platform. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[007] In some embodiments, the gene-editing process is carried out after the first TIL expansion step. In some embodiments, the gene-editing process is carried out after the first TIL expansion step and before the second expansion step. In some embodiments, the gene-editing process is carried out after the TILs are activated. In some embodiments, the gene-editing process is carried out after the first expansion step and after the TILs are activated, but before the second expansion step. In some embodiments, the gene-editing process is carried out after the first expansion step and after the TILs are activated, and the TILs are rested after gene-editing and before the second expansion step. In some embodiments, the TILs are rested for about 1 to 2 days after gene-editing and before the second expansion step. In some embodiments, the TILs are activated by exposure to an anti-CD3 agonist and an anti-CD28 agonist. In some embodiments, the anti-CD3 agonist is an anti-CD3 agonist antibody and the anti-CD28 agonist is an anti-CD28 agonist antibody. In some embodiments, the anti-CD3 agonist antibody is OKT-3. In some embodiments, the TILs are activated by exposure to anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads. In some embodiments, the anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads are the TransAct™ product of Miltenyi. In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction. In some embodiments, the gene-editing process is carried out by lentiviral transduction. In some embodiments, the immunomodulatory composition is a membrane anchored immunomodulatory fusion protein. In some embodiments, the immunomodulatory fusion protein comprises IL-15. In some embodiments, the immunomodulatory fusion protein comprises IL-21. In some embodiments, the immunomodulatory composition comprises two or more different membrane bound fusion proteins. In some embodiments, the immunomodulatory composition comprises a first immunomodulatory protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21. In some embodiments, the TILs are gene-edited to express the immunomodulatory composition under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-15 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express a first immunomodulatory fusion protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter.

[008] In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction. In some embodiments, the gene-editing process is carried out by lentiviral transduction.

[009] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3 (*e.g.*, OKT-3 may be present in the culture medium beginning on the start date of the expansion process), to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (b) to step (c) occurs without opening the system;

(d) gene-editing at least a portion of the TIL cells in the second population of TILs to express an immunomodulatory composition comprising an immunomodulatory agent (e.g., a membrane anchored immunomodulatory fusion protein described herein) on the surface of the TIL cells;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (c) to step (d) occurs without opening the system;

(f) harvesting the therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

[0010] (g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the TILs are rested after the gene-editing step and before the second expansion step. In some embodiments, the TILs are rested for about 1 to 2 days after the gene-editing step and before the second expansion step. In some embodiments, the TILs are activated by exposure to an anti-CD3

agonist and an anti-CD28 agonist. In some embodiments, the anti-CD3 agonist is an anti-CD3 agonist antibody and the anti-CD28 agonist is an anti-CD28 agonist antibody. In some embodiments, the anti-CD3 agonist antibody is OKT-3. In some embodiments, the TILs are activated by exposure to anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads. In some embodiments, the anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads are the TransAct™ product of Miltenyi. In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction of the TILs, optionally for about 2 days. In some embodiments, the gene-editing process is carried out by lentiviral transduction of the TILs, optionally for about 2 days. In some embodiments, the immunomodulatory composition is a membrane anchored immunomodulatory fusion protein. In some embodiments, the immunomodulatory fusion protein comprises IL-15. In some embodiments, the immunomodulatory fusion protein comprises IL-21. In some embodiments, the immunomodulatory composition comprises two or more different membrane bound fusion proteins. In some embodiments, the immunomodulatory composition comprises a first immunomodulatory protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21. In some embodiments, the TILs are gene-edited to express the immunomodulatory composition under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-15 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express a first immunomodulatory fusion protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter.

[0011] It should be noted that alternative embodiments of the expansion process may differ from the method shown above; *e.g.*, alternative embodiments may not have the same steps (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two expansions, and it is possible that gene-editing may be conducted on the TILs during a third or fourth expansion, etc.

[0012] According to other embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3 (*e.g.*, OKT-3 may be present in the culture medium beginning on the start date of the expansion process), to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (b) to step (c) occurs without opening the system;

(d) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) harvesting the therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system;

(f) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(g) at any time during the method prior to the transfer to the infusion bag in step (f), introducing a transient phenotypic alteration in at least a portion of the TIL cells to express an immunomodulatory composition comprising an immunomodulatory agent on the surface of the TIL cells (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, nucleic acids for transient phenotypic alteration are delivered to the TILs using a microfluidic platform. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0013] As stated in step (g) of the embodiments described above, the transient phenotypic alteration process may be carried out at any time during the TIL expansion method prior to the transfer to the infusion bag in step (f), which means that the transient phenotypic alteration may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(f) outlined in the method above, or before or after any of steps (a)-(e) outlined

in the method above. According to certain embodiments, TILs are collected during the expansion method (*e.g.*, the expansion method is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a transient modification process, and, in some cases, subsequently reintroduced back into the expansion method (*e.g.*, back into the culture medium) to continue the expansion process, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are transiently altered to express the immunomodulatory composition on the surface of the TIL cells. In some embodiments, the transient cellular modification process may be carried out before expansion by activating TILs, performing a transient phenotypic alteration step on the activated TILs, and expanding the modified TILs according to the processes described herein.

[0014] It should be noted that alternative embodiments of the expansion process may differ from the method shown above; *e.g.*, alternative embodiments may not have the same steps (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the transient cellular modification process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two expansions, and it is possible that transient cellular modification process may be conducted on the TILs during a third or fourth expansion, etc.

[0015] According to some embodiments, the gene-editing process is carried out on TILs from one or more of the first population, the second population, and the third population. For example, gene-editing may be carried out on the first population of TILs, or on a portion of TILs collected from the first population, and following the gene-editing process those TILs may subsequently be placed back into the expansion process (*e.g.,* back into the culture medium). Alternatively, gene-editing may be carried out on TILs from the second or third population, or on a portion of TILs collected from the second or third population, respectively, and following the gene-editing process those TILs may subsequently be placed back into the expansion process (*e.g.,* back into the culture medium). According to other embodiments, gene-editing is performed while the TILs are still in the culture medium and while the expansion is being carried out, *i.e.,* they are not necessarily "removed" from the expansion in order to conduct gene-editing.

[0016] According to some embodiments, the transient cellular modification process is carried out on TILs from one or more of the first population, the second population, and the third population. For example, transient cellular modification may be carried out on the first population of TILs, or on a portion of TILs collected from the first population, and following the gene-editing process those transiently modified TILs may subsequently be placed back into the expansion process (*e.g.,* back into the culture medium). Alternatively, transient cellular modification may be carried out on TILs from the second or third population, or on a portion of TILs collected from the second or third population, respectively, and following the transient cellular modification process those modified TILs may subsequently be placed back into the expansion process (*e.g.,* back into the culture medium).

According to other embodiments, transient cellular modification is performed while the TILs are still in the culture medium and while the expansion is being carried out, *i.e.*, they are not necessarily "removed" from the expansion in order to effect transient cellular modification.

[0017] According to other embodiments, the gene-editing process is carried out on TILs from the first expansion, or TILs from the second expansion, or both. For example, during the first expansion or second expansion, gene-editing may be carried out on TILs that are collected from the culture medium, and following the gene-editing process those TILs may subsequently be placed back into the expansion method, *e.g.*, by reintroducing them back into the culture medium.

[0018] According to other embodiments, the transient cellular modification process is carried out on TILs from the first expansion, or TILs from the second expansion, or both. For example, during the first expansion or second expansion, transient cellular modification may be carried out on TILs that are collected from the culture medium, and following the transient cellular modification process those modified TILs may subsequently be placed back into the expansion method, *e.g.*, by reintroducing them back into the culture medium.

[0019] According to other embodiments, the gene-editing process is carried out on at least a portion of the TILs after the first expansion and before the second expansion. For example, after the first expansion, gene-editing may be carried out on TILs that are collected from the culture medium, and following the gene-editing process those TILs may subsequently be placed back into the expansion method, *e.g.*, by reintroducing them back into the culture medium for the second expansion.

[0020] According to other embodiments, the transient cellular modification process is carried out on at least a portion of the TILs after the first expansion and before the second expansion. For example, after the first expansion, transient cellular modification may be carried out on TILs that are collected from the culture medium, and following the transient cellular modification process those modified TILs may subsequently be placed back into the expansion method, *e.g.*, by reintroducing them back into the culture medium for the second expansion.

[0021] According to alternative embodiments, the gene-editing process is carried out before step (c) (*e.g.*, before, during, or after any of steps (a)-(b)), before step (d) (*e.g.*, before, during, or after any of steps (a)-(c)), before step (e) (*e.g.*, before, during, or after any of steps (a)-(d)), or before step (f) (*e.g.*, before, during, or after any of steps (a)-(e)).

[0022] According to alternative embodiments, the transient cellular modification process is carried out before step (c) (*e.g.*, before, during, or after any of steps (a)-(b)), before step (d) (*e.g.*, before, during, or after any of steps (a)-(c)), before step (e) (*e.g.*, before, during, or after any of steps (a)-(d)), or before step (f) (*e.g.*, before, during, or after any of steps (a)-(e)).

[0023] It should be noted with regard to OKT-3, according to certain embodiments, that the cell culture medium may comprise OKT-3 beginning on the start day (Day 0), or on Day 1 of the first expansion, such that the gene-editing or transient cellular modification is carried out on TILs after they have been exposed to OKT-3 in the cell culture medium on Day 0 and/or Day 1. According to other embodiments, the cell culture medium comprises OKT-3 during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out before the OKT-3 is introduced into the cell culture medium. Alternatively, the cell culture medium may comprise OKT-3 during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out after the OKT-3 is introduced into the cell culture medium.

[0024] It should also be noted with regard to a 4-1BB agonist, according to certain embodiments, that the cell culture medium may comprise a 4-1BB agonist beginning on the start day (Day 0), or on Day 1 of the first expansion, such that the gene-editing or transient cellular modification is carried out on TILs after they have been exposed to a 4-1BB agonist in the cell culture medium on Day 0 and/or Day 1. According to other embodiments, the cell culture medium comprises a 4-1BB agonist during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out before the 4-1BB agonist is introduced into the cell culture medium. Alternatively, the cell culture medium may comprise a 4-1BB agonist during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out after the 4-1BB agonist is introduced into the cell culture medium.

[0025] It should also be noted with regard to IL-2, according to certain embodiments, that the cell culture medium may comprise IL-2 beginning on the start day (Day 0), or on Day 1 of the first expansion, such that the gene-editing or transient cellular modification is carried out on TILs after they have been exposed to IL-2 in the cell culture medium on Day 0 and/or Day 1. According to other embodiments, the cell culture medium comprises IL-2 during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out before the IL-2 is introduced into the cell culture medium. Alternatively, the cell culture medium may comprise IL-2 during the first expansion and/or during the second expansion, and the gene-editing or transient cellular modification is carried out after the IL-2 is introduced into the cell culture medium.

[0026] As discussed above, one or more of OKT-3, 4-1BB agonist and IL-2 may be included in the cell culture medium beginning on Day 0 or Day 1 of the first expansion. According to some embodiments, OKT-3 is included in the cell culture medium beginning on Day 0 or Day 1 of the first expansion, and/or a 4-1BB agonist is included in the cell culture medium beginning on Day 0 or Day 1 of the first expansion, and/or IL-2 is included in the cell culture medium beginning on Day 0 or Day 1 of the first expansion. According to other examples, the cell culture medium comprises OKT-3 and

a 4-1BB agonist beginning on Day 0 or Day 1 of the first expansion. According to other examples, the cell culture medium comprises OKT-3, a 4-1BB agonist and IL-2 beginning on Day 0 or Day 1 of the first expansion. Of course, one or more of OKT-3, 4-1BB agonist and IL-2 may be added to the cell culture medium at one or more additional time points during the expansion process, as set forth in various embodiments described herein.

[0027] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) activating the second population of TILs by adding OKT-3 and culturing for about 1 to 2 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) gene-editing at least a portion of the TIL cells in the second population of TILs to express an immunomodulatory composition comprising an immunomodulatory agent (e.g., a membrane anchored immunomodulatory fusion protein described herein) on the surface of the TIL cells;

(f) optionally resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the

immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the TILs are rested after the gene-editing step and before the second expansion step. In some embodiments, the TILs are rested for about 1 to 2 days after the gene-editing step and before the second expansion step. In some embodiments, the TILs are activated by exposure to an anti-CD3 agonist and an anti-CD28 agonist for about 2 days. In some embodiments, the anti-CD3 agonist is an anti-CD3 agonist antibody and the anti-CD28 agonist is an anti-CD28 agonist antibody. In some embodiments, the anti-CD3 agonist antibody is OKT-3. In some embodiments, the TILs are activated by exposure to anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads. In some embodiments, the anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads are the TransAct™ product of Miltenyi. In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction of the TILs, optionally for about 2 days. In some embodiments, the gene-editing process is carried out by lentiviral transduction of the TILs, optionally for about 2 days. In some embodiments, the immunomodulatory composition is a membrane anchored immunomodulatory fusion protein. In some embodiments, the immunomodulatory fusion protein comprises IL-15. In some embodiments, the immunomodulatory fusion protein comprises IL-21. In some embodiments, the immunomodulatory composition comprises two or more different membrane bound fusion proteins. In some embodiments, the immunomodulatory composition comprises a first immunomodulatory protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21. In some embodiments, the TILs are gene-edited to express the immunomodulatory composition under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-15 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express a first immunomodulatory fusion protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter.

[0028] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for

about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0029] According to other embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the sterile electroporation of the at least one nucleic acid molecule into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0030] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the

immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0031] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the at least one gene editor delivered into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored

immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0032] According to other embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the at least one nucleic acid molecule delivered into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18 , IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0033] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second

expansion is performed for about 7 to 11 days to obtain a third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs; and

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system,

wherein the at least one gene editor delivered into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0034] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) sterile electroporating the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0035] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the TIL cells in the second population of TILs to express an immunomodulatory composition comprising an immunomodulatory agent (e.g., a membrane anchored immunomodulatory fusion protein described herein) on the surface of the TIL cells; and

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In

some embodiments, the TILs are rested after the gene-editing step and before the second expansion step. In some embodiments, the TILs are rested for about 1 to 2 days after the gene-editing step and before the second expansion step. In some embodiments, the TILs are activated by exposure to an anti-CD3 agonist and an anti-CD28 agonist for about 2 days. In some embodiments, the anti-CD3 agonist is an anti-CD3 agonist antibody and the anti-CD28 agonist is an anti-CD28 agonist antibody. In some embodiments, the anti-CD3 agonist antibody is OKT-3. In some embodiments, the TILs are activated by exposure to anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads. In some embodiments, the anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads are the TransAct™ product of Miltenyi. In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction of the TILs, optionally for about 2 days. In some embodiments, the gene-editing process is carried out by lentiviral transduction of the TILs, optionally for about 2 days. In some embodiments, the immunomodulatory composition is a membrane anchored immunomodulatory fusion protein. In some embodiments, the immunomodulatory fusion protein comprises IL-15. In some embodiments, the immunomodulatory fusion protein comprises IL-21. In some embodiments, the immunomodulatory composition comprises two or more different membrane bound fusion proteins. In some embodiments, the immunomodulatory composition comprises a first immunomodulatory protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21. In some embodiments, the TILs are gene-edited to express the immunomodulatory composition under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-15 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express a first immunomodulatory fusion protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter.

[0036] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) sterile electroporating the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(c) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the at least one nucleic acid molecule delivered into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0037] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the TIL cells in the second population of TILs to express an immunomodulatory composition comprising an immunomodulatory agent (e.g., a membrane anchored immunomodulatory fusion protein described herein) on the surface of the TIL cells; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the TILs are rested after the gene-editing step and before the second expansion step. In some embodiments, the TILs are rested for about 1 to 2 days after the gene-editing step and before the second expansion step. In some embodiments, the TILs are activated by exposure to an anti-CD3 agonist and an anti-CD28 agonist for about 2 days. In some embodiments, the anti-CD3 agonist is an anti-CD3 agonist antibody and the anti-CD28 agonist is an anti-CD28 agonist antibody. In some embodiments, the anti-CD3 agonist antibody is OKT-3. In some embodiments, the TILs are activated by exposure to anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads. In some embodiments, the anti-CD3 agonist antibody- and anti-CD28 agonist antibody-conjugated beads are the TransAct™ product of Miltenyi. In some embodiments, the gene-editing process is carried out by viral transduction. In some embodiments, the gene-editing process is carried out by retroviral transduction of the TILs, optionally for about 2 days. In some embodiments, the gene-editing process is carried out by lentiviral transduction of the TILs, optionally for about 2 days. In some embodiments, the immunomodulatory composition is a membrane anchored immunomodulatory fusion protein. In some embodiments, the immunomodulatory fusion protein comprises IL-15. In some embodiments, the immunomodulatory fusion protein comprises IL-21. In some embodiments, the immunomodulatory composition comprises two or more different membrane bound fusion proteins. In some embodiments, the immunomodulatory composition comprises a first immunomodulatory protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21. In some embodiments, the TILs are gene-edited to express the immunomodulatory composition under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-15 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express an immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter. In some embodiments, the TILs are gene-edited to express a first immunomodulatory fusion protein comprising IL-15 and a second immunomodulatory fusion protein comprising IL-21 under the control of an NFAT promoter.

[0038] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) sterile electroporating the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0039] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) sterile electroporating the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the at least one nucleic acid molecule delivered into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0040] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a

CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0041] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0042] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0043] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0044] In some embodiments, any of the foregoing methods is modified such that the step of culturing the fourth population of TILs is replaced with the steps of:

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(g) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide an expanded number of TILs.

[0045] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days or 7 days.

[0046] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2-7 days.

[0047] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 3-7 days.

[0048] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 4-7 days.

[0049] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 5-7 days.

[0050] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 6-7 days.

[0051] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1-6 days.

[0052] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1-5 days.

[0053] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1-4 days.

[0054] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1-3 days.

[0055] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1-2 days.

[0056] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2-6 days.

[0057] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 3-6 days.

[0058] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 4-6 days.

[0059] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 5-6 days.

[0060] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 3-5 days.

[0061] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 3-4 days.

[0062] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2-5 days.

[0063] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2-4 days.

[0064] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2-3 days.

[0065] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 4-5 days.

[0066] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 1 day.

[0067] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 2 days.

[0068] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 3 days.

[0069] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 4 days.

[0070] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 5 days.

[0071] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 6 days.

[0072] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of activating the second population of TILs is performed for about 7 days.

[0073] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(c) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs to produce a third population of TILs; and

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0074] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(c) sterile electroporating the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs to produce a third population of TILs; and

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the

group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[0075] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the cytokine is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the cytokine is selected from the group consisting of IL-2, IL-12, IL-15, IL-18 and IL-21. In some embodiments, the cytokine is selected from the group consisting of IL-12, IL-15, IL-18, IL-21 and a CD40 agonist.

[0076] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) sterile electroporating the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one nucleic acid molecule into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(c) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs to produce a third population of TILs; and

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0077] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(c) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs to produce a third population of TILs; and

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-

10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0078] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a portion of cells of the second population of TILs to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0079] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the second population of TILs to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one nucleic acid molecule into the portion of cells of the second population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[0080] In some embodiments, the step of culturing the third population of TILs is performed by culturing the third population of TILs in the second cell culture medium for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3-7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[0081] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or 11 days.

[0082] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-11 days.

[0083] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-11 days.

[0084] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-11 days.

[0085] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-11 days.

[0086] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8-11 days.

[0087] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 9-11 days.

[0088] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 10-11 days.

[0089] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-10 days.

[0090] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-10 days.

[0091] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-10 days.

[0092] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-10 days.

[0093] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8-10 days.

[0094] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 9-10 days.

[0095] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-9 days.

[0096] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 5-9 days.

[0097] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 6-9 days.

[0098] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 7-9 days.

[0099] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 8-9 days.

[00100] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3-8 days.

[00101] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3-7 days.

[00102] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3-6 days.

[00103] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3-5 days.

[00104] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3-4 days.

[00105] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-8 days.

[00106] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-7 days.

[00107] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-6 days.

[00108] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-6 days.

[00109] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 5-8 days.

[00110] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 5-7 days.

[00111] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 5-6 days.

[00112] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 6-8 days.

[00113] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 6-7 days.

[00114] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 7-8 days.

[00115] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4-5 days.

[00116] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 3 days.

[00117] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 4 days.

[00118] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 5 days.

[00119] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 6 days.

[00120] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 7 days.

[00121] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 8 days.

[00122] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 9 days.

[00123] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 10 days.

[00124] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs in the first cell culture medium is performed for about 11 days.

[00125] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d)) sterile electroporating the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group

consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00126] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d)) sterile electroporating the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00127] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) sterile electroporating the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00128] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) sterile electroporating the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the sterile electroporation of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00129] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d)) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00130] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d)) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the

immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00131] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one gene editor into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one gene editor into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent

is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00132] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) temporarily disrupting the cell membranes of the third population of TILs to effect transfer of at least one nucleic acid molecule into a portion of cells of the third population of TILs to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs,

wherein the transfer of the at least one nucleic acid molecule into the portion of cells of the third population of TILs modifies a plurality of cells in the portion to transiently express an immunomodulatory composition on the surface of the cells. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21 and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the second population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00133] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the third cell culture medium for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a fourth culture medium comprising IL-2 for a second period of about 3-7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00134] In some embodiments, in the step of culturing the first population of TILs in the first culture medium the first culture medium further comprises anti-CD3 and anti-CD28 beads or antibodies.

[00135] In some embodiments, the anti-CD3 and anti-CD28 beads or antibodies comprise the OKT-3 in the first culture medium.

[00136] In some embodiments, in the step of culturing the second population of TILs in the second culture medium the second culture medium further comprises anti-CD3 and anti-CD28 beads or antibodies.

[00137] In some embodiments, the anti-CD3 and anti-CD28 beads or antibodies comprise the OKT-3 in the second culture medium.

[00138] According to some embodiments, the foregoing method further comprises cryopreserving the harvested TIL population using a cryopreservation medium. In some embodiments, the cryopreservation medium is a dimethylsulfoxide-based cryopreservation medium. In other embodiments, the cryopreservation medium is CS10.

[00139] In some embodiments, the invention provides the method described in any preceding paragraph above modified as applicable such that the step of culturing the second population of TILs in the second culture medium is performed for about 2-3 days.

[00140] In some embodiments, the invention provides the method described in any preceding paragraph above modified as applicable such that the step of culturing the second population of TILs in the second culture medium is performed for about 3-4 days.

[00141] In some embodiments, the invention provides the method described in any preceding paragraph above modified as applicable such that the step of culturing the second population of TILs in the second culture medium is performed for about 2 days.

[00142] In some embodiments, the invention provides the method described in any preceding paragraph above modified as applicable such that the step of culturing the second population of TILs in the second culture medium is performed for about 3 days.

[00143] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the second population of TILs in the second culture medium is performed for about 4 days.

[00144] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs, as applicable, in the second or third cell culture medium, applicable, is performed for about 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days or 15 days.

[00145] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-15 days.

[00146] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-15 days.

[00147] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-15 days.

[00148] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-15 days.

[00149] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10-15 days.

[00150] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 11-15 days.

[00151] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 12-15 days.

[00152] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 13-15 days.

[00153] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 14-15 days.

[00154] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-14 days.

[00155] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-14 days.

[00156] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-14 days.

[00157] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-14 days.

[00158] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-14 days.

[00159] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10-14 days.

[00160] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 11-14 days.

[00161] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 12-14 days.

[00162] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 13-14 days.

[00163] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-13 days.

[00164] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-12 days.

[00165] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-11 days.

[00166] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-10 days.

[00167] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-9 days.

[00168] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-8 days.

[00169] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-7 days.

[00170] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5-6 days.

[00171] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-13 days.

[00172] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-12 days.

[00173] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-11 days.

[00174] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-10 days.

[00175] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-9 days.

[00176] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-8 days.

[00177] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6-7 days.

[00178] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-13 days.

[00179] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-12 days.

[00180] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-11 days.

[00181] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-10 days.

[00182] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-9 days.

[00183] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7-8 days.

[00184] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-13 days.

[00185] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-12 days.

[00186] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-11 days.

[00187] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-10 days.

[00188] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8-9 days.

[00189] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-13 days.

[00190] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-12 days.

[00191] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-11 days.

[00192] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9-10 days.

[00193] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10-13 days.

[00194] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10-12 days.

[00195] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10-11 days.

[00196] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 11-13 days.

[00197] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 11-12 days.

[00198] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 12-13 days.

[00199] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 5 days.

[00200] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 6 days.

[00201] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 7 days.

[00202] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 8 days.

[00203] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 9 days.

[00204] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 10 days.

[00205] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 11 days.

[00206] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 12 days.

[00207] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 13 days.

[00208] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 14 days.

[00209] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs in the second or third cell culture medium is performed for about 15 days.

[00210] According to some embodiments, any of the foregoing methods may be used to provide an autologous harvested TIL population for the treatment of a human subject with cancer.

C. PD-1 TALEN knockdown

[00211] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3- 9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00212] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00213] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(e) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(f) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide an expanded number of TILs.

[00214] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(g) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide an expanded number of TILs.

[00215] In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days, about 3-8 days, about 4-8 days, about 5-8 days, about 6-8 days, about 7-8 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3 days. In some embodiments, the step of culturing the first population of TILs is performed for about 4 days. In some embodiments, the step of culturing the first population of TILs is performed for about 5 days. In some embodiments, the step of culturing the first population of TILs is performed for about 6 days. In some embodiments, the step of culturing the first population of TILs is performed for about 7 days. In some embodiments, the step of culturing the first population of TILs is performed for about 8 days. In some embodiments, the step of culturing the first population of TILs is performed for about 9 days.

[00216] In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days. In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, about 1-2 days. In some embodiments, the step of activating the second population of TILs is performed for about 1 day. In some embodiments, the step of activating the second population of TILs is performed for about 2 days. In some embodiments, the step of activating the second population of TILs is performed for about 3 days. In some embodiments, the step of activating the second population of TILs is performed for about 4 days. In some embodiments, the step of activating the second population of TILs is performed for about 5 days. In some embodiments, the step of activating the second population of TILs is performed for about 6 days. In some embodiments, the step of activating the second population of TILs is performed for about 7 days.

[00217] In some embodiments, the step of culturing the fourth population of TILs is performed for about 5-15 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 5-15 days, about 6-15 days, about 7-15 days, about 8-15 days, about 9-15 days, about 10-15 days, about 11-15 days, about 12-15 days, about 13-15 days, about 14-15 days, about 5-14 days, about 6-14 days, about 7-14 days, about 8-14 days, about 9-14 days, about 10-14 days, about 11-14 days, about 12-14 days, about 13-14 days, about 5-13 days, about 6-13 days, about 7-13 days, about 8-13 days, about 9-13 days, about 10-13 days, about 11-13 days, about 12-13 days, about 5-12 days, about 6-12 days, about 7-12 days, about 8-12 days, about 9-12 days, about 10-12 days, about 11-12 days, about 5-11 days, 6-11 days, 7-11 days, about 8-11 days, about 9-11 days, about 10-11 days, about 5-10 days, 6-10 days, 7-10 days, about 8-10 days, about 9-10 days, about 5-9 days, 6-9 days, 7-9 days, about 8-9 days, about 5-8 days, about 6-8 days, 7-8 days, about 5-7 days, about 6-7 days, about 5-6 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 5 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 6 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 7 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 8 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 9 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 10 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 11 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 12 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 13 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 14 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 15 days.

[00218] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 23 days. In some embodiments, the steps of the method are completed within a period of about 24 days. In some embodiments, the steps of the method are completed within a period of about 25 days. In some embodiments, the steps of the method are completed within a period of about 26 days. In some embodiments, the steps of the method are completed within a period of about 27 days. In some embodiments, the steps of the method are completed within a period of about 28 days. In some embodiments, the steps of the method are completed within a period of about 29 days. In some embodiments, the steps of the method are completed within a period of about 30 days. In some embodiments, the steps of the method are completed within a period of about 31 days.

[00219] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00220] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00221] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00222] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00223] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00224] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00225] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00226] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2

days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00227] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00228] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00229] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00230] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00231] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00232] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00233] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00234] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00235] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00236] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00237] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00238] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00239] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00240] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00241] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00242] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00243] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5

days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00244] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00245] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00246] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00247] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00248] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00249] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00250] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00251] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00252] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00253] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00254] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00255] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00256] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(e), (a)-(f), or (a)-(g) outlined in the methods above, or before or after any of steps (a)-(e), (a)-(f), or (a)-(g) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00257] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(e), (a)-(f), or (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00258] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00259] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3- 9 days to produce a second population of TILs;

(c) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00260] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00261] In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days, about 3-8 days, about 4-8 days, about 5-8 days, about 6-8 days, about 7-8 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3 days. In some embodiments, the step of culturing the first population of TILs is performed for about 4 days. In some embodiments, the step of culturing the first population of TILs 5 days. In some embodiments, the step of culturing the first population of TILs is performed for about 6 days. In some embodiments, the step of culturing the first population of TILs is performed for about 7 days. In some embodiments, the step of culturing the first population of TILs is performed for about 8 days. In some embodiments, the step of culturing the first population of TILs is performed for about 9 days.

[00262] In some embodiments, the step of culturing the third population of TILs is performed for about 5-15 days. In some embodiments, the step of culturing the third population of TILs is performed

for about 5-15 days, about 6-15 days, about 7-15 days, about 8-15 days, about 9-15 days, about 10-15 days, about 11-15 days, about 12-15 days, about 13-15 days, about 14-15 days, about 5-14 days, about 6-14 days, about 7-14 days, about 8-14 days, about 9-14 days, about 10-14 days, about 11-14 days, about 12-14 days, about 13-14 days, about 5-13 days, about 6-13 days, about 7-13 days, about 8-13 days, about 9-13 days, about 10-13 days, about 11-13 days, about 12-13 days, about 5-12 days, about 6-12 days, about 7-12 days, about 8-12 days, about 9-12 days, about 10-12 days, about 11-12 days, about 5-11 days, 6-11 days, 7-11 days, about 8-11 days, about 9-11 days, about 10-11 days, about 5-10 days, 6-10 days, 7-10 days, about 8-10 days, about 9-10 days, about 5-9 days, 6-9 days, 7-9 days, about 8-9 days, about 5-8 days, about 6-8 days, 7-8 days, about 5-7 days, about 6-7 days, about 5-6 days. In some embodiments, the step of culturing the third population of TILs is performed for about 5 days. In some embodiments, the step of culturing the third population of TILs is performed for about 6 days. In some embodiments, the step of culturing the third population of TILs is performed for about 7 days. In some embodiments, the step of culturing the third population of TILs is performed for about 8 days. In some embodiments, the step of culturing the third population of TILs is performed for about 9 days. In some embodiments, the step of culturing the third population of TILs is performed for about 10 days. In some embodiments, the step of culturing the third population of TILs is performed for about 11 days. In some embodiments, the step of culturing the third population of TILs is performed for about 12 days. In some embodiments, the step of culturing the third population of TILs is performed for about 13 days. In some embodiments, the step of culturing the third population of TILs is performed for about 14 days. In some embodiments, the step of culturing the third population of TILs is performed for about 15 days.

[00263] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some

embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 23 days. In some embodiments, the steps of the method are completed within a period of about 24 days.

[00264] In some embodiments, the step of culturing the third population of TILs is performed by culturing the third population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00265] In some embodiments, the step of culturing the third population of TILs is performed by culturing the third population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00266] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(d) or (a)-(e) outlined in the method above, or before or after any of steps (a)-(d) or (a)-(c) outlined in the method above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00267] It should be noted that alternative embodiments of the expansion process may differ from the method shown above; e.g., alternative embodiments may not have the same steps (a)-(d) or (a)-(e), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00268] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily

"removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00269] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(c) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;

(d) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(e) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00270] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(f) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and

combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00271] In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3-9 days, about 3-8 days, about 4-8 days, about 5-8 days, about 6-8 days, about 7-8 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the step of culturing the first population of TILs is performed for about 3 days. In some embodiments, the step of culturing the first population of TILs is performed for about 4 days. In some embodiments, the step of culturing the first population of TILs is performed for about 5 days. In some embodiments, the step of culturing the first population of TILs is performed for about 6 days. In some embodiments, the step of culturing the first population of TILs is performed for about 7 days. In some embodiments, the step of culturing the first population of TILs is performed for about 8 days. In some embodiments, the step of culturing the first population of TILs is performed for about 9 days.

[00272] In some embodiments, the step of culturing the third population of TILs is performed for about 1-7 days. In some embodiments, the step of culturing the third population of TILs is performed for about 1-7 days, about 2-7 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4 days, about 2-4 days, about 3-4 days, about 1-3 days, about 2-3 days, about 1-2 days. In some embodiments, the step of culturing the third population of TILs is performed for about 1 day. In some embodiments, the step of culturing the third population of TILs is performed for about 2 days. In some embodiments, the step of culturing the third population of TILs is performed for about 3 days. In some embodiments, the step of culturing the third population of TILs is performed for about 4 days. In some embodiments, the step of culturing the third population of TILs is performed for about 5 days. In some embodiments, the step of culturing the third population of TILs is performed for about 6 days. In some embodiments, the step of culturing the third population of TILs is performed for about 7 days.

[00273] In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 3-6 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 3 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 4 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 5 days. In some embodiments, the step of culturing each of the

plurality of subcultures is performed for about 6 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 7 days.

[00274] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 23 days.

[00275] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(e) or (a)-(f) outlined in the methods above, or before or after any of steps (a)-(e) or (a)-(f) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00276] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(e) or (a)-(f), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative

embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00277] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00278] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(e) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00279] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and

(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

[00280] In some embodiments, the step of culturing the second population of TILs is performed for about 2-4 days. In some embodiments, the step of culturing the third population of TILs is performed for about 2-4 days, about 3-4 days, about 2-3 days. In some embodiments, the step of culturing the second population of TILs is performed for about 2 days. In some embodiments, the step of culturing the second population of TILs is performed for about 3 days. In some embodiments, the step of culturing the second population of TILs is performed for about 4 days.

[00281] In some embodiments, the step of culturing the fourth population of TILs is performed for about 5-15 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 5-15 days, about 6-15 days, about 7-15 days, about 8-15 days, about 9-15 days, about 10-15 days, about 11-15 days, about 12-15 days, about 13-15 days, about 14-15 days, about 5-14 days, about 6-14 days, about 7-14 days, about 8-14 days, about 9-14 days, about 10-14 days, about 11-14 days, about 12-14 days, about 13-14 days, about 5-13 days, about 6-13 days, about 7-13 days, about 8-13 days, about 9-13 days, about 10-13 days, about 11-13 days, about 12-13 days, about 5-12 days, about 6-12 days, about 7-12 days, about 8-12 days, about 9-12 days, about 10-12 days, about 11-12 days, about 5-11 days, 6-11 days, 7-11 days, about 8-11 days, about 9-11 days, about 10-11 days, about 5-10 days, 6-10 days, 7-10 days, about 8-10 days, about 9-10 days, about 5-9 days, 6-9 days, 7-9 days, about 8-9 days, about 5-8 days, about 6-8 days, 7-8 days, about 5-7 days, about 6-7 days, about 5-6 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 5 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 6 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 7 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 8 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 9 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 10 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 11 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 12 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 13 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 14 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 15 days.

[00282] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of

subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00283] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00284] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00285] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00286] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00287] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00288] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00289] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00290] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00291] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00292] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00293] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00294] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00295] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00296] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00297] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00298] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00299] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4

days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00300] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00301] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00302] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00303] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00304] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00305] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00306] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00307] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00308] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00309] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00310] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00311] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00312] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00313] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00314] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00315] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00316] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7

days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00317] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some embodiments, the steps of the method are completed within a period of about 22 days.

[00318] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(f) or (a)-(g) outlined in the methods above, or before or after any of steps (a)-(f) or (a)-(g) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00319] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(f) or (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative

embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00320] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00321] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(c) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(f) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00322] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;

(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(g) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

[00323] In some embodiments, the step of culturing the second population of TILs is performed for about 2-4 days. In some embodiments, the step of culturing the third population of TILs is performed for about 2-4 days, about 3-4 days, about 2-3 days. In some embodiments, the step of culturing the second population of TILs is performed for about 2 days. In some embodiments, the step of culturing the second population of TILs is performed for about 3 days. In some embodiments, the step of culturing the second population of TILs is performed for about 4 days.

[00324] In some embodiments, the step of culturing the fourth population of TILs is performed for about 1-7 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 1-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, about 1-2 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 1 day. In some embodiments, the step of culturing the fourth population of TILs is performed for about 2 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 3 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 4 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 5 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 6 days. In some embodiments, the step of culturing the fourth population of TILs is performed for about 7 days.

[00325] In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 3-6 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed

for about 3 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 4 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 5 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 6 days. In some embodiments, the step of culturing each of the plurality of subcultures is performed for about 7 days.

[00326] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days.

[00327] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(f) or (a)-(g) outlined in the methods above, or before or after any of steps (a)-(f) or (a)-(g) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00328] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(f) or (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative

embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00329] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00330] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 9 days;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(e) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00331] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 9 days;

(c) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(d) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00332] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 9 days;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00333] In some embodiments, a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium

comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 9 days;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(e) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

[00334] In some embodiments, the initial expansion is performed for about 3-9 days. In some embodiments, the initial expansion is performed for about 1-9 days, 2-9 days, 3-9 days, about 4-9 days, about 5-9 days, about 6-9 days, about 7-9 days, about 8-9 days, about 1-8 days, about 2-8 days, about 3-8 days, about 4-8 days, about 5-8 days, about 6-8 days, about 7-8 days, about 1-7 days, about 2-7 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4 days, about 2-4 days, about 3-4 days, about 1-3 days, about 2-3 days, or about 1-2 days. In some embodiments, the initial expansion is performed for about 1 day. In some embodiments, the initial expansion is performed for about 2 days. In some embodiments, the initial expansion is performed for about 3 days. In some embodiments, the initial expansion is performed for about 4 days. In some embodiments, the initial expansion is performed for about 5 days. In some embodiments, the initial expansion is performed for about 6 days. In some embodiments, the initial expansion is performed for about 7 days. In some embodiments, the initial expansion is performed for about 8 days. In some embodiments, the initial expansion is performed for about 9 days.

[00335] In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days. In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days, about 2-7 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, or about 1-2 days. In some embodiments, the step of activating the second population of TILs is performed for about 1 day. In some embodiments, the step of activating the second population of TILs is performed for about 2 days. In some embodiments, the step of activating the second population of TILs is performed for about 3 days. In some embodiments, the step of activating the second population of TILs is performed for about 4 days. In some embodiments, the step of activating the second population of TILs is performed for about 5 days. In some embodiments, the step of activating the second population of TILs is performed for about 6

days. In some embodiments, the step of activating the second population of TILs is performed for about 7 days.

[00336] In some embodiments, the rapid second expansion is performed for about 5-15 days. In some embodiments, the rapid second expansion is performed for about 5-15 days, about 6-15 days, about 7-15 days, about 8-15 days, about 9-15 days, about 10-15 days, about 11-15 days, about 12-15 days, about 13-15 days, about 14-15 days, about 5-14 days, about 6-14 days, about 7-14 days, about 8-14 days, about 9-14 days, about 10-14 days, about 11-14 days, about 12-14 days, about 13-14 days, about 5-13 days, about 6-13 days, about 7-13 days, about 8-13 days, about 9-13 days, about 10-13 days, about 11-13 days, about 12-13 days, about 5-12 days, about 6-12 days, about 7-12 days, about 8-12 days, about 9-12 days, about 10-12 days, about 11-12 days, about 5-11 days, 6-11 days, 7-11 days, about 8-11 days, about 9-11 days, about 10-11 days, about 5-10 days, 6-10 days, 7-10 days, about 8-10 days, about 9-10 days, about 5-9 days, 6-9 days, 7-9 days, about 8-9 days, about 5-8 days, about 6-8 days, 7-8 days, about 5-7 days, about 6-7 days, about 5-6 days. In some embodiments, the rapid second expansion is performed for about 5 days. In some embodiments, the rapid second expansion is performed for about 6 days. In some embodiments, the rapid second expansion is performed for about 7 days. In some embodiments, the rapid second expansion is performed for about 8 days. In some embodiments, the rapid second expansion is performed for about 9 days. In some embodiments, the rapid second expansion is performed for about 10 days. In some embodiments, the rapid second expansion is performed for about 11 days. In some embodiments, the rapid second expansion is performed for about 12 days. In some embodiments, the rapid second expansion is performed for about 13 days. In some embodiments, the rapid second expansion is performed for about 14 days. In some embodiments, the rapid second expansion is performed for about 15 days.

[00337] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some

embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 23 days. In some embodiments, the steps of the method are completed within a period of about 24 days. In some embodiments, the steps of the method are completed within a period of about 25 days. In some embodiments, the steps of the method are completed within a period of about 26 days. In some embodiments, the steps of the method are completed within a period of about 27 days. In some embodiments, the steps of the method are completed within a period of about 28 days. In some embodiments, the steps of the method are completed within a period of about 29 days. In some embodiments, the steps of the method are completed within a period of about 30 days. In some embodiments, the steps of the method are completed within a period of about 31 days.

[00338] In some embodiments, the rapid second expansion is performed by culturing the third population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00339] In some embodiments, the rapid second expansion is performed by culturing the third population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00340] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(e) or (a)-(f) outlined in the methods above, or before or after any of steps (a)-(e) or (a)-(f) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00341] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(e) or (a)-(f), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00342] According to some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00343] In some embodiments, a method for expanding tumor infiltrating lymphocytes into a therapeutic population of TILs comprises:

(a) obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;

(b) adding the tumor tissue into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(c) activating the second population of TILs using CD3 and CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(e) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(f) harvesting the therapeutic population of TILs obtained from step (e), wherein each of steps (b) to (f) is performed in a closed, sterile system, and wherein the transition from step (b) to step (c), the

transition from step (c) to step (d), the transition from step (d) to step (e) and/or the transition from step (e) to step (f) occurs without opening the system.

[00344] In some embodiments, a method for expanding tumor infiltrating lymphocytes into a therapeutic population of TILs comprises:

(a) obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;

(b) digesting the sample of tumor tissue or tumor fragments in an enzymatic media to produce a tumor digest;

(c) adding the tumor tissue into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(d) activating the second population of TILs using CD3 and CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(g) harvesting the therapeutic population of TILs obtained from step (e), wherein each of steps (c) to (g) is performed in a closed, sterile system, and wherein the transition from step (c) to step (d), the transition from step (d) to step (e), the transition from step (e) to step (f) and/or the transition from step (f) to step (g) occurs without opening the system.

[00345] In some embodiments, the first expansion is performed for about 3-9 days. In some embodiments, the first expansion is performed for about 3-9 days, about 3-8 days, about 3-7 days, about 3-6 days, about 3-5 days, about 3-4 days, about 4-9 days, about 4-8 days, about 5-9 days, about 5-8 days, about 6-9 days, about 6-8 days, about 7-9 days, about 7-8 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 3-6 days, about 4-6 days, about 5-6 days, about 3-5 days, about 4-5 days, about 3-4 days. In some embodiments, the first expansion is performed for about 3

days. In some embodiments, the first expansion is performed for about 4 days. In some embodiments, the first expansion is performed for about 5 days. In some embodiments, the first expansion is performed for about 6 days. In some embodiments, the first expansion is performed for about 7 days. In some embodiments, the first expansion is performed for about 8 days. In some embodiments, the first expansion is performed for about 9 days.

[00346] In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days. In some embodiments, the step of activating the second population of TILs is performed for about 1-7 days, about 2-7 days, about 3-7 days, 4-7 days, about 5-7 days, about 6-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, about 1-2 days. In some embodiments, the step of activating the second population of TILs is performed for about 1 day. In some embodiments, the step of activating the second population of TILs is performed for about 2 days. In some embodiments, the step of activating the second population of TILs is performed for about 3 days. In some embodiments, the step of activating the second population of TILs is performed for about 4 days. In some embodiments, the step of activating the second population of TILs is performed for about 5 days. In some embodiments, the step of activating the second population of TILs is performed for about 6 days. In some embodiments, the step of activating the second population of TILs is performed for about 7 days.

[00347] In some embodiments, the second expansion is performed for about 5-15 days. In some embodiments, the second expansion is performed for about 5-15 days, about 6-15 days, about 7-15 days, about 8-15 days, about 9-15 days, about 10-15 days, about 11-15 days, about 12-15 days, about 13-15 days, about 14-15 days, about 5-14 days, about 6-14 days, about 7-14 days, about 8-14 days, about 9-14 days, about 10-14 days, about 11-14 days, about 12-14 days, about 13-14 days, about 5-13 days, about 6-13 days, about 7-13 days, about 8-13 days, about 9-13 days, about 10-13 days, about 11-13 days, about 12-13 days, about 5-12 days, about 6-12 days, about 7-12 days, about 8-12 days, about 9-12 days, about 10-12 days, about 11-12 days, about 5-11 days, 6-11 days, 7-11 days, about 8-11 days, about 9-11 days, about 10-11 days, about 5-10 days, 6-10 days, 7-10 days, about 8-10 days, about 9-10 days, about 5-9 days, 6-9 days, 7-9 days, about 8-9 days, about 5-8 days, about 6-8 days, 7-8 days, about 5-7 days, about 6-7 days, about 5-6 days. In some embodiments, the second expansion is performed for about 5 days. In some embodiments, the second expansion is performed for about 6 days. In some embodiments, the second expansion is performed for about 7 days. In some embodiments, the second expansion is performed for about 8 days. In some embodiments, the second expansion is performed for about 9 days. In some embodiments, the second expansion is performed for about 10 days. In some embodiments, the second expansion is performed for about 11 days. In

some embodiments, the second expansion is performed for about 12 days. In some embodiments, the second expansion is performed for about 13 days. In some embodiments, the second expansion is performed for about 14 days. In some embodiments, the second expansion is performed for about 15 days.

[00348] In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 8 days. In some embodiments, the steps of the method are completed within a period of about 9 days. In some embodiments, the steps of the method are completed within a period of about 10 days. In some embodiments, the steps of the method are completed within a period of about 11 days. In some embodiments, the steps of the method are completed within a period of about 12 days. In some embodiments, the steps of the method are completed within a period of about 13 days. In some embodiments, the steps of the method are completed within a period of about 14 days. In some embodiments, the steps of the method are completed within a period of about 15 days. In some embodiments, the steps of the method are completed within a period of about 16 days. In some embodiments, the steps of the method are completed within a period of about 17 days. In some embodiments, the steps of the method are completed within a period of about 18 days. In some embodiments, the steps of the method are completed within a period of about 19 days. In some embodiments, the steps of the method are completed within a period of about 20 days. In some embodiments, the steps of the method are completed within a period of about 21 days. In some embodiments, the steps of the method are completed within a period of about 22 days. In some embodiments, the steps of the method are completed within a period of about 23 days. In some embodiments, the steps of the method are completed within a period of about 24 days. In some embodiments, the steps of the method are completed within a period of about 25 days. In some embodiments, the steps of the method are completed within a period of about 26 days. In some embodiments, the steps of the method are completed within a period of about 27 days. In some embodiments, the steps of the method are completed within a period of about 28 days. In some embodiments, the steps of the method are completed within a period of about 29 days. In some embodiments, the steps of the method are completed within a period of about 30 days. In some embodiments, the steps of the method are completed within a period of about 31 days. In some embodiments, the steps of the method are completed within a period of about 32 days.

[00349] In some embodiments, the second expansion is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end

of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00350] In some embodiments, the second expansion is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00351] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00352] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00353] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00354] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00355] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 1 day,

at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00356] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00357] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00358] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00359] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00360] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 2 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00361] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00362] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00363] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00364] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00365] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 3 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00366] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00367] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00368] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00369] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00370] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 4 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00371] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00372] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5

days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00373] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00374] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00375] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 5 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00376] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00377] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00378] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00379] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00380] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 6 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00381] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00382] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 4 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00383] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of

about 5 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00384] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00385] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second culture medium for a first period of about 7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00386] In some embodiments, the gene-editing process can be carried out at any time during the TIL expansion method, which means that the gene-editing may be carried out on TILs before, during, or after any of the steps in the expansion method; for example, during any of steps (a)-(f) or (a)-(g) outlined in the methods above, or before or after any of steps (a)-(f) or (a)-(g) outlined in the methods above. In some embodiments, the gene-editing process can be carried out more than once at any time during the TIL expansion method. According to certain embodiments, TILs are collected during a culturing step (e.g., the culturing step is "paused" for at least a portion of the TILs), and the collected TILs are subjected to a gene-editing process, and, in some cases, subsequently reintroduced back into the culturing step (e.g., back into the culture medium) to continue the culturing step, so that at least a portion of the therapeutic population of TILs that are eventually transferred to the infusion bag are permanently gene-edited.

[00387] It should be noted that alternative embodiments of the expansion process may differ from the methods shown above; e.g., alternative embodiments may not have the same steps (a)-(f) or (a)-(g), or may have a different number of steps. Regardless of the specific embodiment, the gene-editing process may be carried out at any time during the TIL expansion method. For example, alternative embodiments may include more than two culturing steps, and it is possible that gene-editing may be conducted on the TILs during a third or fourth culturing step, etc.

[00388] In some embodiments, gene-editing is performed while the TILs are still in the culture medium and while the culturing step is being carried out, i.e., they are not necessarily "removed" from the culturing step in order to conduct gene-editing. According to some embodiments, gene-

editing is performed on TILs that are collected from the culture medium, and following the gene-editing process those TILs are subsequently be placed back into the culture medium.

[00389] In some embodiments, the step of gene-editing at least a portion of the second or third population of TILs comprises performing a sterile electroporation step on the second or third population of TILs.

[00390] In some embodiments, the sterile electroporation step mediates the transfer of at least one gene editor. According to some embodiments, the gene editor is a TALE nuclease system for modulating the expression of at least one protein. According to some embodiments, the TALE nuclease system downmodulates expression of PD-1. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CTLA-4. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of LAG-3. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CISH. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CBL-B. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of TIGIT. According to some embodiments, the resulting TILs are PD-1 knockout TILs. According to some embodiments, the resulting TILs are CTLA-4 knockout TILs. According to some embodiments, the resulting TILs are LAG-3 knockout TILs. According to some embodiments, the resulting TILs are CISH knockout TILs. According to some embodiments, the resulting TILs are CBL-B knockout TILs. According to some embodiments, the resulting TILs are TIGIT knockout TILs. According to some embodiments, the resulting TILs exhibit downmodulated expression of PD-1 and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CTLA-4 and downmodulated expression of one or more of PD-1, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of LAG-3 and downmodulated expression of one or more of PD-1, CTLA-4, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CISH and downmodulated expression of one or more of PD-1, LAG-3, CTLA-4, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CBL-B and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and PD-1. According to some embodiments, the resulting TILs are PD-1/CTLA-4 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CISH double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are PD-1/TIGIT double knockout

TILs. According to some embodiments, the resulting TILs are CTLA-4/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CISH double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CISH double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CISH/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CISH/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CBL-B/TIGIT double knockout TILs.

[00391] In some embodiments, the step of gene-editing further comprises a resting step. According to some embodiments, the resting step comprises incubating the fourth population of TILs at about 30-40 °C with about 5% CO2. According to some embodiments, the resting step is carried out at about 30°C, about 30.5°C, about 31°C, about 31.5°C, about 32°C, about 32.5°C, about 33°C, about 33.5°C, about 34°C, about 34.5°C, about 35°C, about 35.5°C, about 36°C, about 36.5°C, about 37°C, about 37.5°C, about 38°C, about 38.5°C, about 39°C, about 39.5°C, about 40°C. According to some embodiments, the resting step is carried out for about 1 hour, about 2 hours, about 3 hours, about 4 hours, about 5 hours, about 6 hours, about 7 hours, about 8 hours, about 9 hours, about 10 hours, about 11 hours, about 12 hours, about 13 hours, about 14 hours, about 15 hours, about 16 hours, about 17 hours, about 18 hours, about 19 hours, about 20 hours, about 21 hours, about 22 hours, about 23 hours, about 24 hours. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 16 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 17 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 18 hours at about 30°C. According to some embodiments, the resting step comprises incubating

the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 19 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 20 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 21 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 22 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 23 hours at about 30°C.

[00392] In some embodiments, the antigen presenting cells (APCs) are PBMCs. According to some embodiments, the PBMCs are irradiated. According to some embodiments, the PBMCs are allogeneic. According to some embodiments, the PBMCs are irradiated and allogeneic. According to some embodiments, the antigen-presenting cells are artificial antigen-presenting cells.

[00393] In some embodiments, the tumor tissue is from a dissected tumor.

[00394] In some embodiments, the dissected tumor is less than 8 hours old.

[00395] In some embodiments, the tumor tissue is selected from the group consisting of melanoma tumor tissue, head and neck tumor tissue, breast tumor tissue, renal tumor tissue, pancreatic tumor tissue, glioblastoma tumor tissue, lung tumor tissue, colorectal tumor tissue, sarcoma tumor tissue, triple negative breast tumor tissue, cervical tumor tissue, ovarian tumor tissue, and HPV-positive tumor tissue.

[00396] In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2.5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3.5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 4 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 4.5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into

approximately spherical fragments having a diameter of about 5.5 mm to 6 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2.5 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3.5 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 4 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 4.5 mm to 5 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to 4 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2 mm to 4 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2.5 mm to 4 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3 mm to 4 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 3.5 mm to 4 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to 3 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2 mm to 3 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 2.5 mm to 3 mm. In some embodiments, the tumor tissue is fragmented into approximately spherical fragments having a diameter of about 1.5 mm to 2 mm.

[00397] In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 1.5 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 2 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 2.5 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 3 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 3.5 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 4 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular

fragments having a shortest edge length of at least 4.5 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 5 mm and a longest edge length of about 6 mm. In some embodiments, the tumor tissue is fragmented into generally rectangular fragments having a shortest edge length of at least 5.5 mm and a longest edge length of about 6 mm.

[00398] In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 3 mm or about 6 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 3 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 3.5 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 4 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 4.5 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 5 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 5.5 mm. In some embodiments, the tumor tissue is fragmented into generally cubical fragments having edge lengths of about 6 mm.

[00399] In some embodiments, the present invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) product produced by a method as described herein.

[00400] In some embodiments, the present invention provides a method for treatment cancer in a patient comprising administering to the patient an effective amount of the therapeutic population of TILs produced by a method as described herein. In some embodiments, the cancer is selected from the group consisting of glioblastoma (GBM), gastrointestinal cancer, melanoma, metastatic melanoma, ovarian cancer, endometrial cancer, thyroid cancer, colorectal cancer, cervical cancer, non-small-cell lung cancer (NSCLC), metastatic NSCLC, lung cancer, bladder cancer, breast cancer, endometrial cancer, cholangiocarcinoma, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), renal cancer, renal cell carcinoma, multiple myeloma, chronic lymphocytic leukemia, acute lymphoblastic leukemia, diffuse large B cell lymphoma, non-Hodgkin's lymphoma, Hodgkin's lymphoma, follicular lymphoma, and mantle cell lymphoma. In some embodiments, the cancer is selected from the group consisting of cutaneous melanoma, ocular melanoma, uveal melanoma, conjunctival malignant melanoma, metastatic melanoma, pleomorphic xanthoastrocytoma, dysembryoplastic neuroepithelial tumor, ganglioglioma, and pilocytic astrocytoma, endometrioid adenocarcinoma with significant mucinous differentiation (ECMD), papillary thyroid carcinoma, serous low-grade or borderline ovarian carcinoma, hairy cell leukemia, and Langerhans cell histiocytosis.

[00401] In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1500 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2000 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2500 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 3000 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 3500 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 4000 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 4500 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 5000 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 5500 IU/mL and 6000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1500 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2000 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2500 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 3000 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 3500 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 4000 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 4500 IU/mL and 5000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1500 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2000 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2500 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of

between 3000 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 3500 IU/mL and 4000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 3000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1500 IU/mL and 3000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2000 IU/mL and 3000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 2500 IU/mL and 3000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1000 IU/mL and 2000 IU/mL in the cell culture medium in the first expansion. In some embodiments, the IL-2 is present at an initial concentration of between 1500 IU/mL and 2000 IU/mL in the cell culture medium in the first expansion.

[00402] In some embodiments, the second expansion step, the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL and the OKT-3 antibody is present at an initial concentration of about 30 ng/mL.

[00403] In some embodiments, the first cell culture medium and/or the second cell culture medium further comprises a 4-1BB agonist and/or an OX40 agonist.

[00404] In some embodiments, the first expansion is performed using a gas permeable container. In some embodiments, the second expansion is performed using a gas permeable container.

[00405] In some embodiments, the first cell culture medium further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof. In some embodiments, the second cell culture medium and/or third culture medium further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof.

[00406] In some embodiments, the method further comprises the step of treating the patient with a non-myeloablative lymphodepletion regimen prior to administering the TILs or PBL product to the patient. In some embodiments, the method further comprises the step of treating the patient with an IL-2 regimen starting on the day after the administration of the TILs or PBL product to the patient. In some embodiments, the method further comprises the step of treating the patient with an IL-2 regimen starting on the same day as administration of the TILs or PBL product to the patient. In some embodiments, the IL-2 regimen comprises aldesleukin, nemvaleukin, or a biosimilar or variant thereof.

[00407] In some embodiments, the therapeutically effective amount of TILs product comprises from about 2.3×1010 to about 13.7×1010 TILs.

[00408] In some embodiments, the second population of TILs is at least 50-fold greater in number than the first population of TILs.

[00409] Exemplary disclosures of the PD-1 TALEN knockdown are provided in U.S. Provisional Application No. 63/242,373, which is incorporated herein by reference in its entirety for all related purposes.

D. Gene Editing Methods

[00410] As discussed above, embodiments of the present invention provide tumor infiltrating lymphocytes (TILs) that have been genetically modified via gene-editing to enhance their therapeutic effect (*e.g.*, expression of an immunomodulatory fusion protein on its cell surface). Embodiments of the present invention embrace genetic editing through nucleotide insertion (RNA or DNA) into a population of TILs for both promotion of the expression of one or more proteins and inhibition of the expression of one or more proteins, as well as combinations thereof. Embodiments of the present invention also provide methods for expanding TILs into a therapeutic population, wherein the methods comprise gene-editing the TILs. There are several gene-editing technologies that may be used to genetically modify a population of TILs, which are suitable for use in accordance with the present invention.

[00411] In some embodiments, a method of genetically modifying a population of TILs includes the step of stable incorporation of genes for production of one or more proteins. In some embodiments, a method of genetically modifying a population of TILs includes the step of retroviral transduction. In some embodiments, a method of genetically modifying a population of TILs includes the step of lentiviral transduction. Lentiviral transduction systems are known in the art and are described, e.g., in Levine, et al., Proc. Nat'l Acad. Sci. 2006, 103, 17372-77; Zufferey, et al., Nat. Biotechnol. 1997, 15, 871-75; Dull, et al., J. Virology 1998, 72, 8463-71, and U.S. Patent No. 6,627,442, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of gamma-retroviral transduction. Gamma-retroviral transduction systems are known in the art and are described, e.g., Cepko and Pear, Cur. Prot. Mol. Biol. 1996, 9.9.1-9.9.16, the disclosure of which is incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of transposon-mediated gene transfer. Transposon-mediated gene transfer systems are known in the art and include systems wherein the transposase is provided as DNA expression vector or as an expressible RNA or a protein such that long-term expression of the transposase does not occur in the transgenic cells, for example, a transposase provided as an mRNA (*e.g.*, an mRNA comprising a cap and poly-A tail). Suitable transposon-mediated gene transfer systems, including the salmonid-type Tel-like transposase (SB or Sleeping Beauty transposase), such as SB10, SB11, and SB100x, and

engineered enzymes with increased enzymatic activity, are described in, *e.g.*, Hackett, *et al.*, *Mol. Therapy* **2010,** *18,* 674-83 and U.S. Patent No. 6,489,458, the disclosures of each of which are incorporated by reference herein.

[00412] In some embodiments, a method of genetically modifying a population of TILs includes the step of stable incorporation of genes for production or inhibition (*e.g.*, silencing) of one or more proteins. In some embodiments, a method of genetically modifying a population of TILs includes the step of electroporation. Electroporation methods are known in the art and are described, *e.g.*, in Tsong, *Biophys. J.* **1991,** *60,* 297-306, and U.S. Patent Application Publication No. 2014/0227237 A1, the disclosures of each of which are incorporated by reference herein. Other electroporation methods known in the art, such as those described in U.S. Patent Nos. 5,019,034; 5,128,257; 5,137,817; 5,173,158; 5,232,856; 5,273,525; 5,304,120; 5,318,514; 6,010,613 and 6,078,490, the disclosures of which are incorporated by reference herein, may be used. In some embodiments, the electroporation method is a sterile electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of the at least three pulses differ from each other in pulse amplitude. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of the at least three pulses differ from each other in pulse width. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary

changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to induce pore formation in the TILs, comprising the step of applying a sequence of at least three DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses, such that induced pores are sustained for a relatively long period of time, and such that viability of the TILs is maintained. In some embodiments, a method of genetically modifying a population of TILs includes the step of calcium phosphate transfection. Calcium phosphate transfection methods (calcium phosphate DNA precipitation, cell surface coating, and endocytosis) are known in the art and are described in Graham and van der Eb, *Virology* **1973,** *52,* 456-467; Wigler, *et al.*, *Proc. Natl. Acad. Sci.* **1979,** *76,* 1373-1376; and Chen and Okayarea, *Mol. Cell. Biol.* **1987,** *7,* 2745-2752; and in U.S. Patent No. 5,593,875, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of liposomal transfection. Liposomal transfection methods, such as methods that employ a 1:1 (w/w) liposome formulation of the cationic lipid *N*-[1-(2,3-dioleyloxy)propyl]-*n,n,n*-trimethylammonium chloride (DOTMA) and dioleoyl phophotidylethanolamine (DOPE) in filtered water, are known in the art and are described in Rose, *et al.*, *Biotechniques* **1991,** *10,* 520-525 and Felgner, *et al.*, *Proc. Natl. Acad. Sci. USA*, **1987,** *84,* 7413-7417 and in U.S. Patent Nos. 5,279,833; 5,908,635; 6,056,938; 6,110,490; 6,534,484; and 7,687,070, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of transfection using methods described in U.S. Patent Nos. 5,766,902; 6,025,337; 6,410,517; 6,475,994; and 7,189,705; the disclosures of each of which are incorporated by reference herein.

[00413] According to some embodiments, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at one or more immune checkpoint genes. Such programmable nucleases enable precise genome editing by introducing breaks at specific genomic loci, *i.e.,* they rely on the recognition of a specific DNA sequence within the genome to target a nuclease domain to this location and mediate the generation of a double-strand break at the target sequence. A double-strand break in the DNA subsequently recruits endogenous repair machinery to the break site to mediate genome editing by either non-homologous

end-joining (NHEJ) or homology-directed repair (HDR). Thus, the repair of the break can result in the introduction of insertion/deletion mutations that disrupt (*e.g.*, silence, repress, or enhance) the target gene product.

[00414] Major classes of nucleases that have been developed to enable site-specific genomic editing include zinc finger nucleases (ZFNs), transcription activator-like nucleases (TALENs), and CRISPR-associated nucleases (*e.g.*, CRISPR/Cas9). These nuclease systems can be broadly classified into two categories based on their mode of DNA recognition: ZFNs and TALENs achieve specific DNA binding via protein-DNA interactions, whereas CRISPR systems, such as Cas9, are targeted to specific DNA sequences by a short RNA guide molecule that base-pairs directly with the target DNA and by protein-DNA interactions. *See, e.g.,* Cox *et al.*, *Nature Medicine,* 2015, Vol. 21, No. 2.

[00415] Non-limiting examples of gene-editing methods that may be used in accordance with TIL expansion methods of the present invention include CRISPR methods, TALE methods, and ZFN methods, embodiments of which are described in more detail below. According to some embodiments, a method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A) or as described in PCT/US2017/058610, PCT/US2018/012605, or PCT/US2018/012633, wherein the method further comprises gene-editing at least a portion of the TILs by one or more of a CRISPR method, a TALE method or a ZFN method, in order to generate TILs that can provide an enhanced therapeutic effect. According to some embodiments, gene-edited TILs can be evaluated for an improved therapeutic effect by comparing them to non-modified TILs *in vitro, e.g.,* by evaluating *in vitro* effector function, cytokine profiles, etc. compared to unmodified TILs.

[00416] In some embodiments of the present invention, electroporation is used for delivery of a gene editing system, such as CRISPR, TALEN, and ZFN systems. In some embodiments of the present invention, the electroporation system is a flow electroporation system. An example of a suitable flow electroporation system suitable for use with some embodiments of the present invention is the commercially-available MaxCyte STX system. There are several alternative commercially-available electroporation instruments which may be suitable for use with the present invention, such as the AgilePulse system or ECM 830 available from BTX-Harvard Apparatus, Cellaxess Elektra (Cellectricon), Nucleofector (Lonza/Amaxa), GenePulser MXcell (BIORAD), iPorator-96 (Primax) or siPORTer96 (Ambion). In some embodiments of the present invention, the electroporation system forms a closed, sterile system with the remainder of the TIL expansion method. In some embodiments of the present invention, the electroporation system is a pulsed electroporation system as described herein, and forms a closed, sterile system with the remainder of the TIL expansion method.

[00417] In some embodiments, a microfluidic platform is used for delivery of the gene editing system. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

a. CRISPR Methods

[00418] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A) or as described in PCT/US2017/058610, PCT/US2018/012605, or PCT/US2018/012633, wherein the method further comprises gene-editing at least a portion of the TILs by a CRISPR method (*e.g.*, CRISPR/Cas9 or CRISPR/Cpf1). According to particular embodiments, the use of a CRISPR method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface of, and optionally causes one or more immune checkpoint genes to be silenced or reduced in, at least a portion of the therapeutic population of TILs. Alternatively, the use of a CRISPR method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface of, and optionally causes one or more immune checkpoint genes to be enhanced in, at least a portion of the therapeutic population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00419] CRISPR stands for "Clustered Regularly Interspaced Short Palindromic Repeats." A method of using a CRISPR system for gene editing is also referred to herein as a CRISPR method. CRISPR systems can be divided into two main classes, Class 1 and Class 2, which are further classified into different types and sub-types. The classification of the CRISPR systems is based on the effector Cas proteins that are capable of cleaving specific nucleic acids. In Class 1 CRISPR systems the effector module consists of a multi-protein complex, whereas Class 2 systems only use one effector protein. Class 1 CRISPR includes Types I, III, and IV and Class 2 CRISPR includes Types II, V, and VI. While any of these types of CRISPR systems may be used in accordance with the present invention, there are three types of CRISPR systems which incorporate RNAs and Cas proteins that are preferred for use in accordance with the present invention: Types I (exemplified by Cas3), II (exemplified by Cas9), and III (exemplified by Cas10). The Type II CRISPR is one of the most well-characterized systems.

[00420] CRISPR technology was adapted from the natural defense mechanisms of bacteria and archaea (the domain of single-celled microorganisms). These organisms use CRISPR-derived RNA and various Cas proteins, including Cas9, to foil attacks by viruses and other foreign bodies by chopping up and destroying the DNA of a foreign invader. A CRISPR is a specialized region of DNA with two distinct characteristics: the presence of nucleotide repeats and spacers. Repeated sequences of nucleotides are distributed throughout a CRISPR region with short segments of foreign DNA (spacers) interspersed among the repeated sequences. In the type II CRISPR/Cas system, spacers are integrated within the CRISPR genomic loci and transcribed and processed into short CRISPR RNA (crRNA). These crRNAs anneal to trans-activating crRNAs (tracrRNAs) and direct sequence-specific cleavage and silencing of pathogenic DNA by Cas proteins. Target recognition by the Cas9 protein requires a "seed" sequence within the crRNA and a conserved dinucleotide-containing protospacer adjacent motif (PAM) sequence upstream of the crRNA-binding region. The CRISPR/Cas system can thereby be retargeted to cleave virtually any DNA sequence by redesigning the crRNA. Thus, according to certain embodiments, Cas9 serves as an RNA-guided DNA endonuclease that cleaves DNA upon crRNA-tracrRNA recognition. The crRNA and tracrRNA in the native system can be simplified into a single guide RNA (sgRNA) of approximately 100 nucleotides for use in genetic engineering. The sgRNA is a synthetic RNA that includes a scaffold sequence necessary for Cas-binding and a user-defined approximately 17- to 20-nucleotide spacer that defines the genomic target to be modified. Thus, a user can change the genomic target of the Cas protein by changing the target sequence present in the sgRNA. The CRISPR/Cas system is directly portable to human cells by co-delivery of plasmids expressing the Cas9 endo-nuclease and the RNA components (*e.g.*, sgRNA). Different variants of Cas proteins may be used to reduce targeting limitations (*e.g.*, orthologs of Cas9, such as Cpf1).

[00421] According to some embodiments, an engineered, programmable, non-naturally occurring Type II CRISPR-Cas system comprises a Cas9 protein and at least one guide RNA that targets and hybridizes to a target sequence of a DNA molecule in a TIL, wherein the DNA molecule encodes and the TIL expresses at least one immune checkpoint molecule, and the Cas9 protein cleaves the DNA molecules, whereby expression of the at least one immune checkpoint molecule is altered; and, wherein the Cas9 protein and the guide RNA do not naturally occur together. According to some embodiments, the expression of two or more immune checkpoint molecules is altered. According to some embodiments, the guide RNA(s) comprise a guide sequence fused to a tracr sequence. For example, the guide RNA may comprise crRNA-tracrRNA or sgRNA. According to aspects of the present invention, the terms "guide RNA", "single guide RNA" and "synthetic guide RNA" may be used interchangeably and refer to the polynucleotide sequence comprising the guide sequence, which is the approximately 17-20 bp sequence within the guide RNA that specifies the target site.

[00422] Variants of Cas9 having improved on-target specificity compared to Cas9 may also be used in accordance with embodiments of the present invention. Such variants may be referred to as high-fidelity Cas-9s. According to some embodiments, a dual nickase approach may be utilized, wherein two nickases targeting opposite DNA strands generate a DSB within the target DNA (often referred to as a double nick or dual nickase CRISPR system). For example, this approach may involve the mutation of one of the two Cas9 nuclease domains, turning Cas9 from a nuclease into a nickase. Non-limiting examples of high-fidelity Cas9s include eSpCas9, SpCas9-HF1 and HypaCas9. Such variants may reduce or eliminate unwanted changes at non-target DNA sites. *See, e.g.*, Slaymaker IM, et al. *Science*. **2015** Dec 1, Kleinstiver BP, et al. *Nature*. **2016** Jan 6, and Ran et al., *Nat Protoc.* 2013 Nov; 8(11):2281-2308, the disclosures of which are incorporated by reference herein.

[00423] Additionally, according to particular embodiments, Cas9 scaffolds may be used that improve gene delivery of Cas9 into cells and improve on-target specificity, such as those disclosed in U.S. Patent Application Publication No. 2016/0102324, which is incorporated by reference herein. For example, Cas9 scaffolds may include a RuvC motif as defined by (D-[I/L]-G-X-X-S-X-G-W-A) and/or a HNH motif defined by (Y-X-X-D-H-X-X-P-X-S-X-X-X-D-X-S), where X represents any one of the 20 naturally occurring amino acids and [I/L] represents isoleucine or leucine. The HNH domain is responsible for nicking one strand of the target dsDNA and the RuvC domain is involved in cleavage of the other strand of the dsDNA. Thus, each of these domains nick a strand of the target DNA within the protospacer in the immediate vicinity of PAM, resulting in blunt cleavage of the DNA. These motifs may be combined with each other to create more compact and/or more specific Cas9 scaffolds. Further, the motifs may be used to create a split Cas9 protein (*i.e.*, a reduced or truncated form of a Cas9 protein or Cas9 variant that comprises either a RuvC domain or a HNH domain) that is divided into two separate RuvC and HNH domains, which can process the target DNA together or separately.

[00424] According to particular embodiments, a CRISPR method comprises silencing or reducing the expression of one or more immune checkpoint genes in TILs by introducing a Cas9 nuclease and a guide RNA (*e.g.*, crRNA-tracrRNA or sgRNA) containing a sequence of approximately 17-20 nucleotides specific to a target DNA sequence of the immune checkpoint gene(s). The guide RNA may be delivered as RNA or by transforming a plasmid with the guide RNA-coding sequence under a promoter. The CRISPR/Cas enzymes introduce a double-strand break (DSB) at a specific location based on a sgRNA-defined target sequence. DSBs may be repaired in the cells by non-homologous end joining (NHEJ), a mechanism which frequently causes insertions or deletions (indels) in the DNA. Indels often lead to frameshifts, creating loss of function alleles; for example, by causing premature stop codons within the open reading frame (ORF) of the targeted gene. According to

certain embodiments, the result is a loss-of-function mutation within the targeted immune checkpoint gene.

[00425] Alternatively, DSBs induced by CRISPR/Cas enzymes may be repaired by homology-directed repair (HDR) instead of NHEJ. While NHEJ-mediated DSB repair often disrupts the open reading frame of the gene, homology directed repair (HDR) can be used to generate specific nucleotide changes ranging from a single nucleotide change to large insertions. According to some embodiments, HDR is used for gene editing immune checkpoint genes by delivering a DNA repair template containing the desired sequence into the TILs with the sgRNA(s) and Cas9 or Cas9 nickase. The repair template preferably contains the desired edit as well as additional homologous sequence immediately upstream and downstream of the target gene (often referred to as left and right homology arms).

[00426] According to particular embodiments, an enzymatically inactive version of Cas9 (deadCas9 or dCas9) may be targeted to transcription start sites in order to repress transcription by blocking initiation. Thus, targeted immune checkpoint genes may be repressed without the use of a DSB. A dCas9 molecule retains the ability to bind to target DNA based on the sgRNA targeting sequence. According to some embodiments of the present invention, a CRISPR method comprises silencing or reducing the expression of one or more immune checkpoint genes by inhibiting or preventing transcription of the targeted gene(s). For example, a CRISPR method may comprise fusing a transcriptional repressor domain, such as a Kruppel-associated box (KRAB) domain, to an enzymatically inactive version of Cas9, thereby forming, *e.g.*, a dCas9-KRAB, that targets the immune checkpoint gene's transcription start site, leading to the inhibition or prevention of transcription of the gene. Preferably, the repressor domain is targeted to a window downstream from the transcription start site, *e.g.*, about 500 bp downstream. This approach, which may be referred to as CRISPR interference (CRISPRi), leads to robust gene knockdown via transcriptional reduction of the target RNA.

[00427] According to particular embodiments, an enzymatically inactive version of Cas9 (deadCas9 or dCas9) may be targeted to transcription start sites in order to activate transcription. This approach may be referred to as CRISPR activation (CRISPRa). According to some embodiments, a CRISPR method comprises increasing the expression of one or more immune checkpoint genes by activating transcription of the targeted gene(s). According to such embodiments, targeted immune checkpoint genes may be activated without the use of a DSB. A CRISPR method may comprise targeting transcriptional activation domains to the transcription start site; for example, by fusing a transcriptional activator, such as VP64, to dCas9, thereby forming, *e.g.*, a dCas9-VP64, that targets the immune checkpoint gene's transcription start site, leading to activation of transcription of the

gene. Preferably, the activator domain is targeted to a window upstream from the transcription start site, *e.g.*, about 50-400 bp downstream

[00428] Additional embodiments of the present invention may utilize activation strategies that have been developed for potent activation of target genes in mammalian cells. Non-limiting examples include co-expression of epitope-tagged dCas9 and antibody-activator effector proteins (*e.g.*, the SunTag system), dCas9 fused to a plurality of different activation domains in series (*e.g.*, dCas9-VPR) or co-expression of dCas9-VP64 with a modified scaffold gRNA and additional RNA-binding helper activators (*e.g.*, SAM activators).

[00429] According to other embodiments, a CRISPR-mediated genome editing method referred to as CRISPR assisted rational protein engineering (CARPE) may be used in accordance with embodiments of the present invention, as disclosed in US Patent No. 9,982,278, which is incorporated by reference herein. CARPE involves the generation of "donor" and "destination" libraries that incorporate directed mutations from single-stranded DNA (ssDNA) or double-stranded DNA (dsDNA) editing cassettes directly into the genome. Construction of the donor library involves cotransforming rationally designed editing oligonucleotides into cells with a guide RNA (gRNA) that hybridizes to a target DNA sequence. The editing oligonucleotides are designed to couple deletion or mutation of a PAM with the mutation of one or more desired codons in the adjacent gene. This enables the entire donor library to be generated in a single transformation. The donor library is retrieved by amplification of the recombinant chromosomes, such as by a PCR reaction, using a synthetic feature from the editing oligonucleotide, namely, a second PAM deletion or mutation that is simultaneously incorporated at the 3' terminus of the gene. This covalently couples the codon target mutations directed to a PAM deletion. The donor libraries are then co-transformed into cells with a destination gRNA vector to create a population of cells that express a rationally designed protein library.

[00430] According to other embodiments, methods for trackable, precision genome editing using a CRISPR-mediated system referred to as Genome Engineering by Trackable CRISPR Enriched Recombineering (GEn-TraCER) may be used in accordance with embodiments of the present invention, as disclosed in US Patent No. 9,982,278, which is incorporated by reference herein. The GEn-TraCER methods and vectors combine an editing cassette with a gene encoding gRNA on a single vector. The cassette contains a desired mutation and a PAM mutation. The vector, which may also encode Cas9, is the introduced into a cell or population of cells. This activates expression of the CRISPR system in the cell or population of cells, causing the gRNA to recruit Cas9 to the target region, where a dsDNA break occurs, allowing integration of the PAM mutation.

[00431] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a CRISPR method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ,

PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, **SOCS1,** ANKRD11, and BCOR.

[00432] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a CRISPR method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-18, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[00433] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a CRISPR method, and which may be used in accordance with embodiments of the present invention, are described in U.S. Patent Nos. 8,697,359; 8,993,233; 8,795,965; 8,771,945; 8,889,356; 8,865,406; 8,999,641; 8,945,839; 8,932,814; 8,871,445; 8,906,616; and 8,895,308, which are incorporated by reference herein. Resources for carrying out CRISPR methods, such as plasmids for expressing CRISPR/Cas9 and CRISPR/Cpf1, are commercially available from companies such as GenScript.

[00434] In some embodiments, genetic modifications of populations of TILs, as described herein, may be performed using the CRISPR/Cpf1 system as described in U.S. Patent No. US 9,790,490, the disclosure of which is incorporated by reference herein. The CRISPR/Cpf1 system is functionally distinct from the CRISPR-Cas9 system in that Cpf1-associated CRISPR arrays are processed into mature crRNAs without the need for an additional tracrRNA. The crRNAs used in the CRISPR/Cpf1 system have a spacer or guide sequence and a direct repeat sequence. The Cpf1p-crRNA complex that is formed using this method is sufficient by itself to cleave the target DNA.

[00435] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 system and a CRISPR/Cpf1 system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and modulates expression of at least one checkpoint protein in the plurality of cells of the second population of TILs.

[00436] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(c) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 system and a CRISPR/Cpf1 system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of PD-1 and LAG-3 in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

b. TALE Methods

[00437] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A) or as described in WO2018081473, WO2018129332, or WO2018182817, wherein the method further comprises gene-editing at least a portion of the TILs by a TALE method. According to particular embodiments, the use of a TALE method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface, and optionally causes expression of one or more immune checkpoint genes to be silenced or reduced, in at least a portion of the therapeutic population of TILs. Alternatively, the use of a TALE method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface, and optionally causes expression of one or more immune checkpoint genes to be enhanced, in at least a portion of the therapeutic population of TILs.

[00438] TALE stands for "Transcription Activator-Like Effector" proteins, which include TALENs ("Transcription Activator-Like Effector Nucleases"). A method of using a TALE system for gene editing may also be referred to herein as a TALE method. TALEs are naturally occurring proteins from the plant pathogenic bacteria genus *Xanthomonas*, and contain DNA-binding domains composed of a series of 33–35-amino-acid repeat domains that each recognizes a single base pair. TALE specificity is determined by two hypervariable amino acids that are known as the repeat-variable di-residues (RVDs). Modular TALE repeats are linked together to recognize contiguous DNA sequences. A specific RVD in the DNA-binding domain recognizes a base in the target locus, providing a structural feature to assemble predictable DNA-binding domains. The DNA binding domains of a TALE are fused to the catalytic domain of a type IIS FokI endonuclease to make a targetable TALE nuclease. To induce site-specific mutation, two individual TALEN arms, separated by a 14-20 base pair spacer region, bring FokI monomers in close proximity to dimerize and produce a targeted double-strand break.

[00439] Several large, systematic studies utilizing various assembly methods have indicated that TALE repeats can be combined to recognize virtually any user-defined sequence. Strategies that enable the rapid assembly of custom TALE arrays include Golden Gate molecular cloning, high-throughput solid-phase assembly, and ligation-independent cloning techniques. Custom-designed TALE arrays are also commercially available through Cellectis Bioresearch (Paris, France), Transposagen Biopharmaceuticals (Lexington, KY, USA), and Life Technologies (Grand Island, NY, USA). Additionally web-based tools, such as TAL Effector-Nucleotide Target 2.0, are available that enable the design of custom TAL effector repeat arrays for desired targets and also provides predicted TAL effector binding sites. *See* Doyle, *et al.*, *Nucleic Acids Research*, **2012**, Vol. 40, W117-W122. Examples of TALE and TALEN methods suitable for use in the present invention are described in U.S. Patent Application Publication Nos. US 2011/0201118 A1; US 2013/0117869 A1; US

2013/0315884 A1; US 2015/0203871 A1 and US 2016/0120906 A1, the disclosures of which are incorporated by reference herein.

[00440] According to some embodiments of the present invention, a TALE method comprises silencing or reducing the expression of one or more immune checkpoint genes by inhibiting or preventing transcription of the targeted gene(s). For example, a TALE method may include utilizing KRAB-TALEs, wherein the method comprises fusing a transcriptional Kruppel-associated box (KRAB) domain to a DNA binding domain that targets the gene's transcription start site, leading to the inhibition or prevention of transcription of the gene.

[00441] According to other embodiments, a TALE method comprises silencing or reducing the expression of one or more immune checkpoint genes by introducing mutations in the targeted gene(s). For example, a TALE method may include fusing a nuclease effector domain, such as FokI, to the TALE DNA binding domain, resulting in a TALEN. FokI is active as a dimer; hence, the method comprises constructing pairs of TALENs to position the FOKL nuclease domains to adjacent genomic target sites, where they introduce DNA double strand breaks. A double strand break may be completed following correct positioning and dimerization of FokI. Once the double strand break is introduced, DNA repair can be achieved via two different mechanisms: the high-fidelity homologous recombination pair (HRR) (also known as homology-directed repair or HDR) or the error-prone non-homologous end joining (NHEJ). Repair of double strand breaks via NHEJ preferably results in DNA target site deletions, insertions or substitutions, *i.e.*, NHEJ typically leads to the introduction of small insertions and deletions at the site of the break, often inducing frameshifts that knockout gene function. According to particular embodiments, the TALEN pairs are targeted to the most 5' exons of the genes, promoting early frame shift mutations or premature stop codons. The genetic mutation(s) introduced by TALEN are preferably permanent. Thus, according to some embodiments, the method comprises silencing or reducing expression of an immune checkpoint gene by utilizing dimerized TALENs to induce a site-specific double strand break that is repaired via error-prone NHEJ, leading to one or more mutations in the targeted immune checkpoint gene.

[00442] According to additional embodiments, TALENs are utilized to introduce genetic alterations via HRR, such as non-random point mutations, targeted deletion, or addition of DNA fragments. The introduction of DNA double strand breaks enables gene editing via homologous recombination in the presence of suitable donor DNA. According to some embodiments, the method comprises co-delivering dimerized TALENs and a donor plasmid bearing locus-specific homology arms to induce a site-specific double strand break and integrate one or more transgenes into the DNA.

[00443] According to other embodiments, a TALEN that is a hybrid protein derived from FokI and AvrXa7, as disclosed in U.S. Patent Publication No. 2011/0201118, may be used in accordance with embodiments of the present invention. This TALEN retains recognition specificity for target

nucleotides of AvrXa7 and the double-stranded DNA cleaving activity of FokI. The same methods can be used to prepare other TALEN having different recognition specificity. For example, compact TALENs may be generated by engineering a core TALE scaffold having different sets of RVDs to change the DNA binding specificity and target a specific single dsDNA target sequence. *See* U.S. Patent Publication No. 2013/0117869. A selection of catalytic domains can be attached to the scaffold to effect DNA processing, which may be engineered to ensure that the catalytic domain is capable of processing DNA near the single dsDNA target sequence when fused to the core TALE scaffold. A peptide linker may also be engineered to fuse the catalytic domain to the scaffold to create a compact TALEN made of a single polypeptide chain that does not require dimerization to target a specific single dsDNA sequence. A core TALE scaffold may also be modified by fusing a catalytic domain, which may be a TAL monomer, to its N-terminus, allowing for the possibility that this catalytic domain might interact with another catalytic domain fused to another TAL monomer, thereby creating a catalytic entity likely to process DNA in the proximity of the target sequences. *See* U.S. Patent Publication No. 2015/0203871. This architecture allows only one DNA strand to be targeted, which is not an option for classical TALEN architectures.

[00444] According to some embodiments of the present invention, conventional RVDs may be used create TALENs that are capable of significantly reducing gene expression. In some embodiments, four RVDs, NI, HD, NN, and NG, are used to target adenine, cytosine, guanine, and thymine, respectively. These conventional RVDs can be used to, for instance, create TALENs targeting the PD-1 gene. Examples of TALENs using conventional RVDs include the T3v1 and T1 TALENs disclosed in Gautron *et al.*, *Molecular Therapy: Nucleic Acids* Dec. 2017, Vol. 9:312-321 (Gautron), which is incorporated by reference herein. The T3v1 and T1 TALENs target the second exon of the *PDCD1* locus where the PD-L1 binding site is located and are able to considerably reduce PD-1 production. In some embodiments, the T1 TALEN does so by using target SEQ ID NO:256 and the T3v1 TALEN does so by using target SEQ ID NO:257.

[00445] According to other embodiments, TALENs are modified using non-conventional RVDs to improve their activity and specificity for a target gene, such as disclosed in Gautron. Naturally occurring RVDs only cover a small fraction of the potential diversity repertoire for the hypervariable amino acid locations. Non-conventional RVDs provide an alternative to natural RVDs and have novel intrinsic targeting specificity features that can be used to exclude the targeting of off-site targets (sequences within the genome that contain a few mismatches relative to the targeted sequence) by TALEN. Non-conventional RVDs may be identified by generating and screening collections of TALEN containing alternative combinations of amino acids at the two hypervariable amino acid locations at defined positions of an array as disclosed in Juillerat, *et al.*, *Scientific Reports* 5, Article Number 8150 (2015), which is incorporated by reference herein. Next, non-conventional RVDs may

be selected that discriminate between the nucleotides present at the position of mismatches, which can prevent TALEN activity at off-site sequences while still allowing appropriate processing of the target location. The selected non-conventional RVDs may then be used to replace the conventional RVDs in a TALEN. Examples of TALENs where conventional RVDs have been replaced by non-conventional RVDs include the T3v2 and T3v3 PD-1 TALENs produced by Gautron. These TALENs had increased specificity when compared to TALENs using conventional RVDs.

[00446] According to additional embodiments, TALEN may be utilized to introduce genetic alterations to silence or reduce the expression of two genes. For instance, two separate TALEN may be generated to target two different genes and then used together. The molecular events generated by the two TALEN at their respective loci and potential off-target sites may be characterized by high-throughput DNA sequencing. This enables the analysis of off-target sites and identification of the sites that might result from the use of both TALEN. Based on this information, appropriate conventional and non-conventional RVDs may be selected to engineer TALEN that have increased specificity and activity even when used together. For example, Gautron discloses the combined use of T3v4 PD-1 and TRAC TALEN to produce double knockout CAR T cells, which maintained a potent *in vitro* anti-tumor function.

[00447] In some embodiments, the method of Gautron or other methods described herein may be employed to genetically-edit TILs, which may then be expanded by any of the procedures described herein. In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs using electroporation of transcription activator-like effector nuclease-encoding nucleic acids to obtain a second population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of at least one immune checkpoint protein, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3 to 14 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to

produce a fourth population of TILs, wherein the second expansion is performed for about 7 to 14 days to obtain the fourth population of TILs, wherein the fourth population of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00448] In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs using electroporation of transcription activator-like effector nuclease-encoding nucleic acids in cytoporation medium to obtain a second population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of at least one immune checkpoint protein, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 6 to 9 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fourth population of TILs, wherein the second expansion is performed for about 9 to 11 days to obtain the fourth population of TILs, wherein the fourth population of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00449] In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs using electroporation of transcription activator-like effector nuclease-encoding nucleic acids in cytoporation medium to obtain a second population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of at least one immune checkpoint protein, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 6 to 9 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fourth population of TILs, wherein the second expansion is performed for about 9 to 11 days to obtain the fourth population of TILs, wherein the fourth population of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the

transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00450] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs using electroporation of transcription activator-like effector nuclease-encoding nucleic acids in cytoporation medium to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface;

(e) optionally incubating the fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21,

and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00451] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs using electroporation of transcription activator-like effector nuclease-encoding nucleic acids in cytoporation medium to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface;

(f) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00452] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing the third population of TILs by temporarily disrupting the cell membranes of the third population of TILs to effect transfer of transcription activator-like effector nuclease-encoding nucleic acids into the third population of TILs to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface;

(e) optionally incubating the fourth population of TILs; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00453] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing the third population of TILs by temporarily disrupting the cell membranes of the third population of TILs to effect transfer of transcription activator-like effector nuclease-encoding nucleic acids into the third population of TILs to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[00454] In some embodiments, the step of culturing the fourth population of TILs is performed by culturing the fourth population of TILs in the second cell culture medium for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3-7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

[00455] According to other embodiments, TALENs may be specifically designed, which allows higher rates of DSB events within the target cell(s) that are able to target a specific selection of genes. *See* U.S. Patent Publication No. 2013/0315884. The use of such rare cutting endonucleases increases the chances of obtaining double inactivation of target genes in transfected cells, allowing for the production of engineered cells, such as T-cells. Further, additional catalytic domains can be introduced with the TALEN to increase mutagenesis and enhance target gene inactivation. The TALENs described in U.S. Patent Publication No. 2013/0315884 were successfully used to engineer T-cells to make them suitable for immunotherapy. TALENs may also be used to inactivate various immune checkpoint genes in T-cells, including the inactivation of at least two genes in a single T-cell. *See* U.S. Patent Publication No. 2016/0120906. Additionally, TALENs may be used to inactivate genes encoding targets for immunosuppressive agents and T-cell receptors, as disclosed in U.S. Patent Publication No. 2018/0021379, which is incorporated by reference herein. Further, TALENs may be used to inhibit the expression of beta 2-microglobulin (B2M) and/or class II major histocompatibility complex transactivator (CIITA), as disclosed in U.S. Patent Publication No. 2019/0010514, which is incorporated by reference herein.

[00456] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a TALE method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3**, TOX, SOCS1,** ANKRD11, and BCOR.

[00457] Non-limiting examples of TALE-nucleases targeting the PD-1 gene are provided in the following table. In these examples, the targeted genomic sequences contain two 17-base pair (bp)

long sequences (referred to as half targets, shown in upper case letters) separated by a 15-bp spacer (shown in lower case letters). Each half target is recognized by repeats of half TALE-nucleases listed in Table 11. Thus, according to particular embodiments, TALE-nucleases according to the invention recognize and cleave the target sequence selected from the group consisting of: SEQ ID NO: 286 and SEQ ID NO: 287. TALEN sequences and gene-editing methods are also described in Gautron, discussed above.

TABLE 11 – TALEN PD-1 Sequences.

TALEN PD-1 No. 1 Sequences	
Target PD-1 Sequence (SEQ ID NO:286)	TTCTCCCCAGCCCTGCT cgtggtgaccgaagg GGACAACGCCACCTTCA
Repeat PD-1-left (SEQ ID NO:288)	LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAI ASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQ ALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLL PVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGL TPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIAS HDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE TVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVL CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPE QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHD GGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETV QRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQ AHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQV VAIASNGGGRPALE
Repeat PD-1-right (SEQ ID NO: 289)	LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI ASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASNIGGKQAL ETVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPV LCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTP QQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN NGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALET VQRLLPVLCQAHGLTPEQVVAIASNGGKQALETVQRLLPVLCQ

	AHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQV VAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGG KQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQR LLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAH GLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVA IASNGGGRPALE
PD-1-left TALEN (SEQ ID NO:290)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATTACCCA TACGATGTTCCAGATTACGCTATCGATATCGCCGATCTACGC ACGCTCGGCTACAGCCAGCAGCAACAGGAGAAGATCAAACC GAAGGTTCGTTCGACAGTGGCGCAGCACCACGAGGCACTGGT CGGCCACGGGTTTACACACGCGCACATCGTTGCGTTAAGCCA ACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGTATCAGGA CATGATCGCAGCGTTGCCAGAGGCGACACACGAAGCGATCG TTGGCGTCGGCAAACAGTGGTCCGGCGCACGCGCTCTGGAGG CCTTGCTCACGGTGGCGGGAGAGTTGAGAGGTCCACCGTTAC AGTTGGACACAGGCCAACTTCTCAAGATTGCAAAACGTGGCG GCGTGACCGCAGTGGAGGCAGTGCATGCATGGCGCAATGCA CTGACGGGTGCCCCGCTCAACTTGACCCCCCAGCAGGTGGTG GCCATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAGAC GGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTT GACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCG GCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG CTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCC ATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAGACGGT CCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGAC CCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCA AGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGT GCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCG CCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAG CGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCG GAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCA GGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCA GGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCGCCAG CCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGC

	TGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGC
	AGGTGGTGGCCATCGCCAGCAATATTGGTGGCAAGCAGGCG
	CTGGAGACGGTGCAGGCGCTGTTGCCGGTGCTGTGCCAGGCC
	CACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAAT
	AATGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTT
	GCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGT
	GGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGG
	AGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACG
	GCTTGACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATG
	GCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCG
	GTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTG
	GCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGAC
	GGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTT
	GACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATGGCGGTG
	GCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG
	CTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCC
	ATCGCCAGCAATAATGGTGGCAAGCAGGCGCTGGAGACGGT
	CCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGAC
	CCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCA
	AGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGT
	GCCAGGCCCACGGCTTGACCCCTCAGCAGGTGGTGGCCATCG
	CCAGCAATGGCGGCGGCAGGCCGGCGCTGGAGAGCATTGTT
	GCCCAGTTATCTCGCCCTGATCCGGCGTTGGCCGCGTTGACC
	AACGACCACCTCGTCGCCTTGGCCTGCCTCGGCGGGCGTCCT
	GCGCTGGATGCAGTGAAAAAGGGATTGGGGGATCCTATCAG
	CCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAAT
	CCGAGTTGAGGCACAAGCTGAAGTACGTGCCCCACGAGTAC
	ATCGAGCTGATCGAGATCGCCCGGAACAGCACCCAGGACCG
	TATCCTGGAGATGAAGGTGATGGAGTTCTTCATGAAGGTGTA
	CGGCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCG
	ACGGCGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCG
	TGATCGTGGACACCAAGGCCTACTCCGGCGGCTACAACCTGC
	CCATCGGCCAGGCCGACGAAATGCAGAGGTACGTGGAGGAG
	AACCAGACCAGGAACAAGCACATCAACCCCAACGAGTGGTG
	GAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTT
	CGTGTCCGGCCACTTCAAGGGCAACTACAAGGCCCAGCTGAC

	CAGGCTGAACCACATCACCAACTGCAACGGCGCCGTGCTGTC CGTGGAGGAGCTCCTGATCGGCGGCGAGATGATCAAGGCCG GCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAAC GGCGAGATCAACTTCGCGGCCGACTGATAA
PD-1-right TALEN (SEQ ID NO:291)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATAAGGA GACCGCCGCTGCCAAGTTCGAGAGACAGCACATGGACAGCA TCGATATCGCCGATCTACGCACGCTCGGCTACAGCCAGCAGC AACAGGAGAAGATCAAACCGAAGGTTCGTTCGACAGTGGCG CAGCACCACGAGGCACTGGTCGGCCACGGGTTTACACACGCG CACATCGTTGCGTTAAGCCAACACCCGGCAGCGTTAGGGACC GTCGCTGTCAAGTATCAGGACATGATCGCAGCGTTGCCAGAG GCGACACACGAAGCGATCGTTGGCGTCGGCAAACAGTGGTC CGGCGCACGCGCTCTGGAGGCCTTGCTCACGGTGGCGGGAGA GTTGAGAGGTCCACCGTTACAGTTGGACACAGGCCAACTTCT CAAGATTGCAAAACGTGGCGGCGTGACCGCAGTGGAGGCAG TGCATGCATGGCGCAATGCACTGACGGGTGCCCCGCTCAACT TGACCCCCCAGCAAGTCGTCGCAATCGCCAGCAATAACGGAG GGAAGCAAGCCCTCGAAACCGTGCAGCGGTTGCTTCCTGTGC TCTGCCAGGCCCACGGCCTTACCCCTGAGCAGGTGGTGGCCA TCGCAAGTAACATTGGAGGAAAGCAAGCCTTGGAGACAGTG CAGGCCCTGTTGCCCGTGCTGTGCCAGGCACACGGCCTCACA CCAGAGCAGGTCGTGGCCATTGCCTCCAACATCGGGGGGAA ACAGGCTCTGGAGACCGTCCAGGCCCTGCTGCCCGTCCTCTG TCAAGCTCACGGCCTGACTCCCCAACAAGTGGTCGCCATCGC CTCTAATAACGGCGGGAAGCAGGCACTGGAAACAGTGCAGA GACTGCTCCCTGTGCTTTGCCAAGCTCATGGGTTGACCCCCCA ACAGGTCGTCGCTATTGCCTCAAACAACGGGGGCAAGCAGG CCCTTGAGACTGTGCAGAGGCTGTTGCCAGTGCTGTGTCAGG CTCACGGGCTCACTCCACAACAGGTGGTCGCAATTGCCAGCA ACGGCGGCGGAAAGCAAGCTCTTGAAACCGTGCAACGCCTC CTGCCCGTGCTCTGTCAGGCTCATGGCCTGACACCACAACAA GTCGTGGCCATCGCCAGTAATAATGGCGGGAAACAGGCTCTT GAGACCGTCCAGAGGCTGCTCCCAGTGCTCTGCCAGGCACAC GGGCTGACCCCCCAGCAGGTGGTGGCTATCGCCAGCAATAAT

	GGGGGCAAGCAGGCCCTGGAAACAGTCCAGCGCCTGCTGCC
	AGTGCTTTGCCAGGCTCACGGGCTCACTCCCGAACAGGTCGT
	GGCAATCGCCTCCAACGGAGGGAAGCAGGCTCTGGAGACCG
	TGCAGAGACTGCTGCCCGTCTTGTGCCAGGCCCACGGACTCA
	CACCTCAGCAGGTCGTCGCCATTGCCTCTAACAACGGGGGCA
	AACAAGCCCTGGAGACAGTGCAGCGGCTGTTGCCTGTGTTGT
	GCCAAGCCCACGGCTTGACTCCTCAACAAGTGGTCGCCATCG
	CCTCAAATGGCGGCGGAAAACAAGCTCTGGAGACAGTGCAG
	AGGTTGCTGCCCGTCCTCTGCCAAGCCCACGGCCTGACTCCC
	CAACAGGTCGTCGCCATTGCCAGCAACGGCGGAGGAAAGCA
	GGCTCTCGAAACTGTGCAGCGGCTGCTTCCTGTGCTGTGTCA
	GGCTCATGGGCTGACCCCCCAGCAAGTGGTGGCTATTGCCTC
	TAACAATGGAGGCAAGCAAGCCCTTGAGACAGTCCAGAGGC
	TGTTGCCAGTGCTGTGCCAGGCCCACGGGCTCACACCCCAGC
	AGGTGGTCGCCATCGCCAGTAACGGCGGGGGCAAACAGGCA
	TTGGAAACCGTCCAGCGCCTGCTTCCAGTGCTCTGCCAGGCA
	CACGGACTGACACCCGAACAGGTGGTGGCCATTGCATCCCAT
	GATGGGGGCAAGCAGGCCCTGGAGACCGTGCAGAGACTCCT
	GCCAGTGTTGTGCCAAGCTCACGGCCTCACCCCTCAGCAAGT
	CGTGGCCATCGCCTCAAACGGGGGGGGCCGGCCTGCACTGG
	AGAGCATTGTTGCCCAGTTATCTCGCCCTGATCCGGCGTTGG
	CCGCGTTGACCAACGACCACCTCGTCGCCTTGGCCTGCCTCG
	GCGGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGG
	GATCCTATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAG
	GAGAAGAAATCCGAGTTGAGGCACAAGCTGAAGTACGTGCC
	CCACGAGTACATCGAGCTGATCGAGATCGCCCGGAACAGCA
	CCCAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTCA
	TGAAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCC
	AGGAAGCCCGACGGCGCCATCTACACCGTGGGCTCCCCCATC
	GACTACGGCGTGATCGTGGACACCAAGGCCTACTCCGGCGGC
	TACAACCTGCCCATCGGCCAGGCCGACGAAATGCAGAGGTA
	CGTGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCA
	ACGAGTGGTGGAAGGTGTACCCCTCCAGCGTGACCGAGTTCA
	AGTTCCTGTTCGTGTCCGGCCACTTCAAGGGCAACTACAAGG
	CCCAGCTGACCAGGCTGAACCACATCACCAACTGCAACGGCG
	CCGTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGA

	TCAAGGCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAG TTCAACAACGGCGAGATCAACTTCGCGGCCGACTGATAA
TALEN PD-1 No. 2 Sequences	
Target PD-1 Sequence (SEQ ID NO:287)	TACCTCTGTGGGGCCATctccctggcccccaaGGCGCAGATCAAAGA GA
Repeat PD-1-left (SEQ ID NO:292)	LTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIA SHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQAL ETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV LCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTP QQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN NGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALET VQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLC QAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQ VVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNG GKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQ RLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQA HGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVV AIASNGGGRPALE
Repeat PD-1-right (SEQ ID NO: 293)	LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAI ASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQA LETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLP VLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLT PQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIAS NNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALE TVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVL CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQ QVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNN GGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGKQALETVQ RLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQA

	HGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVV AIASNGGGRPALE
PD-1-left TALEN (SEQ ID NO:294)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATTACCCA TACGATGTTCCAGATTACGCTATCGATATCGCCGATCTACGC ACGCTCGGCTACAGCCAGCAGCAACAGGAGAAGATCAAACC GAAGGTTCGTTCGACAGTGGCGCAGCACCACGAGGCACTGGT CGGCCACGGGTTTACACACGCGCACATCGTTGCGTTAAGCCA ACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGTATCAGGA CATGATCGCAGCGTTGCCAGAGGCGACACACGAAGCGATCG TTGGCGTCGGCAAACAGTGGTCCGGCGCACGCGCTCTGGAGG CCTTGCTCACGGTGGCGGGAGAGTTGAGAGGTCCACCGTTAC AGTTGGACACAGGCCAACTTCTCAAGATTGCAAAACGTGGCG GCGTGACCGCAGTGGAGGCAGTGCATGCATGGCGCAATGCA CTGACGGGTGCCCCGCTCAACTTGACCCCGGAGCAGGTGGTG GCCATCGCCAGCAATATTGGTGGCAAGCAGGCGCTGGAGAC GGTGCAGGCGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTT GACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCG GCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG CTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCC ATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGT CCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGAC CCCCCAGCAGGTGGTGGCCATCGCCAGCAATGGCGGTGGCA AGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGT GCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCG CCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAG CGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCC CAGCAGGTGGTGGCCATCGCCAGCAATGGCGGTGGCAAGCA GGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCA GGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAG CAATAATGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGC TGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGC AGGTGGTGGCCATCGCCAGCAATGGCGGTGGCAAGCAGGCG CTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCC CACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAAT

	AATGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTT
	GCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGT
	GGTGGCCATCGCCAGCAATAATGGTGGCAAGCAGGCGCTGG
	AGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACG
	GCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATAATG
	GTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCG
	GTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTG
	GCCATCGCCAGCAATAATGGTGGCAAGCAGGCGCTGGAGAC
	GGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTT
	GACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCG
	GCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG
	CTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCC
	ATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGT
	CCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGAC
	CCCGGAGCAGGTGGTGGCCATCGCCAGCAATATTGGTGGCAA
	GCAGGCGCTGGAGACGGTGCAGGCGCTGTTGCCGGTGCTGTG
	CCAGGCCCACGGCTTGACCCCTCAGCAGGTGGTGGCCATCGC
	CAGCAATGGCGGCGGCAGGCCGGCGCTGGAGAGCATTGTTG
	CCCAGTTATCTCGCCCTGATCCGGCGTTGGCCGCGTTGACCA
	ACGACCACCTCGTCGCCTTGGCCTGCCTCGGCGGGCGTCCTG
	CGCTGGATGCAGTGAAAAAGGGATTGGGGGATCCTATCAGC
	CGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAATC
	CGAGTTGAGGCACAAGCTGAAGTACGTGCCCCACGAGTACAT
	CGAGCTGATCGAGATCGCCCGGAACAGCACCCAGGACCGTA
	TCCTGGAGATGAAGGTGATGGAGTTCTTCATGAAGGTGTACG
	GCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCGAC
	GGCGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCGTG
	ATCGTGGACACCAAGGCCTACTCCGGCGGCTACAACCTGCCC
	ATCGGCCAGGCCGACGAAATGCAGAGGTACGTGGAGGAGAA
	CCAGACCAGGAACAAGCACATCAACCCCAACGAGTGGTGGA
	AGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTTCG
	TGTCCGGCCACTTCAAGGGCAACTACAAGGCCCAGCTGACCA
	GGCTGAACCACATCACCAACTGCAACGGCGCCGTGCTGTCCG
	TGGAGGAGCTCCTGATCGGCGGCGAGATGATCAAGGCCGGC

	ACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAACGG CGAGATCAACTTCGCGGCCGACTGATAA
PD-1-right TALEN (SEQ ID NO:295)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATAAGGA GACCGCCGCTGCCAAGTTCGAGAGACAGCACATGGACAGCA TCGATATCGCCGATCTACGCACGCTCGGCTACAGCCAGCAGC AACAGGAGAAGATCAAACCGAAGGTTCGTTCGACAGTGGCG CAGCACCACGAGGCACTGGTCGGCCACGGGTTTACACACGCG CACATCGTTGCGTTAAGCCAACACCCGGCAGCGTTAGGGACC GTCGCTGTCAAGTATCAGGACATGATCGCAGCGTTGCCAGAG GCGACACACGAAGCGATCGTTGGCGTCGGCAAACAGTGGTC CGGCGCACGCGCTCTGGAGGCCTTGCTCACGGTGGCGGGAGA GTTGAGAGGTCCACCGTTACAGTTGGACACAGGCCAACTTCT CAAGATTGCAAAACGTGGCGGCGTGACCGCAGTGGAGGCAG TGCATGCATGGCGCAATGCACTGACGGGTGCCCCGCTCAACT TGACCCCCGAGCAAGTCGTCGCAATCGCCAGCCATGATGGAG GGAAGCAAGCCCTCGAAACCGTGCAGCGGTTGCTTCCTGTGC TCTGCCAGGCCCACGGCCTTACCCCTCAGCAGGTGGTGGCCA TCGCAAGTAACGGAGGAGGAAAGCAAGCCTTGGAGACAGTG CAGCGCCTGTTGCCCGTGCTGTGCCAGGCACACGGCCTCACA CCAGAGCAGGTCGTGGCCATTGCCTCCCATGACGGGGGGAA ACAGGCTCTGGAGACCGTCCAGAGGCTGCTGCCCGTCCTCTG TCAAGCTCACGGCCTGACTCCCCAACAAGTGGTCGCCATCGC CTCTAATGGCGGCGGGAAGCAGGCACTGGAAACAGTGCAGA GACTGCTCCCTGTGCTTTGCCAAGCTCATGGGTTGACCCCCCA ACAGGTCGTCGCTATTGCCTCAAACGGGGGGGGCAAGCAGG CCCTTGAGACTGTGCAGAGGCTGTTGCCAGTGCTGTGTCAGG CTCACGGGCTCACTCCACAACAGGTGGTCGCAATTGCCAGCA ACGGCGGCGGAAAGCAAGCTCTTGAAACCGTGCAACGCCTC CTGCCCGTGCTCTGTCAGGCTCATGGCCTGACACCACAACAA GTCGTGGCCATCGCCAGTAATAATGGCGGGAAACAGGCTCTT GAGACCGTCCAGAGGCTGCTCCCAGTGCTCTGCCAGGCACAC GGGCTGACCCCCGAGCAGGTGGTGGCTATCGCCAGCAATATT GGGGGCAAGCAGGCCCTGGAAACAGTCCAGGCCCTGCTGCC AGTGCTTTGCCAGGCTCACGGGCTCACTCCCCAGCAGGTCGT GGCAATCGCCTCCAACGGCGGAGGGAAGCAGGCTCTGGAGA

	CCGTGCAGAGACTGCTGCCCGTCTTGTGCCAGGCCCACGGAC TCACACCTGAACAGGTCGTCGCCATTGCCTCTCACGATGGGG GCAAACAAGCCCTGGAGACAGTGCAGCGGCTGTTGCCTGTGT TGTGCCAAGCCCACGGCTTGACTCCTCAACAAGTGGTCGCCA TCGCCTCAAATGGCGGCGGAAAACAAGCTCTGGAGACAGTG CAGAGGTTGCTGCCCGTCCTCTGCCAAGCCCACGGCCTGACT CCCCAACAGGTCGTCGCCATTGCCAGCAACAACGGAGGAAA GCAGGCTCTCGAAACTGTGCAGCGGCTGCTTCCTGTGCTGTG TCAGGCTCATGGGCTGACCCCCGAGCAAGTGGTGGCTATTGC CTCTAATGGAGGCAAGCAAGCCCTTGAGACAGTCCAGAGGCT GTTGCCAGTGCTGTGCCAGGCCCACGGGCTCACACCCCAGCA GGTGGTCGCCATCGCCAGTAACAACGGGGGCAAACAGGCAT TGGAAACCGTCCAGCGCCTGCTTCCAGTGCTCTGCCAGGCAC ACGGACTGACACCCGAACAGGTGGTGGCCATTGCATCCCATG ATGGGGGCAAGCAGGCCCTGGAGACCGTGCAGAGACTCCTG CCAGTGTTGTGCCAAGCTCACGGCCTCACCCCTCAGCAAGTC GTGGCCATCGCCTCAAACGGGGGGGGCCGGCCTGCACTGGA GAGCATTGTTGCCCAGTTATCTCGCCCTGATCCGGCGTTGGCC GCGTTGACCAACGACCACCTCGTCGCCTTGGCCTGCCTCGGC GGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGGGA TCCTATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGA GAAGAAATCCGAGTTGAGGCACAAGCTGAAGTACGTGCCCC ACGAGTACATCGAGCTGATCGAGATCGCCCGGAACAGCACC CAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTCATG AAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCCAG GAAGCCCGACGGCGCCATCTACACCGTGGGCTCCCCCATCGA CTACGGCGTGATCGTGGACACCAAGGCCTACTCCGGCGGCTA CAACCTGCCCATCGGCCAGGCCGACGAAATGCAGAGGTACG TGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCAAC GAGTGGTGGAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAG TTCCTGTTCGTGTCCGGCCACTTCAAGGGCAACTACAAGGCC CAGCTGACCAGGCTGAACCACATCACCAACTGCAACGGCGCC GTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGATC AAGGCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTT CAACAACGGCGAGATCAACTTCGCGGCCGACTGATAA

[00458] In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding nucleic acids targeting PD-1 in cytoporation medium to obtain a second population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 6 to 9 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fourth population of TILs, wherein the second expansion is performed for about 9 to 11 days to obtain the fourth population of TILs, wherein the fourth population of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00459] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding nucleic acids targeting PD-1 in cytoporation medium to obtain a fourth population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00460] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs by temporarily disrupting the cell membranes of the third population of TILs to effect transfer of transcription activator-like effector nuclease-encoding nucleic acids targeting PD-1 into the third population of TILs to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00461] In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding nucleic acids targeting SEQ ID NO:149 or SEQ ID NO:150 in cytoporation medium to obtain a second population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs, wherein the incubation is performed

at about 30-40 °C with about 5% CO_2;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 6 to 9 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fourth population of TILs, wherein the second expansion is performed for about 9 to 11 days to obtain the fourth population of TILs, wherein the fourth population of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00462] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding nucleic acids targeting SEQ ID NO: 149 or SEQ ID NO:150 in cytoporation medium to

obtain a fourth population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(c) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00463] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs by temporarily disrupting the cell membranes of the third population of TILs to effect transfer of transcription activator-like effector nuclease-encoding nucleic acids targeting SEQ ID NO: 149 or SEQ ID NO:150 into the third population of TILs to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00464] In some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises the steps of:

(a) activating a first population of TILs obtained from a tumor resected from a patient using CD3 and CD28 activating beads or antibodies for 1 to 5 days;

(b) gene-editing at least a portion of the first population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding mRNAs according to SEQ ID NO:157 and SEQ ID NO:158 or SEQ ID NO: 153 and SEQ ID NO:154 in cytoporation medium to obtain a second population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the second population of TILs;

(c) optionally incubating the second population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2;

(d) performing a first expansion by culturing the second population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a third population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 6 to 9 days to obtain the third population of TILs;

(e) performing a second expansion by supplementing the cell culture medium of the third population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fourth population of TILs, wherein the second expansion is performed for about 9 to 11 days to obtain the fourth population of TILs, wherein the fourth population

of TILs is a therapeutic population of TILs;

(f) harvesting the therapeutic population of TILs obtained from step (e);

(g) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system; and

(h) wherein one or more of steps (a) to (g) are performed in a closed, sterile system.

In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00465] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs, wherein the gene-editing comprises using electroporation of transcription activator-like effector nuclease-encoding mRNAs according to SEQ ID NO:157 and SEQ ID NO:158 or SEQ ID NO: 153 and SEQ ID NO:154 in cytoporation medium to obtain a fourth population of TILs, and wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00466] In some embodiments, provided herein is a method for preparing expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(c) activating the second population of TILs using anti-CD3 and anti-CD28 beads or antibodies for 1-7 days, to produce a third population of TILs;

(d) gene-editing at least a portion of the third population of TILs by temporarily disrupting the cell membranes of the third population of TILs to effect transfer of transcription activator-like effector nuclease-encoding mRNAs according to SEQ ID NO:157 and SEQ ID NO:158 or SEQ ID NO: 153 and SEQ ID NO:154 into the third population of TILs to obtain a fourth population of TILs, wherein the gene-editing effects expression of at least one immunomodulatory composition at the cell surface, and inhibits expression of PD-1, in the portion of the cells of the third population of TILs;

(e) optionally incubating the fourth population of TILs, wherein the incubation is performed at about 30-40 °C with about 5% CO_2; and

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory

agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00467] Other non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a TALE method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[00468] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a TALE method, and which may be used in accordance with embodiments of the present invention, are described in U.S. Patent No. 8,586,526, which is incorporated by reference herein. These disclosed examples include the use of a non-naturally occurring DNA-binding polypeptide that has two or more TALE-repeat units containing a repeat RVD, an N-cap polypeptide made of residues of a TALE protein, and a C-cap polypeptide made of a fragment of a full length C-terminus region of a TALE protein.

[00469] Examples of TALEN designs and design strategies, activity assessments, screening strategies, and methods that can be used to efficiently perform TALEN-mediated gene integration and inactivation, and which may be used in accordance with embodiments of the present invention, are described in Valton, *et al.*, *Methods*, **2014**, 69, 151-170, which is incorporated by reference herein.

[00470] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of a TALE nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and modulates expression of at least one immune checkpoint protein and/or adhesion molecule, in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00471] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for

about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the transfer of the at least one gene editor step comprises the delivery of a TALE nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and modulates expression of at least one immune checkpoint protein and/or adhesion molecule, in the plurality of cells of the second population of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00472] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating step on the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of a TALE nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and suppresses the expression of PD-1 and LAG-3 in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises a cytokine fused to a membrane anchor. In some embodiments, the at least one immunomodulatory composition comprises

an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00473] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the transfer of the at least one gene editor step comprises the delivery of a TALE nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and suppresses the expression of PD-1 and LAG-3 in the plurality of cells of the second population of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

c. Zinc Finger Methods

[00474] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A) or as described in PCT/US2017/058610, PCT/US2018/012605, or PCT/US2018/012633, wherein the method further comprises gene-editing at least a portion of the TILs by a zinc finger or zinc finger nuclease method. According to particular embodiments, the use of a zinc finger method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface, and optionally causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs. Alternatively, the use of a zinc finger method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface, and optionally causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs.

[00475] An individual zinc finger contains approximately 30 amino acids in a conserved $\beta\beta\alpha$ configuration. Several amino acids on the surface of the α-helix typically contact 3 bp in the major groove of DNA, with varying levels of selectivity. Zinc fingers have two protein domains. The first domain is the DNA binding domain, which includes eukaryotic transcription factors and contain the zinc finger. The second domain is the nuclease domain, which includes the FokI restriction enzyme and is responsible for the catalytic cleavage of DNA.

[00476] The DNA-binding domains of individual ZFNs typically contain between three and six individual zinc finger repeats and can each recognize between 9 and 18 base pairs. If the zinc finger domains are specific for their intended target site then even a pair of 3-finger ZFNs that recognize a total of 18 base pairs can, in theory, target a single locus in a mammalian genome. One method to generate new zinc-finger arrays is to combine smaller zinc-finger "modules" of known specificity. The most common modular assembly process involves combining three separate zinc fingers that can each recognize a 3 base pair DNA sequence to generate a 3-finger array that can recognize a 9 base pair target site. Alternatively, selection-based approaches, such as oligomerized pool engineering (OPEN) can be used to select for new zinc-finger arrays from randomized libraries that take into consideration context-dependent interactions between neighboring fingers. Engineered zinc fingers are available commercially; Sangamo Biosciences (Richmond, CA, USA) has developed a propriety platform (CompoZr®) for zinc-finger construction in partnership with Sigma–Aldrich (St. Louis, MO, USA).

[00477] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a zinc finger method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3**, TOX, SOCS1,** ANKRD11, and BCOR.

[00478] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a zinc finger method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-18, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[00479] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a zinc finger method, which may be used in accordance with embodiments of the present invention, are described in U.S. Patent Nos. 6,534,261, 6,607,882, 6,746,838, 6,794,136, 6,824,978, 6,866,997, 6,933,113, 6,979,539, 7,013,219, 7,030,215, 7,220,719, 7,241,573, 7,241,574, 7,585,849, 7,595,376, 6,903,185, and 6,479,626, which are incorporated by reference herein.

[00480] Other examples of systems, methods, and compositions for altering the expression of a target gene sequence by a zinc finger method, which may be used in accordance with embodiments of the present invention, are described in Beane, *et al.*, *Mol. Therapy*, **2015,** 23 1380-1390, the disclosure of which is incorporated by reference herein.

[00481] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of a zinc finger nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and modulates the expression of at least one immune checkpoint protein and/or adhesion molecule in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane

anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00482] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the transfer of the at least one gene editor step comprises the delivery of a zinc finger nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and modulates the expression of at least one immune checkpoint protein and/or adhesion molecule in the plurality of cells of the second population of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00483] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second

expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of a zinc finger nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and suppresses the expression of PD-1 and LAG-3 in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00484] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) temporarily disrupting the cell membranes of the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the transfer of the at least one gene editor step comprises the delivery of a zinc finger nuclease system that effects expression of at least one immunomodulatory composition at the cell surface of and suppresses the expression of PD-1 and LAG-3 in the plurality of cells of the second population of TILs. In some embodiments, a microfluidic platform is used to temporarily disrupt the cell membranes of the third population of TILs. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist. In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-12, IL-15, IL-18, IL-21, and a CD40 agonist.

[00485] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed by culturing the third or fourth population of TILs or performing the second expansion for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures

is cultured with additional IL-2 for a second period of about 3-7 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs or the therapeutic population of TILs.

[00486] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, or 11 days.

[00487] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-11 days.

[00488] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-11 days.

[00489] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-11 days.

[00490] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-11 days.

[00491] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8-11 days.

[00492] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 9-11 days.

[00493] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 10-11 days.

[00494] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-10 days.

[00495] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-10 days.

[00496] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-10 days.

[00497] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-10 days.

[00498] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8-10 days.

[00499] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 9-10 days.

[00500] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-9 days.

[00501] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-9 days.

[00502] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-9 days.

[00503] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-9 days.

[00504] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8-9 days.

[00505] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3-8 days.

[00506] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3-7 days.

[00507] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3-6 days.

[00508] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3-5 days.

[00509] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3-4 days.

[00510] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-8 days.

[00511] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-7 days.

[00512] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-6 days.

[00513] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-6 days.

[00514] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-8 days.

[00515] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-7 days.

[00516] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5-6 days.

[00517] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-8 days.

[00518] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6-7 days.

[00519] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7-8 days.

[00520] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4-5 days.

[00521] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 3 days.

[00522] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 4 days.

[00523] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 5 days.

[00524] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 6 days.

[00525] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 7 days.

[00526] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 8 days.

[00527] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 9 days.

[00528] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 10 days.

[00529] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the first population of TILs or the first expansion step is performed for about 11 days.

[00530] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days or 7 days.

[00531] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2-7 days.

[00532] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 3-7 days.

[00533] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 4-7 days.

[00534] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 5-7 days.

[00535] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 6-7 days.

[00536] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1-6 days.

[00537] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1-5 days.

[00538] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1-4 days.

[00539] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1-3 days.

[00540] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1-2 days.

[00541] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2-6 days.

[00542] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 3-6 days.

[00543] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 4-6 days.

[00544] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 5-6 days.

[00545] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 3-5 days.

[00546] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 3-4 days.

[00547] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2-5 days.

[00548] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2-4 days.

[00549] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2-3 days.

[00550] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 4-5 days.

[00551] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 1 day.

[00552] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 2 days.

[00553] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 3 days.

[00554] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 4 days.

[00555] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 5 days.

[00556] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 6 days.

[00557] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the activating step is performed for about 7 days.

[00558] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 1 day, 2 days or 3 days.

[00559] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 1-2 days.

[00560] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 2-3 days.

[00561] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 1 day.

[00562] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 2 days.

[00563] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the stimulating step is performed from about 3 days.

[00564] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days or 15 days.

[00565] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-15 days.

[00566] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-15 days.

[00567] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-15 days.

[00568] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-15 days.

[00569] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10-15 days.

[00570] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 11-15 days.

[00571] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 12-15 days.

[00572] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 13-15 days.

[00573] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 14-15 days.

[00574] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-14 days.

[00575] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-14 days.

[00576] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-14 days.

[00577] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-14 days.

[00578] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-14 days.

[00579] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10-14 days.

[00580] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 11-14 days.

[00581] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 12-14 days.

[00582] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 13-14 days.

[00583] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-13 days.

[00584] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-12 days.

[00585] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-11 days.

[00586] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-10 days.

[00587] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-9 days.

[00588] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-8 days.

[00589] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-7 days.

[00590] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5-6 days.

[00591] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-13 days.

[00592] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-12 days.

[00593] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-11 days.

[00594] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-10 days.

[00595] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-9 days.

[00596] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-8 days.

[00597] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6-7 days.

[00598] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-13 days.

[00599] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-12 days.

[00600] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-11 days.

[00601] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-10 days.

[00602] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-9 days.

[00603] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7-8 days.

[00604] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-13 days.

[00605] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-12 days.

[00606] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-11 days.

[00607] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-10 days.

[00608] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8-9 days.

[00609] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-13 days.

[00610] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-12 days.

[00611] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-11 days.

[00612] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9-10 days.

[00613] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10-13 days.

[00614] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10-12 days.

[00615] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10-11 days.

[00616] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 11-13 days.

[00617] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 11-12 days.

[00618] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 12-13 days.

[00619] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 5 days.

[00620] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 6 days.

[00621] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 7 days.

[00622] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 8 days.

[00623] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 9 days.

[00624] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 10 days.

[00625] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 11 days.

[00626] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 12 days.

[00627] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 13 days.

[00628] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 14 days.

[00629] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of culturing the third or fourth population of TILs or the second expansion step is performed for about 15 days.

E. Transient Cellular Modification

[00630] In some embodiments, the expanded TILs of the present invention are further manipulated before, during, or after an expansion step, including during closed, sterile manufacturing processes, each as provided herein, in order to alter protein expression in a transient manner. In some embodiments, the present invention includes transient cellular modification through nucleotide insertion, such as through ribonucleic acid (RNA) insertion, including insertion of messenger RNA (mRNA), into a population of TILs for promotion of the expression of one or more proteins or inhibition of the expression of one or more proteins, as well as simultaneous combinations of both promotion of one set of proteins with inhibition of another set of proteins.

[00631] In some embodiments, the expanded TILs of the present invention undergo transient alteration of protein expression. In some embodiments, the transient alteration of protein expression occurs in the bulk TIL population prior to first expansion. In some embodiments, the transient alteration of protein expression occurs after the first expansion. In some embodiments, the transient alteration of protein expression occurs in the bulk TIL population prior to second expansion. In some embodiments, the transient alteration of protein expression occurs after the second expansion.

[00632] In some embodiments, the transient alteration of protein expression results in transient expression of an immunomodulatory composition. In some embodiments, the immunomodulatory composition is an immunomodulatory fusion protein. In some embodiments, the immunomodulatory

fusion protein comprises a membrane anchor fused to an immunomodulatory agent. In some embodiments, the immunomodulatory agent is selected from the group consisting of: IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18 and IL-21. In some embodiments, the immunomodulatory agent is an interleukin selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, the immunomodulatory agent is an interleukin selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

[00633] As discussed herein, embodiments of the present invention provide tumor infiltrating lymphocytes (TILs) that have been transiently modified via transient alteration of protein expression to enhance their therapeutic effect. Embodiments of the present invention embrace transient modification through nucleotide insertion (e.g., RNA) into a population of TILs for expression of an immunomodulatory composition. Embodiments of the present invention also provide methods for expanding TILs into a therapeutic population, wherein the methods comprise transient modification of the TILs. There are several gene-editing technologies that may be used to transiently modify a population of TILs, which are suitable for use in accordance with the present invention.

[00634] In some embodiments, a method of transiently altering protein expression in a population of TILs includes contacting the TILs with nucleic acid (e.g., mRNA) encoding the immunomodulatory composition and then subjecting the cells to the step of electroporation. Electroporation methods are known in the art and are described, e.g., in Tsong, Biophys. J. 1991, 60, 297-306, and U.S. Patent Application Publication No. 2014/0227237 A1, the disclosures of each of which are incorporated by reference herein. Other electroporation methods known in the art, such as those described in U.S. Patent Nos. 5,019,034; 5,128,257; 5,137,817; 5,173,158; 5,232,856; 5,273,525; 5,304,120; 5,318,514; 6,010,613 and 6,078,490, the disclosures of which are incorporated by reference herein, may be used. In some embodiments, the electroporation method is a sterile electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different

from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of the at least three pulses differ from each other in pulse amplitude. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of the at least three pulses differ from each other in pulse width. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to induce pore formation in the TILs, comprising the step of applying a sequence of at least three DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses, such that induced pores are sustained for a relatively long period of time, and such that viability of the TILs is maintained.

[00635] In some embodiments, a method of transiently altering protein expression in population of TILs includes the step of calcium phosphate transfection. Calcium phosphate transfection methods (calcium phosphate nucleic acid precipitation, cell surface coating, and endocytosis) are known in the art and are described in Graham and van der Eb, Virology 1973, 52, 456-467; Wigler, et al., Proc. Natl. Acad. Sci. 1979, 76, 1373-1376; and Chen and Okayarea, Mol. Cell. Biol. 1987, 7, 2745-2752; and in U.S. Patent No. 5,593,875, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of transiently altering protein expression in a population of TILs includes the step of liposomal transfection. Liposomal transfection methods, such as methods

that employ a 1:1 (w/w) liposome formulation of the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-n,n,n-trimethylammonium chloride (DOTMA) and dioleoyl phophotidylethanolamine (DOPE) in filtered water, are known in the art and are described in Rose, et al., Biotechniques 1991, 10, 520-525 and Felgner, et al., Proc. Natl. Acad. Sci. USA, 1987, 84, 7413-7417 and in U.S. Patent Nos. 5,279,833; 5,908,635; 6,056,938; 6,110,490; 6,534,484; and 7,687,070, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of transiently altering protein expression in a population of TILs includes the step of transfection using methods described in U.S. Patent Nos. 5,766,902; 6,025,337; 6,410,517; 6,475,994; and 7,189,705; the disclosures of each of which are incorporated by reference herein. The TILs may be a first population, a second population and/or a third population of TILs as described herein.

[00636] In some embodiments, a SQZ vector-free microfluidic platform is used for transiently altering protein expression. See, e.g., International Patent Application Publication Nos. WO 2013/059343A1, WO 2017/008063A1, or WO 2017/123663A1, or U.S. Patent Application Publication Nos. US 2014/0287509A1, US 2018/0201889A1, or US 2018/0245089A1, all of which are incorporated by reference herein in their entireties, and particularly for disclosures of microfluidic platforms for nucleic acid delivery. In the SQZ platform, the cell membranes of the TILs for modification are temporarily disrupted by microfluidic constriction, thereby allowing the delivery of nucleic acids encoding the transiently expressed protein. The TILs may be a first population, a second population and/or a third population of TILs as described herein.

F. Immune Checkpoints

[00637] According to particular embodiments of the present invention, a TIL population is gene-edited to express one or more immunomodulatory compositions at the cell surface of TIL cells in the TIL population and to genetically modify one or more immune checkpoint genes in the TIL population. Stated another way, in addition to modification of a TIL population to express one or more immunomodulatory compositions at the cell surface, a DNA sequence within the TIL that encodes one or more of the TIL's immune checkpoints is permanently modified, *e.g.*, inserted, deleted or replaced, in the TIL's genome. Immune checkpoints are molecules expressed by lymphocytes that regulate an immune response via inhibitory or stimulatory pathways. In the case of cancer, immune checkpoint pathways are often activated to inhibit the anti-tumor response, *i.e.*, the expression of certain immune checkpoints by malignant cells inhibits the anti-tumor immunity and favors the growth of cancer cells. *See, e.g.,* Marin-Acevedo *et al., Journal of Hematology & Oncology* (2018) 11:39. Thus, certain inhibitory checkpoint molecules serve as targets for immunotherapies of the present invention. According to particular embodiments, TILs are gene-edited to block or stimulate certain immune checkpoint pathways and thereby enhance the body's immunological activity against tumors.

[00638] As used herein, an immune checkpoint gene comprises a DNA sequence encoding an immune checkpoint molecule. According to particular embodiments of the present invention, gene-editing TILs during the TIL expansion method causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs. For example, gene-editing may cause the expression of an inhibitory receptor, such as PD-1 or CTLA-4, to be silenced or reduced in order to enhance an immune reaction.

[00639] The most broadly studied checkpoints include programmed cell death receptor-1 (PD-1) and cytotoxic T lymphocyte-associated molecule-4 (CTLA-4), which are inhibitory receptors on immune cells that inhibit key effector functions (*e.g.*, activation, proliferation, cytokine release, cytotoxicity, etc.) when they interact with an inhibitory ligand. Numerous checkpoint molecules, in addition to PD-1 and CTLA-4, have emerged as potential targets for immunotherapy, as discussed in more detail below.

[00640] Non-limiting examples of immune checkpoint genes that may be silenced or inhibited by permanently gene-editing TILs of the present invention include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR. For example, immune checkpoint genes that may be silenced or inhibited in TILs of the present invention may be selected from the group comprising PD-1, CTLA-4, LAG-3, TIM-3, Cish, CBL-B, TIGIT, TET2, TGFβ, and PKA. BAFF (BR3) is described in Bloom, *et al.*, *J. Immunother.*, **2018,** in press. According to another example, immune checkpoint genes that may be silenced or inhibited in TILs of the present invention may be selected from the group comprising PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof.

[00641] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for

about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the third population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) system, a Transcription Activator-Like Effector (TALE) system, or a zinc finger system, wherein the at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of a molecule selected from the group consisting of PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof, in the plurality of cells of the second population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

1. PD-1

[00642] One of the most studied targets for the induction of checkpoint blockade is the programmed death receptor (PD1 or PD-1, also known as PDCD1), a member of the CD28 super family of T-cell regulators. Its ligands, PD-L1 and PD-L2, are expressed on a variety of tumor cells, including melanoma. The interaction of PD-1 with PD-L1 inhibits T-cell effector function, results in T-cell exhaustion in the setting of chronic stimulation, and induces T-cell apoptosis in the tumor microenvironment. PD1 may also play a role in tumor-specific escape from immune surveillance.

[00643] According to particular embodiments, expression of PD1 in TILs is silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs by silencing or repressing the expression of PD1. As described in more detail below, the gene-editing process may involve the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as PD1. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or reduce the expression of PD1 in the TILs.

2. CTLA-4

[00644] CTLA-4 expression is induced upon T-cell activation on activated T-cells, and competes for binding with the antigen presenting cell activating antigens CD80 and CD86. Interaction of CTLA-4 with CD80 or CD86 causes T-cell inhibition and serves to maintain balance of the immune response. However, inhibition of the CTLA-4 interaction with CD80 or CD86 may prolong T-cell activation and thus increase the level of immune response to a cancer antigen.

[00645] According to particular embodiments, expression of CTLA-4 in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and CTLA-4 in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of CTLA-4 in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as CTLA-4. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the

expression of CTLA-4 in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and CTLA-4 in the TILs.

3. LAG-3

[00646] Lymphocyte activation gene-3 (LAG-3, CD223) is expressed by T cells and natural killer (NK) cells after major histocompatibility complex (MHC) class II ligation. Although its mechanism remains unclear, its modulation causes a negative regulatory effect over T cell function, preventing tissue damage and autoimmunity. LAG-3 and PD-1 are frequently co-expressed and upregulated on TILs, leading to immune exhaustion and tumor growth. Thus, LAG-3 blockade improves anti-tumor responses. *See, e.g.,* Marin-Acevedo *et al., Journal of Hematology & Oncology* (2018) 11:39.

[00647] According to particular embodiments, expression of LAG-3 in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and LAG-3 in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of LAG-3 in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as LAG-3. According to particular embodiments, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of LAG-3 in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and LAG-3 in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

4. TIM-3

[00648] T cell immunoglobulin-3 (TIM-3) is a direct negative regulator of T cells and is expressed on NK cells and macrophages. TIM-3 indirectly promotes immunosuppression by inducing expansion

of myeloid-derived suppressor cells (MDSCs). Its levels have been found to be particularly elevated on dysfunctional and exhausted T-cells, suggesting an important role in malignancy.

[00649] According to particular embodiments, expression of TIM-3 in TILs is silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of TIM-3 in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as TIM-3. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of TIM-3 in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

5. Cish

[00650] Cish, a member of the suppressor of cytokine signaling (SOCS) family, is induced by TCR stimulation in CD8+ T cells and inhibits their functional avidity against tumors. Genetic deletion of Cish in CD8+ T cells may enhance their expansion, functional avidity, and cytokine polyfunctionality, resulting in pronounced and durable regression of established tumors. *See, e.g.,* Palmer *et al.*, *Journal of Experimental Medicine*, 212 (12): 2095 (2015).

[00651] According to particular embodiments, expression of Cish in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and Cish in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of Cish in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as Cish. For example, a CRISPR

method, a TALE method, or a zinc finger method may be used to silence or repress the expression of Cish in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and Cish in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

6. TGFβ

[00652] The TGFβ signaling pathway has multiple functions in regulating cell growth, differentiation, apoptosis, motility and invasion, extracellular matrix production, angiogenesis, and immune response. TGFβ signaling deregulation is frequent in tumors and has crucial roles in tumor initiation, development and metastasis. At the microenvironment level, the TGFβ pathway contributes to generate a favorable microenvironment for tumor growth and metastasis throughout carcinogenesis. *See, e.g.*, Neuzillet *et al.*, *Pharmacology & Therapeutics*, Vol. 147, pp. 22-31 (2015).

[00653] According to particular embodiments, expression of TGFβ in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and TGFβ in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or reduce the expression of TGFβ in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as TGFβ. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of TGFβ in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and TGFβ in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

[00654] In some embodiments, TGFβR2 (TGF beta receptor 2) may be suppressed by silencing TGFβR2 using a CRISPR/Cas9 system or by using a TGFβR2 dominant negative extracellular trap, using methods known in the art.

7. PKA

[00655] Protein Kinase A (PKA) is a well-known member of the serine-threonine protein kinase superfamily. PKA, also known as cAMP-dependent protein kinase, is a multi-unit protein kinase that mediates signal transduction of G-protein coupled receptors through its activation upon cAMP binding. It is involved in the control of a wide variety of cellular processes from metabolism to ion channel activation, cell growth and differentiation, gene expression and apoptosis. Importantly, PKA has been implicated in the initiation and progression of many tumors. *See, e.g.,* Sapio *et al., EXCLI Journal*; 2014; 13: 843–855.

[00656] According to particular embodiments, expression of PKA in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and PKA in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of PKA in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as PKA. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of PKA in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and PKA in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

8. CBLB

[00657] CBLB (or CBL-B) is a E3 ubiquitin-protein ligase and is a negative regulator of T cell activation. Bachmaier, *et al., Nature*, 2000, 403, 211–216; Wallner, et al., *Clin. Dev. Immunol.* **2012,** 692639.

[00658] According to particular embodiments, expression of CBLB in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and CBL-B in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silencing or repressing the expression of CBLB in TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as CBLB. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of PKA in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and CBL-B in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). In some embodiments, CBLB is silenced using a TALEN knockout. In some embodiments, CBLB is silenced using a TALE-KRAB transcriptional inhibitor knock in. More details on these methods can be found in Boettcher and McManus, *Mol. Cell Review*, **2015,** *58,* 575-585.

9. TIGIT

[00659] T-cell immunoreceptor with Ig and ITIM (immunoreceptor tyrosine-based inhibitory motif) domain or TIGIT is a transmembrane glycoprotein receptor with an Ig-like V-type domain and an ITIM in its cytoplasmic domain. Khalil, *et al.*, *Advances in Cancer Research*, **2015**, 128, 1-68; Yu, *et al.*, *Nature Immunology*, **2009**, Vol. 10, No. 1, 48-57. TIGIT is expressed by some T cells and Natural Killer Cells. Additionally, TIGIT has been shown to be overexpressed on antigen-specific CD8+ T cells and CD8+ TILs, particularly from individuals with melanoma. Studies have shown that the TIGIT pathway contributes to tumor immune evasion and TIGIT inhibition has been shown to increase T-cell activation and proliferation in response to polyclonal and antigen-specific stimulation. Khalil, *et al.*, *Advances in Cancer Research*, **2015**, 128, 1-68. Further, coblockade of TIGIT with either PD-1 or TIM3 has shown synergistic effects against solid tumors in mouse models. *Id.*; *see also* Kurtulus, *et al.*, *The Journal of Clinical Investigation*, **2015**, Vol. 125, No. 11, 4053-4062.

[00660] According to particular embodiments, expression of TIGIT in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular

embodiments, expression of both PD-1 and TIGIT in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of TIGIT in the TILs. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as TIGIT. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of TIGIT in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and TIGIT in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain). TIGIT is silenced using a TALEN knockout. In some embodiments, TIGIT is silenced using a TALE-KRAB transcriptional inhibitor knock in. More details on these methods can be found in Boettcher and McManus, Mol. Cell Review, 2015, 58, 575-585. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and TIGIT in the TILs.

10. TOX

[00661] Thymocyte selection associated high mobility group (HMG) box (TOX) is a transcription factor containing an HMG box DNA binding domain. TOX is a member of the HMG box superfamily that is thought to bind DNA in a sequence-independent but structure-dependent manner.

[00662] TOX was identified as a critical regulator of tumor-specific $CD8^+$ T cell dysfunction or T cell exhaustion and was found to transcriptionally and epigenetically program $CD8^+$ T cell exhaustion, as described, for example in Scott, et al., *Nature*, **2019**, 571, 270-274 and Khan, et al., *Nature*, **2019**, 571, 211-218, both of which are herein incorporated by reference in their entireties. TOX was also found to be critical factor for progression of T cell dysfunction and maintenance of exhausted T cells during chronic infection, as described in Alfei, et al., *Nature*, **2019**, 571, 265-269, which is herein incorporated by reference in its entirety. TOX is highly expressed in dysfunctional or exhausted T cells from tumors and chronic viral infection. Ectopic expression of TOX in effector T cells *in vitro* induced a transcriptional program associated with T cell exhaustion, whereas deletion of TOX in T cells abrogated the T exhaustion program.

[00663] According to particular embodiments, expression of TOX in TILs is silenced or reduced in accordance with compositions and methods of the present invention. According to particular embodiments, expression of both PD-1 and TOX in TILs are silenced or reduced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and silence or repress the expression of TOX. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an immune checkpoint gene, such as TOX. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to silence or repress the expression of TOX in the TILs. In some embodiments, a TALEN method may be used to silence or reduce the expression of PD-1 and TOX in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

G. Overexpression of Co-Stimulatory Receptors or Adhesion Molecules

[00664] According to additional embodiments, gene-editing TILs during the TIL expansion method causes expression of at least one immunomodulatory composition at the cell surface and causes expression of one or more co-stimulatory receptors, adhesion molecules and/or cytokines to be enhanced in at least a portion of the therapeutic population of TILs. For example, gene-editing may cause the expression of a co-stimulatory receptor, adhesion molecule or cytokine to be enhanced, which means that it is overexpressed as compared to the expression of a co-stimulatory receptor, adhesion molecule or cytokine that has not been genetically modified. Non-limiting examples of co-stimulatory receptor, adhesion molecule or cytokine genes that may exhibit enhanced expression by permanently gene-editing TILs of the present invention include certain chemokine receptors and interleukins, such as CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-18, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

1. CCRs

[00665] For adoptive T cell immunotherapy to be effective, T cells need to be trafficked properly into tumors by chemokines. A match between chemokines secreted by tumor cells, chemokines

present in the periphery, and chemokine receptors expressed by T cells is important for successful trafficking of T cells into a tumor bed.

[00666] According to particular embodiments, gene-editing methods of the present invention may be used to increase the expression of certain chemokine receptors in the TILs, such as one or more of CCR2, CCR4, CCR5, CXCR2, CXCR3 and CX3CR1. Over-expression of CCRs may help promote effector function and proliferation of TILs following adoptive transfer.

[00667] According to particular embodiments, expression of one or more of CCR2, CCR4, CCR5, CXCR2, CXCR3 and CX3CR1 in TILs is enhanced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs to express at least one immunomodulatory composition at the cell surface of and enhance the expression of one or more of CCR2, CCR4, CCR5, CXCR2, CXCR3 and CX3CR1 in the TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

[00668] As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at a chemokine receptor gene. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to enhance the expression of certain chemokine receptors in the TILs.

[00669] In some embodiments, CCR4 and/or CCR5 adhesion molecules are inserted into a TIL population using a gamma-retroviral or lentiviral method as described herein. In some embodiments, CXCR2 adhesion molecule are inserted into a TIL population using a gamma-retroviral or lentiviral method as described in Forget, *et al., Frontiers Immunology* **2017**, *8*, 908 or Peng, *et al., Clin. Cancer Res.* **2010**, *16*, 5458, the disclosures of which are incorporated by reference herein.

[00670] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the third population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) system, a Transcription Activator-Like Effector (TALE) system, or a zinc finger system, wherein the at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of PD-1 and, optionally, LAG-3, in the plurality of cells of the second population of TILs, and further wherein the at least one gene editor system effects expression of a CXCR2 adhesion molecule at the cell surface of the plurality of cells of the second population of TILs or the CXCR2 adhesion molecule is inserted by a gammaretroviral or lentiviral method into the first population of TILs, second population of TILs, or harvested population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored

immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

[00671] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the third population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) system, a Transcription Activator-Like Effector (TALE) system, or a zinc finger system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of PD-1 and, optionally, LAG-3, in the plurality of cells of the second population of TILs and further wherein the at least one gene editor system effects expression of a CCR4 and/or CCR5 adhesion molecule at the cell surface of the plurality of cells of the second population of TILs or the CXCR2 adhesion molecule is inserted by a gammaretroviral or lentiviral method into the first population of TILs, second population of TILs, or harvested population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

[00672] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor into a plurality of cells in the second population of TILs;

(f) resting the second population of TILs for about 1 day;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11 days, wherein the second expansion is performed in a closed

container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the third population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) system, a Transcription Activator-Like Effector (TALE) system, or a zinc finger system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of PD-1 and, optionally, LAG-3, in the plurality of cells of the second population of TILs, and further wherein the at least one gene editor system effects expression of an adhesion molecule selected from the group consisting of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof, at the cell surface of the plurality of cells of the second population of TILs or the adhesion molecule is inserted by a gammaretroviral or lentiviral method into the first population of TILs, second population of TILs, or harvested population of TILs. In some embodiments, the at least one immunomodulatory composition comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein). In some embodiments, the immunomodulatory agent is selected from the group consisting of IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., a CD40L or an agonistic CD40 binding domain).

2. Interleukins

[00673] According to additional embodiments, gene-editing methods of the present invention may be used to increase the expression of certain interleukins, such as one or more of IL-2, IL-4, IL-7, IL-10, IL-15, IL-18 and IL-21. Certain interleukins have been demonstrated to augment effector functions of T cells and mediate tumor control.

[00674] According to particular embodiments, expression of one or more of IL-2, IL-4, IL-7, IL-10, IL-15, IL-18 and IL-21 in TILs is enhanced in accordance with compositions and methods of the present invention. For example, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs may be carried out in accordance with any embodiment of the methods

described herein (*e.g.*, process 2A, process Gen 3, or the methods shown in Figures 34 and 35), wherein the method comprises gene-editing at least a portion of the TILs by enhancing the expression of one or more of IL-2, IL-4, IL-7, IL-10, IL-15, IL-18 and IL-21. As described in more detail below, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at an interleukin gene. For example, a CRISPR method, a TALE method, or a zinc finger method may be used to enhance the expression of certain interleukins in the TILs.

[00675] According to some embodiments, a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from a tumor resected from a patient by processing a tumor sample obtained from the patient into multiple tumor fragments;

(b) adding the tumor fragments into a closed system;

(c) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and optionally comprising OKT-3 and/or a 4-1BB agonist antibody for about 3 to 11 days to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area;

(d) stimulating the second population of TILs by adding OKT-3 and culturing for about 1 to 3 days to obtain the second population of TILs, wherein the transition from step (c) to step (d) occurs without opening the system;

(e) sterile electroporating the second population of TILs to effect transfer of at least one gene editor;

(f) resting the second population of TILs for about 1 day into a plurality of cells in the second population of TILs;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, optionally OKT-3 antibody, optionally an OX40 antibody, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7 to 11, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting the therapeutic population of TILs obtained from step (g) to provide a harvested TIL population, wherein the transition from step (g) to step (h) occurs without opening the system, wherein the harvested population of TILs is a therapeutic population of TILs;

(i) transferring the harvested TIL population to an infusion bag, wherein the transfer from step (h) to (i) occurs without opening the system; and

(j) optionally cryopreserving the harvested TIL population using a cryopreservation medium,

wherein the electroporation step comprises the delivery of at least one gene editor system selected from the group consisting of a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) system, a Transcription Activator-Like Effector (TALE) system, or a zinc finger system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of and inhibits expression of PD-1 and, optionally, LAG-3, in the plurality of cells of the second population of TILs and further wherein the at least one gene editor system effects expression of an interleukin selected from the group consisting of IL-2, IL-4, IL-7, IL-10, IL-15, IL-18, IL-21, and combinations thereof, at the cell surface of the plurality of cells of the second population of TILs or the interleukin is inserted by a gammaretroviral or lentiviral method into the first population of TILs, second population of TILs, or harvested population of TILs. In some embodiments, the at least one immunomodulatory composition comprises a cytokine fused to a membrane anchor. In some embodiments, the cytokine is selected from the group consisting of IL-12, IL-15, IL-18 and IL-21.

V. Gen 2 TIL Manufacturing Processes

[00837] In some embodiments, after the making of the cryopreserved TIL preparation as described herein, the the patient is monitored for exhibitions of progressive disease on or after ICI and/or standard of care treatment. In some embodiments, the patient exhibits progressive cancer on or after ICI and/or standard of care treatment and is indicated for autologous TIL therapy. In some embodiments, after progression, the cryopreserved TIL preparation is thawed and expanded according to expansion methods described in the sections below.

[00838] An exemplary family of TIL processes known as Gen 2 (also known as process 2A) containing some of these features is depicted in Figures 1 and 2. An embodiment of Gen 2 is shown in Figure 2.

[00839] As discussed herein, the present invention can include a step relating to the restimulation of cryopreserved TILs to increase their metabolic activity and thus relative health prior to transplant into a patient, and methods of testing said metabolic health. As generally outlined herein, TILs are generally taken from a patient sample and manipulated to expand their number prior to transplant into a patient. In some embodiments, the TILs may be optionally genetically manipulated as discussed below.

[00840] In some embodiments, the TILs may be cryopreserved. Once thawed, they may also be restimulated to increase their metabolism prior to infusion into a patient.

[00841] In some embodiments, the first expansion (including processes referred to as the preREP as well as processes shown in Figure 1 as Step A) is shortened to 3 to 14 days and the second expansion (including processes referred to as the REP as well as processes shown in Figure 1 as Step B) is shorted to 7 to 14 days, as discussed in detail below as well as in the examples and figures. In some embodiments, the first expansion (for example, an expansion described as Step B in Figure 1) is shortened to 11 days and the second expansion (for example, an expansion as described in Step D in Figure 1) is shortened to 11 days. In some embodiments, the combination of the first expansion and second expansion (for example, expansions described as Step B and Step D in Figure 1) is shortened to 22 days, as discussed in detail below and in the examples and figures.

[00842] The "Step" Designations A, B, C, *etc.*, below are in reference to Figure 1 and in reference to certain embodiments described herein. The ordering of the Steps below and in Figure 1 is exemplary and any combination or order of steps, as well as additional steps, repetition of steps, and/or omission of steps is contemplated by the present application and the methods disclosed herein.

A. STEP A: Obtain Patient Tumor Sample

[00843] In general, TILs are initially obtained from a patient tumor sample and then expanded into a larger population for further manipulation as described herein, optionally cryopreserved, restimulated as outlined herein and optionally evaluated for phenotype and metabolic parameters as an indication of TIL health.

[00844] A patient tumor sample may be obtained using methods known in the art, generally via surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells. In some embodiments, multilesional sampling is used. In some embodiments, surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells includes multilesional sampling (*i.e.*, obtaining samples from one or more tumor sites and/or locations in the patient, as well as one or more tumors in the same location or in close proximity). In general, the tumor sample may be from any solid tumor, including primary tumors, invasive tumors or metastatic tumors. The tumor sample may also be a liquid tumor, such as a tumor obtained from a hematological malignancy. The solid tumor may be of lung tissue. In some embodiments, useful TILs are obtained from non-small cell lung carcinoma (NSCLC). The solid tumor may be of skin tissue. In some embodiments, useful TILs are obtained from a melanoma.

[00845] Once obtained, the tumor sample is generally fragmented using sharp dissection into small pieces of between 1 to about 8 mm^3, with from about 2-3 mm^3 being particularly useful. In some embdoiments, the TILs are cultured from these fragments using enzymatic tumor digests. Such tumor digests may be produced by incubation in enzymatic media (*e.g.*, Roswell Park Memorial Institute

(RPMI) 1640 buffer, 2 mM glutamate, 10 mcg/mL gentamicine, 30 units/mL of DNase and 1.0 mg/mL of collagenase) followed by mechanical dissociation (*e.g.*, using a tissue dissociator). Tumor digests may be produced by placing the tumor in enzymatic media and mechanically dissociating the tumor for approximately 1 minute, followed by incubation for 30 minutes at 37 °C in 5% CO_2, followed by repeated cycles of mechanical dissociation and incubation under the foregoing conditions until only small tissue pieces are present. At the end of this process, if the cell suspension contains a large number of red blood cells or dead cells, a density gradient separation using FICOLL branched hydrophilic polysaccharide may be performed to remove these cells. Alternative methods known in the art may be used, such as those described in U.S. Patent Application Publication No. 2012/0244133 A1, the disclosure of which is incorporated by reference herein. Any of the foregoing methods may be used in any of the embodiments described herein for methods of expanding TILs or methods treating a cancer.

[00846] Tumor dissociating enzyme mixtures can include one or more dissociating (digesting) enzymes such as, but not limited to, collagenase (including any blend or type of collagenase), Accutase™, Accumax™, hyaluronidase, neutral protease (dispase), chymotrypsin, chymopapain, trypsin, caseinase, elastase, papain, protease type XIV (pronase), deoxyribonuclease I (DNase), trypsin inhibitor, any other dissociating or proteolytic enzyme, and any combination thereof.

[00847] In some embodiments, the dissociating enzymes are reconstituted from lyophilized enzymes. In some embodiments, lyophilized enzymes are reconstituted in an amount of sterile buffer such as HBSS.

[00848] In some instances, collagenase (such as animal free- type 1 collagenase) is reconstitued in 10 mL of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 2892 PZ U/vial. In some embodiments, collagenase is reconstituted in 5 mL to 15 mL buffer. In some embodiment, after reconstitution the collagenase stock ranges from about 100 PZ U/mL-about 400 PZ U/mL, *e.g.*, about 100 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL-about 350 PZ U/mL, about 100 PZ U/mL-about 300 PZ U/mL, about 150 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL, about 150 PZ U/mL, about 200 PZ U/mL, about 210 PZ U/mL, about 220 PZ U/mL, about 230 PZ U/mL, about 240 PZ U/mL, about 250 PZ U/mL, about 260 PZ U/mL, about 270 PZ U/mL, about 280 PZ U/mL, about 289.2 PZ U/mL, about 300 PZ U/mL, about 350 PZ U/mL, or about 400 PZ U/mL.

[00849] In some embodiments, neutral protease is reconstituted in 1-ml of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 175 DMC U/vial. In some embodiments, after reconstitution the neutral protease stock ranges from about 100 DMC/mL-about 400 DMC/mL, *e.g.*, about 100 DMC/mL-about 400 DMC/mL, about 100 DMC/mL-about 350 DMC/mL, about 100 DMC/mL-about 300 DMC/mL, about 150 DMC/mL-about 400 DMC/mL, about

100 DMC/mL, about 110 DMC/mL, about 120 DMC/mL, about 130 DMC/mL, about 140 DMC/mL, about 150 DMC/mL, about 160 DMC/mL, about 170 DMC/mL, about 175 DMC/mL, about 180 DMC/mL, about 190 DMC/mL, about 200 DMC/mL, about 250 DMC/mL, about 300 DMC/mL, about 350 DMC/mL, or about 400 DMC/mL.

[00850] In some embodiments, DNAse I is reconstituted in 1-ml of sterile HBSS or another buffer. The lyophilized stock enzyme was at a concentration of 4 KU/vial. In some embodiments, after reconstitution the DNase I stock ranges from about 1 KU/mL-10 KU/mL, *e.g.*, about 1 KU/mL, about 2 KU/mL, about 3 KU/mL, about 4 KU/mL, about 5 KU/mL, about 6 KU/mL, about 7 KU/mL, about 8 KU/mL, about 9 KU/mL, or about 10 KU/mL.

[00851] In some embodiments, the stock of enzymes is variable and the concentrations may need to be determined. In some embodiments, the the concentration of the lyophilized stock can be verified. In some embodiments, the final amount of enzyme added to the digest cocktail is adjusted based on the determined stock concentration.

[00852] In some embodiment, the enzyme mixture includes about 10.2-ul of neutral protease (0.36 DMC U/mL), 21.3-ul of collagenase (1.2 PZ/mL) and 250-ul of DNAse I (200 U/mL) in about 4.7-ml of sterile HBSS.

[00853] As indicated above, in some embodiments, the TILs are derived from solid tumors. In some embodiments, the solid tumors are not fragmented. In some embodiments, the solid tumors are not fragmented and are subjected to enzymatic digestion as whole tumors. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours at 37°C, 5% CO_2. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours at 37°C, 5% CO_2 with rotation. In some embodiments, the tumors are digested overnight with constant rotation. In some embodiments, the tumors are digested overnight at 37°C, 5% CO_2 with constant rotation. In some embodiments, the whole tumor is combined with the enzymes to form a tumor digest reaction mixture.

[00854] In some embodiments, the tumor is reconstituted with the lyophilized enzymes in a sterile buffer. In some embodiments, the buffer is sterile HBSS.

[00855] In some embodiments, the enzyme mixture comprises collagenase. In some embodiments, the collagenase is collagenase IV. In some embodiments, the working stock for the collagenase is a 100 mg/mL 10X working stock.

[00856] In some embodiments, the enzyme mixture comprises DNAse. In some embodiments, the working stock for the DNAse is a 10,000IU/mL 10X working stock.

[00857] In some embodiments, the enzyme mixture comprises hyaluronidase. In some embodiments, the working stock for the hyaluronidase is a 10-mg/mL 10X working stock.

[00858] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 1000 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[00859] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 500 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[00860] In general, the harvested cell suspension is called a "primary cell population" or a "freshly harvested" cell population.

[00861] In some embodiments, fragmentation includes physical fragmentation, including for example, dissection as well as digestion. In some embodiments, the fragmentation is physical fragmentation. In some embodiments, the fragmentation is dissection. In some embodiments, the fragmentation is by digestion. In some embodiments, TILs can be initially cultured from enzymatic tumor digests and tumor fragments obtained from digesting or fragmenting a tumor sample obtained from a patient.

[00862] In some embodiments, where the tumor is a solid tumor, the tumor undergoes physical fragmentation after the tumor sample is obtained in, for example, Step A (as provided in Figure 1). In some embodiments, the fragmentation occurs before cryopreservation. In some embodiments, the fragmentation occurs after cryopreservation. In some embodiments, the fragmentation occurs after obtaining the tumor and in the absence of any cryopreservation. In some embodiments, the tumor is fragmented and 10, 20, 30, 40 or more fragments or pieces are placed in each container for the first expansion. In some embodiments, the tumor is fragmented and 30 or 40 fragments or pieces are placed in each container for the first expansion. In some embodiments, the tumor is fragmented and 40 fragments or pieces are placed in each container for the first expansion. In some embodiments, the multiple fragments comprise about 4 to about 50 fragments, wherein each fragment has a volume of about 27 mm^3. In some embodiments, the multiple fragments comprise about 30 to about 60 fragments with a total volume of about 1300 mm^3 to about 1500 mm^3. In some embodiments, the multiple fragments comprise about 50 fragments with a total volume of about 1350 mm^3. In some embodiments, the multiple fragments comprise about 50 fragments with a total mass of about 1 gram to about 1.5 grams. In some embodiments, the multiple fragments comprise about 4 fragments.

[00863] In some embodiments, the TILs are obtained from tumor fragments. In some embodiments, the tumor fragment is obtained by sharp dissection. In some embodiments, the tumor fragment is

between about 1 mm^3 and 10 mm^3. In some embodiments, the tumor fragment is between about 1 mm^3 and 8 mm^3. In some embodiments, the tumor fragment is about 1 mm^3. In some embodiments, the tumor fragment is about 2 mm^3. In some embodiments, the tumor fragment is about 3 mm^3. In some embodiments, the tumor fragment is about 4 mm^3. In some embodiments, the tumor fragment is about 5 mm^3. In some embodiments, the tumor fragment is about 6 mm^3. In some embodiments, the tumor fragment is about 7 mm^3. In some embodiments, the tumor fragment is about 8 mm^3. In some embodiments, the tumor fragment is about 9 mm^3. In some embodiments, the tumor fragment is about 10 mm^3. In some embodiments, the tumors are 1-4 mm × 1-4 mm × 1-4 mm. In some embodiments, the tumors are 1 mm × 1 mm × 1 mm. In some embodiments, the tumors are 2 mm × 2 mm × 2 mm. In some embodiments, the tumors are 3 mm × 3 mm × 3 mm. In some embodiments, the tumors are 4 mm × 4 mm × 4 mm.

[00864] In some embodiments, the tumors are resected in order to minimize the amount of hemorrhagic, necrotic, and/or fatty tissues on each piece. In some embodiments, the tumors are resected in order to minimize the amount of hemorrhagic tissue on each piece. In some embodiments, the tumors are resected in order to minimize the amount of necrotic tissue on each piece. In some embodiments, the tumors are resected in order to minimize the amount of fatty tissue on each piece.

[00865] In some embodiments, the tumor fragmentation is performed in order to maintain the tumor internal structure. In some embodiments, the tumor fragmentation is performed without preforming a sawing motion with a scalpel. In some embodiments, the TILs are obtained from tumor digests. In some embodiments, tumor digests were generated by incubation in enzyme media, for example but not limited to RPMI 1640, 2 mM GlutaMAX, 10 mg/mL gentamicin, 30 U/mL DNase, and 1.0 mg/mL collagenase, followed by mechanical dissociation (GentleMACS, Miltenyi Biotec, Auburn, CA). After placing the tumor in enzyme media, the tumor can be mechanically dissociated for approximately 1 minute. The solution can then be incubated for 30 minutes at 37 °C in 5% CO_2 and it then mechanically disrupted again for approximately 1 minute. After being incubated again for 30 minutes at 37 °C in 5% CO_2, the tumor can be mechanically disrupted a third time for approximately 1 minute. In some embodiments, after the third mechanical disruption if large pieces of tissue were present, 1 or 2 additional mechanical dissociations were applied to the sample, with or without 30 additional minutes of incubation at 37 °C in 5% CO_2. In some embodiments, at the end of the final incubation if the cell suspension contained a large number of red blood cells or dead cells, a density gradient separation using Ficoll can be performed to remove these cells.

[00866] In some embodiments, the harvested cell suspension prior to the first expansion step is called a "primary cell population" or a "freshly harvested" cell population.

[00867] In some embodiments, cells can be optionally frozen after sample harvest and stored frozen prior to entry into the expansion described in Step B, which is described in further detail below, as well as exemplified in Figure 1, as well as Figure 8.

1. Pleural effusion T-cells or TILs

[00868] In some embodiments, the sample is a pleural fluid sample. In some embodiments, the source of the T-cells or TILs for expansion according to the processes described herein is a pleural fluid sample. In some embodiments, the sample is a pleural effusion derived sample. In some embodiments, the source of the T-cells or TILs for expansion according to the processes described herein is a pleural effusion derived sample. See, for example, methods described in U.S. Patent Publication US 2014/0295426, incorporated herein by reference in its entirety for all purposes.

[00869] In some embodiments, any pleural fluid or pleural effusion suspected of and/or containing TILs can be employed. Such a sample may be derived from a primary or metastatic lung cancer, such as NSCLC or SCLC. In some embodiments, the sample may be secondary metastatic cancer cells which originated from another organ, *e.g.*, breast, ovary, colon or prostate. In some embodiments, the sample for use in the expansion methods described herein is a pleural exudate. In some embodiments, the sample for use in the expansion methods described herein is a pleural transudate. Other biological samples may include other serous fluids containing TILs, including, *e.g.*, ascites fluid from the abdomen or pancreatic cyst fluid. Ascites fluid and pleural fluids involve very similar chemical systems; both the abdomen and lung have mesothelial lines and fluid forms in the pleural space and abdominal spaces in the same matter in malignancies and such fluids in some embodiments contain TILs. In some embodiments, wherein the disclosure exemplifies pleural fluid, the same methods may be performed with similar results using ascites or other cyst fluids containing TILs.

[00870] In some embodiments, the pleural fluid is in unprocessed form, directly as removed from the patient. In some embodiments, the unprocessed pleural fluid is placed in a standard blood collection tube, such as an EDTA or Heparin tube, prior to the contacting step. In some embodiments, the unprocessed pleural fluid is placed in a standard CellSave® tube (Veridex) prior to the contacting step. In some embodiments, the sample is placed in the CellSave tube immediately after collection from the patient to avoid a decrease in the number of viable TILs. The number of viable TILs can decrease to a significant extent within 24 hours, if left in the untreated pleural fluid, even at 4°C. In some embodiments, the sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, or up to 24 hours after removal from the patient. In some embodiments, the sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, or up to 24 hours after removal from the patient at 4°C.

[00871] In some embodiments, the pleural fluid sample from the chosen subject may be diluted. In one embodiment, the dilution is 1:10 pleural fluid to diluent. In some embodiments, the dilution is 1:9 pleural fluid to diluent. In some embodiments, the dilution is 1:8 pleural fluid to diluent. In some embodiments, the dilution is 1:5 pleural fluid to diluent. In some embodiments, the dilution is 1:2 pleural fluid to diluent. In some embodiments, the dilution is 1:1 pleural fluid to diluent. In some embodiments, diluents include saline, phosphate buffered saline, another buffer or a physiologically acceptable diluent. In some embodiments, the sample is placed in the CellSave tube immediately after collection from the patient and dilution to avoid a decrease in the viable TILs, which may occur to a significant extent within 24-48 hours, if left in the untreated pleural fluid, even at 4°C. In some embodiments, the pleural fluid sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, 24 hours, 36 hours, up to 48 hours after removal from the patient, and dilution. In some embodiments, the pleural fluid sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, 24 hours, 36 hours, up to 48 hours after removal from the patient, and dilution at 4°C.

[00872] In still another embodiment, pleural fluid samples are concentrated by conventional means prior further processing steps. In some embodiments, this pre-treatment of the pleural fluid is preferable in circumstances in which the pleural fluid must be cryopreserved for shipment to a laboratory performing the method or for later analysis (*e.g.*, later than 24-48 hours post-collection). In some embodiments, the pleural fluid sample is prepared by centrifuging the pleural fluid sample after its withdrawal from the subject and resuspending the centrifugate or pellet in buffer. In some embodiments, the pleural fluid sample is subjected to multiple centrifugations and resuspensions, before it is cryopreserved for transport or later analysis and/or processing.

[00873] In some embodiments, pleural fluid samples are concentrated prior to further processing steps by using a filtration method. In some embodiments, the pleural fluid sample used in the contacting step is prepared by filtering the fluid through a filter containing a known and essentially uniform pore size that allows for passage of the pleural fluid through the membrane but retains the tumor cells. In some embodiments, the diameter of the pores in the membrane may be at least 4 μM. In some embodiments the pore diameter may be 5 μM or more, and in other embodiment, any of 6, 7, 8, 9, or 10 μM. After filtration, the cells, including TILs, retained by the membrane may be rinsed off the membrane into a suitable physiologically acceptable buffer. Cells, including TILs, concentrated in this way may then be used in the contacting step of the method.

[00874] In some embodiment, pleural fluid sample (including, for example, the untreated pleural fluid), diluted pleural fluid, or the resuspended cell pellet, is contacted with a lytic reagent that differentially lyses non-nucleated red blood cells present in the sample. In some embodiments, this step is performed prior to further processing steps in circumstances in which the pleural fluid contains

substantial numbers of RBCs. Suitable lysing reagents include a single lytic reagent or a lytic reagent and a quench reagent, or a lytic agent, a quench reagent and a fixation reagent. Suitable lytic systems are marketed commercially and include the BD Pharm Lyse™ system (Becton Dickenson). Other lytic systems include the Versalyse™ system, the FACSlyse™ system (Becton Dickenson), the Immunoprep™ system or Erythrolyse II system (Beckman Coulter, Inc.), or an ammonium chloride system. In some embodiments, the lytic reagent can vary with the primary requirements being efficient lysis of the red blood cells, and the conservation of the TILs and phenotypic properties of the TILs in the pleural fluid. In addition to employing a single reagent for lysis, the lytic systems useful in methods described herein can include a second reagent, *e.g.*, one that quenches or retards the effect of the lytic reagent during the remaining steps of the method, *e.g.*, Stabilyse™ reagent (Beckman Coulter, Inc.). A conventional fixation reagent may also be employed depending upon the choice of lytic reagents or the preferred implementation of the method.

[00875] In some embodiments, the pleural fluid sample, unprocessed, diluted or multiply centrifuged or processed as described herein above is cryopreserved at a temperature of about −140°C prior to being further processed and/or expanded as provided herein.

A1. STEP A1: Pre-Progression Cryopreservation

[00876] In some embodiments, the present methods provide for cryopreserving the harvested tumor sample obtained from Step A to make a cryopreserved TIL preparation for future TIL manufacturing, after the patient exhibits cancer progression on or after receiving immune-check point inhibitor (ICI) and/or standard of care treatment.

[00877] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor in the subject or patient,

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample.

[00878] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments; and

(b) cryopreserving the tumor fragments comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments.

[00879] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into a tumor digest; and

(b) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor digest.

[00880] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, resecting a NSCLC tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor; and

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample.

[00881] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, resecting a NSCLC tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor;

(b) fragmenting the tumor into tumor fragments; and

(c) cryopreserving the tumor fragments comprising the first population of TILs from step (b) to produce cryopreserved tumor fragments.

[00882] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest; and

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest.

[00883] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) dissociate tumor tissue to produce a dissociated tumor material and

(c) cryopreserving the dissociated tumor material comprising the first population of TILs from step (a) to produce a cryopreserved dissociated tumor material.

B. STEP B: First Expansion

[00884] In some embodiments, the present methods provide for obtaining young TILs, which are capable of increased replication cycles upon administration to a subject/patient and as such may provide additional therapeutic benefits over older TILs (*i.e.*, TILs which have further undergone more rounds of replication prior to administration to a subject/patient). Features of young TILs have been described in the literature, for example Donia, *et al.*, *Scand. J. Immunol.* **2012,** *75,* 157–167; Dudley, *et al.*, *Clin. Cancer Res.* **2010,** *16,* 6122-6131; Huang, *et al.*, *J. Immunother.* **2005,** *28*, 258–267; Besser, *et al.*, *Clin. Cancer Res.* **2013,** *19*, OF1-OF9; Besser, *et al.*, *J. Immunother.* **2009**, *32*:415–423; Robbins, *et al.*, *J. Immunol.* **2004**, *173,* 7125-7130; Shen, *et al.*, *J. Immunother.*, **2007,** *30,* 123–129; Zhou, *et al.*, *J. Immunother.* **2005,** *28,* 53–62; and Tran, *et al.*, *J. Immunother.*, **2008**, *31*, 742–751, each of which is incorporated herein by reference.

[00885] The diverse antigen receptors of T and B lymphocytes are produced by somatic recombination of a limited, but large number of gene segments. These gene segments: V (variable), D (diversity), J (joining), and C (constant), determine the binding specificity and downstream applications of immunoglobulins and T-cell receptors (TCRs). The present invention provides a method for generating

[00886] TILs which exhibit and increase the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity as compared to freshly harvested TILs and/or TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity as compared to freshly harvested TILs and/or TILs prepared using methods referred to as process 1C, as exemplified in Figure 5 and/or Figure 6. In some embodiments, the TILs obtained in the first expansion exhibit an increase in the T-cell repertoire diversity. In some embodiments, the increase in diversity is an increase in the immunoglobulin diversity and/or the T-cell receptor diversity. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin heavy chain. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin light chain. In some embodiments, the diversity is in the T-cell receptor. In some embodiments, the diversity is in one of the T-cell receptors selected from the group consisting of alpha, beta, gamma, and delta receptors. In some embodiments, there is an increase in the expression of T-cell receptor

(TCR) alpha and/or beta. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) beta. In some embodiments, there is an increase in the expression of TCRab (*i.e.*, TCRα/β).

[00887] After dissection or digestion of tumor fragments, for example such as described in Step A of Figure 1, the resulting cells are cultured in serum containing IL-2 under conditions that favor the growth of TILs over tumor and other cells. In some embodiments, the tumor digests are incubated in 2 mL wells in media comprising inactivated human AB serum with 6000 IU/mL of IL-2. This primary cell population is cultured for a period of days, generally from 3 to 14 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this primary cell population is cultured for a period of 7 to 14 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this primary cell population is cultured for a period of 10 to 14 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this primary cell population is cultured for a period of about 11 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells.

[00888] In some embodiments, expansion of TILs may be performed using an initial bulk TIL expansion step (for example such as those described in Step B of Figure 1, which can include processes referred to as pre-REP) as described below and herein, followed by a second expansion (Step D, including processes referred to as rapid expansion protocol (REP) steps) as described below under Step D and herein, followed by optional cryopreservation, and followed by a second Step D (including processes referred to as restimulation REP steps) as described below and herein. The TILs obtained from this process may be optionally characterized for phenotypic characteristics and metabolic parameters as described herein.

[00889] In embodiments where TIL cultures are initiated in 24-well plates, for example, using Costar 24-well cell culture cluster, flat bottom (Corning Incorporated, Corning, NY, each well can be seeded with 1×10^6 tumor digest cells or one tumor fragment in 2 mL of complete medium (CM) with IL-2 (6000 IU/mL; Chiron Corp., Emeryville, CA). In some embodiments, the tumor fragment is between about 1 mm^3 and 10 mm^3.

[00890] In some embodiments, the first expansion culture medium is referred to as "CM", an abbreviation for culture media. In some embodiments, CM for Step B consists of RPMI 1640 with GlutaMAX, supplemented with 10% human AB serum, 25 mM Hepes, and 10 mg/mL gentamicin. In embodiments where cultures are initiated in gas-permeable flasks with a 40 mL capacity and a 10 cm^2 gas-permeable silicon bottom (for example, G-REX10; Wilson Wolf Manufacturing, New Brighton, MN), each flask was loaded with 10–40 $\times 10^6$ viable tumor digest cells or 5–30 tumor fragments in 10–40 mL of CM with IL-2. Both the G-REX10 and 24-well plates were incubated in a humidified

incubator at 37°C in 5% CO_2 and 5 days after culture initiation, half the media was removed and replaced with fresh CM and IL-2 and after day 5, half the media was changed every 2–3 days.

[00891] In some embodiments, the culture medium used in the expansion processes disclosed herein is a serum-free medium or a defined medium. In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or a serum replacement. In some embodiments, the serum-free or defined medium is used to prevent and/or decrease experimental variation due in part to the lot-to-lot variation of serum-containing media.

[00892] In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or serum replacement. In some embodiments, the basal cell medium includes, but is not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium , CTS™ OpTmizer™ T-Cell Expansion SFM, CTS™ AIM-V Medium, CTS™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00893] In some embodiments, the serum supplement or serum replacement includes, but is not limited to one or more of CTS™ OpTmizer T-Cell Expansion Serum Supplement, CTS™ Immune Cell Serum Replacement, one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more antibiotics, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L- histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or 2-mercaptoethanol.

[00894] In some embodiments, the CTS™OpTmizer™ T-cell Immune Cell Serum Replacement is used with conventional growth media, including but not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium, CTS™ OpTmizer™ T-cell Expansion SFM, CTS™ AIM-V Medium, CST™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00895] In some embodiments, the total serum replacement concentration (vol%) in the serum-free or defined medium is from about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, or 20% by volume of the total serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 3% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 5% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 10% of the total volume of the serum-free or defined medium.

[00896] In some embodiments, the serum-free or defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific). In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55μM.

[00897] In some embodiments, the defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 3000

IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55µM.

[00898] In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of from about 0.1mM to about 10mM, 0.5mM to about 9mM, 1mM to about 8mM, 2mM to about 7mM, 3mM to about 6mM, or 4mM to about 5 mM. In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of about 2mM.

[00899] In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of from about 5mM to about 150mM, 10mM to about 140mM, 15mM to about 130mM, 20mM to about 120mM, 25mM to about 110mM, 30mM to about 100mM, 35mM to about 95mM, 40mM to about 90mM, 45mM to about 85mM, 50mM to about 80mM, 55mM to about 75mM, 60mM to about 70mM, or about 65mM. In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of about 55mM. In some embodiments, the final concentration of 2-mercaptoethanol in the media is 55µM.

[00900] In some embodiments, the defined media described in International PCT Publication No. WO/1998/030679, which is herein incorporated by reference, are useful in the present invention. In that publication, serum-free eukaryotic cell culture media are described. The serum-free, eukaryotic cell culture medium includes a basal cell culture medium supplemented with a serum-free supplement capable of supporting the growth of cells in serum- free culture. The serum-free eukaryotic cell culture medium supplement comprises or is obtained by combining one or more ingredients selected from the group consisting of one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more trace elements, and one or more antibiotics. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or beta-mercaptoethanol. In some embodiments, the defined medium comprises an albumin or an albumin substitute and one or more ingredients selected from group consisting of one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L-histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the basal cell media is selected from the group consisting of Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00901] In some embodiments, the concentration of glycine in the defined medium is in the range of from about 5-200 mg/L, the concentration of L- histidine is about 5-250 mg/L, the concentration of L-isoleucine is about 5-300 mg/L, the concentration of L-methionine is about 5-200 mg/L, the concentration of L-phenylalanine is about 5-400 mg/L, the concentration of L-proline is about 1-1000 mg/L, the concentration of L- hydroxyproline is about 1-45 mg/L, the concentration of L-serine is about 1-250 mg/L, the concentration of L-threonine is about 10-500 mg/L, the concentration of L-tryptophan is about 2-110 mg/L, the concentration of L-tyrosine is about 3-175 mg/L, the concentration of L-valine is about 5-500 mg/L, the concentration of thiamine is about 1-20 mg/L, the concentration of reduced glutathione is about 1-20 mg/L, the concentration of L-ascorbic acid-2-phosphate is about 1-200 mg/L, the concentration of iron saturated transferrin is about 1-50 mg/L, the concentration of insulin is about 1-100 mg/L, the concentration of sodium selenite is about 0.000001-0.0001 mg/L, and the concentration of albumin (*e.g.*, AlbuMAX® I) is about 5000-50,000 mg/L.

[00902] In some embodiments, the non-trace element moiety ingredients in the defined medium are present in the concentration ranges listed in the column under the heading "Concentration Range in 1X Medium" in Table 4. In other embodiments, the non-trace element moiety ingredients in the defined medium are present in the final concentrations listed in the column under the heading "A Preferred Embodiment of the 1X Medium" in Table 4. In other embodiments, the defined medium is a basal cell medium comprising a serum free supplement. In some of these embodiments, the serum free supplement comprises non-trace moiety ingredients of the type and in the concentrations listed in the column under the heading "A Preferred Embodiment in Supplement" in Table 4 below.

Table 4: Concentrations of Non-Trace Element Moiety Ingredients

Ingredient	A preferred embodiment in supplement (mg/L) (About)	Concentration range in 1X medium (mg/L) (About)	A preferred embodiment in 1X medium (mg/L) (About)
Glycine	150	5-200	53
L-Histidine	940	5-250	183
L-Isoleucine	3400	5-300	615
L-Methionine	90	5-200	44
L-Phenylalanine	1800	5-400	336
L-Proline	4000	1-1000	600
L-Hydroxyproline	100	1-45	15
L-Serine	800	1-250	162
L-Threonine	2200	10-500	425
L-Tryptophan	440	2-110	82
L-Tyrosine	77	3-175	84
L-Valine	2400	5-500	454
Thiamine	33	1-20	9
Reduced Glutathione	10	1-20	1.5
Ascorbic Acid-2-PO_4 (Mg Salt)	330	1-200	50
Transferrin (iron saturated)	55	1-50	8
Insulin	100	1-100	10
Sodium Selenite	0.07	0.000001-0.0001	0.00001

AlbuMAX®I	83,000	5000-50,000	12,500

[00903] In some embodiments, the osmolarity of the defined medium is between about 260 and 350 mOsmol. In some embodiments, the osmolarity is between about 280 and 310 mOsmol. In some embodiments, the defined medium is supplemented with up to about 3.7 g/L, or about 2.2 g/L sodium bicarbonate. The defined medium can be further supplemented with L-glutamine (final concentration of about 2 mM), one or more antibiotics, non-essential amino acids (NEAA; final concentration of about 100 μM), 2-mercaptoethanol (final concentration of about 100 μM).

[00904] In some embodiments, the defined media described in Smith, *et al.*, *Clin Transl Immunology*, 4(1) 2015 (doi: 10.1038/cti.2014.31) are useful in the present invention. Briefly, RPMI or CTS™ OpTmizer™ was used as the basal cell medium, and supplemented with either 0, 2%, 5%, or 10% CTS™ Immune Cell Serum Replacement.

[00905] In some embodiments, the cell medium in the first and/or second gas permeable container is unfiltered. The use of unfiltered cell medium may simplify the procedures necessary to expand the number of cells. In some embodiments, the cell medium in the first and/or second gas permeable container lacks beta-mercaptoethanol (BME or βME; also known as 2-mercaptoethanol, CAS 60-24-2).

[00906] After preparation of the tumor fragments, the resulting cells (*i.e.*, fragments) are cultured in serum containing IL-2 under conditions that favor the growth of TILs over tumor and other cells. In some embodiments, the tumor digests are incubated in 2 mL wells in media comprising inactivated human AB serum (or, in some cases, as outlined herein, in the presence of an APC cell population) with 6000 IU/mL of IL-2. This primary cell population is cultured for a period of days, generally from 10 to 14 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, the growth media during the first expansion comprises IL-2 or a variant thereof. In some embodiments, the IL is recombinant human IL-2 (rhIL-2). In some embodiments the IL-2 stock solution has a specific activity of $20\text{-}30\times10^6$ IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 20×10^6 IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 25×10^6 IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 30×10^6 IU/mg for a 1 mg vial. In some embodiments, the IL- 2 stock solution has a final concentration of $4\text{-}8\times10^6$ IU/mg of IL-2. In some embodiments, the IL- 2 stock solution has a final concentration of $5\text{-}7\times10^6$ IU/mg of IL-2. In some embodiments, the IL- 2 stock solution has a final concentration of 6×10^6 IU/mg of IL-2. In some embodiments, the IL-2 stock solution is prepare as described in Example 5. In some embodiments, the first expansion culture media comprises about 10,000 IU/mL of IL-2, about 9,000 IU/mL of IL-2, about 8,000 IU/mL of IL-

2, about 7,000 IU/mL of IL-2, about 6000 IU/mL of IL-2 or about 5,000 IU/mL of IL-2. In some embodiments, the first expansion culture media comprises about 9,000 IU/mL of IL-2 to about 5,000 IU/mL of IL-2. In some embodiments, the first expansion culture media comprises about 8,000 IU/mL of IL-2 to about 6,000 IU/mL of IL-2. In some embodiments, the first expansion culture media comprises about 7,000 IU/mL of IL-2 to about 6,000 IU/mL of IL-2. In some embodiments, the first expansion culture media comprises about 6,000 IU/mL of IL-2. In some embodiments, the cell culture medium further comprises IL-2. In some embodiments, the cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the cell culture medium further comprises IL-2. In some embodiments, the cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises about 1000 IU/mL, about 1500 IU/mL, about 2000 IU/mL, about 2500 IU/mL, about 3000 IU/mL, about 3500 IU/mL, about 4000 IU/mL, about 4500 IU/mL, about 5000 IU/mL, about 5500 IU/mL, about 6000 IU/mL, about 6500 IU/mL, about 7000 IU/mL, about 7500 IU/mL, or about 8000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises between 1000 and 2000 IU/mL, between 2000 and 3000 IU/mL, between 3000 and 4000 IU/mL, between 4000 and 5000 IU/mL, between 5000 and 6000 IU/mL, between 6000 and 7000 IU/mL, between 7000 and 8000 IU/mL, or about 8000 IU/mL of IL-2.

[00907] In some embodiments, first expansion culture media comprises about 500 IU/mL of IL-15, about 400 IU/mL of IL-15, about 300 IU/mL of IL-15, about 200 IU/mL of IL-15, about 180 IU/mL of IL-15, about 160 IU/mL of IL-15, about 140 IU/mL of IL-15, about 120 IU/mL of IL-15, or about 100 IU/mL of IL-15. In some embodiments, the first expansion culture media comprises about 500 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the first expansion culture media comprises about 400 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the first expansion culture media comprises about 300 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the first expansion culture media comprises about 200 IU/mL of IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15. In some embodiments, the cell culture medium further comprises IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15.

[00908] In some embodiments, first expansion culture media comprises about 20 IU/mL of IL-21, about 15 IU/mL of IL-21, about 12 IU/mL of IL-21, about 10 IU/mL of IL-21, about 5 IU/mL of IL-21, about 4 IU/mL of IL-21, about 3 IU/mL of IL-21, about 2 IU/mL of IL-21, about 1 IU/mL of IL-21, or about 0.5 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 20 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 15 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 12 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 10 IU/mL

of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 5 IU/mL of IL-21 to about 1 IU/mL of IL-21. In some embodiments, the first expansion culture media comprises about 2 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 0.5 IU/mL of IL-21. In some embodiments, the cell culture medium further comprises IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21.

[00909] In some embodiments, the cell culture medium comprises an anti-CD3 agonist antibody, *e.g.*, OKT-3 antibody. In some embodiments, the cell culture medium comprises about 30 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises about 0.1 ng/mL, about 0.5 ng/mL, about 1 ng/mL, about 2.5 ng/mL, about 5 ng/mL, about 7.5 ng/mL, about 10 ng/mL, about 15 ng/mL, about 20 ng/mL, about 25 ng/mL, about 30 ng/mL, about 35 ng/mL, about 40 ng/mL, about 50 ng/mL, about 60 ng/mL, about 70 ng/mL, about 80 ng/mL, about 90 ng/mL, about 100 ng/mL, about 200 ng/mL, about 500 ng/mL, and about 1 μg/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 0.1 ng/mL and 1 ng/mL, between 1 ng/mL and 5 ng/mL, between 5 ng/mL and 10 ng/mL, between 10 ng/mL and 20 ng/mL, between 20 ng/mL and 30 ng/mL, between 30 ng/mL and 40 ng/mL, between 40 ng/mL and 50 ng/mL, and between 50 ng/mL and 100 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium does not comprise OKT-3 antibody. In some embodiments, the OKT-3 antibody is muromonab. *See*, for example, Table 1.

[00910] In some embodiments, OKT-3 is present in the cell culture medium at the initiation (day 0) of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium at any time during the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 1 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 2 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 3 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 4 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 5 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 6 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 7 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 8 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 9 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 10 of the first expansion. In some embodiments, OKT-3 is added to the cell culture medium on day 11 of the first expansion.

[00911] In some embodiments, OKT-3 is added at one or more times between day 0 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and

day 3 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and day 2 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and day 1 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 1 and day 2 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 1 and day 3 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 2 and day 3 of the first expansion.

[00912] In some embodiments, OKT-3 is added at one or more times between day 1 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 2 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 3 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 4 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 5 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 6 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 7 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 8 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 9 and day 11 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 10 and day 11 of the first expansion.

[00913] In some embodiments, OKT-3 is added at one or more times between day 0 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and day 6 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and day 5 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 0 and day 4 of the first expansion.

[00914] In some embodiments, OKT-3 is added at one or more times between day 1 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 1 and day 6 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 1 and day 5 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 1 and day 4 of the first expansion.

[00915] In some embodiments, OKT-3 is added at one or more times between day 2 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 2 and day 6 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 2 and day 5 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 2 and day 4 of the first expansion.

[00916] In some embodiments, OKT-3 is added at one or more times between day 3 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 3 and day 6 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 3 and day 5 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 3 and day 4 of the first expansion.

[00917] In some embodiments, OKT-3 is added at one or more times between day 4 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 4 and day 6 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 4 and day 5 of the first expansion.

[00918] In some embodiments, OKT-3 is added at one or more times between day 5 and day 7 of the first expansion. In some embodiments, OKT-3 is added at one or more times between day 5 and day 6 of the first expansion.

[00919] In some embodiments, OKT-3 is added at one or more times between day 6 and day 7 of the first expansion.

[00920] In some embodiments, the cell culture medium comprises one or more TNFRSF agonists in a cell culture medium. In some embodiments, the TNFRSF agonist comprises a 4-1BB agonist. In some embodiments, the TNFRSF agonist is a 4-1BB agonist, and the 4-1BB agonist is selected from the group consisting of urelumab, utomilumab, EU-101, a fusion protein, and fragments, derivatives, variants, biosimilars, and combinations thereof. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 0.1 μg/mL and 100 μg/mL. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 20 μg/mL and 40 μg/mL.

[00921] In some embodiments, in addition to one or more TNFRSF agonists, the cell culture medium further comprises IL-2 at an initial concentration of about 3000 IU/mL and OKT-3 antibody at an initial concentration of about 30 ng/mL, and wherein the one or more TNFRSF agonists comprises a 4-1BB agonist.

[00922] In some embodiments, the first expansion culture medium is referred to as "CM", an abbreviation for culture media. In some embodiments, it is referred to as CM1 (culture medium 1). In some embodiments, CM consists of RPMI 1640 with GlutaMAX, supplemented with 10% human AB serum, 25 mM Hepes, and 10 mg/mL gentamicin. In embodiments where cultures are initiated in gas-permeable flasks with a 40 mL capacity and a $10cm^2$ gas-permeable silicon bottom (for example, G-REX10; Wilson Wolf Manufacturing, New Brighton, MN), each flask was loaded with $10–40x10^6$ viable tumor digest cells or 5–30 tumor fragments in 10–40mL of CM with IL-2. Both the G-REX10

and 24-well plates were incubated in a humidified incubator at 37°C in 5% CO_2 and 5 days after culture initiation, half the media was removed and replaced with fresh CM and IL-2 and after day 5, half the media was changed every 2–3 days. In some embodiments, the CM is the CM1 described in the Examples, *see*, Example 1. In some embodiments, the first expansion occurs in an initial cell culture medium or a first cell culture medium. In some embodiments, the initial cell culture medium or the first cell culture medium comprises IL-2.

[00923] In some embodiments, the first expansion (including processes such as for example those described in Step B of Figure 1, which can include those sometimes referred to as the pre-REP) process is shortened to 3-14 days, as discussed in the examples and figures. In some embodiments, the first expansion (including processes such as for example those described in Step B of Figure 1, which can include those sometimes referred to as the pre-REP) is shortened to 7 to 14 days, as discussed in the Examples and shown in Figures 4 and 5, as well as including for example, an expansion as described in Step B of Figure 1. In some embodiments, the first expansion of Step B is shortened to 10-14 days. In some embodiments, the first expansion is shortened to 11 days, as discussed in, for example, an expansion as described in Step B of Figure 1.

[00924] In some embodiments, the first TIL expansion can proceed for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days. In some embodiments, the first TIL expansion can proceed for 1 day to 14 days. In some embodiments, the first TIL expansion can proceed for 2 days to 14 days. In some embodiments, the first TIL expansion can proceed for 3 days to 14 days. In some embodiments, the first TIL expansion can proceed for 4 days to 14 days. In some embodiments, the first TIL expansion can proceed for 5 days to 14 days. In some embodiments, the first TIL expansion can proceed for 6 days to 14 days. In some embodiments, the first TIL expansion can proceed for 7 days to 14 days. In some embodiments, the first TIL expansion can proceed for 8 days to 14 days. In some embodiments, the first TIL expansion can proceed for 9 days to 14 days. In some embodiments, the first TIL expansion can proceed for 10 days to 14 days. In some embodiments, the first TIL expansion can proceed for 11 days to 14 days. In some embodiments, the first TIL expansion can proceed for 12 days to 14 days. In some embodiments, the first TIL expansion can proceed for 13 days to 14 days. In some embodiments, the first TIL expansion can proceed for 14 days. In some embodiments, the first TIL expansion can proceed for 1 day to 11 days. In some embodiments, the first TIL expansion can proceed for 2 days to 11 days. In some embodiments, the first TIL expansion can proceed for 3 days to 11 days. In some embodiments, the first TIL expansion can proceed for 4 days to 11 days. In some embodiments, the first TIL expansion can proceed for 5 days to 11 days. In some embodiments, the first TIL expansion can proceed for 6 days to 11 days. In some embodiments, the first TIL expansion can proceed for 7 days to 11 days. In some embodiments, the first TIL expansion can proceed for 8 days to 11 days. In some embodiments,

the first TIL expansion can proceed for 9 days to 11 days. In some embodiments, the first TIL expansion can proceed for 10 days to 11 days. In some embodiments, the first TIL expansion can proceed for 11 days.

[00925] In some embodiments, a combination of IL-2, IL-7, IL-15, and/or IL-21 are employed as a combination during the first expansion. In some embodiments, IL-2, IL-7, IL-15, and/or IL-21 as well as any combinations thereof can be included during the first expansion, including for example during a Step B processes according to Figure 1, as well as described herein. In some embodiments, a combination of IL-2, IL-15, and IL-21 are employed as a combination during the first expansion. In some embodiments, IL-2, IL-15, and IL-21 as well as any combinations thereof can be included during Step B processes according to Figure 1 and as described herein.

[00926] In some embodiments, the first expansion (including processes referred to as the pre-REP; for example, Step B according to Figure 1) process is shortened to 3 to 14 days, as discussed in the examples and figures. In some embodiments, the first expansion of Step B is shortened to 7 to 14 days. In some embodiments, the first expansion of Step B is shortened to 10 to 14 days. In some embodiments, the first expansion is shortened to 11 days.

[00927] In some embodiments, the first expansion, for example, Step B according to Figure 1, is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX-10 or a G-REX-100. In some embodiments, the closed system bioreactor is a single bioreactor.

1. Cytokines and Other Additives

[00928] The expansion methods described herein generally use culture media with high doses of a cytokine, in particular IL-2, as is known in the art.

Alternatively, using combinations of cytokines for the rapid expansion and or second expansion of TILs is additionally possible, with combinations of two or more of IL-2, IL-15 and IL-21 as is described in U.S. Patent Application Publication No. US 2017/0107490 A1, the disclosure of which is incorporated by reference herein. Thus, possible combinations include IL-2 and IL-15, IL-2 and IL-21, IL-15 and IL-21 and IL-2, or IL-15 and IL-21, with the latter finding particular use in many embodiments. The use of combinations of cytokines specifically favors the generation of lymphocytes, and in particular T-cells as described therein.

[0001] In some embodiments, Step B may also include the addition of OKT-3 antibody or muromonab to the culture media, as described elsewhere herein. In some embodiments, Step B may also include the addition of a 4-1BB agonist to the culture media, as described elsewhere herein. In

some embodiments, Step B may also include the addition of an OX-40 agonist to the culture media, as described elsewhere herein. In other embodiments, additives such as peroxisome proliferator-activated receptor gamma coactivator I-alpha agonists, including proliferator-activated receptor (PPAR)-gamma agonists such as a thiazolidinedione compound, may be used in the culture media during Step B, as described in U.S. Patent Application Publication No. US 2019/0307796 A1, the disclosure of which is incorporated by reference herein.

C. STEP C: First Expansion to Second Expansion Transition

[00929] In some cases, the bulk TIL population obtained from the first expansion, including for example the TIL population obtained from for example, Step B as indicated in Figure 1, can be cryopreserved immediately, using the protocols discussed herein below. Alternatively, the TIL population obtained from the first expansion, referred to as the second TIL population, can be subjected to a second expansion (which can include expansions sometimes referred to as REP) and then cryopreserved as discussed below. Similarly, in the case where genetically modified TILs will be used in therapy, the first TIL population (sometimes referred to as the bulk TIL population) or the second TIL population (which can in some embodiments include populations referred to as the REP TIL populations) can be subjected to genetic modifications for suitable treatments prior to expansion or after the first expansion and prior to the second expansion.

[00930] In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 1) are stored until phenotyped for selection. In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 1) are not stored and proceed directly to the second expansion. In some embodiments, the TILs obtained from the first expansion are not cryopreserved after the first expansion and prior to the second expansion. In some embodiments, the transition from the first expansion to the second expansion occurs at about 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs at about 3 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs at about 4 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs at about 4 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs at about 7 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs at about 14 days from when fragmentation occurs.

[00931] In some embodiments, the transition from the first expansion to the second expansion occurs at 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 1 day to 14 days from when fragmentation occurs. In some embodiments, the first TIL expansion can proceed for 2 days to 14 days. In some embodiments, the transition from the first expansion to the second expansion occurs 3 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 4 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 5 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 6 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 7 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 8 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 9 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 10 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 11 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 12 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 13 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 1 day to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 2 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 3 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 4 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 5 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 6 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 7 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 8 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 9 days to 11 days from when fragmentation occurs. In some embodiments, the

transition from the first expansion to the second expansion occurs 10 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the second expansion occurs 11 days from when fragmentation occurs.

[00932] In some embodiments, the TILs are not stored after the first expansion and prior to the second expansion, and the TILs proceed directly to the second expansion (for example, in some embodiments, there is no storage during the transition from Step B to Step D as shown in Figure 1). In some embodiments, the transition occurs in closed system, as described herein. In some embodiments, the TILs from the first expansion, the second population of TILs, proceeds directly into the second expansion with no transition period.

[00933] In some embodiments, the transition from the first expansion to the second expansion, for example, Step C according to Figure 1, is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX -10 or a G-REX -100. In some embodiments, the closed system bioreactor is a single bioreactor.

[00934] In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 48A-D) are transitioned to an activation or a gene-editing step. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion

to the activation or gene-editing step occurs at about 3 days to 5 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 4 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 5 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 14 days from when fragmentation

occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 7 days from when fragmentation occurs.

[00935] In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs in a closed system, as described herein.

[00936] In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 and/or anti-CD38 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD38 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 and anti-CD38 beads for about 1-7 days. In some embodiments, the activation step is performed for about 1-7 days. In some embodiments, the activation step is performed for about 1-7 days, about 2-7 days, about 3-7 days, about 4-7 days, about 5-7 days, about 6-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, or about 1-2 days. In some embodiments, the activation step is performed for about 1 day. In some embodiments, the activation step is performed for about 2 days. In some embodiments, the activation step is performed for about 3 days. In some embodiments, the activation step is performed for about 4 days. In some embodiments, the activation step is performed for about 5 days. In some embodiments, the activation step is performed for about 6 days. In some embodiments, the activation step is performed for about 7 days.

[00937] Any suitable anti-CD3/anti-CD38 beads known to those in the art in view of the instant specification can be used. Suitable anti-CD3/anti-CD38 beads include, but are not limited to, commercially available products including, but not limited to, Dynabeads™ Human T-Activator CD3/CD28 for T Cell Expansion and Activation (available commercially from Invitrogen),

ImmunoCult™ Human CD3/CD28 T Cell Activator (available commercially from StemCell Technologies), and T Cell TransAct™ (available commercially from Miltenyi Biotec).

[00938] In some embodiments, the activation step is optional. In some embodiments, the activation step is optional if the first expansion included OKT-3.

[00939] In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 48C-D) or from the activation step (for example, from Step C as indicated in Figure 48A-B) are transitioned to a gene-editing step.

[00940] In some embodiments, the gene-editing step comprises performing a sterile electroporation step on the population of TILs. In some embodiments, the sterile electroporation step mediates the transfer of at least one gene editor. According to some embodiments, the gene editor is a TALE nuclease system for modulating the expression of at least one protein. According to some embodiments, the TALE nuclease system downmodulates expression of PD-1. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CTLA-4. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of LAG-3. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CISH. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of TIGIT. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CBL-B. According to some embodiments, the resulting TILs are PD-1 knockout TILs. According to some embodiments, the resulting TILs are CTLA-4 knockout TILs. According to some embodiments, the resulting TILs are LAG-3 knockout TILs. According to some embodiments, the resulting TILs are CISH knockout TILs. According to some embodiments, the resulting TILs are CBL-B knockout TILs. According to some embodiments, the resulting TILs are TIGIT knockout TILs. According to some embodiments, the resulting TILs exhibit downmodulated expression of PD-1 and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CTLA-4 and downmodulated expression of one or more of PD-1, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of LAG-3 and downmodulated expression of one or more of PD-1, CTLA-4, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CISH and downmodulated expression of one or more of PD-1, LAG-3, CTLA-4, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CBL-B and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and PD-1. According to some embodiments, the resulting TILs exhibit downmodulated expression of TIGIT and downmodulated expression of one or more of CTLA-4,

LAG-3, CISH, CBL-B and PD-1. According to some embodiments, the resulting TILs are PD-1/CTLA-4 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CISH double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are PD-1/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CISH double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CISH double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CISH/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CISH/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CBL-B/TIGIT double knockout TILs.

[00941] In some embodiments, the step of gene-editing further comprises a resting step. According to some embodiments, the resting step comprises incubating the fourth population of TILs at about 30-40 °C with about 5% CO2. According to some embodiments, the resting step is carried out at about 30°C, about 30.5°C, about 31°C, about 31.5°C, about 32°C, about 32.5°C, about 33°C, about 33.5°C, about 34°C, about 34.5°C, about 35°C, about 35.5°C, about 36°C, about 36.5°C, about 37°C, about 37.5°C, about 38°C, about 38.5°C, about 39°C, about 39.5°C, about 40°C. According to some embodiments, the resting step is carried out for about 1 hour, about 2 hours, about 3 hours, about 4 hours, about 5 hours, about 6 hours, about 7 hours, about 8 hours, about 9 hours, about 10 hours, about 11 hours, about 12 hours, about 13 hours, about 14 hours, about 15 hours, about 16 hours, about 17 hours, about 18 hours, about 19 hours, about 20 hours, about 21 hours, about 22 hours, about 23 hours, about 24 hours. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 16 hours at about 30°C. According to some

embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 17 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 18 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 19 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 20 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 21 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 22 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 23 hours at about 30°C.

[00942] In some embodiments, the TILs obtained from the gene-editing step or the resting step (for example, from Step C as indicated in Figure 48A-D) are transitioned to a second expansion step (for example, from Step D as indicated in Figure 48A-D). In some embodiments, the transition from the gene-editing step or the resting step to the second expansion step occurs at about 0.5 days, 1 day, 2 days, 3 days, or 4 days from the gene-editing step or the resting step.

[00943] In some embodiments, the transition from the gene-editing step or the resting step to the second expansion step occurs in a closed system, as described herein.

[00944] In some embodiments, the TILs are not stored after the gene-editing step or the resting step and prior to the second expansion, and the TILs proceed directly to the second expansion (for example, in some embodiments, there is no storage during the transition from Step C to Step D as shown in Figure 48A-D).

[00945] In some embodiments, the transition from the first expansion to the second expansion, for example, Step C according to Figure 48, is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX-10 or a G-REX-100 bioreactor.

D. STEP D: Second Expansion

[00946] In some embodiments, the TIL cell population is expanded in number after harvest and initial bulk processing for example, after Step A and Step B, and the transition referred to as Step C, as indicated in Figure 1). This further expansion is referred to herein as the second expansion, which can include expansion processes generally referred to in the art as a rapid expansion process (REP; as well as processes as indicated in Step D of Figure 1). The second expansion is generally accomplished using a culture media comprising a number of components, including feeder cells, a cytokine source, and an anti-CD3 antibody, in a gas-permeable container.

[00947] In some embodiments, the second expansion or second TIL expansion (which can include expansions sometimes referred to as REP; as well as processes as indicated in Step D of Figure 1) of TIL can be performed using any TIL flasks or containers known by those of skill in the art. In some embodiments, the second TIL expansion can proceed for 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days. In some embodiments, the second TIL expansion can proceed for about 7 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 8 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 9 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 10 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 11 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 12 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 13 days to about 14 days. In some embodiments, the second TIL expansion can proceed for about 14 days.

[00948] In some embodiments, the second expansion can be performed in a gas permeable container using the methods of the present disclosure (including for example, expansions referred to as REP; as well as processes as indicated in Step D of Figure 1). For example, TILs can be rapidly expanded using non-specific T-cell receptor stimulation in the presence of interleukin-2 (IL-2) or interleukin-15 (IL-15). The non-specific T-cell receptor stimulus can include, for example, an anti-CD3 antibody, such as about 30 ng/mL of OKT3, a mouse monoclonal anti-CD3 antibody (commercially available from Ortho-McNeil, Raritan, NJ or Miltenyi Biotech, Auburn, CA) or UHCT-1 (commercially available from BioLegend, San Diego, CA, USA). TILs can be expanded to induce further stimulation of the TILs *in vitro* by including one or more antigens during the second expansion, including antigenic portions thereof, such as epitope(s), of the cancer, which can be optionally expressed from a vector, such as a human leukocyte antigen A2 (HLA-A2) binding peptide, *e.g.*, 0.3 μM MART-1 :26-35 (27 L) or gpl 00:209-217 (210M), optionally in the presence of a T-cell growth factor, such as 300 IU/mL IL-2 or IL-15. Other suitable antigens may include, *e.g.*, NY-ESO-1, TRP-1, TRP-2, tyrosinase cancer antigen, MAGE-A3, SSX-2, and VEGFR2, or antigenic portions thereof. TIL may also be rapidly expanded by re-stimulation with the same antigen(s) of the cancer pulsed onto HLA-A2-expressing antigen-presenting cells. Alternatively, the TILs can be further re-stimulated with, *e.g.*,

example, irradiated, autologous lymphocytes or with irradiated HLA-A2+ allogeneic lymphocytes and IL-2. In some embodiments, the re-stimulation occurs as part of the second expansion. In some embodiments, the second expansion occurs in the presence of irradiated, autologous lymphocytes or with irradiated HLA-A2+ allogeneic lymphocytes and IL-2.

[00949] In some embodiments, the cell culture medium further comprises IL-2. In some embodiments, the cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises about 1000 IU/mL, about 1500 IU/mL, about 2000 IU/mL, about 2500 IU/mL, about 3000 IU/mL, about 3500 IU/mL, about 4000 IU/mL, about 4500 IU/mL, about 5000 IU/mL, about 5500 IU/mL, about 6000 IU/mL, about 6500 IU/mL, about 7000 IU/mL, about 7500 IU/mL, or about 8000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises between 1000 and 2000 IU/mL, between 2000 and 3000 IU/mL, between 3000 and 4000 IU/mL, between 4000 and 5000 IU/mL, between 5000 and 6000 IU/mL, between 6000 and 7000 IU/mL, between 7000 and 8000 IU/mL, or between 8000 IU/mL of IL-2.

[00950] In some embodiments, the cell culture medium comprises OKT-3 antibody. In some embodiments, the cell culture medium comprises about 30 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises about 0.1 ng/mL, about 0.5 ng/mL, about 1 ng/mL, about 2.5 ng/mL, about 5 ng/mL, about 7.5 ng/mL, about 10 ng/mL, about 15 ng/mL, about 20 ng/mL, about 25 ng/mL, about 30 ng/mL, about 35 ng/mL, about 40 ng/mL, about 50 ng/mL, about 60 ng/mL, about 70 ng/mL, about 80 ng/mL, about 90 ng/mL, about 100 ng/mL, about 200 ng/mL, about 500 ng/mL, and about 1 µg/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 0.1 ng/mL and 1 ng/mL, between 1 ng/mL and 5 ng/mL, between 5 ng/mL and 10 ng/mL, between 10 ng/mL and 20 ng/mL, between 20 ng/mL and 30 ng/mL, between 30 ng/mL and 40 ng/mL, between 40 ng/mL and 50 ng/mL, and between 50 ng/mL and 100 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium does not comprise OKT-3 antibody. In some embodiments, the OKT-3 antibody is muromonab.

[00951] In some embodiments, the cell culture medium comprises one or more TNFRSF agonists in a cell culture medium. In some embodiments, the TNFRSF agonist comprises a 4-1BB agonist. In some embodiments, the TNFRSF agonist is a 4-1BB agonist, and the 4-1BB agonist is selected from the group consisting of urelumab, utomilumab, EU-101, a fusion protein, and fragments, derivatives, variants, biosimilars, and combinations thereof. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 0.1 µg/mL and 100 µg/mL. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 20 µg/mL and 40 µg/mL.

[00952] In some embodiments, in addition to one or more TNFRSF agonists, the cell culture medium further comprises IL-2 at an initial concentration of about 3000 IU/mL and OKT-3 antibody at an initial concentration of about 30 ng/mL, and wherein the one or more TNFRSF agonists comprises a 4-1BB agonist.

[00953] In some embodiments, a combination of IL-2, IL-7, IL-15, and/or IL-21 are employed as a combination during the second expansion. In some embodiments, IL-2, IL-7, IL-15, and/or IL-21 as well as any combinations thereof can be included during the second expansion, including for example during a Step D processes according to Figure 1, as well as described herein. In some embodiments, a combination of IL-2, IL-15, and IL-21 are employed as a combination during the second expansion. In some embodiments, IL-2, IL-15, and IL-21 as well as any combinations thereof can be included during Step D processes according to Figure 1 and as described herein.

[00954] In some embodiments, the second expansion can be conducted in a supplemented cell culture medium comprising IL-2, OKT-3, antigen-presenting feeder cells, and optionally a TNFRSF agonist. In some embodiments, the second expansion occurs in a supplemented cell culture medium. In some embodiments, the supplemented cell culture medium comprises IL-2, OKT-3, and antigen-presenting feeder cells. In some embodiments, the second cell culture medium comprises IL-2, OKT-3, and antigen-presenting cells (APCs; also referred to as antigen-presenting feeder cells). In some embodiments, the second expansion occurs in a cell culture medium comprising IL-2, OKT-3, and antigen-presenting feeder cells (*i.e.*, antigen presenting cells).

[00955] In some embodiments, the second expansion culture media comprises about 500 IU/mL of IL-15, about 400 IU/mL of IL-15, about 300 IU/mL of IL-15, about 200 IU/mL of IL-15, about 180 IU/mL of IL-15, about 160 IU/mL of IL-15, about 140 IU/mL of IL-15, about 120 IU/mL of IL-15, or about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 500 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 400 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 300 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 200 IU/mL of IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15. In some embodiments, the cell culture medium further comprises IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15.

[00956] In some embodiments, the second expansion culture media comprises about 20 IU/mL of IL-21, about 15 IU/mL of IL-21, about 12 IU/mL of IL-21, about 10 IU/mL of IL-21, about 5 IU/mL of IL-21, about 4 IU/mL of IL-21, about 3 IU/mL of IL-21, about 2 IU/mL of IL-21, about 1 IU/mL of IL-21, or about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media

comprises about 20 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 15 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 12 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 10 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 5 IU/mL of IL-21 to about 1 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 2 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 0.5 IU/mL of IL-21. In some embodiments, the cell culture medium further comprises IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21.

[00957] In some embodiments the antigen-presenting feeder cells (APCs) are PBMCs. In some embodiments, the ratio of TILs to PBMCs and/or antigen-presenting cells in the rapid expansion and/or the second expansion is about 1 to 25, about 1 to 50, about 1 to 100, about 1 to 125, about 1 to 150, about 1 to 175, about 1 to 200, about 1 to 225, about 1 to 250, about 1 to 275, about 1 to 300, about 1 to 325, about 1 to 350, about 1 to 375, about 1 to 400, or about 1 to 500. In some embodiments, the ratio of TILs to PBMCs in the rapid expansion and/or the second expansion is between 1 to 50 and 1 to 300. In some embodiments, the ratio of TILs to PBMCs in the rapid expansion and/or the second expansion is between 1 to 100 and 1 to 200.

[00958] In some embodiments, REP and/or the second expansion is performed in flasks with the bulk TILs being mixed with a 100- or 200-fold excess of inactivated feeder cells, 30 mg/mL OKT3 anti-CD3 antibody and 3000 IU/mL IL-2 in 150 mL media. Media replacement is done (generally 2/3 media replacement via respiration with fresh media) until the cells are transferred to an alternative growth chamber. Alternative growth chambers include G-REX flasks and gas permeable containers as more fully discussed below.

[00959] In some embodiments, the second expansion (which can include processes referred to as the REP process) is shortened to 7-14 days, as discussed in the examples and figures. In some embodiments, the second expansion is shortened to 11 days.

[00960] In some embodiments, REP and/or the second expansion may be performed using T-175 flasks and gas permeable bags as previously described (Tran, *et al.*, *J. Immunother.* **2008,** *31,* 742-51; Dudley, *et al.*, *J. Immunother.* **2003,** *26,* 332-42) or gas permeable cultureware (G-REX flasks). In some embodiments, the second expansion (including expansions referred to as rapid expansions) is performed in T-175 flasks, and about 1×10^6 TILs suspended in 150 mL of media may be added to each T-175 flask. The TILs may be cultured in a 1 to 1 mixture of CM and AIM-V medium, supplemented with 3000 IU per mL of IL-2 and 30 ng per mL of anti-CD3. The T-175 flasks may be

incubated at 37° C in 5% CO_2. Half the media may be exchanged on day 5 using 50/50 medium with 3000 IU per mL of IL-2. In some embodiments, on day 7 cells from two T-175 flasks may be combined in a 3 L bag and 300 mL of AIM V with 5% human AB serum and 3000 IU per mL of IL-2 was added to the 300 mL of TIL suspension. The number of cells in each bag was counted every day or two and fresh media was added to keep the cell count between 0.5 and 2.0 × 10^6 cells/mL.

[00961] In some embodiments, the second expansion (which can include expansions referred to as REP, as well as those referred to in Step D of Figure 1) may be performed in 500 mL capacity gas permeable flasks with 100 cm gas-permeable silicon bottoms (G-REX 100, commercially available from Wilson Wolf Manufacturing Corporation, New Brighton, MN, USA), 5 × 10^6 or 10 × 10^6 TIL may be cultured with PBMCs in 400 mL of 50/50 medium, supplemented with 5% human AB serum, 3000 IU per mL of IL-2 and 30 ng per mL of anti-CD3 (OKT3). The G-REX 100 flasks may be incubated at 37°C in 5% CO_2. On day 5, 250 mL of supernatant may be removed and placed into centrifuge bottles and centrifuged at 1500 rpm (491 × g) for 10 minutes. The TIL pellets may be re-suspended with 150 mL of fresh medium with 5% human AB serum, 3000 IU per mL of IL-2, and added back to the original G-REX 100 flasks. When TIL are expanded serially in G-REX 100 flasks, on day 7 the TIL in each G-REX 100 may be suspended in the 300 mL of media present in each flask and the cell suspension may be divided into 3 100 mL aliquots that may be used to seed 3 G-REX 100 flasks. Then 150 mL of AIM-V with 5% human AB serum and 3000 IU per mL of IL-2 may be added to each flask. The G-REX 100 flasks may be incubated at 37° C in 5% CO_2 and after 4 days 150 mL of AIM-V with 3000 IU per mL of IL-2 may be added to each G-REX 100 flask. The cells may be harvested on day 14 of culture.

[00962] In some embodiments, the second expansion (including expansions referred to as REP) is performed in flasks with the bulk TILs being mixed with a 100- or 200-fold excess of inactivated feeder cells, 30 mg/mL OKT3 anti-CD3 antibody and 3000 IU/mL IL-2 in 150 mL media. In some embodiments, media replacement is done until the cells are transferred to an alternative growth chamber. In some embodiments, 2/3 of the media is replaced by respiration with fresh media. In some embodiments, alternative growth chambers include G-REX flasks and gas permeable containers as more fully discussed below.

[00963] In some embodiments, the second expansion (including expansions referred to as REP) is performed and further comprises a step wherein TILs are selected for superior tumor reactivity. Any selection method known in the art may be used. For example, the methods described in U.S. Patent Application Publication No. 2016/0010058 A1, the disclosures of which are incorporated herein by reference, may be used for selection of TILs for superior tumor reactivity.

[00964] Optionally, a cell viability assay can be performed after the second expansion (including expansions referred to as the REP expansion), using standard assays known in the art. For example, a trypan blue exclusion assay can be done on a sample of the bulk TILs, which selectively labels dead cells and allows a viability assessment. In some embodiments, TIL samples can be counted and viability determined using a Cellometer K2 automated cell counter (Nexcelom Bioscience, Lawrence, MA). In some embodiments, viability is determined according to the standard Cellometer K2 Image Cytometer Automatic Cell Counter protocol.

[00965] In some embodiments, the second expansion (including expansions referred to as REP) of TIL can be performed using T-175 flasks and gas-permeable bags as previously described (Tran, *et al.*, **2008**, *J Immunother.*, 31:742–751, and Dudley, *et al.*, 2003, *J Immunother.*, 26:332–342) or gas-permeable G-REX flasks. In some embodiments, the second expansion is performed using flasks. In some embodiments, the second expansion is performed using gas-permeable G-REX flasks. In some embodiments, the second expansion is performed in T-175 flasks, and about 1×10^6 TIL are suspended in about 150 mL of media and this is added to each T-175 flask. The TIL are cultured with irradiated (50 Gy) allogeneic PBMC as "feeder" cells at a ratio of 1 to 100 and the cells were cultured in a 1 to 1 mixture of CM and AIM-V medium (50/50 medium), supplemented with 3000 IU/mL of IL-2 and 30 ng/mL of anti-CD3. The T-175 flasks are incubated at 37°C in 5% CO_2. In some embodiments, half the media is changed on day 5 using 50/50 medium with 3000 IU/mL of IL-2. In some embodiments, on day 7, cells from 2 T-175 flasks are combined in a 3 L bag and 300 mL of AIM-V with 5% human AB serum and 3000 IU/mL of IL-2 is added to the 300 mL of TIL suspension. The number of cells in each bag can be counted every day or two and fresh media can be added to keep the cell count between about 0.5 and about 2.0×10^6 cells/mL.

[00966] In some embodiments, the second expansion (including expansions referred to as REP) are performed in 500 mL capacity flasks with 100 cm^2 gas-permeable silicon bottoms (G-REX 100, Wilson Wolf), about 5×10^6 or 10×10^6 TIL are cultured with irradiated allogeneic PBMC at a ratio of 1 to 100 in 400 mL of 50/50 medium, supplemented with 3000 IU/mL of IL-2 and 30 ng/ mL of anti-CD3. The G-REX 100 flasks are incubated at 37°C in 5% CO_2. In some embodiments, on day 5, 250mL of supernatant is removed and placed into centrifuge bottles and centrifuged at 1500 rpm (491g) for 10 minutes. The TIL pellets can then be resuspended with 150 mL of fresh 50/50 medium with 3000 IU/ mL of IL-2 and added back to the original G-REX 100 flasks. In embodiments where TILs are expanded serially in G-REX 100 flasks, on day 7 the TIL in each G-REX 100 are suspended in the 300 mL of media present in each flask and the cell suspension was divided into three 100 mL aliquots that are used to seed 3 G-REX 100 flasks. Then 150 mL of AIM-V with 5% human AB serum and 3000 IU/mL of IL-2 is added to each flask. The G-REX 100 flasks are incubated at 37°C in

5% CO_2 and after 4 days 150 mL of AIM-V with 3000 IU/mL of IL-2 is added to each G-REX 100 flask. The cells are harvested on day 14 of culture.

[00967] The diverse antigen receptors of T and B lymphocytes are produced by somatic recombination of a limited, but large number of gene segments. These gene segments: V (variable), D (diversity), J (joining), and C (constant), determine the binding specificity and downstream applications of immunoglobulins and T-cell receptors (TCRs). The present invention provides a method for generating TILs which exhibit and increase the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity. In some embodiments, the TILs obtained in the second expansion exhibit an increase in the T-cell repertoire diversity. In some embodiments, the increase in diversity is an increase in the immunoglobulin diversity and/or the T-cell receptor diversity. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin heavy chain. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin light chain. In some embodiments, the diversity is in the T-cell receptor. In some embodiments, the diversity is in one of the T-cell receptors selected from the group consisting of alpha, beta, gamma, and delta receptors. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha and/or beta. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) beta. In some embodiments, there is an increase in the expression of TCRab (*i.e.*, TCRα/β).

[00968] In some embodiments, the second expansion culture medium (*e.g.*, sometimes referred to as CM2 or the second cell culture medium), comprises IL-2, OKT-3, as well as the antigen-presenting feeder cells (APCs), as discussed in more detail below.

[00969] In some embodiments, the culture medium used in the expansion processes disclosed herein is a serum-free medium or a defined medium. In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or a serum replacement. In some embodiments, the serum-free or defined medium is used to prevent and/or decrease experimental variation due in part to the lot-to-lot variation of serum-containing media.

[00970] In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or serum replacement. In some embodiments, the basal cell medium includes, but is not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium , CTS™ OpTmizer™ T-Cell Expansion SFM, CTS™ AIM-V Medium, CTS™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential

Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00971] In some embodiments, the serum supplement or serum replacement includes, but is not limited to one or more of CTS™ OpTmizer T-Cell Expansion Serum Supplement, CTS™ Immune Cell Serum Replacement, one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more antibiotics, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L- histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or 2-mercaptoethanol.

[00972] In some embodiments, the CTS™OpTmizer™ T-cell Immune Cell Serum Replacement is used with conventional growth media, including but not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium, CTS™ OpTmizer™ T-cell Expansion SFM, CTS™ AIM-V Medium, CST™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00973] In some embodiments, the total serum replacement concentration (vol%) in the serum-free or defined medium is from about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, or 20% by volume of the total serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 3% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 5% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 10% of the total volume of the serum-free or defined medium.

[00974] In some embodiments, the serum-free or defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-

cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific). In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55μM.

[00975] In some embodiments, the defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine,

and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55µM.

[00976] In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of from about 0.1mM to about 10mM, 0.5mM to about 9mM, 1mM to about 8mM, 2mM to about 7mM, 3mM to about 6mM, or 4mM to about 5 mM. In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of about 2mM.

[00977] In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of from about 5mM to about 150mM, 10mM to about 140mM, 15mM to about 130mM, 20mM to about 120mM, 25mM to about 110mM, 30mM to about 100mM, 35mM to about 95mM, 40mM to about 90mM, 45mM to about 85mM, 50mM to about 80mM, 55mM to about 75mM, 60mM to about 70mM, or about 65mM. In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of about 55mM. In some embodiments, the final concentration of 2-mercaptoethanol in the media is 55µM.

[00978] In some embodiments, the defined media described in International PCT Publication No. WO/1998/030679, which is herein incorporated by reference, are useful in the present invention. In that publication, serum-free eukaryotic cell culture media are described. The serum-free, eukaryotic cell culture medium includes a basal cell culture medium supplemented with a serum-free supplement capable of supporting the growth of cells in serum- free culture. The serum-free eukaryotic cell culture medium supplement comprises or is obtained by combining one or more ingredients selected from the group consisting of one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more trace elements, and one or more antibiotics. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or beta-mercaptoethanol. In some embodiments, the defined medium comprises an albumin or an albumin substitute and one or more ingredients selected from group consisting of one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or

more collagen precursors, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L-histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the basal cell media is selected from the group consisting of Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[00979] In some embodiments, the concentration of glycine in the defined medium is in the range of from about 5-200 mg/L, the concentration of L- histidine is about 5-250 mg/L, the concentration of L-isoleucine is about 5-300 mg/L, the concentration of L-methionine is about 5-200 mg/L, the concentration of L-phenylalanine is about 5-400 mg/L, the concentration of L-proline is about 1-1000 mg/L, the concentration of L- hydroxyproline is about 1-45 mg/L, the concentration of L-serine is about 1-250 mg/L, the concentration of L-threonine is about 10-500 mg/L, the concentration of L-tryptophan is about 2-110 mg/L, the concentration of L-tyrosine is about 3-175 mg/L, the concentration of L-valine is about 5-500 mg/L, the concentration of thiamine is about 1-20 mg/L, the concentration of reduced glutathione is about 1-20 mg/L, the concentration of L-ascorbic acid-2-phosphate is about 1-200 mg/L, the concentration of iron saturated transferrin is about 1-50 mg/L, the concentration of insulin is about 1-100 mg/L, the concentration of sodium selenite is about 0.000001-0.0001 mg/L, and the concentration of albumin (*e.g.*, AlbuMAX® I) is about 5000-50,000 mg/L.

[00980] In some embodiments, the non-trace element moiety ingredients in the defined medium are present in the concentration ranges listed in the column under the heading "Concentration Range in 1X Medium" in Table 4. In other embodiments, the non-trace element moiety ingredients in the defined medium are present in the final concentrations listed in the column under the heading "A Preferred Embodiment of the 1X Medium" in Table 4. In other embodiments, the defined medium is a basal cell medium comprising a serum free supplement. In some of these embodiments, the serum free supplement comprises non-trace moiety ingredients of the type and in the concentrations listed in the column under the heading "A Preferred Embodiment in Supplement" in Table 4.

[00981] In some embodiments, the osmolarity of the defined medium is between about 260 and 350 mOsmol. In some embodiments, the osmolarity is between about 280 and 310 mOsmol. In some embodiments, the defined medium is supplemented with up to about 3.7 g/L, or about 2.2 g/L sodium bicarbonate. The defined medium can be further supplemented with L-glutamine (final concentration

of about 2 mM), one or more antibiotics, non-essential amino acids (NEAA; final concentration of about 100 μM), 2-mercaptoethanol (final concentration of about 100 μM).

[00982] In some embodiments, the defined media described in Smith, *et al.*, *Clin Transl Immunology*, 4(1) 2015 (doi: 10.1038/cti.2014.31) are useful in the present invention. Briefly, RPMI or CTS™ OpTmizer™ was used as the basal cell medium, and supplemented with either 0, 2%, 5%, or 10% CTS™ Immune Cell Serum Replacement.

[00983] In some embodiments, the cell medium in the first and/or second gas permeable container is unfiltered. The use of unfiltered cell medium may simplify the procedures necessary to expand the number of cells. In some embodiments, the cell medium in the first and/or second gas permeable container lacks beta-mercaptoethanol (BME or βME; also known as 2-mercaptoethanol, CAS 60-24-2).

[00984] In some embodiments, the second expansion, for example, Step D according to Figure 1, is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX -10 or a G-REX -100. In some embodiments, the closed system bioreactor is a single bioreactor.

[00985] In some embodiments, the step of rapid or second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (a) performing the rapid or second expansion by culturing TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer of the TILs in the small scale culture to a second container larger than the first container, *e.g.*, a G-REX-500-MCS container, and culturing the TILs from the small scale culture in a larger scale culture in the second container for a period of about 4 to 7 days.

[00986] In some embodiments, the step of rapid or second expansion is split into a plurality of steps to achieve a scaling out of the culture by: (a) performing the rapid or second expansion by culturing TILs in a first small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer and apportioning of the TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the TILs from first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days.

[00987] In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations of TILs.

[00988] In some embodiments, the step of rapid or second expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid or second expansion by culturing TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer and apportioning of the TILs from the small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX-500MCS containers, wherein in each second container the portion of the TILs from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 4 to 7 days.

[00989] In some embodiments, the step of rapid or second expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid or second expansion by culturing TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 5 days, and then (b) effecting the transfer and apportioning of the TILs from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX-500 MCS containers, wherein in each second container the portion of the TILs from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 6 days.

[00990] In some embodiments, upon the splitting of the rapid or second expansion, each second container comprises at least 10^8 TILs. In some embodiments, upon the splitting of the rapid or second expansion, each second container comprises at least 10^8 TILs, at least 10^9 TILs, or at least 10^{10} TILs. In one exemplary embodiment, each second container comprises at least 10^{10} TILs.

[00991] In some embodiments, the first small scale TIL culture is apportioned into a plurality of subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2, 3, 4, or 5 subpopulations.

[00992] In some embodiments, after the completion of the rapid or second expansion, the plurality of subpopulations comprises a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid or second expansion, one or more subpopulations of TILs are pooled together to produce a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid expansion, each subpopulation of TILs comprises a therapeutically effective amount of TILs.

[00993] In some embodiments, the rapid or second expansion is performed for a period of about 3 to 7 days before being split into a plurality of steps. In some embodiments, the splitting of the

rapid or second expansion occurs at about day 3, day 4, day 5, day 6, or day 7 after the initiation of the rapid or second expansion.

[00994] In some embodiments, the splitting of the rapid or second expansion occurs at about day 7, day 8, day 9, day 10, day 11, day 12, day 13, day 14, day 15, or day 16 day 17, or day 18 after the initiation of the first expansion (*i.e.*, pre-REP expansion). In one exemplary embodiment, the splitting of the rapid or second expansion occurs at about day 16 after the initiation of the first expansion.

[00995] In some embodiments, the rapid or second expansion is further performed for a period of about 7 to 11 days after the splitting. In some embodiments, the rapid or second expansion is further performed for a period of about 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, or 11 days after the splitting.

[00996] In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting comprises the same components as the cell culture medium used for the rapid or second expansion after the splitting. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting comprises different components from the cell culture medium used for the rapid or second expansion after the splitting.

[00997] In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting comprises IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting comprises IL-2, OKT-3, and further optionally APCs. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting comprises IL-2, OKT-3 and APCs.

[00998] In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, OKT-3 and APCs. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid or second expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, OKT-3 and APCs.

[00999] In some embodiments, the cell culture medium used for the rapid or second expansion after the splitting comprises IL-2, and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid or second expansion after the splitting comprises IL-2, and OKT-3. In some embodiments, the cell culture medium used for the rapid or second expansion after the splitting is generated by replacing the cell culture medium used for the rapid or second expansion before the splitting with fresh culture medium comprising IL-2 and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid or second expansion after the splitting is generated by replacing the cell culture medium used for the rapid or second expansion before the splitting with fresh culture medium comprising IL-2 and OKT-3.

[001000] In some embodiments, the splitting of the rapid expansion occurs in a closed system.

[001001] In some embodiments, the scaling up of the TIL culture during the rapid or second expansion comprises adding fresh cell culture medium to the TIL culture (also referred to as feeding the TILs). In some embodiments, the feeding comprises adding fresh cell culture medium to the TIL culture frequently. In some embodiments, the feeding comprises adding fresh cell culture medium to the TIL culture at a regular interval. In some embodiments, the fresh cell culture medium is supplied to the TILs via a constant flow. In some embodiments, an automated cell expansion system such as Xuri W25 is used for the rapid expansion and feeding.

1. Feeder Cells and Antigen Presenting Cells

[001002] In some embodiments, the second expansion procedures described herein (for example including expansion such as those described in Step D from Figure 1, as well as those referred to as REP) require an excess of feeder cells during REP TIL expansion and/or during the second expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation.

[001003] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the REP procedures, as described in the examples, which provides an exemplary protocol for evaluating the replication incompetence of irradiate allogeneic PBMCs.

[001004] In some embodiments, PBMCs are considered replication incompetent and accepted for use in the TIL expansion procedures described herein if the total number of viable cells on day 14 is less than the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion).

[001005] In some embodiments, PBMCs are considered replication incompetent and accepted for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in the

presence of OKT3 and IL-2, on day 7 and day 14 has not increased from the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion). In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 3000 IU/mL IL-2.

[001006] In some embodiments, PBMCs are considered replication incompetent and accepted for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in the presence of OKT3 and IL-2, on day 7 and day 14 has not increased from the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion). In some embodiments, the PBMCs are cultured in the presence of 5-60 ng/mL OKT3 antibody and 1000-6000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 10-50 ng/mL OKT3 antibody and 2000-5000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 20-40 ng/mL OKT3 antibody and 2000-4000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 25-35 ng/mL OKT3 antibody and 2500-3500 IU/mL IL-2.

[001007] In some embodiments, the antigen-presenting feeder cells are PBMCs. In some embodiments, the antigen-presenting feeder cells are artificial antigen-presenting feeder cells. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is about 1 to 25, about 1 to 50, about 1 to 100, about 1 to 125, about 1 to 150, about 1 to 175, about 1 to 200, about 1 to 225, about 1 to 250, about 1 to 275, about 1 to 300, about 1 to 325, about 1 to 350, about 1 to 375, about 1 to 400, or about 1 to 500. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is between 1 to 50 and 1 to 300. In some embodiments, the ratio of TIL to antigen-presenting feeder cells in the second expansion is between 1 to 100 and 1 to 200.

[001008] In some embodiments, the second expansion procedures described herein require a ratio of about $2.5x10^9$ feeder cells to about $100x10^6$ TIL. In some embodiments, the second expansion procedures described herein require a ratio of about $2.5x10^9$ feeder cells to about $50x10^6$ TIL. In yet another embodiment, the second expansion procedures described herein require about $2.5x10^9$ feeder cells to about $25x10^6$ TIL.

[001009] In some embodiments, the second expansion procedures described herein require an excess of feeder cells during the second expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation. In some embodiments, artificial antigen-presenting (aAPC) cells are used in place of PBMCs.

[001010] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the TIL expansion procedures described herein, including the exemplary procedures described in the figures and examples.

[001011] In some embodiments, artificial antigen presenting cells are used in the second expansion as a replacement for, or in combination with, PBMCs.

2. Cytokines

[001012] The expansion methods described herein generally use culture media with high doses of a cytokine, in particular IL-2, as is known in the art.

[001013] Alternatively, using combinations of cytokines for the rapid expansion and or second expansion of TILs is additionally possible, with combinations of two or more of IL-2, IL-15 and IL-21 as is described in U.S. Patent Application US 2017/0107490 A1, the disclosure of which is incorporated by reference herein. Thus, possible combinations include IL-2 and IL-15, IL-2 and IL-21, IL-15 and IL-21 and IL-2, IL-15 and IL-21, with the latter finding particular use in many embodiments. The use of combinations of cytokines specifically favors the generation of lymphocytes, and in particular T-cells as described therein.

[001014] In some embodiments, Step D may also include the addition of OKT-3 antibody or muromonab to the culture media, as described elsewhere herein. In some embodiments, Step D may also include the addition of a 4-1BB agonist to the culture media, as described elsewhere herein. In some embodiments, Step D may also include the addition of an OX-40 agonist to the culture media, as described elsewhere herein. In addition, additives such as peroxisome proliferator-activated receptor gamma coactivator I-alpha agonists, including proliferator-activated receptor (PPAR)-gamma agonists such as a thiazolidinedione compound, may be used in the culture media during Step D, as described in U.S. Patent Application Publication No. US 2019/0307796 A1, the disclosure of which is incorporated by reference herein.

E. STEP E: Harvest TILs

[001015] After the second expansion step, cells can be harvested. In some embodiments the TILs are harvested after one, two, three, four or more expansion steps, for example as provided in Figure 1. In some embodiments the TILs are harvested after two expansion steps, for example as provided in Figure 1.

[001016] TILs can be harvested in any appropriate and sterile manner, including for example by centrifugation. Methods for TIL harvesting are well known in the art and any such know methods can

be employed with the present process. In some embodiments, TILs are harvested using an automated system.

[001017] Cell harvesters and/or cell processing systems are commercially available from a variety of sources, including, for example, Fresenius Kabi, Tomtec Life Science, Perkin Elmer, and Inotech Biosystems International, Inc. Any cell based harvester can be employed with the present methods. In some embodiments, the cell harvester and/or cell processing systems is a membrane-based cell harvester. In some embodiments, cell harvesting is via a cell processing system, such as the LOVO system (manufactured by Fresenius Kabi). The term "LOVO cell processing system" also refers to any instrument or device manufactured by any vendor that can pump a solution comprising cells through a membrane or filter such as a spinning membrane or spinning filter in a sterile and/or closed system environment, allowing for continuous flow and cell processing to remove supernatant or cell culture media without pelletization. In some embodiments, the cell harvester and/or cell processing system can perform cell separation, washing, fluid-exchange, concentration, and/or other cell processing steps in a closed, sterile system.

[001018] In some embodiments, the harvest, for example, Step E according to Figure 1, is performed from a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX -10 or a G-REX -100. In some embodiments, the closed system bioreactor is a single bioreactor.

[001019] In some embodiments, Step E according to Figure 1, is performed according to the processes described herein. In some embodiments, the closed system is accessed via syringes under sterile conditions in order to maintain the sterility and closed nature of the system. In some embodiments, a closed system as described in the Examples is employed.

[001020] In some embodiments, TILs are harvested according to the methods described in the Examples. In some embodiments, TILs between days 1 and 11 are harvested using the methods as described in the steps referred herein, such as in the day 11 TIL harvest in the Examples. In some embodiments, TILs between days 12 and 24 are harvested using the methods as described in the steps referred herein, such as in the Day 22 TIL harvest in the Examples. In some embodiments, TILs between days 12 and 22 are harvested using the methods as described in the steps referred herein, such as in the Day 22 TIL harvest in the Examples.

F. STEP F: Final Formulation and Transfer to Infusion Container

[001021] After Steps A through E as provided in an exemplary order in Figure 1 and as outlined in detailed above and herein are complete, cells are transferred to a container for use in administration to

a patient, such as an infusion bag or sterile vial. In some embodiments, once a therapeutically sufficient number of TILs are obtained using the expansion methods described above, they are transferred to a container for use in administration to a patient.

[001022] In some embodiments, TILs expanded using APCs of the present disclosure are administered to a patient as a pharmaceutical composition. In some embodiments, the pharmaceutical composition is a suspension of TILs in a sterile buffer. TILs expanded using PBMCs of the present disclosure may be administered by any suitable route as known in the art. In some embodiments, the T-cells are administered as a single intra-arterial or intravenous infusion, which preferably lasts approximately 30 to 60 minutes. Other suitable routes of administration include intraperitoneal, intrathecal, and intralymphatic administration.

VI. Gen 3 TIL Manufacturing Processes

[001023] In some embodiments, after the making of the cryopreserved TIL preparation as described herein, the the patient is monitored for exhibitions of progressive disease on or after ICI and/or standard of care treatment. In some embodiments, the patient exhibits progressive cancer on or after ICI and/or standard of care treatment and is indicated for autologous TIL therapy. In some embodiments, after progression, the cryopreserved TIL preparation is thawed and expanded according to expansion methods described in the sections below.

[001024] Without being limited to any particular theory, it is believed that the priming first expansion that primes an activation of T cells followed by the rapid second expansion that boosts the activation of T cells as described in the methods of the invention allows the preparation of expanded T cells that retain a "younger" phenotype, and as such the expanded T cells of the invention are expected to exhibit greater cytotoxicity against cancer cells than T cells expanded by other methods. In particular, it is believed that an activation of T cells that is primed by exposure to an anti-CD3 antibody (*e.g.* OKT-3), IL-2 and optionally antigen-presenting cells (APCs) and then boosted by subsequent exposure to additional anti-CD-3 antibody (*e.g.* OKT-3), IL-2 and APCs as taught by the methods of the invention limits or avoids the maturation of T cells in culture, yielding a population of T cells with a less mature phenotype, which T cells are less exhausted by expansion in culture and exhibit greater cytotoxicity against cancer cells. In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (a) performing the rapid second expansion by culturing T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer of the T cells in the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, and culturing the T cells from the small scale culture in a larger scale culture in the second container for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split

into a plurality of steps to achieve a scaling out of the culture by: (a) performing the rapid second expansion by culturing T cells in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the T cells from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the T cells from first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the T cells from the small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 4 days, and then (b) effecting the transfer and apportioning of the T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 5 days.

[001025] In some embodiments, upon the splitting of the rapid expansion, each second container comprises at least 10^8 TILs. In some embodiments, upon the splitting of the rapid expansion, each second container comprises at least 10^8 TILs, at least 10^9 TILs, or at least 10^{10} TILs. In one exemplary embodiment, each second container comprises at least 10^{10} TILs.

[001026] In some embodiments, the first small scale TIL culture is apportioned into a plurality of subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2, 3, 4, or 5 subpopulations.

[001027] In some embodiments, after the completion of the rapid expansion, the plurality of subpopulations comprises a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid expansion, one or more subpopulations of TILs are pooled together to produce a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid expansion, each subpopulation of TILs comprises a therapeutically effective amount of TILs.

[001028] In some embodiments, the rapid expansion is performed for a period of about 1 to 5 days before being split into a plurality of steps. In some embodiments, the splitting of the rapid expansion occurs at about day 1, day 2, day 3, day 4, or day 5 after the initiation of the rapid expansion.

[001029] In some embodiments, the splitting of the rapid expansion occurs at about day 8, day 9, day 10, day 11, day 12, or day 13 after the initiation of the first expansion (*i.e.*, pre-REP expansion). In one exemplary embodiment, the splitting of the rapid expansion occurs at about day 10 after the initiation of the priming first expansion. In another exemplary embodiment, the splitting of the rapid expansion occurs at about day 11 after the initiation of the priming first expansion.

[001030] In some embodiments, the rapid expansion is further performed for a period of about 4 to 11 days after the splitting. In some embodiments, the rapid expansion is further performed for a period of about 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, or 11 days after the splitting.

[001031] In some embodiments, the cell culture medium used for the rapid expansion before the splitting comprises the same components as the cell culture medium used for the rapid expansion after the splitting. In some embodiments, the cell culture medium used for the rapid expansion before the splitting comprises different components from the cell culture medium used for the rapid expansion after the splitting.

[001032] In some embodiments, the cell culture medium used for the rapid expansion before the splitting comprises IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid expansion before the splitting comprises IL-2, OKT-3, and further optionally APCs. In some embodiments, the cell culture medium used for the rapid expansion before the splitting comprises IL-2, OKT-3 and APCs.

[001033] In some embodiments, the cell culture medium used for the rapid expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, OKT-3 and APCs. In some embodiments, the cell culture medium used for the rapid expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, OKT-3 and APCs.

[001034] In some embodiments, the cell culture medium used for the rapid expansion after the splitting comprises IL-2, and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid expansion after the splitting comprises IL-2, and OKT-3. In some embodiments, the cell culture medium used for the rapid expansion after the splitting is generated by replacing the cell culture medium used for the rapid expansion before the splitting with fresh culture medium comprising IL-2 and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid expansion after the splitting is generated by replacing the cell culture medium used for the rapid expansion before the splitting with fresh culture medium comprising IL-2 and OKT-3.

[001035] In some embodiments, the splitting of the rapid expansion occurs in a closed system.

[001036] In some embodiments, the scaling up of the TIL culture during the rapid expansion comprises adding fresh cell culture medium to the TIL culture (also referred to as feeding the TILs). In some embodiments, the feeding comprises adding fresh cell culture medium to the TIL culture frequently. In some embodiments, the feeding comprises adding fresh cell culture medium to the TIL culture at a regular interval. In some embodiments, the fresh cell culture medium is supplied to the TILs via a constant flow. In some embodiments, an automated cell expansion system such as Xuri W25 is used for the rapid expansion and feeding.

[001037] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion begins to decrease, abate, decay or subside.

[001038] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion has decreased by at or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%.

[001039] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion has decreased by a percentage in the range of at or about 1% to 100%.

[001040] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion has decreased by a percentage in the range of at or about 1% to 10%, 10% to 20%, 20% to 30%, 30% to 40%, 40% to 50%, 50% to 60%, 60% to 70%, 70% to 80%, 80% to 90%, or 90% to 100%.

[001041] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion has decreased by at least at or about 1, 2, 3, 4, 5, 6, 7, 8,

9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99%.

[001042] In some embodiments, the rapid second expansion is performed after the activation of T cells effected by the priming first expansion has decreased by up to at or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100%.

[001043] In some embodiments, the decrease in the activation of T cells effected by the priming first expansion is determined by a reduction in the amount of interferon gamma released by the T cells in response to stimulation with antigen.

[001044] In some embodiments, the priming first expansion of T cells is performed during a period of up to at or about 7 days or about 8 days.

[001045] In some embodiments, the priming first expansion of T cells is performed during a period of up to at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, or 8 days.

[001046] In some embodiments, the priming first expansion of T cells is performed during a period of 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, or 8 days.

[001047] In some embodiments, the rapid second expansion of T cells is performed during a period of up to at or about 11 days.

[001048] In some embodiments, the rapid second expansion of T cells is performed during a period of up to at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or 11 days.

[001049] In some embodiments, the rapid second expansion of T cells is performed during a period of 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or 11 days.

[001050] In some embodiments, the priming first expansion of T cells is performed during a period of from at or about 1 day to at or about 7 days and the rapid second expansion of T cells is performed during a period of from at or about 1 day to at or about 11 days.

[001051] In some embodiments, the priming first expansion of T cells is performed during a period of up to at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, or 8 days and the rapid second

expansion of T cells is performed during a period of up to at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or 11 days.

[001052] In some embodiments, the priming first expansion of T cells is performed during a period of from at or about 1 day to at or about 8 days and the rapid second expansion of T cells is performed during a period of from at or about 1 day to at or about 9 days.

[001053] In some embodiments, the priming first expansion of T cells is performed during a period of 8 days and the rapid second expansion of T cells is performed during a period of 9 days.

[001054] In some embodiments, the priming first expansion of T cells is performed during a period of from at or about 1 day to at or about 7 days and the rapid second expansion of T cells is performed during a period of from at or about 1 day to at or about 9 days.

[001055] In some embodiments, the priming first expansion of T cells is performed during a period of 7 days and the rapid second expansion of T cells is performed during a period of 9 days.

[001056] In some embodiments, the T cells are tumor infiltrating lymphocytes (TILs).

[001057] In some embodiments, the T cells are marrow infiltrating lymphocytes (MILs).

[001058] In some embodiments, the T cells are peripheral blood lymphocytes (PBLs).

[001059] In some embodiments, the T cells are obtained from a donor suffering from a cancer.

[001060] In some embodiments, the T cells are TILs obtained from a tumor excised from a patient suffering from a cancer.

[001061] In some embodiments, the T cells are MILs obtained from bone marrow of a patient suffering from a hematologic malignancy.

[001062] In some embodiments, the T cells are PBLs obtained from peripheral blood mononuclear cells (PBMCs) from a donor. In some embodiments, the donor is suffering from a cancer. In some embodiments, the cancer is the cancer is selected from the group consisting of melanoma, ovarian cancer, endometrial cancer, thyroid cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, and renal cell carcinoma. In some embodiments, the cancer is selected from the group consisting of melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, and renal cell carcinoma. In some

embodments, the donor is suffering from a tumor. In some embodiments, the tumor is a liquid tumor. In some embodiments, the tumor is a solid tumor. In some embodiments, the donor is suffering from a hematologic malignancy.

[001063] In certain aspects of the present disclosure, immune effector cells, *e.g.*, T cells, can be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as FICOLL separation. In one preferred aspect, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. In one aspect, the cells collected by apheresis may be washed to remove the plasma fraction and, optionally, to place the cells in an appropriate buffer or media for subsequent processing steps. In one embodiment, the cells are washed with phosphate buffered saline (PBS). In an alternative embodiment, the wash solution lacks calcium and may lack magnesium or may lack many if not all divalent cations. In one aspect, T cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL gradient or by counterflow centrifugal elutriation.

[001064] In some embodiments, the T cells are PBLs separated from whole blood or apheresis product enriched for lymphocytes from a donor. In some embodiments, the donor is suffering from a cancer. In some embodiments, the cancer is the cancer is selected from the group consisting of melanoma, ovarian cancer, endometrial cancer, thyroid cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, and renal cell carcinoma. In some embodiments, the cancer is selected from the group consisting of melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, and renal cell carcinoma. In some embodments, the donor is suffering from a tumor. In some embodiments, the tumor is a liquid tumor. In some embodiments, the tumor is a solid tumor. In some embodiments, the donor is suffering from a hematologic malignancy. In some embodiments, the PBLs are isolated from whole blood or apheresis product enriched for lymphocytes by using positive or negative selection methods, i.e., removing the PBLs using a marker(s), *e.g.*, CD3+ CD45+, for T cell phenotype, or removing non-T cell phenotype cells, leaving PBLs. In other embodiments, the PBLs are isolated by gradient centrifugation. Upon isolation of PBLs from donor tissue, the priming first expansion of PBLs can be initiated by seeding a suitable number of isolated PBLs (in some embodiments,

approximately 1×10^7 PBLs) in the priming first expansion culture according to the priming first expansion step of any of the methods described herein.

[001065] An exemplary TIL process known as process 3 (also referred to herein as Gen 3) containing some of these features is depicted in Figure 8 and as well as the exemplary process provided in Figure 48 (KO TIL TALEN process) (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), and some of the advantages of this embodiment of the present invention over Gen 2 are described in Figures 1, 2, 8, 30, and 31 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). Embodiments of Gen 3 are shown in Figures 1, 8, and 30 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). Process 2A or Gen 2 or Gen 2A is also described in U.S. Patent Publication No. 2018/0280436, incorporated by reference herein in its entirety. The Gen 3 process is also described in International Patent Publication WO 2020/096988.

[001066] As discussed and generally outlined herein, TILs are taken from a patient sample and manipulated to expand their number prior to transplant into a patient using the TIL expansion process described herein and referred to as Gen 3. In some embodiments, the TILs may be optionally genetically manipulated as discussed below. In some embodiments, the TILs may be cryopreserved prior to or after expansion. Once thawed, they may also be restimulated to increase their metabolism prior to infusion into a patient.

[001067] In some embodiments, the priming first expansion (including processes referred herein as the pre-Rapid Expansion (Pre-REP), as well as processes shown in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step B) is shortened to 1 to 8 days and the rapid second expansion (including processes referred to herein as Rapid Expansion Protocol (REP) as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step D) is shortened to 1 to 9 days, as discussed in detail below as well as in the examples and figures. In some embodiments, the priming first expansion (including processes referred herein as the pre-Rapid Expansion (Pre-REP), as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step B) is shortened to 1 to 8 days and the rapid second expansion (including processes referred to herein as Rapid Expansion Protocol (REP) as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step D) is shortened to 1 to 8 days, as

discussed in detail below as well as in the examples and figures. In some embodiments, the priming first expansion (including processes referred herein as the pre-Rapid Expansion (Pre-REP), as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step B) is shortened to 1 to 7 days and the rapid second expansion (including processes referred to herein as Rapid Expansion Protocol (REP) as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step D) is shortened to 1 to 9 days, as discussed in detail below as well as in the examples and figures. In some embodiments, the priming first expansion (including processes referred herein as the pre-Rapid Expansion (Pre-REP), as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 1B and/or Figure 8C) as Step B) is 1 to 7 days and the rapid second expansion (including processes referred to herein as Rapid Expansion Protocol (REP) as well as processes shown in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) as Step D) is 1 to 10 days, as discussed in detail below as well as in the examples and figures. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is shortened to 8 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 to 9 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 to 9 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is shortened to 7 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 to 8 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is shortened to 8 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C

and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 9 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 10 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 to 10 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 8 to 10 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 9 to 10 days. In some embodiments, the priming first expansion (for example, an expansion described as Step B in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is shortened to 7 days and the rapid second expansion (for example, an expansion as described in Step D in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) is 7 to 9 days. In some embodiments, the combination of the priming first expansion and rapid second expansion (for example, expansions described as Step B and Step D in Figure 8 (in particular,

e.g., Figure 1B and/or Figure 8C)) is 14-16 days, as discussed in detail below and in the examples and figures. Particularly, it is considered that certain embodiments of the present invention comprise a priming first expansion step in which TILs are activated by exposure to an anti-CD3 antibody, *e.g.*, OKT-3 in the presence of IL-2 or exposure to an antigen in the presence of at least IL-2 and an anti-CD3 antibody *e.g.* OKT-3. In certain embodiments, the TILs which are activated in the priming first expansion step as described above are a first population of TILs *i.e.*, which are a primary cell population.

[001068] The "Step" Designations A, B, C, *etc.*, below are in reference to the non-limiting example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and in reference to certain non-limiting embodiments described herein. The ordering of the Steps below and in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) is exemplary and any combination or order of steps, as well as additional steps, repetition of steps, and/or omission of steps is contemplated by the present application and the methods disclosed herein.

A. STEP A: Obtain Patient Tumor Sample

[001069] In general, TILs are initially obtained from a patient tumor sample ("primary TILs") or from circulating lymphocytes, such as peripheral blood lymphocytes, including peripheral blood lymphocytes having TIL-like characteristics, and are then expanded into a larger population for further manipulation as described herein, optionally cryopreserved, and optionally evaluated for phenotype and metabolic parameters as an indication of TIL health.

[001070] A patient tumor sample may be obtained using methods known in the art, generally via surgical resection, needle biopsy or other means for obtaining a sample that contains a mixture of tumor and TIL cells. In general, the tumor sample may be from any solid tumor, including primary tumors, invasive tumors or metastatic tumors. The tumor sample may also be a liquid tumor, such as a tumor obtained from a hematological malignancy. The solid tumor may be of any cancer type, including, but not limited to, breast, pancreatic, prostate, colorectal, lung, brain, renal, stomach, and skin (including but not limited to squamous cell carcinoma, basal cell carcinoma, and melanoma). In some embodiments, the cancer is selected from cervical cancer, head and neck cancer (including, for example, head and neck squamous cell carcinoma (HNSCC)), glioblastoma (GBM), gastrointestinal cancer, ovarian cancer, sarcoma, pancreatic cancer, bladder cancer, breast cancer, triple negative breast cancer, and non-small cell lung carcinoma. In some embodiments, the cancer is melanoma. In some embodiments, useful TILs are obtained from malignant melanoma tumors, as these have been reported to have particularly high levels of TILs.

[001071] Once obtained, the tumor sample is generally fragmented using sharp dissection into small pieces of between 1 to about 8 mm^3, with from about 2-3 mm^3 being particularly useful. The TILs are cultured from these fragments using enzymatic tumor digests. Such tumor digests may be produced by incubation in enzymatic media (*e.g.*, Roswell Park Memorial Institute (RPMI) 1640 buffer, 2 mM glutamate, 10 mcg/mL gentamicine, 30 units/mL of DNase and 1.0 mg/mL of collagenase) followed by mechanical dissociation (*e.g.*, using a tissue dissociator). Tumor digests may be produced by placing the tumor in enzymatic media and mechanically dissociating the tumor for approximately 1 minute, followed by incubation for 30 minutes at 37 °C in 5% CO_2, followed by repeated cycles of mechanical dissociation and incubation under the foregoing conditions until only small tissue pieces are present. At the end of this process, if the cell suspension contains a large number of red blood cells or dead cells, a density gradient separation using FICOLL branched hydrophilic polysaccharide may be performed to remove these cells. Alternative methods known in the art may be used, such as those described in U.S. Patent Application Publication No. 2012/0244133 A1, the disclosure of which is incorporated by reference herein. Any of the foregoing methods may be used in any of the embodiments described herein for methods of expanding TILs or methods treating a cancer.

[001072] Tumor dissociating enzyme mixtures can include one or more dissociating (digesting) enzymes such as, but not limited to, collagenase (including any blend or type of collagenase), Accutase™, Accumax™, hyaluronidase, neutral protease (dispase), chymotrypsin, chymopapain, trypsin, caseinase, elastase, papain, protease type XIV (pronase), deoxyribonuclease I (DNase), trypsin inhibitor, any other dissociating or proteolytic enzyme, and any combination thereof.

[001073] In some embodiments, the dissociating enzymes are reconstituted from lyophilized enzymes. In some embodiments, lyophilized enzymes are reconstituted in an amount of sterile buffer such as HBSS.

[001074] In some instances, collagenase (such as animal free- type 1 collagenase) is reconstituted in 10 mL of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 2892 PZ U/vial. In some embodiments, collagenase is reconstituted in 5 mL to 15 mL buffer. In some embodiment, after reconstitution the collagenase stock ranges from about 100 PZ U/mL-about 400 PZ U/mL, e.g., about 100 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL-about 350 PZ U/mL, about 100 PZ U/mL-about 300 PZ U/mL, about 150 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL, about 150 PZ U/mL, about 200 PZ U/mL, about 210 PZ U/mL, about 220 PZ U/mL, about 230 PZ U/mL, about 240 PZ U/mL, about 250 PZ U/mL, about 260 PZ U/mL, about 270 PZ U/mL, about 280 PZ U/mL, about 289.2 PZ U/mL, about 300 PZ U/mL, about 350 PZ U/mL, or about 400 PZ U/mL.

[001075] In some embodiments, neutral protease is reconstituted in 1 mL of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 175 DMC U/vial. In some embodiments, after reconstitution the neutral protease stock ranges from about 100 DMC/mL-about 400 DMC/mL, e.g., about 100 DMC/mL-about 400 DMC/mL, about 100 DMC/mL-about 350 DMC/mL, about 100 DMC/mL-about 300 DMC/mL, about 150 DMC/mL-about 400 DMC/mL, about 100 DMC/mL, about 110 DMC/mL, about 120 DMC/mL, about 130 DMC/mL, about 140 DMC/mL, about 150 DMC/mL, about 160 DMC/mL, about 170 DMC/mL, about 175 DMC/mL, about 180 DMC/mL, about 190 DMC/mL, about 200 DMC/mL, about 250 DMC/mL, about 300 DMC/mL, about 350 DMC/mL, or about 400 DMC/mL.

[001076] In some embodiments, DNAse I is reconstituted in 1 mL of sterile HBSS or another buffer. The lyophilized stock enzyme was at a concentration of 4 KU/vial. In some embodiments, after reconstitution the DNase I stock ranges from about 1 KU/mL-10 KU/mL, e.g., about 1 KU/mL, about 2 KU/mL, about 3 KU/mL, about 4 KU/mL, about 5 KU/mL, about 6 KU/mL, about 7 KU/mL, about 8 KU/mL, about 9 KU/mL, or about 10 KU/mL.

[001077] In some embodiments, the stock of enzymes is variable and the concentrations may need to be determined. In some embodiments, the concentration of the lyophilized stock can be verified. In some embodiments, the final amount of enzyme added to the digest cocktail is adjusted based on the determined stock concentration.

[001078] In some embodiment, the enzyme mixture includes about 10.2-ul of neutral protease (0.36 DMC U/mL), 21.3 µL of collagenase (1.2 PZ/mL) and 250-ul of DNAse I (200 U/mL) in about 4.7 mL of sterile HBSS.

[001079] As indicated above, in some embodiments, the TILs are derived from solid tumors. In some embodiments, the solid tumors are not fragmented. In some embodiments, the solid tumors are not fragmented and are subjected to enzymatic digestion as whole tumors. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours at 37°C, 5% CO_2. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and hyaluronidase for 1-2 hours at 37°C, 5% CO_2 with rotation. In some embodiments, the tumors are digested overnight with constant rotation. In some embodiments, the tumors are digested overnight at 37°C, 5% CO_2 with constant rotation. In some embodiments, the whole tumor is combined with the enzymes to form a tumor digest reaction mixture.

[001080] In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours at 37°C, 5% CO2. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours at 37°C, 5% CO2 with rotation. In some embodiments, the tumors are digested overnight with constant rotation. In some embodiments, the tumors are digested overnight at 37°C, 5% CO2 with constant rotation. In some embodiments, the whole tumor is combined with the enzymes to form a tumor digest reaction mixture.

[001081] In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours at 37°C, 5% CO2. In some embodiments, the tumors are digested in in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours at 37°C, 5% CO2 with rotation. In some embodiments, the tumors are digested overnight with constant rotation. In some embodiments, the tumors are digested overnight at 37°C, 5% CO2 with constant rotation. In some embodiments, the whole tumor is combined with the enzymes to form a tumor digest reaction mixture.

[001082] In some embodiments, the tumor is reconstituted with the lyophilized enzymes in a sterile buffer. In some embodiments, the buffer is sterile HBSS.

[001083] In some embodiments, the enzyme mixture comprises collagenase. In some embodiments, the collagenase is collagenase IV. In some embodiments, the working stock for the collagenase is a 100 mg/mL 10X working stock.

[001084] In some embodiments, the enzyme mixture comprises DNAse. In some embodiments, the working stock for the DNAse is a 10,000IU/mL 10X working stock.

[001085] In some embodiments, the enzyme mixture comprises hyaluronidase. In some embodiments, the working stock for the hyaluronidase is a 10-mg/mL 10X working stock.

[001086] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 1000 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[001087] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 500 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[001088] In general, the cell suspension obtained from the tumor is called a "primary cell population" or a "freshly obtained" or a "freshly isolated" cell population. In certain embodiments, the freshly obtained cell population of TILs is exposed to a cell culture medium comprising antigen presenting cells, IL-12 and OKT-3.

[001089] In some embodiments, fragmentation includes physical fragmentation, including, for example, dissection as well as digestion. In some embodiments, the fragmentation is physical fragmentation. In some embodiments, the fragmentation is dissection. In some embodiments, the fragmentation is by digestion. In some embodiments, TILs can be initially cultured from enzymatic tumor digests and tumor fragments obtained from patients. In some embodiments, TILs can be initially cultured from enzymatic tumor digests and tumor fragments obtained from patients.

[001090] In some embodiments, where the tumor is a solid tumor, the tumor undergoes physical fragmentation after the tumor sample is obtained in, for example, Step A (as provided in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)). In some embodiments, the fragmentation occurs before cryopreservation. In some embodiments, the fragmentation occurs after cryopreservation. In some embodiments, the fragmentation occurs after obtaining the tumor and in the absence of any cryopreservation. In some embodiments, the step of fragmentation is an *in vitro* or *ex-vivo* process. In some embodiments, the tumor is fragmented and 10, 20, 30, 40 or more fragments or pieces are placed in each container for the priming first expansion. In some embodiments, the tumor is fragmented and 30 or 40 fragments or pieces are placed in each container for the priming first expansion. In some embodiments, the tumor is fragmented and 40 fragments or pieces are placed in each container for the priming first expansion. In some embodiments, the multiple fragments comprise about 4 to about 50 fragments, wherein each fragment has a volume of about 27 mm^3. In some embodiments, the multiple fragments comprise about 30 to about 60 fragments with a total volume of about 1300 mm^3 to about 1500 mm^3. In some embodiments, the multiple fragments comprise about 50 fragments with a total volume of about 1350 mm^3. In some embodiments, the multiple fragments comprise about 50 fragments with a total mass of about 1 gram to about 1.5 grams. In some embodiments, the multiple fragments comprise about 4 fragments.

[001091] In some embodiments, the TILs are obtained from tumor fragments. In some embodiments, the tumor fragment is obtained by sharp dissection. In some embodiments, the tumor fragment is between about 1 mm^3 and 10 mm^3. In some embodiments, the tumor fragment is between about 1 mm^3 and 8 mm^3. In some embodiments, the tumor fragment is about 1 mm^3. In some embodiments, the tumor fragment is about 2 mm^3. In some embodiments, the tumor fragment is about 3 mm^3. In some embodiments, the tumor fragment is about 4 mm^3. In some embodiments, the tumor fragment is about 5 mm^3. In some embodiments, the tumor fragment is about 6 mm^3. In some embodiments, the

tumor fragment is about 7 mm^3. In some embodiments, the tumor fragment is about 8 mm^3. In some embodiments, the tumor fragment is about 9 mm^3. In some embodiments, the tumor fragment is about 10 mm^3. In some embodiments, the tumor fragments are 1-4 mm × 1-4 mm × 1-4 mm. In some embodiments, the tumor fragments are 1 mm × 1 mm × 1 mm. In some embodiments, the tumor fragments are 2 mm × 2 mm × 2 mm. In some embodiments, the tumor fragments are 3 mm × 3 mm × 3 mm. In some embodiments, the tumor fragments are 4 mm × 4 mm × 4 mm.

[001092] In some embodiments, the tumors are fragmented in order to minimize the amount of hemorrhagic, necrotic, and/or fatty tissues on each piece. In some embodiments, the tumors are fragmented in order to minimize the amount of hemorrhagic tissue on each piece. In some embodiments, the tumors are fragmented in order to minimize the amount of necrotic tissue on each piece. In some embodiments, the tumors are fragmented in order to minimize the amount of fatty tissue on each piece. In certain embodiments, the step of fragmentation of the tumor is an *in vitro* or *ex-vivo* method.

[001093] In some embodiments, the tumor fragmentation is performed in order to maintain the tumor internal structure. In some embodiments, the tumor fragmentation is performed without performing a sawing motion with a scalpel. In some embodiments, the TILs are obtained from tumor digests. In some embodiments, tumor digests were generated by incubation in enzyme media, for example but not limited to RPMI 1640, 2 mM GlutaMAX, 10 mg/mL gentamicin, 30 U/mL DNase, and 1.0 mg/mL collagenase, followed by mechanical dissociation (GentleMACS, Miltenyi Biotec, Auburn, CA). After placing the tumor in enzyme media, the tumor can be mechanically dissociated for approximately 1 minute. The solution can then be incubated for 30 minutes at 37 °C in 5% CO_2 and it then mechanically disrupted again for approximately 1 minute. After being incubated again for 30 minutes at 37 °C in 5% CO_2, the tumor can be mechanically disrupted a third time for approximately 1 minute. In some embodiments, after the third mechanical disruption if large pieces of tissue were present, 1 or 2 additional mechanical dissociations were applied to the sample, with or without 30 additional minutes of incubation at 37 °C in 5% CO_2. In some embodiments, at the end of the final incubation if the cell suspension contains a large number of red blood cells or dead cells, a density gradient separation using Ficoll can be performed to remove these cells.

[001094] In some embodiments, the cell suspension prior to the priming first expansion step is called a "primary cell population" or a "freshly obtained" or "freshly isolated" cell population.

[001095] In some embodiments, cells can be optionally frozen after sample isolation (*e.g.*, after obtaining the tumor sample and/or after obtaining the cell suspension from the tumor sample) and stored frozen prior to entry into the expansion described in Step B, which is described in further detail below, as well as exemplified in Figure 8 (in particular, *e.g.*, Figure 8B).

1. Core/Small Biopsy Derived TILs

[001096] In some embodiments, TILs are initially obtained from a patient tumor sample ("primary TILs") obtained by a core biopsy or similar procedure and then expanded into a larger population for further manipulation as described herein, optionally cryopreserved, and optionally evaluated for phenotype and metabolic parameters.

[001097] In some embodiments, a patient tumor sample may be obtained using methods known in the art, generally via small biopsy, core biopsy, needle biopsy or other means for obtaining a sample that contains a mixture of tumor and TIL cells. In general, the tumor sample may be from any solid tumor, including primary tumors, invasive tumors or metastatic tumors. The tumor sample may also be a liquid tumor, such as a tumor obtained from a hematological malignancy. In some embodiments, the sample can be from multiple small tumor samples or biopsies. In some embodiments, the sample can comprise multiple tumor samples from a single tumor from the same patient. In some embodiments, the sample can comprise multiple tumor samples from one, two, three, or four tumors from the same patient. In some embodiments, the sample can comprise multiple tumor samples from multiple tumors from the same patient. The solid tumor may of lung and/or non-small cell lung carcinoma (NSCLC).

[001098] In general, the cell suspension obtained from the tumor core or fragment is called a "primary cell population" or a "freshly obtained" or a "freshly isolated" cell population. In certain embodiments, the freshly obtained cell population of TILs is exposed to a cell culture medium comprising antigen presenting cells, IL-2 and OKT-3.

[001099] In some embodiments, if the tumor is metastatic and the primary lesion has been efficiently treated/removed in the past, removal of one of the metastatic lesions may be needed. In some embodiments, the least invasive approach is to remove a skin lesion, or a lymph node on the neck or axillary area when available. In some embodiments, a skin lesion is removed or small biopsy thereof is removed. In some embodiments, a lymph node or small biopsy thereof is removed. In some embodiments, a lung or liver metastatic lesion, or an intra-abdominal or thoracic lymph node or small biopsy is removed. In some embodiments, the tumor is a melanoma. In some embodiments, the small biopsy for a melanoma comprises a mole or portion thereof.

[001100] In some embodiments, the small biopsy is a punch biopsy. In some embodiments, the punch biopsy is obtained with a circular blade pressed into the skin. In some embodiments, the punch biopsy is obtained with a circular blade pressed into the skin. around a suspicious mole. In some embodiments, the punch biopsy is obtained with a circular blade pressed into the skin, and a round piece of skin is removed. In some embodiments, the small biopsy is a punch biopsy and round portion of the tumor is removed.

[001101] In some embodiments, the small biopsy is an excisional biopsy. In some embodiments, the small biopsy is an excisional biopsy and the entire mole or growth is removed. In some embodiments, the small biopsy is an excisional biopsy and the entire mole or growth is removed along with a small border of normal-appearing skin.

[001102] In some embodiments, the small biopsy is an incisional biopsy. In some embodiments, the small biopsy is an incisional biopsy and only the most irregular part of a mole or growth is taken. In some embodiments, the small biopsy is an incisional biopsy and the incisional biopsy is used when other techniques can't be completed, such as if a suspicious mole is very large.

[001103] In some embodiments, the small biopsy is a lung biopsy. In some embodiments, the small biopsy is obtained by bronchoscopy. Generally, bronchoscopy, the patient is put under anesthesia, and a small tool goes through the nose or mouth, down the throat, and into the bronchial passages, where small tools are used to remove some tissue. In some embodiments, where the tumor or growth cannot be reached via bronchoscopy, a transthoracic needle biopsy can be employed. Generally, for a transthoracic needle biopsy, the patient is also under anesthesia and a needle is inserted through the skin directly into the suspicious spot to remove a small sample of tissue. In some embodiments, a transthoracic needle biopsy may require interventional radiology (for example, the use of x-rays or CT scan to guide the needle). In some embodiments, the small biopsy is obtained by needle biopsy. In some embodiments, the small biopsy is obtained endoscopic ultrasound (for example, an endoscope with a light and is placed through the mouth into the esophagus). In some embodiments, the small biopsy is obtained surgically.

[001104] In some embodiments, the small biopsy is a head and neck biopsy. In some embodiments, the small biopsy is an incisional biopsy. In some embodiments, the small biopsy is an incisional biopsy, wherein a small piece of tissue is cut from an abnormal-looking area. In some embodiments, if the abnormal region is easily accessed, the sample may be taken without hospitalization. In some embodiments, if the tumor is deeper inside the mouth or throat, the biopsy may need to be done in an operating room, with general anesthesia. In some embodiments, the small biopsy is an excisional biopsy. In some embodiments, the small biopsy is an excisional biopsy, wherein the whole area is removed. In some embodiments, the small biopsy is a fine needle aspiration (FNA). In some embodiments, the small biopsy is a fine needle aspiration (FNA), wherein a very thin needle attached to a syringe is used to extract (aspirate) cells from a tumor or lump. In some embodiments, the small biopsy is a punch biopsy. In some embodiments, the small biopsy is a punch biopsy, wherein punch forceps are used to remove a piece of the suspicious area.

[001105] In some embodiments, the small biopsy is a cervical biopsy. In some embodiments, the small biopsy is obtained via colposcopy. Generally, colposcopy methods employ the use of a lighted

magnifying instrument attached to magnifying binoculars (a colposcope) which is then used to biopsy a small section of the surface of the cervix. In some embodiments, the small biopsy is a conization/cone biopsy. In some embodiments, the small biopsy is a conization/cone biopsy, wherein an outpatient surgery may be needed to remove a larger piece of tissue from the cervix. In some embodiments, the cone biopsy, in addition to helping to confirm a diagnosis, a cone biopsy can serve as an initial treatment.

[001106] The term "solid tumor" refers to an abnormal mass of tissue that usually does not contain cysts or liquid areas. Solid tumors may be benign or malignant. The term "solid tumor cancer refers to malignant, neoplastic, or cancerous solid tumors. Solid tumor cancers include cancers of the lung. In some embodiments, the cancer is melanoma. In some embodiments,the cancer is non-small cell lung carcinoma (NSCLC). The tissue structure of solid tumors includes interdependent tissue compartments including the parenchyma (cancer cells) and the supporting stromal cells in which the cancer cells are dispersed and which may provide a supporting microenvironment.

[001107] In some embodiments, the sample from the tumor is obtained as a fine needle aspirate (FNA), a core biopsy, a small biopsy (including, for example, a punch biopsy). In some embodiments, sample is placed first into a G-REX 10. In some embodiments, sample is placed first into a G-REX 10 when there are 1 or 2 core biopsy and/or small biopsy samples. In some embodiments, sample is placed first into a G-REX 100 when there are 3, 4, 5, 6, 8, 9, or 10 or more core biopsy and/or small biopsy samples. In some embodiments, sample is placed first into a G-REX 500 when there are 3, 4, 5, 6, 8, 9, or 10 or more core biopsy and/or small biopsy samples.

[001108] The FNA can be obtained from a skin tumor, including, for example, a melanoma. In some embodiments, the FNA is obtained from a skin tumor, such as a skin tumor from a patient with metastatic melanoma. In some cases, the patient with melanoma has previously undergone a surgical treatment.

[001109] The FNA can be obtained from a lung tumor, including, for example, an NSCLC. In some embodiments, the FNA is obtained from a lung tumor, such as a lung tumor from a patient with non-small cell lung cancer (NSCLC). In some cases, the patient with NSCLC has previously undergone a surgical treatment.

[001110] TILs described herein can be obtained from an FNA sample. In some cases, the FNA sample is obtained or isolated from the patient using a fine gauge needle ranging from an 18 gauge needle to a 25 gauge needle. The fine gauge needle can be 18 gauge, 19 gauge, 20 gauge, 21 gauge, 22 gauge, 23 gauge, 24 gauge, or 25 gauge. In some embodiments, the FNA sample from the patient can contain at least 400,000 TILs, *e.g.*, 400,000 TILs, 450,000 TILs, 500,000 TILs, 550,000 TILs,

600,000 TILs, 650,000 TILs, 700,000 TILs, 750,000 TILs, 800,000 TILs, 850,000 TILs, 900,000 TILs, 950,000 TILs, or more.

[001111] In some cases, the TILs described herein are obtained from a core biopsy sample. In some cases, the core biopsy sample is obtained or isolated from the patient using a surgical or medical needle ranging from an 11 gauge needle to a 16 gauge needle. The needle can be 11 gauge, 12 gauge, 13 gauge, 14 gauge, 15 gauge, or 16 gauge. In some embodiments, the core biopsy sample from the patient can contain at least 400,000 TILs, *e.g.*, 400,000 TILs, 450,000 TILs, 500,000 TILs, 550,000 TILs, 600,000 TILs, 650,000 TILs, 700,000 TILs, 750,000 TILs, 800,000 TILs, 850,000 TILs, 900,000 TILs, 950,000 TILs, or more.

[001112] In general, the harvested cell suspension is called a "primary cell population" or a "freshly harvested" cell population.

[001113] In some embodiments, the TILs are not obtained from tumor digests. In some embodiments, the solid tumor cores are not fragmented.

[001114] In some embodiments, the TILs are obtained from tumor digests. In some embodiments, tumor digests were generated by incubation in enzyme media, for example but not limited to RPMI 1640, 2mM GlutaMAX, 10 mg/mL gentamicin, 30 U/mL DNase, and 1.0 mg/mL collagenase, followed by mechanical dissociation (GentleMACS, Miltenyi Biotec, Auburn, CA). After placing the tumor in enzyme media, the tumor can be mechanically dissociated for approximately 1 minute. The solution can then be incubated for 30 minutes at 37 °C in 5% CO_2 and it then mechanically disrupted again for approximately 1 minute. After being incubated again for 30 minutes at 37 °C in 5% CO_2, the tumor can be mechanically disrupted a third time for approximately 1 minute. In some embodiments, after the third mechanical disruption if large pieces of tissue were present, 1 or 2 additional mechanical dissociations were applied to the sample, with or without 30 additional minutes of incubation at 37 °C in 5% CO_2. In some embodiments, at the end of the final incubation if the cell suspension contained a large number of red blood cells or dead cells, a density gradient separation using Ficoll can be performed to remove these cells.

[001115] In some embodiments, obtaining the first population of TILs comprises a multilesional sampling method.

[001116] Tumor dissociating enzyme mixtures can include one or more dissociating (digesting) enzymes such as, but not limited to, collagenase (including any blend or type of collagenase), Accutase™, Accumax™, hyaluronidase, neutral protease (dispase), chymotrypsin, chymopapain, trypsin, caseinase, elastase, papain, protease type XIV (pronase), deoxyribonuclease I (DNase), trypsin inhibitor, any other dissociating or proteolytic enzyme, and any combination thereof.

[001117] In some embodiments, the dissociating enzymes are reconstituted from lyophilized enzymes. In some embodiments, lyophilized enzymes are reconstituted in an amount of sterile buffer such as Hank's balance salt solution (HBSS).

[001118] In some instances, collagenase (such as animal free- type 1 collagenase) is reconstituted in 10 mL of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 2892 PZ U/vial. In some embodiments, collagenase is reconstituted in 5 mL to 15 mL buffer. In some embodiment, after reconstitution the collagenase stock ranges from about 100 PZ U/mL-about 400 PZ U/mL, *e.g.*, about 100 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL-about 350 PZ U/mL, about 100 PZ U/mL-about 300 PZ U/mL, about 150 PZ U/mL-about 400 PZ U/mL, about 100 PZ U/mL, about 150 PZ U/mL, about 200 PZ U/mL, about 210 PZ U/mL, about 220 PZ U/mL, about 230 PZ U/mL, about 240 PZ U/mL, about 250 PZ U/mL, about 260 PZ U/mL, about 270 PZ U/mL, about 280 PZ U/mL, about 289.2 PZ U/mL, about 300 PZ U/mL, about 350 PZ U/mL, or about 400 PZ U/mL.

[001119] In some embodiments neutral protease is reconstituted in 1-ml of sterile HBSS or another buffer. The lyophilized stock enzyme may be at a concentration of 175 DMC U/vial. In some embodiments, after reconstitution the neutral protease stock ranges from about 100 DMC/mL-about 400 DMC/mL, *e.g.*, about 100 DMC/mL-about 400 DMC/mL, about 100 DMC/mL-about 350 DMC/mL, about 100 DMC/mL-about 300 DMC/mL, about 150 DMC/mL-about 400 DMC/mL, about 100 DMC/mL, about 110 DMC/mL, about 120 DMC/mL, about 130 DMC/mL, about 140 DMC/mL, about 150 DMC/mL, about 160 DMC/mL, about 170 DMC/mL, about 175 DMC/mL, about 180 DMC/mL, about 190 DMC/mL, about 200 DMC/mL, about 250 DMC/mL, about 300 DMC/mL, about 350 DMC/mL, or about 400 DMC/mL.

[001120] In some embodiments, DNAse I is reconstituted in 1-ml of sterile HBSS or another buffer. The lyophilized stock enzyme was at a concentration of 4 KU/vial. In some embodiments, after reconstitution the DNase I stock ranges from about 1 KU/mL-10 KU/mL, *e.g.*, about 1 KU/mL, about 2 KU/mL, about 3 KU/mL, about 4 KU/mL, about 5 KU/mL, about 6 KU/mL, about 7 KU/mL, about 8 KU/mL, about 9 KU/mL, or about 10 KU/mL.

[001121] In some embodiments, the stock of enzymes could change so verify the concentration of the lyophilized stock and amend the final amount of enzyme added to the digest cocktail accordingly.

[001122] In some embodiments, the enzyme mixture includes about 10.2-ul of neutral protease (0.36 DMC U/mL), 21.3-ul of collagenase (1.2 PZ/mL) and 250-ul of DNAse I (200 U/mL) in about 4.7-ml of sterile HBSS.

2. Pleural effusion T-cells and TILs

[001123] In some embodiments, the sample is a pleural fluid sample. In some embodiments, the source of the T-cells or TILs for expansion according to the processes described herein is a pleural fluid sample. In some embodiments, the sample is a pleural effusion derived sample. In some embodiments, the source of the T-cells or TILs for expansion according to the processes described herein is a pleural effusion derived sample. See, for example, methods described in U.S. Patent Publication US 2014/0295426, incorporated herein by reference in its entirety for all purposes.

[001124] In some embodiments, any pleural fluid or pleural effusion suspected of and/or containing TILs can be employed. Such a sample may be derived from a primary or metastatic lung cancer, such as NSCLC or SCLC. In some embodiments, the sample may be derived from secondary metastatic cancer cells which originated from another organ, *e.g.*, breast, ovary, colon or prostate. In some embodiments, the sample for use in the expansion methods described herein is a pleural exudate. In some embodiments, the sample for use in the expansion methods described herein is a pleural transudate. Other biological samples may include other serous fluids containing TILs, including, *e.g.*, ascites fluid from the abdomen or pancreatic cyst fluid. Ascites fluid and pleural fluids involve very similar chemical systems; both the abdomen and lung have mesothelial lines and fluid forms in the pleural space and abdominal spaces in the same matter in malignancies and such fluids in some embodiments contain TILs. In some embodiments, wherein the disclosed methods utilize pleural fluid, the same methods may be performed with similar results using ascites or other cyst fluids containing TILs.

[001125] In some embodiments, the pleural fluid is in unprocessed form, directly as removed from the patient. In some embodiments, the unprocessed pleural fluid is placed in a standard blood collection tube, such as an EDTA or Heparin tube, prior to further processing steps. In some embodiments, the unprocessed pleural fluid is placed in a standard CellSave® tube (Veridex) prior to the further processing steps. In some embodiments, the sample is placed in the CellSave tube immediately after collection from the patient to avoid a decrease in the number of viable TILs. The number of viable TILs can decrease to a significant extent within 24 hours, if left in the untreated pleural fluid, even at 4°C. In some embodiments, the sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, or up to 24 hours after removal from the patient. In some embodiments, the sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, or up to 24 hours after removal from the patient at 4°C.

[001126] In some embodiments, the pleural fluid sample from the chosen subject may be diluted. In one embodiment, the dilution is 1:10 pleural fluid to diluent. In some embodiments, the dilution is 1:9 pleural fluid to diluent. In some embodiments, the dilution is 1:8 pleural fluid to diluent. In some

embodiments, the dilution is 1:5 pleural fluid to diluent. In some embodiments, the dilution is 1:2 pleural fluid to diluent. In some embodiments, the dilution is 1:1 pleural fluid to diluent. In some embodiments, diluents include saline, phosphate buffered saline, another buffer or a physiologically acceptable diluent. In some embodiments, the sample is placed in the CellSave tube immediately after collection from the patient and dilution to avoid a decrease in the viable TILs, which may occur to a significant extent within 24-48 hours, if left in the untreated pleural fluid, even at 4°C. In some embodiments, the pleural fluid sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, 24 hours, 36 hours, up to 48 hours after removal from the patient, and dilution. In some embodiments, the pleural fluid sample is placed in the appropriate collection tube within 1 hour, 5 hours, 10 hours, 15 hours, 24 hours, 36 hours, up to 48 hours after removal from the patient, and dilution at 4°C.

[001127] In still another embodiment, pleural fluid samples are concentrated by conventional means prior to further processing steps. In some embodiments, this pre-treatment of the pleural fluid is preferable in circumstances in which the pleural fluid must be cryopreserved for shipment to a laboratory performing the method or for later analysis (*e.g.*, later than 24-48 hours post-collection). In some embodiments, the pleural fluid sample is prepared by centrifuging the pleural fluid sample after its withdrawal from the subject and resuspending the centrifugate or pellet in buffer. In some embodiments, the pleural fluid sample is subjected to multiple centrifugations and resuspensions, before it is cryopreserved for transport or later analysis and/or processing.

[001128] In some embodiments, pleural fluid samples are concentrated prior to further processing steps by using a filtration method. In some embodiments, the pleural fluid sample used in the further processing, is prepared by filtering the fluid through a filter containing a known and essentially uniform pore size that allows for passage of the pleural fluid through the membrane but retains the tumor cells. In some embodiments, the diameter of the pores in the membrane may be at least 4 μM. In some embodiments, the pore diameter may be 5 μM or more, and in other embodiment, any of 6, 7, 8, 9, or 10 μM. After filtration, the cells, including TILs, retained by the membrane may be rinsed off the membrane into a suitable physiologically acceptable buffer. Cells, including TILs, concentrated in this way may then be used in the further processing steps of the method.

[001129] In some embodiment, pleural fluid sample (including, for example, the untreated pleural fluid), diluted pleural fluid, or the resuspended cell pellet, is contacted with a lytic reagent that differentially lyses non-nucleated red blood cells present in the sample. In some embodiments, this step is performed prior to further processing steps in circumstances in which the pleural fluid contains substantial numbers of RBCs. Suitable lysing reagents include a single lytic reagent or a lytic reagent and a quench reagent, or a lytic agent, a quench reagent and a fixation reagent. Suitable lytic systems are marketed commercially and include the BD Pharm Lyse™ system (Becton Dickenson). Other

lytic systems include the Versalyse™ system, the FACSlyse™ system (Becton Dickenson), the Immunoprep™ system or Erythrolyse II system (Beckman Coulter, Inc.), or an ammonium chloride system. In some embodiments, the lytic reagent can vary with the primary requirements being efficient lysis of the red blood cells, and the conservation of the TILs and phenotypic properties of the TILs in the pleural fluid. In addition to employing a single reagent for lysis, the lytic systems useful in methods described herein can include a second reagent, *e.g.*, one that quenches or retards the effect of the lytic reagent during the remaining steps of the method, *e.g.*, Stabilyse™ reagent (Beckman Coulter, Inc.). A conventional fixation reagent may also be employed depending upon the choice of lytic reagents or the preferred implementation of the method.

[001130] In some embodiments, the pleural fluid sample, unprocessed, diluted or multiply centrifuged or processed as described herein above is cryopreserved at a temperature of about −140°C prior to being further processed and/or expanded as provided herein.

1. Methods of Expanding Peripheral Blood Lymphocytes (PBLs) from Peripheral Blood

[001131] PBL Method 1. In some embodiments of the invention, PBLs are expanded using the processes described herein. In some embodiments of the invention, the method comprises obtaining a PBMC sample from whole blood. In some embodiments, the method comprises enriching T-cells by isolating pure T-cells from PBMCs using negative selection of a non-CD19+ fraction. In some embodiments, the method comprises enriching T-cells by isolating pure T-cells from PBMCs using magnetic bead-based negative selection of a non-CD19+ fraction.

[001132] In some embodiments of the invention, PBL Method 1 is performed as follows: On Day 0, a cryopreserved PBMC sample is thawed and PBMCs are counted. T-cells are isolated using a Human Pan T-Cell Isolation Kit and LS columns (Miltenyi Biotec).

[001133] PBL Method 2. In some embodiments of the invention, PBLs are expanded using PBL Method 2, which comprises obtaining a PBMC sample from whole blood. The T-cells from the PBMCs are enriched by incubating the PBMCs for at least three hours at 37°C and then isolating the non-adherent cells.

[001134] In some embodiments of the invention, PBL Method 2 is performed as follows: On Day 0, the cryopreserved PMBC sample is thawed and the PBMC cells are seeded at 6 million cells per well in a 6 well plate in CM-2 media and incubated for 3 hours at 37 degrees Celsius. After 3 hours, the non-adherent cells, which are the PBLs, are removed and counted.

[001135] PBL Method 3. In some embodiments of the invention, PBLs are expanded using PBL Method 3, which comprises obtaining a PBMC sample from peripheral blood. B-cells are isolated

using a CD19+ selection and T-cells are selected using negative selection of the non-CD19+ fraction of the PBMC sample.

[001136] In some embodiments of the invention, PBL Method 3 is performed as follows: On Day 0, cryopreserved PBMCs derived from peripheral blood are thawed and counted. CD19+ B-cells are sorted using a CD19 Multisort Kit, Human (Miltenyi Biotec). Of the non-CD19+ cell fraction, T-cells are purified using the Human Pan T-cell Isolation Kit and LS Columns (Miltenyi Biotec).

[001137] In some embodiments, PBMCs are isolated from a whole blood sample. In some embodiments, the PBMC sample is used as the starting material to expand the PBLs. In some embodiments, the sample is cryopreserved prior to the expansion process. In other embodiments, a fresh sample is used as the starting material to expand the PBLs. In some embodiments of the invention, T-cells are isolated from PBMCs using methods known in the art. In some embodiments, the T-cells are isolated using a Human Pan T-cell isolation kit and LS columns. In some embodiments of the invention, T-cells are isolated from PBMCs using antibody selection methods known in the art, for example, CD19 negative selection.

[001138] In some embodiments of the invention, the PBMC sample is incubated for a period of time at a desired temperature effective to identify the non-adherent cells. In some embodiments of the invention, the incubation time is about 3 hours. In some embodiments of the invention, the temperature is about 37° Celsius. The non-adherent cells are then expanded using the process described above.

[001139] In some embodiments, the PBMC sample is from a subject or patient who has been optionally pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor. In some embodiments, the tumor sample is from a subject or patient who has been pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor. In some embodiments, the PBMC sample is from a subject or patient who has been pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor, has undergone treatment for at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, or 1 year or more. In other embodiments, the PBMCs are derived from a patient who is currently on an ITK inhibitor regimen, such as ibrutinib.

[001140] In some embodiments, the PBMC sample is from a subject or patient who has been pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor and is refractory to treatment with a kinase inhibitor or an ITK inhibitor, such as ibrutinib.

[001141] In some embodiments, the PBMC sample is from a subject or patient who has been pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor but is no longer undergoing treatment with a kinase inhibitor or an ITK inhibitor. In some embodiments, the PBMC sample is

from a subject or patient who has been pre-treated with a regimen comprising a kinase inhibitor or an ITK inhibitor but is no longer undergoing treatment with a kinase inhibitor or an ITK inhibitor and has not undergone treatment for at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, or at least 1 year or more. In other embodiments, the PBMCs are derived from a patient who has prior exposure to an ITK inhibitor, but has not been treated in at least 3 months, at least 6 months, at least 9 months, or at least 1 year.

[001142] In some embodiments of the invention, at Day 0, cells are selected for CD19+ and sorted accordingly. In some embodiments of the invention, the selection is made using antibody binding beads. In some embodiments of the invention, pure T-cells are isolated on Day 0 from the PBMCs.

[001143] In some embodiments of the invention, for patients that are not pre-treated with ibrutinib or other ITK inhibitor, 10-15 mL of Buffy Coat will yield about 5×10^9 PBMC, which, in turn, will yield about 5.5×10^7 PBLs.

[001144] In some embodiments of the invention, for patients that are pre-treated with ibrutinib or other ITK inhibitor, the expansion process will yield about 20×10^9 PBLs. In some embodiments of the invention, 40.3×10^6 PBMCs will yield about 4.7×10^5 PBLs.

[001145] In any of the foregoing embodiments, PBMCs may be derived from a whole blood sample, by apheresis, from the buffy coat, or from any other method known in the art for obtaining PBMCs.

[001146] In some embodiments, PBLs are prepared using the methods described in U.S. Patent Application Publication No. US 2020/0347350 A1, the disclosures of which are incorporated by reference herein.

2. Methods of Expanding Marrow Infiltrating Lymphocytes (MILs) from PBMCs Derived from Bone Marrow

[001147] MIL Method 3. In some embodiments of the invention, the method comprises obtaining PBMCs from the bone marrow. On Day 0, the PBMCs are selected for CD3+/CD33+/CD20+/CD14+ and sorted, and the non-CD3+/CD33+/CD20+/CD14+ cell fraction is sonicated and a portion of the sonicated cell fraction is added back to the selected cell fraction.

[001148] In some embodiments of the invention, MIL Method 3 is performed as follows: On Day 0, a cryopreserved sample of PBMCs is thawed and PBMCs are counted. The cells are stained with CD3, CD33, CD20, and CD14 antibodies and sorted using a S3e cell sorted (Bio-Rad). The cells are sorted into two fractions – an immune cell fraction (or the MIL fraction) (CD3+CD33+CD20+CD14+) and an AML blast cell fraction (non-CD3+CD33+CD20+CD14+).

[001149] In some embodiments of the invention, PBMCs are obtained from bone marrow. In some embodiments, the PBMCs are obtained from the bone marrow through apheresis, aspiration, needle biopsy, or other similar means known in the art. In some embodiments, the PBMCs are fresh. In other embodiments, the PBMCs are cryopreserved.

[001150] In some embodiments of the invention, MILs are expanded from 10-50 mL of bone marrow aspirate. In some embodiments of the invention, 10 mL of bone marrow aspirate is obtained from the patient. In other embodiments, 20 mL of bone marrow aspirate is obtained from the patient. In other embodiments, 30 mL of bone marrow aspirate is obtained from the patient. In other embodiments, 40 mL of bone marrow aspirate is obtained from the patient. In other embodiments, 50 mL of bone marrow aspirate is obtained from the patient.

[001151] In some embodiments of the invention, the number of PBMCs yielded from about 10-50 mL of bone marrow aspirate is about 5×10^7 to about 10×10^7 PBMCs. In other embodiments, the number of PMBCs yielded is about 7×10^7 PBMCs.

[001152] In some embodiments of the invention, about 5×10^7 to about 10×10^7 PBMCs, yields about 0.5×10^6 to about 1.5×10^6 MILs. In some embodiments of the invention, about 1×10^6 MILs is yielded.

[001153] In some embodiments of the invention, 12×10^6 PBMC derived from bone marrow aspirate yields approximately 1.4×10^5 MILs.

[001154] In any of the foregoing embodiments, PBMCs may be derived from a whole blood sample, from bone marrow, by apheresis, from the buffy coat, or from any other method known in the art for obtaining PBMCs.

[001155] In some embodiments, MILs are prepared using the methods described in U.S. Patent Application Publication No. US 2020/0347350 A1, the disclosures of which are incorporated by reference herein.

A1. STEP A1: Pre-Progression Cryopreservation

[001156] In some embodiments, the present methods provide for cryopreserving the harvested tumor sample obtained from Step A to make a cryopreserved TIL preparation for future TIL manufacturing, after the patient exhibits cancer progression on or after receiving immune-check point inhibitor (ICI) and/or standard of care treatment.

[001157] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor in the subject or patient,

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample.

[001158] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments; and

(b) cryopreserving the tumor fragments comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments.

[001159] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into a tumor digest; and

(b) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor digest.

[001160] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, resecting a NSCLC tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor; and

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample.

[001161] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, resecting a NSCLC tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a NSCLC tumor;

(b) fragmenting the tumor into tumor fragments; and

(c) cryopreserving the tumor fragments comprising the first population of TILs from step (b) to produce cryopreserved tumor fragments.

[001162] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest; and

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest.

[001163] In some embodiments, the cryopreserving comprises:

(a) prior to the at least one prior therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) dissociate tumor tissue to produce a dissociated tumor material and

(c) cryopreserving the dissociated tumor material comprising the first population of TILs from step (a) to produce a cryopreserved dissociated tumor material.

B. STEP B: Priming First Expansion

[001164] In some embodiments, the present methods provide for younger TILs, which may provide additional therapeutic benefits over older TILs (*i.e.*, TILs which have further undergone more rounds of replication prior to administration to a subject/patient). Features of young TILs have been described in the literature, for example Donia, *et al.*, *Scand. J. Immunol.* **2012,** *75,* 157–167; Dudley, *et al.*, *Clin. Cancer Res.* **2010,** *16,* 6122-6131; Huang, *et al.*, *J. Immunother.* **2005,** *28*, 258–267; Besser, *et al.*, *Clin. Cancer Res.* **2013,** *19*, OF1-OF9; Besser, *et al.*, *J. Immunother.* **2009**, *32*:415–423; Robbins, *et al.*, *J. Immunol.* **2004**, *173,* 7125-7130; Shen, *et al.*, *J. Immunother.*, **2007,** *30,* 123–129; Zhou, *et al.*, *J. Immunother.* **2005,** *28,* 53–62; and Tran, *et al.*, *J. Immunother.*, **2008**, *31*, 742–751, each of which is incorporated herein by reference.

[001165] After dissection or digestion of tumor fragments and/or tumor fragments, for example such as described in Step A of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), the resulting cells are cultured in serum containing IL-2, OKT-3, and feeder cells (*e.g.*, antigen-presenting feeder cells), under conditions that favor the growth of TILs over tumor and other cells. In some embodiments, the IL-2, OKT-3, and feeder cells are added at culture initiation along with the tumor digest and/or tumor fragments (*e.g.*, at Day 0). In some embodiments, the tumor digests and/or tumor

fragments are incubated in a container with up to 60 fragments per container and with 6000 IU/mL of IL-2. In some embodiments, this primary cell population is cultured for a period of days, generally from 1 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this primary cell population is cultured for a period of days, generally from 1 to 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, priming first expansion occurs for a period of 1 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, priming first expansion occurs for a period of 1 to 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of 5 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of 5 to 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of about 6 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of about 6 to 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of about 7 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of about 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, this priming first expansion occurs for a period of about 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells.

[001166] In some embodiments, expansion of TILs may be performed using a priming first expansion step (for example such as those described in Step B of Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include processes referred to as pre-REP or priming REP and which contains feeder cells from Day 0 and/or from culture initiation) as described below and herein, followed by a rapid second expansion (Step D, including processes referred to as rapid expansion protocol (REP) steps) as described below under Step D and herein, followed by optional cryopreservation, and followed by a second Step D (including processes referred to as restimulation REP steps) as described below and herein. The TILs obtained from this process may be optionally characterized for phenotypic characteristics and metabolic parameters as described herein. In some embodiments, the tumor fragment is between about 1 mm^3 and 10 mm^3.

[001167] In some embodiments, the first expansion culture medium is referred to as "CM", an abbreviation for culture media. In some embodiments, CM for Step B consists of RPMI 1640 with GlutaMAX, supplemented with 10% human AB serum, 25 mM Hepes, and 10 mg/mL gentamicin.

[001168] In some embodiments, there are less than or equal to 240 tumor fragments. In some embodiments, there are less than or equal to 240 tumor fragments placed in less than or equal to 4 containers. In some embodiments, the containers are G-REX100 MCS flasks. In some embodiments, less than or equal to 60 tumor fragments are placed in 1 container. In some embodiments, each container comprises less than or equal to 500 mL of media per container. In some embodiments, the media comprises IL-2. In some embodiments, the media comprises 6000 IU/mL of IL-2. In some embodiments, the media comprises antigen-presenting feeder cells (also referred to herein as "antigen-presenting cells"). In some embodiments, the media comprises 2.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media comprises OKT-3. In some embodiments, the media comprises 30 ng/mL of OKT-3 per container. In some embodiments, the container is a G-REX100 MCS flask. In some embodiments, the media comprises 6000 IU/mL of IL-2, 30 ng of OKT-3, and 2.5×10^8 antigen-presenting feeder cells. In some embodiments, the media comprises 6000 IU/mL of IL-2, 30 ng/mL of OKT-3, and 2.5×10^8 antigen-presenting feeder cells per container.

[001169] After preparation of the tumor fragments, the resulting cells (*i.e.*, fragments which is a primary cell population) are cultured in media containing IL-2, antigen-presenting feeder cells and OKT-3 under conditions that favor the growth of TILs over tumor and other cells and which allow for TIL priming and accelerated growth from initiation of the culture on Day 0. In some embodiments, the tumor digests and/or tumor fragments are incubated in with 6000 IU/mL of IL-2, as well as antigen-presenting feeder cells and OKT-3. This primary cell population is cultured for a period of days, generally from 1 to 8 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, the growth media during the priming first expansion comprises IL-2 or a variant thereof, as well as antigen-presenting feeder cells and OKT-3. In some embodiments, this primary cell population is cultured for a period of days, generally from 1 to 7 days, resulting in a bulk TIL population, generally about 1×10^8 bulk TIL cells. In some embodiments, the growth media during the priming first expansion comprises IL-2 or a variant thereof, as well as antigen-presenting feeder cells and OKT-3. In some embodiments, the IL-2 is recombinant human IL-2 (rhIL-2). In some embodiments the IL-2 stock solution has a specific activity of $20\text{-}30\times10^6$ IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 20×10^6 IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 25×10^6 IU/mg for a 1 mg vial. In some embodiments the IL-2 stock solution has a specific activity of 30×10^6 IU/mg for a 1 mg vial. In some embodiments, the IL- 2 stock solution has a final concentration of $4\text{-}8\times10^6$ IU/mg of IL-2. In some embodiments, the IL- 2 stock solution has a final concentration of $5\text{-}7\times10^6$ IU/mg of IL-2. In some embodiments, the IL- 2 stock solution has a final concentration of 6×10^6 IU/mg of IL-2. In some embodiments, the IL-2 stock solution is prepare as described in Example C. In some embodiments, the priming first expansion culture media comprises about 10,000 IU/mL of IL-2, about 9,000 IU/mL of IL-2, about 8,000 IU/mL of IL-2, about 7,000 IU/mL of IL-2, about 6000 IU/mL of IL-2 or about

5,000 IU/mL of IL-2. In some embodiments, the priming first expansion culture media comprises about 9,000 IU/mL of IL-2 to about 5,000 IU/mL of IL-2. In some embodiments, the priming first expansion culture media comprises about 8,000 IU/mL of IL-2 to about 6,000 IU/mL of IL-2. In some embodiments, the priming first expansion culture media comprises about 7,000 IU/mL of IL-2 to about 6,000 IU/mL of IL-2. In some embodiments, the priming first expansion culture media comprises about 6,000 IU/mL of IL-2. In some embodiments, the cell culture medium further comprises IL-2. In some embodiments, the priming first expansion cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the priming first expansion cell culture medium further comprises IL-2. In some embodiments, the priming first expansion cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the priming first expansion cell culture medium comprises about 1000 IU/mL, about 1500 IU/mL, about 2000 IU/mL, about 2500 IU/mL, about 3000 IU/mL, about 3500 IU/mL, about 4000 IU/mL, about 4500 IU/mL, about 5000 IU/mL, about 5500 IU/mL, about 6000 IU/mL, about 6500 IU/mL, about 7000 IU/mL, about 7500 IU/mL, or about 8000 IU/mL of IL-2. In some embodiments, the priming first expansion cell culture medium comprises between 1000 and 2000 IU/mL, between 2000 and 3000 IU/mL, between 3000 and 4000 IU/mL, between 4000 and 5000 IU/mL, between 5000 and 6000 IU/mL, between 6000 and 7000 IU/mL, between 7000 and 8000 IU/mL, or about 8000 IU/mL of IL-2.

[001170] In some embodiments, priming first expansion culture media comprises about 500 IU/mL of IL-15, about 400 IU/mL of IL-15, about 300 IU/mL of IL-15, about 200 IU/mL of IL-15, about 180 IU/mL of IL-15, about 160 IU/mL of IL-15, about 140 IU/mL of IL-15, about 120 IU/mL of IL-15, or about 100 IU/mL of IL-15. In some embodiments, the priming first expansion culture media comprises about 500 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the priming first expansion culture media comprises about 400 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the priming first expansion culture media comprises about 300 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the priming first expansion culture media comprises about 200 IU/mL of IL-15. In some embodiments, the priming first expansion cell culture medium comprises about 180 IU/mL of IL-15. In some embodiments, the priming first expansion cell culture medium further comprises IL-15. In some embodiments, the priming first expansion cell culture medium comprises about 180 IU/mL of IL-15.

[001171] In some embodiments, priming first expansion culture media comprises about 20 IU/mL of IL-21, about 15 IU/mL of IL-21, about 12 IU/mL of IL-21, about 10 IU/mL of IL-21, about 5 IU/mL of IL-21, about 4 IU/mL of IL-21, about 3 IU/mL of IL-21, about 2 IU/mL of IL-21, about 1 IU/mL of IL-21, or about 0.5 IU/mL of IL-21. In some embodiments, the priming first expansion culture media comprises about 20 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the priming first expansion culture media comprises about 15 IU/mL of IL-21 to about 0.5 IU/mL of IL-

21. In some embodiments, the priming first expansion culture media comprises about 12 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the priming first expansion culture media comprises about 10 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the priming first expansion culture media comprises about 5 IU/mL of IL-21 to about 1 IU/mL of IL-21. In some embodiments, the priming first expansion culture media comprises about 2 IU/mL of IL-21. In some embodiments, the priming first expansion cell culture medium comprises about 1 IU/mL of IL-21. In some embodiments, the priming first expansion cell culture medium comprises about 0.5 IU/mL of IL-21. In some embodiments, the cell culture medium further comprises IL-21. In some embodiments, the priming first expansion cell culture medium comprises about 1 IU/mL of IL-21.

[001172] In some embodiments, the priming first expansion cell culture medium comprises OKT-3 antibody. In some embodiments, the priming first expansion cell culture medium comprises about 30 ng/mL of OKT-3 antibody. In some embodiments, the priming first expansion cell culture medium comprises about 0.1 ng/mL, about 0.5 ng/mL, about 1 ng/mL, about 2.5 ng/mL, about 5 ng/mL, about 7.5 ng/mL, about 10 ng/mL, about 15 ng/mL, about 20 ng/mL, about 25 ng/mL, about 30 ng/mL, about 35 ng/mL, about 40 ng/mL, about 50 ng/mL, about 60 ng/mL, about 70 ng/mL, about 80 ng/mL, about 90 ng/mL, about 100 ng/mL, about 200 ng/mL, about 500 ng/mL, and about 1 µg/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 0.1 ng/mL and 1 ng/mL, between 1 ng/mL and 5 ng/mL, between 5 ng/mL and 10 ng/mL, between 10 ng/mL and 20 ng/mL, between 20 ng/mL and 30 ng/mL, between 30 ng/mL and 40 ng/mL, between 40 ng/mL and 50 ng/mL, and between 50 ng/mL and 100 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 15 ng/mL and 30 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises 30 ng/mL of OKT-3 antibody. In some embodiments, the OKT-3 antibody is muromonab. See, Table 1.

[001173] In some embodiments, the priming first expansion cell culture medium comprises one or more TNFRSF agonists in a cell culture medium. In some embodiments, the TNFRSF agonist comprises a 4-1BB agonist. In some embodiments, the TNFRSF agonist is a 4-1BB agonist, and the 4-1BB agonist is selected from the group consisting of urelumab, utomilumab, EU-101, a fusion protein, and fragments, derivatives, variants, biosimilars, and combinations thereof. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 0.1 µg/mL and 100 µg/mL. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 20 µg/mL and 40 µg/mL.

[001174] In some embodiments, in addition to one or more TNFRSF agonists, the priming first expansion cell culture medium further comprises IL-2 at an initial concentration of about 3000 IU/mL and OKT-3 antibody at an initial concentration of about 30 ng/mL, and wherein the one or more

TNFRSF agonists comprises a 4-1BB agonist. In some embodiments, in addition to one or more TNFRSF agonists, the priming first expansion cell culture medium further comprises IL-2 at an initial concentration of about 6000 IU/mL and OKT-3 antibody at an initial concentration of about 30 ng/mL, and wherein the one or more TNFRSF agonists comprises a 4-1BB agonist.

[001175] In some embodiments, the priming first expansion culture medium is referred to as "CM", an abbreviation for culture media. In some embodiments, it is referred to as CM1 (culture medium 1). In some embodiments, CM consists of RPMI 1640 with GlutaMAX, supplemented with 10% human AB serum, 25 mM Hepes, and 10 mg/mL gentamicin. In some embodiments, the CM is the CM1 described in the Examples, *see*, Example A. In some embodiments, the priming first expansion occurs in an initial cell culture medium or a first cell culture medium. In some embodiments, the priming first expansion culture medium or the initial cell culture medium or the first cell culture medium comprises IL-2, OKT-3 and antigen-presenting feeder cells (also referred to herein as feeder cells).

[001176] In some embodiments, the culture medium used in the expansion processes disclosed herein is a serum-free medium or a defined medium. In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or a serum replacement. In some embodiments, the serum-free or defined medium is used to prevent and/or decrease experimental variation due in part to the lot-to-lot variation of serum-containing media.

[001177] In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or serum replacement. In some embodiments, the basal cell medium includes, but is not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium , CTS™ OpTmizer™ T-Cell Expansion SFM, CTS™ AIM-V Medium, CTS™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001178] In some embodiments, the serum supplement or serum replacement includes, but is not limited to one or more of CTS™ OpTmizer T-Cell Expansion Serum Supplement, CTS™ Immune Cell Serum Replacement, one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more antibiotics, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L- histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated

transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or 2-mercaptoethanol.

[001179] In some embodiments, the CTS™OpTmizer™ T-cell Immune Cell Serum Replacement is used with conventional growth media, including but not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium, CTS™ OpTmizer™ T-cell Expansion SFM, CTS™ AIM-V Medium, CST™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001180] In some embodiments, the total serum replacement concentration (vol%) in the serum-free or defined medium is from about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, or 20% by volume of the total serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 3% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 5% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 10% of the total volume of the serum-free or defined medium.

[001181] In some embodiments, the serum-free or defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific). In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55μM.

[001182] In some embodiments, the defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are

mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and the final concentration of 2-mercaptoethanol in the media is 55μM.

[001183] In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of from about 0.1mM to about 10mM, 0.5mM to

about 9mM, 1mM to about 8mM, 2mM to about 7mM, 3mM to about 6mM, or 4mM to about 5 mM. In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of about 2mM.

[001184] In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of from about 5mM to about 150mM, 10mM to about 140mM, 15mM to about 130mM, 20mM to about 120mM, 25mM to about 110mM, 30mM to about 100mM, 35mM to about 95mM, 40mM to about 90mM, 45mM to about 85mM, 50mM to about 80mM, 55mM to about 75mM, 60mM to about 70mM, or about 65mM. In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of about 55mM. In some embodiments, the final concentration of 2-mercaptoethanol in the media is 55µM.

[001185] In some embodiments, the defined media described in International PCT Publication No. WO/1998/030679, which is herein incorporated by reference, are useful in the present invention. In that publication, serum-free eukaryotic cell culture media are described. The serum-free, eukaryotic cell culture medium includes a basal cell culture medium supplemented with a serum-free supplement capable of supporting the growth of cells in serum- free culture. The serum-free eukaryotic cell culture medium supplement comprises or is obtained by combining one or more ingredients selected from the group consisting of one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more trace elements, and one or more antibiotics. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or beta-mercaptoethanol. In some embodiments, the defined medium comprises an albumin or an albumin substitute and one or more ingredients selected from group consisting of one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L-histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the basal cell media is selected from the group consisting of Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001186] In some embodiments, the concentration of glycine in the defined medium is in the range of from about 5-200 mg/L, the concentration of L- histidine is about 5-250 mg/L, the concentration of L-isoleucine is about 5-300 mg/L, the concentration of L-methionine is about 5-200 mg/L, the concentration of L-phenylalanine is about 5-400 mg/L, the concentration of L-proline is about 1-1000 mg/L, the concentration of L- hydroxyproline is about 1-45 mg/L, the concentration of L-serine is about 1-250 mg/L, the concentration of L-threonine is about 10-500 mg/L, the concentration of L-tryptophan is about 2-110 mg/L, the concentration of L-tyrosine is about 3-175 mg/L, the concentration of L-valine is about 5-500 mg/L, the concentration of thiamine is about 1-20 mg/L, the concentration of reduced glutathione is about 1-20 mg/L, the concentration of L-ascorbic acid-2-phosphate is about 1-200 mg/L, the concentration of iron saturated transferrin is about 1-50 mg/L, the concentration of insulin is about 1-100 mg/L, the concentration of sodium selenite is about 0.000001-0.0001 mg/L, and the concentration of albumin (*e.g.*, AlbuMAX® I) is about 5000-50,000 mg/L.

In some embodiments, the non-trace element moiety ingredients in the defined medium are present in the concentration ranges listed in the column under the heading "Concentration Range in 1X Medium" in Table 4. In other embodiments, the non-trace element moiety ingredients in the defined medium are present in the final concentrations listed in the column under the heading "A Preferred Embodiment of the 1X Medium" in Table 4. In other embodiments, the defined medium is a basal cell medium comprising a serum free supplement. In some of these embodiments, the serum free supplement comprises non-trace moiety ingredients of the type and in the concentrations listed in the column under the heading "A Preferred Embodiment in Supplement" in Table 4.

[001187] In some embodiments, the osmolarity of the defined medium is between about 260 and 350 mOsmol. In some embodiments, the osmolarity is between about 280 and 310 mOsmol. In some embodiments, the defined medium is supplemented with up to about 3.7 g/L, or about 2.2 g/L sodium bicarbonate. The defined medium can be further supplemented with L-glutamine (final concentration of about 2 mM), one or more antibiotics, non-essential amino acids (NEAA; final concentration of about 100 μM), 2-mercaptoethanol (final concentration of about 100 μM).

[001188] In some embodiments, the defined media described in Smith, *et al.*, *Clin Transl Immunology*, 4(1) 2015 (doi: 10.1038/cti.2014.31) are useful in the present invention. Briefly, RPMI or CTS™ OpTmizer™ was used as the basal cell medium, and supplemented with either 0, 2%, 5%, or 10% CTS™ Immune Cell Serum Replacement.

[001189] In some embodiments, the cell medium in the first and/or second gas permeable container is unfiltered. The use of unfiltered cell medium may simplify the procedures necessary to expand the number of cells. In some embodiments, the cell medium in the first and/or second gas permeable

container lacks beta-mercaptoethanol (BME or βME; also known as 2-mercaptoethanol, CAS 60-24-2).

[001190] In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 1 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 2 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 3 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 4 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 5 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 6 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those provided in Step B of Figure 1 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 7 to 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those provided in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those

sometimes referred to as the pre-REP or priming REP) process is 8 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 1 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 2 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 3 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 4 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8B and/or Figure 8C), which can include those sometimes referred to as the pre-REP or priming REP) process is 5 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those described in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 6 to 7 days, as discussed in the examples and figures. In some embodiments, the priming first expansion (including processes such as for example those provided in Step B of Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), which can include those sometimes referred to as the pre-REP or priming REP) process is 7 days, as discussed in the examples and figures.

[001191] In some embodiments, the priming first TIL expansion can proceed for 1 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 1 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 2 days to 8 days from when fragmentation occurs

and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 2 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 3 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 3 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 4 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 4 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 5 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 5 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 6 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated.In some embodiments, the priming first TIL expansion can proceed for 6 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 7 to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the priming first TIL expansion can proceed for 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated.In some embodiments, the priming first TIL expansion can proceed for 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated.

[001192] In some embodiments, the priming first expansion of the TILs can proceed for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, or 8 days. In some embodiments, the first TIL expansion can proceed for 1 day to 8 days. In some embodiments, the first TIL expansion can proceed for 1 day to 7 days. In some embodiments, the first TIL expansion can proceed for 2 days to 8 days. In some embodiments, the first TIL expansion can proceed for 2 days to 7 days. In some embodiments, the first TIL expansion can proceed for 3 days to 8 days. In some embodiments, the first TIL expansion can proceed for 3 days to 7 days. In some embodiments, the first TIL expansion can proceed for 4 days to 8 days. In some embodiments, the first TIL expansion can proceed for 4 days to 7 days. In some embodiments, the first TIL expansion can proceed for 5 days to 8 days. In some embodiments, the first TIL expansion can proceed for 5 days to 7 days. In some embodiments, the first TIL expansion can proceed for 6 days to 8 days. In some embodiments, the first TIL expansion can proceed for 6 days to 7 days. In some embodiments, the first TIL expansion can proceed for 7 to 8 days. In some embodiments, the first TIL expansion can proceed for 8 days. In some embodiments, the first TIL expansion can proceed for 7 days.

[001193] In some embodiments, a combination of IL-2, IL-7, IL-15, and/or IL-21 are employed as a combination during the priming first expansion. In some embodiments, IL-2, IL-7, IL-15, and/or IL-21 as well as any combinations thereof can be included during the priming first expansion, including, for example during Step B processes according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as described herein. In some embodiments, a combination of IL-2, IL-15, and IL-21 are employed as a combination during the priming first expansion. In some embodiments, IL-2, IL-15, and IL-21 as well as any combinations thereof can be included during Step B processes according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and as described herein.

[001194] In some embodiments, the priming first expansion, for example, Step B according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a bioreactor is employed. In some embodiments, a bioreactor is employed as the container. In some embodiments, the bioreactor employed is for example a G-REX-10 or a G-REX-100. In some embodiments, the bioreactor employed is a G-REX-100. In some embodiments, the bioreactor employed is a G-REX-10.

1. Feeder Cells and Antigen Presenting Cells

[001195] In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 4-8. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those

referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 4-7. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 5-8. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 5-7. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 6-8. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during days 6-7. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during day 7 or 8. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those

referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during day 7. In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as pre-REP or priming REP) does not require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion, but rather are added during the priming first expansion at any time during day 8

[001196] In some embodiments, the priming first expansion procedures described herein (for example including expansion such as those described in Step B from Figure 8 (in particular, *e.g.*, Figure 8B), as well as those referred to as pre-REP or priming REP) require feeder cells (also referred to herein as "antigen-presenting cells") at the initiation of the TIL expansion and during the priming first expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from allogeneic healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation. In some embodiments, 2.5×10^8 feeder cells are used during the priming first expansion. In some embodiments, 2.5×10^8 feeder cells per container are used during the priming first expansion. In some embodiments, 2.5×10^8 feeder cells per GREX-10 are used during the priming first expansion. In some embodiments, 2.5×10^8 feeder cells per GREX-100 are used during the priming first expansion.

[001197] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the REP procedures, as described in the examples, which provides an exemplary protocol for evaluating the replication incompetence of irradiate allogeneic PBMCs.

[001198] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells on day 14 is less than the initial viable cell number put into culture on day 0 of the priming first expansion.

[001199] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in the presence of OKT3 and IL-2, on day 7 have not increased from the initial viable cell number put into culture on day 0 of the priming first expansion. In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 3000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 6000 IU/mL IL-2.

[001200] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in

the presence of OKT3 and IL-2, on day 7 have not increased from the initial viable cell number put into culture on day 0 of the priming first expansion. In some embodiments, the PBMCs are cultured in the presence of 5-60 ng/mL OKT3 antibody and 1000-6000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 10-50 ng/mL OKT3 antibody and 2000-5000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 20-40 ng/mL OKT3 antibody and 2000-4000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 25-35 ng/mL OKT3 antibody and 2500-3500 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 6000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 15 ng/mL OKT3 antibody and 3000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 15 ng/mL OKT3 antibody and 6000 IU/mL IL-2.

[001201] In some embodiments, the antigen-presenting feeder cells are PBMCs. In some embodiments, the antigen-presenting feeder cells are artificial antigen-presenting feeder cells. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is about 1 to 25, about 1 to 50, about 1 to 100, about 1 to 125, about 1 to 150, about 1 to 175, about 1 to 200, about 1 to 225, about 1 to 250, about 1 to 275, about 1 to 300, about 1 to 325, about 1 to 350, about 1 to 375, about 1 to 400, or about 1 to 500. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is between 1 to 50 and 1 to 300. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is between 1 to 100 and 1 to 200.

[001202] In some embodiments, the priming first expansion procedures described herein require a ratio of about 2.5×10^8 feeder cells to about 100×10^6 TILs. In some embodiments, the priming first expansion procedures described herein require a ratio of about 2.5×10^8 feeder cells to about 50×10^6 TILs. In yet another embodiment, the priming first expansion described herein require about 2.5×10^8 feeder cells to about 25×10^6 TILs. In yet another embodiment, the priming first expansion described herein require about 2.5×10^8 feeder cells. In yet another embodiment, the priming first expansion requires one-fourth, one-third, five-twelfths, or one-half of the number of feeder cells used in the rapid second expansion.

[001203] In some embodiments, the media in the priming first expansion comprises IL-2. In some embodiments, the media in the priming first expansion comprises 6000 IU/mL of IL-2. In some embodiments, the media in the priming first expansion comprises antigen-presenting feeder cells. In some embodiments, the media in the priming first expansion comprises 2.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media in the priming first expansion comprises OKT-3. In some embodiments, the media comprises 30 ng of OKT-3 per container. In some embodiments, the container is a GREX100 MCS flask. In some embodiments, the media comprises 6000 IU/mL of IL-2, 30 ng/mL of OKT-3, and 2.5×10^8 antigen-presenting feeder cells. In some

embodiments, the media comprises 6000 IU/mL of IL-2, 30 ng/mL of OKT-3, and 2.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media comprises 500 mL of culture medium and 15 μg of OKT-3 per 2.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media comprises 500 mL of culture medium and 15 μg of OKT-3 per container. In some embodiments, the container is a GREX100 MCS flask. In some embodiments, the media comprises 500 mL of culture medium, 6000 IU/mL of IL-2, 30 ng/mL of OKT-3, and 2.5×10^8 antigen-presenting feeder cells. In some embodiments, the media comprises 500 mL of culture medium, 6000 IU/mL of IL-2, 15 μg of OKT-3, and 2.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media comprises 500 mL of culture medium and 15 μg of OKT-3 per 2.5×10^8 antigen-presenting feeder cells per container.

[001204] In some embodiments, the priming first expansion procedures described herein require an excess of feeder cells over TILs during the second expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from allogeneic healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation. In some embodiments, artificial antigen-presenting (aAPC) cells are used in place of PBMCs.

[001205] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the TIL expansion procedures described herein, including the exemplary procedures described in the figures and examples.

[001206] In some embodiments, artificial antigen presenting cells are used in the priming first expansion as a replacement for, or in combination with, PBMCs.

2. Cytokines

[001207] The expansion methods described herein generally use culture media with high doses of a cytokine, in particular IL-2, as is known in the art.

[001208] Alternatively, using combinations of cytokines for the priming first expansion of TILs is additionally possible, with combinations of two or more of IL-2, IL-15 and IL-21 as is generally outlined in International Publication No. WO 2015/189356 and WO 2015/189357, hereby expressly incorporated by reference in their entirety. Thus, possible combinations include IL-2 and IL-15, IL-2 and IL-21, IL-15 and IL-21, and IL-2, IL-15 and IL-21, with the latter finding particular use in many embodiments. The use of combinations of cytokines specifically favors the generation of lymphocytes, and in particular T-cells as described therein. *See*, Table 2.

[001209] In some embodiments, Step B may also include the addition of OKT-3 antibody or muromonab to the culture media, as described elsewhere herein. In some embodiments, Step B may

also include the addition of a 4-1BB agonist to the culture media, as described elsewhere herein. In some embodiments, Step B may also include the addition of an OX-40 agonist to the culture media, as described elsewhere herein. In addition, additives such as peroxisome proliferator-activated receptor gamma coactivator I-alpha agonists, including proliferator-activated receptor (PPAR)-gamma agonists such as a thiazolidinedione compound, may be used in the culture media during Step B, as described in U.S. Patent Application Publication No. US 2019/0307796 A1, the disclosure of which is incorporated by reference herein.

C. STEP C: Priming First Expansion to Rapid Second Expansion Transition

[001210] In some cases, the bulk TIL population obtained from the priming first expansion (which can include expansions sometimes referred to as pre-REP), including, for example the TIL population obtained from for example, Step B as indicated in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), can be subjected to a rapid second expansion (which can include expansions sometimes referred to as Rapid Expansion Protocol (REP)) and then cryopreserved as discussed below. Similarly, in the case where genetically modified TILs will be used in therapy, the expanded TIL population from the priming first expansion or the expanded TIL population from the rapid second expansion can be subjected to genetic modifications for suitable treatments prior to the expansion step or after the priming first expansion and prior to the rapid second expansion.

[001211] In some embodiments, the TILs obtained from the priming first expansion (for example, from Step B as indicated in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) are stored until phenotyped for selection. In some embodiments, the TILs obtained from the priming first expansion (for example, from Step B as indicated in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) are not stored and proceed directly to the rapid second expansion. In some embodiments, the TILs obtained from the priming first expansion are not cryopreserved after the priming first expansion and prior to the rapid second expansion. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, or 8 days from when tumor fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs at about 3 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs at about 3 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 4 days to 7

days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 4 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 5 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 5 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 6 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 6 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 7 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs at about 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated.

[001212] In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs at 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, or 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 1 day to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 1 day to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs 2 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs 2 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs 3 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the second expansion occurs 3 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 4 days to 7 days from when

fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 4 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 5 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 5 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 6 days to 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. . In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 6 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 7 days to 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 7 days from when fragmentation occurs and/or when the first priming expansion step is initiated. In some embodiments, the transition from the priming first expansion to the rapid second expansion occurs 8 days from when fragmentation occurs and/or when the first priming expansion step is initiated

[001213] In some embodiments, the TILs are not stored after the primary first expansion and prior to the rapid second expansion, and the TILs proceed directly to the rapid second expansion (for example, in some embodiments, there is no storage during the transition from Step B to Step D as shown in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)). In some embodiments, the transition occurs in closed system, as described herein. In some embodiments, the TILs from the priming first expansion, the second population of TILs, proceeds directly into the rapid second expansion with no transition period.

[001214] In some embodiments, the transition from the priming first expansion to the rapid second expansion, for example, Step C according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a GREX-10 or a GREX-100. In some embodiments, the closed system bioreactor is a single bioreactor. In some embodiments, the transition from the priming first expansion to the rapid second expansion involves a scale-up in container size. In some embodiments, the priming first expansion is performed in a smaller

container than the rapid second expansion. In some embodiments, the priming first expansion is performed in a GREX-100 and the rapid second expansion is performed in a GREX-500.

[001215] In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 48A-D) are transitioned to an activation or a gene-editing step. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, or 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 5 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 3 days to 4 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 8

days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 4 days to 5 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 7 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 5 days to 6 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 14 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 13 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 12 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 11 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 10 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 9 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 8 days from when fragmentation occurs. In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs at about 6 days to 7 days from when fragmentation occurs.

[001216] In some embodiments, the transition from the first expansion to the activation or gene-editing step occurs in a closed system, as described herein.

[001217] In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 and/or anti-CD38 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD38 beads for about 1-7 days. In some embodiments, the activation step comprises culturing the TILs in medium comprising anti-CD3 and anti-CD38 beads for about 1-7 days. In some embodiments, the activation step is performed for about 1-7 days. In some embodiments, the activation step is performed for about 1-7 days, about 1-6 days, about 2-6 days, about 3-6 days, about 4-6 days, about 5-6 days, about 1-5 days, about 2-5 days, about 3-5 days, about 4-5 days, about 1-4, days, about 2-4, days, about 3-4, days, about 1-3 days, about 2-3 days, about 1-2 days. In some embodiments, the activation step is performed for about 1 day. In some embodiments, the activation step is performed for about 2 days. In some embodiments, the activation step is performed for about 3 days. In some embodiments, the activation step is performed for about 4 days. In some embodiments, the activation step is performed for about 5 days. In some embodiments, the activation step is performed for about 6 days. In some embodiments, the activation step is performed for about 7 days.

[001218] Any suitable anti-CD3/anti-CD38 beads known to those in the art in view of the instant specification can be used. Suitable anti-CD3/anti-CD38 beads include, but are not limited to, commercially available products including, but not limited to, Dynabeads™ Human T-Activator CD3/CD28 for T Cell Expansion and Activation (available commercially from Invitrogen), ImmunoCult™ Human CD3/CD28 T Cell Activator (available commercially from StemCell Technologies), and T Cell TransAct™ (available commercially from Miltenyi Biotec).

[001219] In some embodiments, the activation step is optional. In some embodiments, the activation step is optional if the first expansion included OKT-3.

[001220] In some embodiments, the TILs obtained from the first expansion (for example, from Step B as indicated in Figure 48C-D) or from the activation step (for example, from Step C as indicated in Figure 48A-B) are transitioned to a gene-editing step.

[001221] In some embodiments, the gene-editing step comprises performing a sterile electroporation step on the population of TILs. In some embodiments, the sterile electroporation step mediates the transfer of at least one gene editor. According to some embodiments, the gene editor is a TALE nuclease system for modulating the expression of at least one protein. According to some embodiments, the TALE nuclease system downmodulates expression of PD-1. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CTLA-4. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of LAG-3. According to some embodiments, the

gene editor further comprises a TALE nuclease system that downmodulates expression of CISH. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of CBL-B. According to some embodiments, the gene editor further comprises a TALE nuclease system that downmodulates expression of TIGIT. According to some embodiments, the resulting TILs are PD-1 knockout TILs. According to some embodiments, the resulting TILs are CTLA-4 knockout TILs. According to some embodiments, the resulting TILs are LAG-3 knockout TILs. According to some embodiments, the resulting TILs are CISH knockout TILs. According to some embodiments, the resulting TILs are CBL-B knockout TILs. According to some embodiments, the resulting TILs are TIGIT knockout TILs. According to some embodiments, the resulting TILs exhibit downmodulated expression of PD-1 and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CTLA-4 and downmodulated expression of one or more of PD-1, LAG-3, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of LAG-3 and downmodulated expression of one or more of PD-1, CTLA-4, CISH, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CISH and downmodulated expression of one or more of PD-1, LAG-3, CTLA-4, TIGIT and CBL-B. According to some embodiments, the resulting TILs exhibit downmodulated expression of CBL-B and downmodulated expression of one or more of CTLA-4, LAG-3, CISH, TIGIT and PD-1. According to some embodiments, the resulting TILs are PD-1/CTLA-4 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CISH double knockout TILs. According to some embodiments, the resulting TILs are PD-1/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are PD-1/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/LAG-3 double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CISH double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CTLA-4/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CISH double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are LAG-3/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CISH/CBL-B double knockout TILs. According to some embodiments, the resulting TILs are CISH/TIGIT double knockout TILs. According to some embodiments, the resulting TILs are CBL-B/TIGIT double knockout TILs.

[001222] In some embodiments, the step of gene-editing further comprises a resting step. According to some embodiments, the resting step comprises incubating the fourth population of TILs at about 30-40 °C with about 5% CO2. According to some embodiments, the resting step is carried

out at about 30°C, about 30.5°C, about 31°C, about 31.5°C, about 32°C, about 32.5°C, about 33°C, about 33.5°C, about 34°C, about 34.5°C, about 35°C, about 35.5°C, about 36°C, about 36.5°C, about 37°C, about 37.5°C, about 38°C, about 38.5°C, about 39°C, about 39.5°C, about 40°C. According to some embodiments, the resting step is carried out for about 1 hour, about 2 hours, about 3 hours, about 4 hours, about 5 hours, about 6 hours, about 7 hours, about 8 hours, about 9 hours, about 10 hours, about 11 hours, about 12 hours, about 13 hours, about 14 hours, about 15 hours, about 16 hours, about 17 hours, about 18 hours, about 19 hours, about 20 hours, about 21 hours, about 22 hours, about 23 hours, about 24 hours. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to about 23 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 16 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 17 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 18 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 19 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 20 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 21 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 22 hours at about 30°C. According to some embodiments, the resting step comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 23 hours at about 30°C.

[001223] In some embodiments, the TILs obtained from the gene-editing step or the resting step (for example, from Step C as indicated in Figure 48A-D) are transitioned to a second expansion

step (for example, from Step D as indicated in Figure 48A-D). In some embodiments, the transition from the gene-editing step or the resting step to the second expansion step occurs at about 0.5 days, 1 day, 2 days, 3 days, or 4 days from the gene-editing step or the resting step.

[001224] In some embodiments, the transition from the gene-editing step or the resting step to the second expansion step occurs in a closed system, as described herein.

[001225] In some embodiments, the TILs are not stored after the gene-editing step or the resting step and prior to the second expansion, and the TILs proceed directly to the second expansion (for example, in some embodiments, there is no storage during the transition from Step C to Step D as shown in Figure 48A-D).

[001226] In some embodiments, the transition from the first expansion to the second expansion, for example, Step C according to Figure 48, is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a single bioreactor is employed. In some embodiments, the single bioreactor employed is for example a G-REX-10 or a G-REX-100 bioreactor. In some embodiments, the closed system bioreactor is a single bioreactor.

D. STEP D: Rapid Second Expansion

[001227] In some embodiments, the TIL cell population is further expanded in number after harvest and the priming first expansion, after Step A and Step B, and the transition referred to as Step C, as indicated in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)). This further expansion is referred to herein as the rapid second expansion or a rapid expansion, which can include expansion processes generally referred to in the art as a rapid expansion process (Rapid Expansion Protocol or REP; as well as processes as indicated in Step D of Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). The rapid second expansion is generally accomplished using a culture media comprising a number of components, including feeder cells, a cytokine source, and an anti-CD3 antibody, in a gas-permeable container. In some embodiments, 1 day, 2 days, 3 days, or 4 days after initiation of the rapid second expansion (*i.e.*, at days 8, 9, 10, or 11 of the overall Gen 3 process), the TILs are transferred to a larger volume container.

[001228] In some embodiments, the rapid second expansion (which can include expansions sometimes referred to as REP; as well as processes as indicated in Step D of Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) of TIL can be performed using any TIL flasks or

containers known by those of skill in the art. In some embodiments, the second TIL expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 1 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 1 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 2 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 2 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 3 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 3 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 4 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 4 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 5 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 5 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 6 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 6 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 7 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 7 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 8 days to about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 8 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 9 days to about 10 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 1 day after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 2 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 3 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 4 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 5 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 6 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 7 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion

can proceed for about 8 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 9 days after initiation of the rapid second expansion. In some embodiments, the second TIL expansion can proceed for about 10 days after initiation of the rapid second expansion.

[001229] In some embodiments, the rapid second expansion can be performed in a gas permeable container using the methods of the present disclosure (including, for example, expansions referred to as REP; as well as processes as indicated in Step D of Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the TILs are expanded in the rapid second expansion in the presence of IL-2, OKT-3, and feeder cells (also referred herein as "antigen-presenting cells"). In some embodiments, the TILs are expanded in the rapid second expansion in the presence of IL-2, OKT-3, and feeder cells, wherein the feeder cells are added to a final concentration that is twice, 2.4 times, 2.5 times, 3 times, 3.5 times or 4 times the concentration of feeder cells present in the priming first expansion. For example, TILs can be rapidly expanded using non-specific T-cell receptor stimulation in the presence of interleukin-2 (IL-2) or interleukin-15 (IL-15). The non-specific T-cell receptor stimulus can include, for example, an anti-CD3 antibody, such as about 30 ng/mL of OKT3, a mouse monoclonal anti-CD3 antibody (commercially available from Ortho-McNeil, Raritan, NJ or Miltenyi Biotech, Auburn, CA) or UHCT-1 (commercially available from BioLegend, San Diego, CA, USA). TILs can be expanded to induce further stimulation of the TILs *in vitro* by including one or more antigens during the second expansion, including antigenic portions thereof, such as epitope(s), of the cancer, which can be optionally expressed from a vector, such as a human leukocyte antigen A2 (HLA-A2) binding peptide, *e.g.*, 0.3 μM MART-1 :26-35 (27 L) or gpl 00:209-217 (210M), optionally in the presence of a T-cell growth factor, such as 300 IU/mL IL-2 or IL-15. Other suitable antigens may include, *e.g.*, NY-ESO-1, TRP-1, TRP-2, tyrosinase cancer antigen, MAGE-A3, SSX-2, and VEGFR2, or antigenic portions thereof. TIL may also be rapidly expanded by re-stimulation with the same antigen(s) of the cancer pulsed onto HLA-A2-expressing antigen-presenting cells. Alternatively, the TILs can be further re-stimulated with, *e.g.*, example, irradiated, autologous lymphocytes or with irradiated HLA-A2+ allogeneic lymphocytes and IL-2. In some embodiments, the re-stimulation occurs as part of the second expansion. In some embodiments, the second expansion occurs in the presence of irradiated, autologous lymphocytes or with irradiated HLA-A2+ allogeneic lymphocytes and IL-2.

[001230] In some embodiments, the cell culture medium further comprises IL-2. In some embodiments, the cell culture medium comprises about 3000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises about 1000 IU/mL, about 1500 IU/mL, about 2000 IU/mL, about 2500 IU/mL, about 3000 IU/mL, about 3500 IU/mL, about 4000 IU/mL, about 4500 IU/mL, about

5000 IU/mL, about 5500 IU/mL, about 6000 IU/mL, about 6500 IU/mL, about 7000 IU/mL, about 7500 IU/mL, or about 8000 IU/mL of IL-2. In some embodiments, the cell culture medium comprises between 1000 and 2000 IU/mL, between 2000 and 3000 IU/mL, between 3000 and 4000 IU/mL, between 4000 and 5000 IU/mL, between 5000 and 6000 IU/mL, between 6000 and 7000 IU/mL, between 7000 and 8000 IU/mL, or between 8000 IU/mL of IL-2.

[001231] In some embodiments, the cell culture medium comprises OKT-3 antibody. In some embodiments, the cell culture medium comprises about 30 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises about 0.1 ng/mL, about 0.5 ng/mL, about 1 ng/mL, about 2.5 ng/mL, about 5 ng/mL, about 7.5 ng/mL, about 10 ng/mL, about 15 ng/mL, about 20 ng/mL, about 25 ng/mL, about 30 ng/mL, about 35 ng/mL, about 40 ng/mL, about 50 ng/mL, about 60 ng/mL, about 70 ng/mL, about 80 ng/mL, about 90 ng/mL, about 100 ng/mL, about 200 ng/mL, about 500 ng/mL, and about 1 μg/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 0.1 ng/mL and 1 ng/mL, between 1 ng/mL and 5 ng/mL, between 5 ng/mL and 10 ng/mL, between 10 ng/mL and 20 ng/mL, between 20 ng/mL and 30 ng/mL, between 30 ng/mL and 40 ng/mL, between 40 ng/mL and 50 ng/mL, and between 50 ng/mL and 100 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 15 ng/mL and 30 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises between 30 ng/mL and 60 ng/mL of OKT-3 antibody. In some embodiments, the cell culture medium comprises about 30 ng/mL OKT-3. In some embodiments, the cell culture medium comprises about 60 ng/mL OKT-3. In some embodiments, the OKT-3 antibody is muromonab.

[001232] In some embodiments, the media in the rapid second expansion comprises IL-2. In some embodiments, the media comprises 6000 IU/mL of IL-2. In some embodiments, the media in the rapid second expansion comprises antigen-presenting feeder cells. In some embodiments, the media in the rapid second expansion comprises 7.5×10^8 antigen-presenting feeder cells per container. In some embodiments, the media in the rapid second expansion comprises OKT-3. In some embodiments, the in the rapid second expansion media comprises 500 mL of culture medium and 30 μg of OKT-3 per container. In some embodiments, the container is a GREX100 MCS flask. In some embodiments, the in the rapid second expansion media comprises 6000 IU/mL of IL-2, 60 ng/mL of OKT-3, and 7.5×10^8 antigen-presenting feeder cells. In some embodiments, the media comprises 500 mL of culture medium and 6000 IU/mL of IL-2, 30 μg of OKT-3, and 7.5×10^8 antigen-presenting feeder cells per container.

[001233] In some embodiments, the media in the rapid second expansion comprises IL-2. In some embodiments, the media comprises 6000 IU/mL of IL-2. In some embodiments, the media in the rapid second expansion comprises antigen-presenting feeder cells. In some embodiments, the media comprises between 5×10^8 and 7.5×10^8 antigen-presenting feeder cells per container. In some

embodiments, the media in the rapid second expansion comprises OKT-3. In some embodiments, the media in the rapid second expansion comprises 500 mL of culture medium and 30 μg of OKT-3 per container. In some embodiments, the container is a GREX100 MCS flask. In some embodiments, the media in the rapid second expansion comprises 6000 IU/mL of IL-2, 60 ng/mL of OKT-3, and between 5×10^8 and 7.5×10^8 antigen-presenting feeder cells. In some embodiments, the media in the rapid second expansion comprises 500 mL of culture medium and 6000 IU/mL of IL-2, 30 μg of OKT-3, and between 5×10^8 and 7.5×10^8 antigen-presenting feeder cells per container.

[001234] In some embodiments, the cell culture medium comprises one or more TNFRSF agonists in a cell culture medium. In some embodiments, the TNFRSF agonist comprises a 4-1BB agonist. In some embodiments, the TNFRSF agonist is a 4-1BB agonist, and the 4-1BB agonist is selected from the group consisting of urelumab, utomilumab, EU-101, a fusion protein, and fragments, derivatives, variants, biosimilars, and combinations thereof. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 0.1 μg/mL and 100 μg/mL. In some embodiments, the TNFRSF agonist is added at a concentration sufficient to achieve a concentration in the cell culture medium of between 20 μg/mL and 40 μg/mL.

[001235] In some embodiments, in addition to one or more TNFRSF agonists, the cell culture medium further comprises IL-2 at an initial concentration of about 3000 IU/mL and OKT-3 antibody at an initial concentration of about 30 ng/mL, and wherein the one or more TNFRSF agonists comprises a 4-1BB agonist.

[001236] In some embodiments, a combination of IL-2, IL-7, IL-15, and/or IL-21 are employed as a combination during the second expansion. In some embodiments, IL-2, IL-7, IL-15, and/or IL-21 as well as any combinations thereof can be included during the second expansion, including, for example during a Step D processes according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as described herein. In some embodiments, a combination of IL-2, IL-15, and IL-21 are employed as a combination during the second expansion. In some embodiments, IL-2, IL-15, and IL-21 as well as any combinations thereof can be included during Step D processes according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and as described herein.

[001237] In some embodiments, the second expansion can be conducted in a supplemented cell culture medium comprising IL-2, OKT-3, antigen-presenting feeder cells, and optionally a TNFRSF agonist. In some embodiments, the second expansion occurs in a supplemented cell culture medium. In some embodiments, the supplemented cell culture medium comprises IL-2, OKT-3, and antigen-presenting feeder cells. In some embodiments, the second cell culture medium comprises IL-2, OKT-

3, and antigen-presenting cells (APCs; also referred to as antigen-presenting feeder cells). In some embodiments, the second expansion occurs in a cell culture medium comprising IL-2, OKT-3, and antigen-presenting feeder cells (*i.e.*, antigen presenting cells).

[001238] In some embodiments, the second expansion culture media comprises about 500 IU/mL of IL-15, about 400 IU/mL of IL-15, about 300 IU/mL of IL-15, about 200 IU/mL of IL-15, about 180 IU/mL of IL-15, about 160 IU/mL of IL-15, about 140 IU/mL of IL-15, about 120 IU/mL of IL-15, or about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 500 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 400 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 300 IU/mL of IL-15 to about 100 IU/mL of IL-15. In some embodiments, the second expansion culture media comprises about 200 IU/mL of IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15. In some embodiments, the cell culture medium further comprises IL-15. In some embodiments, the cell culture medium comprises about 180 IU/mL of IL-15.

[001239] In some embodiments, the second expansion culture media comprises about 20 IU/mL of IL-21, about 15 IU/mL of IL-21, about 12 IU/mL of IL-21, about 10 IU/mL of IL-21, about 5 IU/mL of IL-21, about 4 IU/mL of IL-21, about 3 IU/mL of IL-21, about 2 IU/mL of IL-21, about 1 IU/mL of IL-21, or about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 20 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 15 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 12 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 10 IU/mL of IL-21 to about 0.5 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 5 IU/mL of IL-21 to about 1 IU/mL of IL-21. In some embodiments, the second expansion culture media comprises about 2 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21. In some embodiments, the cell culture medium comprises about 0.5 IU/mL of IL-21. In some embodiments, the cell culture medium further comprises IL-21. In some embodiments, the cell culture medium comprises about 1 IU/mL of IL-21.

[001240] In some embodiments, the antigen-presenting feeder cells (APCs) are PBMCs. In some embodiments, the ratio of TILs to PBMCs and/or antigen-presenting cells in the rapid expansion and/or the second expansion is about 1 to 10, about 1 to 15, about 1 to 20, about 1 to 25, about 1 to 30, about 1 to 35, about 1 to 40, about 1 to 45, about 1 to 50, about 1 to 75, about 1 to 100, about 1 to 125, about 1 to 150, about 1 to 175, about 1 to 200, about 1 to 225, about 1 to 250, about 1 to 275, about 1 to 300, about 1 to 325, about 1 to 350, about 1 to 375, about 1 to 400, or about 1 to 500. In some embodiments, the ratio of TILs to PBMCs in the rapid expansion and/or the second expansion is

between 1 to 50 and 1 to 300. In some embodiments, the ratio of TILs to PBMCs in the rapid expansion and/or the second expansion is between 1 to 100 and 1 to 200.

[001241] In some embodiments, REP and/or the rapid second expansion is performed in flasks with the bulk TILs being mixed with a 100- or 200-fold excess of inactivated feeder cells, wherein the feeder cell concentration is at least 1.1 times (1.1X), 1.2X, 1.3X, 1.4X, 1.5X, 1.6X, 1.7X, 1.8X, 1.8X, 2X, 2.1X2.2X, 2.3X, 2.4X, 2.5X, 2.6X, 2.7X, 2.8X, 2.9X, 3.0X, 3.1X, 3.2X, 3.3X, 3.4X, 3.5X, 3.6X, 3.7X, 3.8X, 3.9X or 4.0X the feeder cell concentration in the priming first expansion, 30 ng/mL OKT3 anti-CD3 antibody and 6000 IU/mL IL-2 in 150 mL media. Media replacement is done (generally 2/3 media replacement via aspiration of 2/3 of spent media and replacement with an equal volume of fresh media) until the cells are transferred to an alternative growth chamber. Alternative growth chambers include G-REX flasks and gas permeable containers as more fully discussed below.

[001242] In some embodiments, the rapid second expansion (which can include processes referred to as the REP process) is 7 to 9 days, as discussed in the examples and figures. In some embodiments, the second expansion is 7 days. In some embodiments, the second expansion is 8 days. In some embodiments, the second expansion is 9 days.

[001243] In some embodiments, the second expansion (which can include expansions referred to as REP, as well as those referred to in Step D of Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) may be performed in 500 mL capacity gas permeable flasks with 100 cm gas-permeable silicon bottoms (G-REX 100, commercially available from Wilson Wolf Manufacturing Corporation, New Brighton, MN, USA), 5×10^6 or 10×10^6 TIL may be cultured with PBMCs in 400 mL of 50/50 medium, supplemented with 5% human AB serum, 3000 IU per mL of IL-2 and 30 ng per mL of anti-CD3 (OKT3). The G-REX 100 flasks may be incubated at 37°C in 5% CO_2. On day 5, 250 mL of supernatant may be removed and placed into centrifuge bottles and centrifuged at 1500 rpm ($491 \times g$) for 10 minutes. The TIL pellets may be re-suspended with 150 mL of fresh medium with 5% human AB serum, 6000 IU per mL of IL-2, and added back to the original GREX-100 flasks. When TIL are expanded serially in GREX-100 flasks, on day 10 or 11 the TILs can be moved to a larger flask, such as a GREX-500. The cells may be harvested on day 14 of culture. The cells may be harvested on day 15 of culture. The cells may be harvested on day 16 of culture. In some embodiments, media replacement is done until the cells are transferred to an alternative growth chamber. In some embodiments, 2/3 of the media is replaced by aspiration of spent media and replacement with an equal volume of fresh media. In some embodiments, alternative growth chambers include GREX flasks and gas permeable containers as more fully discussed below.

[001244] In some embodiments, the culture medium used in the expansion processes disclosed herein is a serum-free medium or a defined medium. In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or a serum replacement. In some embodiments, the serum-free or defined medium is used to prevent and/or decrease experimental variation due in part to the lot-to-lot variation of serum-containing media.

[001245] In some embodiments, the serum-free or defined medium comprises a basal cell medium and a serum supplement and/or serum replacement. In some embodiments, the basal cell medium includes, but is not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium , CTS™ OpTmizer™ T-Cell Expansion SFM, CTS™ AIM-V Medium, CTS™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001246] In some embodiments, the serum supplement or serum replacement includes, but is not limited to one or more of CTS™ OpTmizer T-Cell Expansion Serum Supplement, CTS™ Immune Cell Serum Replacement, one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, one or more antibiotics, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L- histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Gc^{4+}, Sc^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or 2-mercaptoethanol.

[001247] In some embodiments, the CTS™OpTmizer™ T-cell Immune Cell Serum Replacement is used with conventional growth media, including but not limited to CTS™ OpTmizer™ T-cell Expansion Basal Medium, CTS™ OpTmizer™ T-cell Expansion SFM, CTS™ AIM-V Medium, CST™ AIM-V SFM, LymphoONE™ T-Cell Expansion Xeno-Free Medium, Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001248] In some embodiments, the total serum replacement concentration (vol%) in the serum-free or defined medium is from about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%,

14%, 15%, 16%, 17%, 18%, 19%, or 20% by volume of the total serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 3% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 5% of the total volume of the serum-free or defined medium. In some embodiments, the total serum replacement concentration is about 10% of the total volume of the serum-free or defined medium.

[001249] In some embodiments, the serum-free or defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM.

[001250] In some embodiments, the defined medium is CTS™ OpTmizer™ T-cell Expansion SFM (ThermoFisher Scientific). Any formulation of CTS™ OpTmizer™ is useful in the present invention. CTS™ OpTmizer™ T-cell Expansion SFM is a combination of 1L CTS™ OpTmizer™ T-cell Expansion Basal Medium and 26 mL CTS™ OpTmizer™ T-Cell Expansion Supplement, which are mixed together prior to use. In some embodiments, the CTS™ OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), along with 2-mercaptoethanol at 55mM. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific), 55mM of 2-mercaptoethanol, and 2mM of L-glutamine, and further comprises about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is

supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and 55mM of 2-mercaptoethanol, and further comprises about 1000 IU/mL to about 6000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 1000 IU/mL to about 8000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 3000 IU/mL of IL-2. In some embodiments, the CTS™OpTmizer™ T-cell Expansion SFM is supplemented with about 3% of the CTS™ Immune Cell Serum Replacement (SR) (ThermoFisher Scientific) and about 2mM glutamine, and further comprises about 6000 IU/mL of IL-2.

[001251] In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of from about 0.1mM to about 10mM, 0.5mM to about 9mM, 1mM to about 8mM, 2mM to about 7mM, 3mM to about 6mM, or 4mM to about 5 mM. In some embodiments, the serum-free medium or defined medium is supplemented with glutamine (i.e., GlutaMAX®) at a concentration of about 2mM.

[001252] In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of from about 5mM to about 150mM, 10mM to about 140mM, 15mM to about 130mM, 20mM to about 120mM, 25mM to about 110mM, 30mM to about 100mM, 35mM to about 95mM, 40mM to about 90mM, 45mM to about 85mM, 50mM to about 80mM, 55mM to about 75mM, 60mM to about 70mM, or about 65mM. In some embodiments, the serum-free medium or defined medium is supplemented with 2-mercaptoethanol at a concentration of about 55mM.

[001253] In some embodiments, the defined media described in International Patent Application Publication No. WO/1998/030679 and U.S. Patent Application Publication No. US 2002/0076747 A1, which is herein incorporated by reference, are useful in the present invention. In that publication, serum-free eukaryotic cell culture media are described. The serum-free, eukaryotic cell culture medium includes a basal cell culture medium supplemented with a serum-free supplement capable of supporting the growth of cells in serum- free culture. The serum-free eukaryotic cell culture medium supplement comprises or is obtained by combining one or more ingredients selected from the group consisting of one or more albumins or albumin substitutes, one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more

insulins or insulin substitutes, one or more collagen precursors, one or more trace elements, and one or more antibiotics. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or beta-mercaptoethanol. In some embodiments, the defined medium comprises an albumin or an albumin substitute and one or more ingredients selected from group consisting of one or more amino acids, one or more vitamins, one or more transferrins or transferrin substitutes, one or more antioxidants, one or more insulins or insulin substitutes, one or more collagen precursors, and one or more trace elements. In some embodiments, the defined medium comprises albumin and one or more ingredients selected from the group consisting of glycine, L- histidine, L-isoleucine, L-methionine, L-phenylalanine, L-proline, L- hydroxyproline, L-serine, L-threonine, L-tryptophan, L-tyrosine, L-valine, thiamine, reduced glutathione, L-ascorbic acid-2-phosphate, iron saturated transferrin, insulin, and compounds containing the trace element moieties Ag^{+}, Al^{3+}, Ba^{2+}, Cd^{2+}, Co^{2+}, Cr^{3+}, Ge^{4+}, Se^{4+}, Br, T, Mn^{2+}, P, Si^{4+}, V^{5+}, Mo^{6+}, Ni^{2+}, Rb^{+}, Sn^{2+} and Zr^{4+}. In some embodiments, the basal cell media is selected from the group consisting of Dulbecco's Modified Eagle's Medium (DMEM), Minimal Essential Medium (MEM), Basal Medium Eagle (BME), RPMI 1640, F-10, F-12, Minimal Essential Medium (αMEM), Glasgow's Minimal Essential Medium (G-MEM), RPMI growth medium, and Iscove's Modified Dulbecco's Medium.

[001254] In some embodiments, the concentration of glycine in the defined medium is in the range of from about 5-200 mg/L, the concentration of L- histidine is about 5-250 mg/L, the concentration of L-isoleucine is about 5-300 mg/L, the concentration of L-methionine is about 5-200 mg/L, the concentration of L-phenylalanine is about 5-400 mg/L, the concentration of L-proline is about 1-1000 mg/L, the concentration of L- hydroxyproline is about 1-45 mg/L, the concentration of L-serine is about 1-250 mg/L, the concentration of L-threonine is about 10-500 mg/L, the concentration of L-tryptophan is about 2-110 mg/L, the concentration of L-tyrosine is about 3-175 mg/L, the concentration of L-valine is about 5-500 mg/L, the concentration of thiamine is about 1-20 mg/L, the concentration of reduced glutathione is about 1-20 mg/L, the concentration of L-ascorbic acid-2-phosphate is about 1-200 mg/L, the concentration of iron saturated transferrin is about 1-50 mg/L, the concentration of insulin is about 1-100 mg/L, the concentration of sodium selenite is about 0.000001-0.0001 mg/L, and the concentration of albumin (*e.g.*, AlbuMAX® I) is about 5000-50,000 mg/L.

[001255] In some embodiments, the non-trace element moiety ingredients in the defined medium are present in the concentration ranges listed in the column under the heading "Concentration Range in 1X Medium" in Table 4. In other embodiments, the non-trace element moiety ingredients in the defined medium are present in the final concentrations listed in the column under the heading "A Preferred Embodiment of the 1X Medium" in Table 4. In other embodiments, the defined medium is a basal cell medium comprising a serum free supplement. In some of these embodiments, the serum free

supplement comprises non-trace moiety ingredients of the type and in the concentrations listed in the column under the heading "A Preferred Embodiment in Supplement" in Table 4.

[001256] In some embodiments, the osmolarity of the defined medium is between about 260 and 350 mOsmol. In some embodiments, the osmolarity is between about 280 and 310 mOsmol. In some embodiments, the defined medium is supplemented with up to about 3.7 g/L, or about 2.2 g/L sodium bicarbonate. The defined medium can be further supplemented with L-glutamine (final concentration of about 2 mM), one or more antibiotics, non-essential amino acids (NEAA; final concentration of about 100 μM), 2-mercaptoethanol (final concentration of about 100 μM).

[001257] In some embodiments, the defined media described in Smith, *et al.*, *Clin Transl Immunology*, 4(1) 2015 (doi: 10.1038/cti.2014.31) are useful in the present invention. Briefly, RPMI or CTS™ OpTmizer™ was used as the basal cell medium, and supplemented with either 0, 2%, 5%, or 10% CTS™ Immune Cell Serum Replacement.

[001258] In some embodiments, the cell medium in the first and/or second gas permeable container is unfiltered. The use of unfiltered cell medium may simplify the procedures necessary to expand the number of cells. In some embodiments, the cell medium in the first and/or second gas permeable container lacks beta-mercaptoethanol (BME or βME; also known as 2-mercaptoethanol, CAS 60-24-2).

[001259] In some embodiments, the rapid second expansion (including expansions referred to as REP) is performed and further comprises a step wherein TILs are selected for superior tumor reactivity. Any selection method known in the art may be used. For example, the methods described in U.S. Patent Application Publication No. 2016/0010058 A1, the disclosures of which are incorporated herein by reference, may be used for selection of TILs for superior tumor reactivity.

[001260] Optionally, a cell viability assay can be performed after the rapid second expansion (including expansions referred to as the REP expansion), using standard assays known in the art. For example, a trypan blue exclusion assay can be done on a sample of the bulk TILs, which selectively labels dead cells and allows a viability assessment. In some embodiments, TIL samples can be counted and viability determined using a Cellometer K2 automated cell counter (Nexcelom Bioscience, Lawrence, MA). In some embodiments, viability is determined according to the standard Cellometer K2 Image Cytometer Automatic Cell Counter protocol.

[001261] The diverse antigen receptors of T and B lymphocytes are produced by somatic recombination of a limited, but large number of gene segments. These gene segments: V (variable), D (diversity), J (joining), and C (constant), determine the binding specificity and downstream applications of immunoglobulins and T-cell receptors (TCRs). The present invention provides a

method for generating TILs which exhibit and increase the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity. In some embodiments, the TILs obtained in the second expansion exhibit an increase in the T-cell repertoire diversity. In some embodiments, the increase in diversity is an increase in the immunoglobulin diversity and/or the T-cell receptor diversity. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin heavy chain. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin light chain. In some embodiments, the diversity is in the T-cell receptor. In some embodiments, the diversity is in one of the T-cell receptors selected from the group consisting of alpha, beta, gamma, and delta receptors. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha and/or beta. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) beta. In some embodiments, there is an increase in the expression of TCRab (*i.e.*, TCRα/β).

[001262] In some embodiments, the rapid second expansion culture medium (*e.g.*, sometimes referred to as CM2 or the second cell culture medium), comprises IL-2, OKT-3, as well as the antigen-presenting feeder cells (APCs), as discussed in more detail below. In some embodiments, the rapid second expansion culture medium (*e.g.*, sometimes referred to as CM2 or the second cell culture medium), comprises 6000 IU/mL IL-2, 30 ug/flask OKT-3, as well as 7.5×10^8 antigen-presenting feeder cells (APCs), as discussed in more detail below. In some embodiments, the rapid second expansion culture medium (*e.g.*, sometimes referred to as CM2 or the second cell culture medium), comprises IL-2, OKT-3, as well as the antigen-presenting feeder cells (APCs), as discussed in more detail below. In some embodiments, the rapid second expansion culture medium (*e.g.*, sometimes referred to as CM2 or the second cell culture medium), comprises 6000 IU/mL IL-2, 30 ug/flask OKT-3, as well as 5×10^8 antigen-presenting feeder cells (APCs), as discussed in more detail below.

[001263] In some embodiments, the rapid second expansion, for example, Step D according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a bioreactor is employed. In some embodiments, a bioreactor is employed as the container. In some embodiments, the bioreactor employed is for example a G-REX-100 or a G-REX-500. In some embodiments, the bioreactor employed is a G-REX-100. In some embodiments, the bioreactor employed is a G-REX-500.

[001264] In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (a) performing the rapid second expansion by culturing

TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer of the TILs in the small scale culture to a second container larger than the first container, *e.g.*, a G-REX-500-MCS container, and culturing the TILs from the small scale culture in a larger scale culture in the second container for a period of about 4 to 7 days.

[001265] In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling out of the culture by: (a) performing the rapid second expansion by culturing TILs in a first small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer and apportioning of the TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the TILs from first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days.

[001266] In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations of TILs.

[001267] In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 3 to 7 days, and then (b) effecting the transfer and apportioning of the TILs from the small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX-500MCS containers, wherein in each second container the portion of the TILs from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 4 to 7 days.

[001268] In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid or second expansion by culturing TILs in a small scale culture in a first container, *e.g.*, a G-REX-100 MCS container, for a period of about 5 days, and then (b) effecting the transfer and apportioning of the TILs from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX-500 MCS containers, wherein in each second container the portion of the TILs from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 6 days.

[001269] In some embodiments, upon the splitting of the rapid second expansion, each second container comprises at least 10^8 TILs. In some embodiments, upon the splitting of the rapid or second

expansion, each second container comprises at least 10^8 TILs, at least 10^9 TILs, or at least 10^{10} TILs. In one exemplary embodiment, each second container comprises at least 10^{10} TILs.

[001270] In some embodiments, the first small scale TIL culture is apportioned into a plurality of subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations. In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2, 3, 4, or 5 subpopulations.

[001271] In some embodiments, after the completion of the rapid second expansion, the plurality of subpopulations comprises a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid or second expansion, one or more subpopulations of TILs are pooled together to produce a therapeutically effective amount of TILs. In some embodiments, after the completion of the rapid expansion, each subpopulation of TILs comprises a therapeutically effective amount of TILs.

[001272] In some embodiments, the rapid second expansion is performed for a period of about 3 to 7 days before being split into a plurality of steps. In some embodiments, the splitting of the rapid second expansion occurs at about day 3, day 4, day 5, day 6, or day 7 after the initiation of the rapid or second expansion.

[001273] In some embodiments, the splitting of the rapid second expansion occurs at about day 7, day 8, day 9, day 10, day 11, day 12, day 13, day 14, day 15, or day 16 day 17, or day 18 after the initiation of the first expansion (*i.e.*, pre-REP expansion). In one exemplary embodiment, the splitting of the rapid or second expansion occurs at about day 16 after the initiation of the first expansion.

[001274] In some embodiments, the rapid second expansion is further performed for a period of about 7 to 11 days after the splitting. In some embodiments, the rapid second expansion is further performed for a period of about 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, or 11 days after the splitting.

[001275] In some embodiments, the cell culture medium used for the rapid second expansion before the splitting comprises the same components as the cell culture medium used for the rapid second expansion after the splitting. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting comprises different components from the cell culture medium used for the rapid second expansion after the splitting.

[001276] In some embodiments, the cell culture medium used for the rapid second expansion before the splitting comprises IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting

comprises IL-2, OKT-3, and further optionally APCs. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting comprises IL-2, OKT-3 and APCs.

[001277] In some embodiments, the cell culture medium used for the rapid second expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting is generated by supplementing the cell culture medium in the first expansion with fresh culture medium comprising IL-2, OKT-3 and APCs. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, optionally OKT-3 and further optionally APCs. In some embodiments, the cell culture medium used for the rapid second expansion before the splitting is generated by replacing the cell culture medium in the first expansion with fresh cell culture medium comprising IL-2, OKT-3 and APCs.

[001278] In some embodiments, the cell culture medium used for the rapid second expansion after the splitting comprises IL-2, and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid second expansion after the splitting comprises IL-2, and OKT-3. In some embodiments, the cell culture medium used for the rapid second expansion after the splitting is generated by replacing the cell culture medium used for the rapid second expansion before the splitting with fresh culture medium comprising IL-2 and optionally OKT-3. In some embodiments, the cell culture medium used for the rapid second expansion after the splitting is generated by replacing the cell culture medium used for the rapid second expansion before the splitting with fresh culture medium comprising IL-2 and OKT-3.

1. Feeder Cells and Antigen Presenting Cells

[001279] In some embodiments, the rapid second expansion procedures described herein (for example including expansion such as those described in Step D from Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as well as those referred to as REP) require an excess of feeder cells during REP TIL expansion and/or during the rapid second expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation.

[001280] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the REP procedures, as described in the examples, which provides an exemplary protocol for evaluating the replication incompetence of irradiate allogeneic PBMCs.

[001281] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells on day 7 or 14 is less than the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion).

[001282] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in the presence of OKT3 and IL-2, on day 7 and day 14 has not increased from the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion). In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 3000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 60 ng/mL OKT3 antibody and 6000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 60 ng/mL OKT3 antibody and 3000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30 ng/mL OKT3 antibody and 6000 IU/mL IL-2.

[001283] In some embodiments, PBMCs are considered replication incompetent and acceptable for use in the TIL expansion procedures described herein if the total number of viable cells, cultured in the presence of OKT3 and IL-2, on day 7 and day 14 has not increased from the initial viable cell number put into culture on day 0 of the REP and/or day 0 of the second expansion (*i.e.*, the start day of the second expansion). In some embodiments, the PBMCs are cultured in the presence of 30-60 ng/mL OKT3 antibody and 1000-6000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30-60 ng/mL OKT3 antibody and 2000-5000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30-60 ng/mL OKT3 antibody and 2000-4000 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30-60 ng/mL OKT3 antibody and 2500-3500 IU/mL IL-2. In some embodiments, the PBMCs are cultured in the presence of 30-60 ng/mL OKT3 antibody and 6000 IU/mL IL-2.

[001284] In some embodiments, the antigen-presenting feeder cells are PBMCs. In some embodiments, the antigen-presenting feeder cells are artificial antigen-presenting feeder cells. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is about 1 to 10, about 1 to 25, about 1 to 50, about 1 to 100, about 1 to 125, about 1 to 150, about 1 to 175, about 1 to 200, about 1 to 225, about 1 to 250, about 1 to 275, about 1 to 300, about 1 to 325, about 1 to 350, about 1 to 375, about 1 to 400, or about 1 to 500. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is between 1 to 50 and 1 to 300. In some embodiments, the ratio of TILs to antigen-presenting feeder cells in the second expansion is between 1 to 100 and 1 to 200.

[001285] In some embodiments, the second expansion procedures described herein require a ratio of about 5×10^8 feeder cells to about 100×10^6 TILs. In some embodiments, the second expansion procedures described herein require a ratio of about 7.5×10^8 feeder cells to about 100×10^6 TILs. In some embodiments, the second expansion procedures described herein require a ratio of about 5×10^8 feeder cells to about 50×10^6 TILs. In some embodiments, the second expansion procedures described herein require a ratio of about 7.5×10^8 feeder cells to about 50×10^6 TILs. In yet another embodiment, the second expansion procedures described herein require about 5×10^8 feeder cells to about 25×10^6 TILs. In yet another embodiment, the second expansion procedures described herein require about 7.5×10^8 feeder cells to about 25×10^6 TILs. In yet another embodiment, the rapid second expansion requires twice the number of feeder cells as the rapid second expansion. In yet another embodiment, when the priming first expansion described herein requires about 2.5×10^8 feeder cells, the rapid second expansion requires about 5×10^8 feeder cells. In yet another embodiment, when the priming first expansion described herein requires about 2.5×10^8 feeder cells, the rapid second expansion requires about 7.5×10^8 feeder cells. In yet another embodiment, the rapid second expansion requires two times (2.0X), 2.5X, 3.0X, 3.5X or 4.0X the number of feeder cells as the priming first expansion.

[001286] In some embodiments, the rapid second expansion procedures described herein require an excess of feeder cells during the rapid second expansion. In many embodiments, the feeder cells are peripheral blood mononuclear cells (PBMCs) obtained from standard whole blood units from allogeneic healthy blood donors. The PBMCs are obtained using standard methods such as Ficoll-Paque gradient separation. In some embodiments, artificial antigen-presenting (aAPC) cells are used in place of PBMCs. In some embodiments, the PBMCs are added to the rapid second expansion at twice the concentration of PBMCs that were added to the priming first expansion.

[001287] In general, the allogenic PBMCs are inactivated, either via irradiation or heat treatment, and used in the TIL expansion procedures described herein, including the exemplary procedures described in the figures and examples.

[001288] In some embodiments, artificial antigen presenting cells are used in the rapid second expansion as a replacement for, or in combination with, PBMCs.

2. Cytokines

[001289] The rapid second expansion methods described herein generally use culture media with high doses of a cytokine, in particular IL-2, as is known in the art.

[001290] Alternatively, using combinations of cytokines for the rapid second expansion of TILs is additionally possible, with combinations of two or more of IL-2, IL-15 and IL-21 as is generally

outlined in WO 2015/189356 and WO 2015/189357, hereby expressly incorporated by reference in their entirety. Thus, possible combinations include IL-2 and IL-15, IL-2 and IL-21, IL-15 and IL-21, and IL-2, IL-15 and IL-21, with the latter finding particular use in many embodiments. The use of combinations of cytokines specifically favors the generation of lymphocytes, and in particular T-cells as described therein.

[001291] In some embodiments, Step D (from in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) may also include the addition of OKT-3 antibody or muromonab to the culture media, as described elsewhere herein. In some embodiments, Step D may also include the addition of a 4-1BB agonist to the culture media, as described elsewhere herein. In some embodiments, Step D (from, in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) may also include the addition of an OX-40 agonist to the culture media, as described elsewhere herein. In addition, additives such as peroxisome proliferator-activated receptor gamma coactivator I-alpha agonists, including proliferator-activated receptor (PPAR)-gamma agonists such as a thiazolidinedione compound, may be used in the culture media during Step D (from, in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as described in U.S. Patent Application Publication No. US 2019/0307796 A1, the disclosure of which is incorporated by reference herein.

E. STEP E: Harvest TILs

[001292] After the rapid second expansion step, cells can be harvested. In some embodiments the TILs are harvested after one, two, three, four or more expansion steps, for example as provided in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments the TILs are harvested after two expansion steps, for example as provided in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments the TILs are harvested after two expansion steps, one priming first expansion and one rapid second expansion, for example as provided in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001293] TILs can be harvested in any appropriate and sterile manner, including, for example by centrifugation. Methods for TIL harvesting are well known in the art and any such known methods can be employed with the present process. In some embodiments, TILs are harvested using an automated system.

[001294] Cell harvesters and/or cell processing systems are commercially available from a variety of sources, including, for example, Fresenius Kabi, Tomtec Life Science, Perkin Elmer, and Inotech Biosystems International, Inc. Any cell based harvester can be employed with the present methods. In some embodiments, the cell harvester and/or cell processing system is a membrane-based cell harvester. In some embodiments, cell harvesting is via a cell processing system, such as the LOVO system (manufactured by Fresenius Kabi). The term "LOVO cell processing system" also refers to any instrument or device manufactured by any vendor that can pump a solution comprising cells through a membrane or filter such as a spinning membrane or spinning filter in a sterile and/or closed system environment, allowing for continuous flow and cell processing to remove supernatant or cell culture media without pelletization. In some embodiments, the cell harvester and/or cell processing system can perform cell separation, washing, fluid-exchange, concentration, and/or other cell processing steps in a closed, sterile system.

[001295] In some embodiments, the rapid second expansion, for example, Step D according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), is performed in a closed system bioreactor. In some embodiments, a closed system is employed for the TIL expansion, as described herein. In some embodiments, a bioreactor is employed. In some embodiments, a bioreactor is employed as the container. In some embodiments, the bioreactor employed is for example a G-REX-100 or a G-REX-500. In some embodiments, the bioreactor employed is a G-REX-100. In some embodiments, the bioreactor employed is a G-REX-500.

[001296] In some embodiments, Step E according to Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), is performed according to the processes described herein. In some embodiments, the closed system is accessed via syringes under sterile conditions in order to maintain the sterility and closed nature of the system. In some embodiments, a closed system as described herein is employed.

[001297] In some embodiments, TILs are harvested according to the methods described in herein. In some embodiments, TILs between days 14 and 16 are harvested using the methods as described herein. In some embodiments, TILs are harvested at 14 days using the methods as described herein. In some embodiments, TILs are harvested at 15 days using the methods as described herein. In some embodiments, TILs are harvested at 16 days using the methods as described herein.

F. STEP F: Final Formulation and Transfer to Infusion Container

[001298] After Steps A through E as provided in an exemplary order in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B

and/or Figure 48C and/or Figure 48D) and as outlined in detailed above and herein are complete, cells are transferred to a container for use in administration to a patient, such as an infusion bag or sterile vial. In some embodiments, once a therapeutically sufficient number of TILs are obtained using the expansion methods described above, they are transferred to a container for use in administration to a patient.

[001299] In some embodiments, TILs expanded using the methods of the present disclosure are administered to a patient as a pharmaceutical composition. In some embodiments, the pharmaceutical composition is a suspension of TILs in a sterile buffer. TILs expanded as disclosed herein may be administered by any suitable route as known in the art. In some embodiments, the TILs are administered as a single intra-arterial or intravenous infusion, which preferably lasts approximately 30 to 60 minutes. Other suitable routes of administration include intraperitoneal, intrathecal, and intralymphatic administration.

VII. Further Gen 2, Gen 3, and Other TIL Manufacturing Process Embodiments

A. PBMC Feeder Cell Ratios

[001300] In some embodiments, the culture media used in expansion methods described herein (see for example, Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D)) include an anti-CD3 antibody *e.g.* OKT-3. An anti-CD3 antibody in combination with IL-2 induces T cell activation and cell division in the TIL population. This effect can be seen with full length antibodies as well as Fab and F(ab')2 fragments, with the former being generally preferred; see, *e.g.,* Tsoukas *et al.*, *J. Immunol.* 1985, *135,* 1719, hereby incorporated by reference in its entirety.

[001301] In some embodiments, the number of PBMC feeder layers is calculated as follows:

A. Volume of a T-cell (10 μm diameter): $V = (4/3)\ \pi r^3 = 523.6\ \mu m^3$

B. Column of G-REX 100 (M) with a 40 μm (4 cells) height: $V = (4/3)\ \pi r^3 = 4\times10^{12}\ \mu m^3$

C. Number cell required to fill column B: $4\times10^{12}\ \mu m^3 / 523.6\ \mu m^3 = 7.6\times10^{8}\ \mu m^3 * 0.64 = 4.86\times10^{8}$

D. Number cells that can be optimally activated in 4D space: $4.86\times10^{8} / 24 = 20.25\times10^{6}$

E. Number of feeders and TIL extrapolated to G-REX 500: TIL: 100×10^{6} and Feeder: 2.5×10^{9}

In this calculation, an approximation of the number of mononuclear cells required to provide an icosahedral geometry for activation of TIL in a cylinder with a 100 cm^2 base is used. The calculation derives the experimental result of ~5×10^{8} for threshold activation of T-cells which closely mirrors NCI experimental data, as described in Jin, *et.al.*, *J. Immunother.* **2012**, *35,* 283–292. In (C), the

multiplier (0.64) is the random packing density for equivalent spheres as calculated by Jaeger and Nagel, *Science*, 1992, *255,* 1523-3. In (D), the divisor 24 is the number of equivalent spheres that could contact a similar object in 4 -dimensional space or "the Newton number" as described in Musin, *Russ. Math. Surv.,* **2003,** *58,* 794–795.

[001302] In other embodiments, the number of antigen-presenting feeder cells exogenously supplied during the priming first expansion is approximately one-half the number of antigen-presenting feeder cells exogenously supplied during the rapid second expansion. In certain embodiments, the method comprises performing the priming first expansion in a cell culture medium which comprises approximately 50% fewer antigen presenting cells as compared to the cell culture medium of the rapid second expansion.

[001303] In other embodiments, the number of antigen-presenting feeder cells (APCs) exogenously supplied during the rapid second expansion is greater than the number of APCs exogenously supplied during the priming first expansion.

[001304] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 20:1.

[001305] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 10:1.

[001306] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 9:1.

[001307] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 8:1.

[001308] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 7:1.

[001309] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 6:1.

[001310] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 5:1.

[001311] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 4:1.

[001312] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion) is selected from a range of from at or about 1.1:1 to at or about 3:1.

[001313] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.9:1.

[001314] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.8:1.

[001315] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.7:1.

[001316] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.6:1.

[001317] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.5:1.

[001318] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.4:1.

[001319] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.3:1.

[001320] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.2:1.

[001321] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.1:1.

[001322] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2:1.

[001323] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 10:1.

[001324] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 5:1.

[001325] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 4:1.

[001326] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 3:1.

[001327] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.9:1.

[001328] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.8:1.

[001329] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.7:1.

[001330] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.6:1.

[001331] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.5:1.

[001332] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.4:1.

[001333] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.3:1.

[001334] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about about 2:1 to at or about 2.2:1.

[001335] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.1:1.

[001336] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is at or about 2:1.

[001337] In other embodiments, the ratio of the number of APCs exogenously supplied during the rapid second expansion to the number of APCs exogenously supplied during the priming first expansion is at or about 1.1:1, 1.2:1, 1.3:1, 1.4:1, 1.5:1, 1.6:1, 1.7:1, 1.8:1, 1.9:1, 2:1, 2.1:1, 2.2:1, 2.3:1, 2.4:1, 2.5:1, 2.6:1, 2.7:1, 2.8:1, 2.9:1, 3:1, 3.1:1, 3.2:1, 3.3:1, 3.4:1, 3.5:1, 3.6:1, 3.7:1, 3.8:1, 3.9:1, 4:1, 4.1:1, 4.2:1, 4.3:1, 4.4:1, 4.5:1, 4.6:1, 4.7:1, 4.8:1, 4.9:1, or 5:1.

[001338] In other embodiments, the number of APCs exogenously supplied during the priming first expansion is at or about 1×10^8, 1.1×10^8, 1.2×10^8, 1.3×10^8, 1.4×10^8, 1.5×10^8, 1.6×10^8, 1.7×10^8, 1.8×10^8, 1.9×10^8, 2×10^8, 2.1×10^8, 2.2×10^8, 2.3×10^8, 2.4×10^8, 2.5×10^8, 2.6×10^8, 2.7×10^8, 2.8×10^8, 2.9×10^8, 3×10^8, 3.1×10^8, 3.2×10^8, 3.3×10^8, 3.4×10^8 or 3.5×10^8 APCs, and the number of APCs exogenously supplied during the rapid second expansion is at or about 3.5×10^8, 3.6×10^8, 3.7×10^8, 3.8×10^8, 3.9×10^8, 4×10^8, 4.1×10^8, 4.2×10^8, 4.3×10^8, 4.4×10^8, 4.5×10^8, 4.6×10^8, 4.7×10^8, 4.8×10^8,

4.9×10^8, 5×10^8, 5.1×10^8, 5.2×10^8, 5.3×10^8, 5.4×10^8, 5.5×10^8, 5.6×10^8, 5.7×10^8, 5.8×10^8, 5.9×10^8, 6×10^8, 6.1×10^8, 6.2×10^8, 6.3×10^8, 6.4×10^8, 6.5×10^8, 6.6×10^8, 6.7×10^8, 6.8×10^8, 6.9×10^8, 7×10^8, 7.1×10^8, 7.2×10^8, 7.3×10^8, 7.4×10^8, 7.5×10^8, 7.6×10^8, 7.7×10^8, 7.8×10^8, 7.9×10^8, 8×10^8, 8.1×10^8, 8.2×10^8, 8.3×10^8, 8.4×10^8, 8.5×10^8, 8.6×10^8, 8.7×10^8, 8.8×10^8, 8.9×10^8, 9×10^8, 9.1×10^8, 9.2×10^8, 9.3×10^8, 9.4×10^8, 9.5×10^8, 9.6×10^8, 9.7×10^8, 9.8×10^8, 9.9×10^8 or 1×10^9 APCs.

[001339] In other embodiments, the number of APCs exogenously supplied during the priming first expansion is selected from the range of at or about 1.5×10^8 APCs to at or about 3×10^8 APCs, and the number of APCs exogenously supplied during the rapid second expansion is selected from the range of at or about 4×10^8 APCs to at or about 7.5×10^8 APCs.

[001340] In other embodiments, the number of APCs exogenously supplied during the priming first expansion is selected from the range of at or about 2×10^8 APCs to at or about 2.5×10^8 APCs, and the number of APCs exogenously supplied during the rapid second expansion is selected from the range of at or about 4.5×10^8 APCs to at or about 5.5×10^8 APCs.

[001341] In other embodiments, the number of APCs exogenously supplied during the priming first expansion is at or about 2.5×10^8 APCs, and the number of APCs exogenously supplied during the rapid second expansion is at or about 5×10^8 APCs.

[001342] In other embodiments, the number of APCs (including, for example, PBMCs) added at day 0 of the priming first expansion is approximately one-half of the number of PBMCs added at day 7 of the priming first expansion (*e.g.*, day 7 of the method). In certain embodiments, the method comprises adding antigen presenting cells at day 0 of the priming first expansion to the first population of TILs and adding antigen presenting cells at day 7 to the second population of TILs, wherein the number of antigen presenting cells added at day 0 is approximately 50% of the number of antigen presenting cells added at day 7 of the priming first expansion (*e.g.*, day 7 of the method).

[001343] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is greater than the number of PBMCs exogenously supplied at day 0 of the priming first expansion.

[001344] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 1.0×10^6 APCs/cm^2 to at or about 4.5×10^6 APCs/cm^2.

[001345] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 1.5×10^6 APCs/cm^2 to at or about 3.5×10^6 APCs/cm^2.

[001346] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 2×10^6 APCs/cm^2 to at or about 3×10^6 APCs/cm^2.

[001347] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density of at or about 2×10^6 APCs/cm^2.

[001348] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density of at or about 1.0×10^6, 1.1×10^6, 1.2×10^6, 1.3×10^6, 1.4×10^6, 1.5×10^6, 1.6×10^6, 1.7×10^6, 1.8×10^6, 1.9×10^6, 2×10^6, 2.1×10^6, 2.2×10^6, 2.3×10^6, 2.4×10^6, 2.5×10^6, 2.6×10^6, 2.7×10^6, 2.8×10^6, 2.9×10^6, 3×10^6, 3.1×10^6, 3.2×10^6, 3.3×10^6, 3.4×10^6, 3.5×10^6, 3.6×10^6, 3.7×10^6, 3.8×10^6, 3.9×10^6, 4×10^6, 4.1×10^6, 4.2×10^6, 4.3×10^6, 4.4×10^6 or 4.5×10^6 APCs/cm^2.

[001349] In other embodiments, the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 2.5×10^6 APCs/cm^2 to at or about 7.5×10^6 APCs/cm^2.

[001350] In other embodiments, the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 3.5×10^6 APCs/cm^2 to about 6.0×10^6 APCs/cm^2.

[001351] In other embodiments, the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 4.0×10^6 APCs/cm^2 to about 5.5×10^6 APCs/cm^2.

[001352] In other embodiments, the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 4.0×10^6 APCs/cm^2.

[001353] In other embodiments, the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density of at or about 2.5×10^6 APCs/cm^2, 2.6×10^6 APCs/cm^2, 2.7×10^6 APCs/cm^2, 2.8×10^6, 2.9×10^6, 3×10^6, 3.1×10^6, 3.2×10^6, 3.3×10^6, 3.4×10^5, 3.5×10^6, 3.6×10^6, 3.7×10^6, 3.8×10^6, 3.9×10^6, 4×10^6, 4.1×10^6, 4.2×10^6, 4.3×10^6, 4.4×10^6, 4.5×10^6, 4.6×10^6, 4.7×10^6, 4.8×10^6, 4.9×10^6, 5×10^6, 5.1×10^6, 5.2×10^6, 5.3×10^6, 5.4×10^6, 5.5×10^6, 5.6×10^6, 5.7×10^6, 5.8×10^6, 5.9×10^6, 6×10^6, 6.1×10^6, 6.2×10^6, 6.3×10^6, 6.4×10^6, 6.5×10^6, 6.6×10^6, 6.7×10^6, 6.8×10^6, 6.9×10^6, 7×10^6, 7.1×10^6, 7.2×10^6, 7.3×10^6, 7.4×10^6 or 7.5×10^6 APCs/cm^2.

[001354] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density of at or about 1.0×10^6, 1.1×10^6, 1.2×10^6, 1.3×10^6, 1.4×10^6, 1.5×10^6, 1.6×10^6, 1.7×10^6, 1.8×10^6, 1.9×10^6, 2×10^6, 2.1×10^6, 2.2×10^6, 2.3×10^6, 2.4×10^6, 2.5×10^6, 2.6×10^6, 2.7×10^6, 2.8×10^6, 2.9×10^6, 3×10^6, 3.1×10^6, 3.2×10^6, 3.3×10^6, 3.4×10^6, 3.5×10^6, 3.6×10^6,

3.7×10^6, 3.8×10^6, 3.9×10^6, 4×10^6, 4.1×10^6, 4.2×10^6, 4.3×10^6, 4.4×10^6 or 4.5×10^6 APCs/cm^2 and the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density of at or about 2.5×10^6 APCs/cm^2, 2.6×10^6 APCs/cm^2, 2.7×10^6 APCs/cm^2, 2.8×10^6, 2.9×10^6, 3×10^6, 3.1×10^6, 3.2×10^6, 3.3×10^6, 3.4×10^6, 3.5×10^6, 3.6×10^6, 3.7×10^6, 3.8×10^6, 3.9×10^6, 4×10^6, 4.1×10^6, 4.2×10^6, 4.3×10^6, 4.4×10^6, 4.5×10^6, 4.6×10^6, 4.7×10^6, 4.8×10^6, 4.9×10^6, 5×10^6, 5.1×10^6, 5.2×10^6, 5.3×10^6, 5.4×10^6, 5.5×10^6, 5.6×10^6, 5.7×10^6, 5.8×10^6, 5.9×10^6, 6×10^6, 6.1×10^6, 6.2×10^6, 6.3×10^6, 6.4×10^6, 6.5×10^6, 6.6×10^6, 6.7×10^6, 6.8×10^6, 6.9×10^6, 7×10^6, 7.1×10^6, 7.2×10^6, 7.3×10^6, 7.4×10^6 or 7.5×10^6 APCs/cm^2.

[001355] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 1.0×10^6 APCs/cm^2 to at or about 4.5×10^6 APCs/cm^2, and the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 2.5×10^6 APCs/cm^2 to at or about 7.5×10^6 APCs/cm^2.

[001356] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 1.5×10^6 APCs/cm^2 to at or about 3.5×10^6 APCs/cm^2, and the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 3.5×10^6 APCs/cm^2 to at or about 6×10^6 APCs/cm^2.

[001357] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density selected from a range of at or about 2×10^6 APCs/cm^2 to at or about 3×10^6 APCs/cm^2, and the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density selected from a range of at or about 4×10^6 APCs/cm^2 to at or about 5.5×10^6 APCs/cm^2.

[001358] In other embodiments, the APCs exogenously supplied in the priming first expansion are seeded in the culture flask at a density at or about 2×10^6 APCs/cm^2 and the APCs exogenously supplied in the rapid second expansion are seeded in the culture flask at a density of at or about 4×10^6 APCs/cm^2.

[001359] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of PBMCs exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 20:1.

[001360] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of PBMCs exogenously

supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 10:1.

[001361] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of PBMCs exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 9:1.

[001362] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 8:1.

[001363] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 7:1.

[001364] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 6:1.

[001365] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 5:1.

[001366] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 4:1.

[001367] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 3:1.

[001368] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for

example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.9:1.

[001369] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.8:1.

[001370] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.7:1.

[001371] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.6:1.

[001372] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.5:1.

[001373] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.4:1.

[001374] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.3:1.

[001375] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.2:1.

[001376] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for

example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2.1:1.

[001377] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 1.1:1 to at or about 2:1.

[001378] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 10:1.

[001379] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 5:1.

[001380] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 4:1.

[001381] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 3:1.

[001382] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.9:1.

[001383] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.8:1.

[001384] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for

example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.7:1.

[001385] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.6:1.

[001386] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.5:1.

[001387] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.4:1.

[001388] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.3:1.

[001389] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about about 2:1 to at or about 2.2:1.

[001390] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from a range of from at or about 2:1 to at or about 2.1:1.

[001391] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is at or about 2:1.

[001392] In other embodiments, the ratio of the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion to the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is at or about 1.1:1,

1.2:1, 1.3:1, 1.4:1, 1.5:1, 1.6:1, 1.7:1, 1.8:1, 1.9:1, 2:1, 2.1:1, 2.2:1, 2.3:1, 2.4:1, 2.5:1, 2.6:1, 2.7:1, 2.8:1, 2.9:1, 3:1, 3.1:1, 3.2:1, 3.3:1, 3.4:1, 3.5:1, 3.6:1, 3.7:1, 3.8:1, 3.9:1, 4:1, 4.1:1, 4.2:1, 4.3:1, 4.4:1, 4.5:1, 4.6:1, 4.7:1, 4.8:1, 4.9:1, or 5:1.

[001393] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is at or about 1×10^8, 1.1×10^8, 1.2×10^8, 1.3×10^8, 1.4×10^8, 1.5×10^8, 1.6×10^8, 1.7×10^8, 1.8×10^8, 1.9×10^8, 2×10^8, 2.1×10^8, 2.2×10^8, 2.3×10^8, 2.4×10^8, 2.5×10^8, 2.6×10^8, 2.7×10^8, 2.8×10^8, 2.9×10^8, 3×10^8, 3.1×10^8, 3.2×10^8, 3.3×10^8, 3.4×10^8 or 3.5×10^8 APCs (including, for example, PBMCs), and the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is at or about 3.5×10^8, 3.6×10^8, 3.7×10^8, 3.8×10^8, 3.9×10^8, 4×10^8, 4.1×10^8, 4.2×10^8, 4.3×10^8, 4.4×10^8, 4.5×10^8, 4.6×10^8, 4.7×10^8, 4.8×10^8, 4.9×10^8, 5×10^8, 5.1×10^8, 5.2×10^8, 5.3×10^8, 5.4×10^8, 5.5×10^8, 5.6×10^8, 5.7×10^8, 5.8×10^8, 5.9×10^8, 6×10^8, 6.1×10^8, 6.2×10^8, 6.3×10^8, 6.4×10^8, 6.5×10^8, 6.6×10^8, 6.7×10^8, 6.8×10^8, 6.9×10^8, 7×10^8, 7.1×10^8, 7.2×10^8, 7.3×10^8, 7.4×10^8, 7.5×10^8, 7.6×10^8, 7.7×10^8, 7.8×10^8, 7.9×10^8, 8×10^8, 8.1×10^8, 8.2×10^8, 8.3×10^8, 8.4×10^8, 8.5×10^8, 8.6×10^8, 8.7×10^8, 8.8×10^8, 8.9×10^8, 9×10^8, 9.1×10^8, 9.2×10^8, 9.3×10^8, 9.4×10^8, 9.5×10^8, 9.6×10^8, 9.7×10^8, 9.8×10^8, 9.9×10^8 or $1x10^9$ APCs (including, for example, PBMCs).

[001394] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from the range of at or about 1×10^8 APCs (including, for example, PBMCs) to at or about 3.5×10^8 APCs (including, for example, PBMCs), and the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is selected from the range of at or about 3.5×10^8 APCs (including, for example, PBMCs) to at or about 1×10^9 APCs (including, for example, PBMCs).

[001395] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from the range of at or about 1.5×10^8 APCs to at or about 3×10^8 APCs (including, for example, PBMCs), and the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is selected from the range of at or about 4×10^8 APCs (including, for example, PBMCs) to at or about 7.5×10^8 APCs (including, for example, PBMCs).

[001396] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is selected from the range of at or about 2×10^8 APCs (including, for example, PBMCs) to at or about 2.5×10^8 APCs (including, for example, PBMCs), and the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is selected from the range of at or about 4.5×10^8 APCs (including, for example, PBMCs) to at or about 5.5×10^8 APCs (including, for example, PBMCs).

[001397] In other embodiments, the number of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion is at or about 2.5×10^8 APCs (including, for example, PBMCs) and the number of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is at or about 5×10^8 APCs (including, for example, PBMCs)

[001398] In other embodiments, the number of layers of APCs (including, for example, PBMCs) added at day 0 of the priming first expansion is approximately one-half of the number of layers of APCs (including, for example, PBMCs) added at day 7 of the rapid second expansion. In certain embodiments, the method comprises adding antigen presenting cell layers at day 0 of the priming first expansion to the first population of TILs and adding antigen presenting cell layers at day 7 to the second population of TILs, wherein the number of antigen presenting cell layer added at day 0 is approximately 50% of the number of antigen presenting cell layers added at day 7.

[001399] In other embodiments, the number of layers of APCs (including, for example, PBMCs) exogenously supplied at day 7 of the rapid second expansion is greater than the number of layers of APCs (including, for example, PBMCs) exogenously supplied at day 0 of the priming first expansion.

[001400] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 2 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 4 cell layers.

[001401] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about one cell layer and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 3 cell layers.

[001402] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 1.5 cell layers to at or about 2.5 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 3 cell layers.

[001403] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about one cell layer and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 2 cell layers.

[001404] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of of at or about 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 or 3 cell layers and day 7 of

the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9 or 8 cell layers.

[001405] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 1 cell layer to at or about 2 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 3 cell layers to at or about 10 cell layers.

[001406] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 2 cell layers to at or about 3 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 4 cell layers to at or about 8 cell layers.

[001407] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 2 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 4 cell layers to at or about 8 cell layers.

[001408] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 1, 2 or 3 cell layers and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with an average thickness of at or about 3, 4, 5, 6, 7, 8, 9 or 10 cell layers.

[001409] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:10.

[001410] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal

to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:8.

[001411] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:7.

[001412] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:6.

[001413] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:5.

[001414] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:4.

[001415] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in

the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:3.

[001416] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.1 to at or about 1:2.

[001417] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.2 to at or about 1:8.

[001418] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.3 to at or about 1:7.

[001419] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.4 to at or about 1:6.

[001420] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number

of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.5 to at or about 1:5.

[001421] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.6 to at or about 1:4.

[001422] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.7 to at or about 1:3.5.

[001423] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.8 to at or about 1:3.

[001424] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from the range of at or about 1:1.9 to at or about 1:2.5.

[001425] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is at or about 1: 2.

[001426] In other embodiments, day 0 of the priming first expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a first average thickness equal to a first number of layers of APCs (including, for example, PBMCs) and day 7 of the rapid second expansion occurs in the presence of layered APCs (including, for example, PBMCs) with a second average thickness equal to a second number of layers of APCs (including, for example, PBMCs), wherein the ratio of the first number of layers of APCs (including, for example, PBMCs) to the second number of layers of APCs (including, for example, PBMCs) is selected from at or about 1:1.1, 1:1.2, 1:1.3, 1:1.4, 1:1.5, 1:1.6, 1:1.7, 1:1.8, 1:1.9, 1:2, 1:2.1, 1:2.2, 1:2.3, 1:2.4, 1:2.5, 1:2.6, 1:2.7, 1:2.8, 1:2.9, 1:3, 1:3.1, 1:3.2, 1:3.3, 1:3.4, 1:3.5, 1:3.6, 1:3.7, 1:3.8, 1:3.9, 1:4, 1:4.1, 1:4.2, 1:4.3, 1:4.4, 1:4.5, 1:4.6, 1:4.7, 1:4.8, 1:4.9, 1:5, 1:5.1, 1:5.2, 1:5.3, 1:5.4, 1:5.5, 1:5.6, 1:5.7, 1:5.8, 1:5.9, 1:6, 1:6.1, 1:6.2, 1:6.3, 1:6.4, 1:6.5, 1:6.6, 1:6.7, 1:6.8, 1:6.9, 1:7, 1:7.1, 1:7.2, 1:7.3, 1:7.4, 1:7.5, 1:7.6, 1:7.7, 1:7.8, 1:7.9, 1:8, 1:8.1, 1:8.2, 1:8.3, 1:8.4, 1:8.5, 1:8.6, 1:8.7, 1:8.8, 1:8.9, 1:9, 1:9.1, 1:9.2, 1:9.3, 1:9.4, 1:9.5, 1:9.6, 1:9.7, 1:9.8, 1:9.9 or 1:10.

[001427] In some embodiments, the number of APCs in the priming first expansion is selected from the range of about 1.0×10^6 APCs/cm^2 to about 4.5×10^6 APCs/cm^2, and the number of APCs in the rapid second expansion is selected from the range of about 2.5×10^6 APCs/cm^2 to about 7.5×10^6 APCs/cm^2.

[001428] In some embodiments, the number of APCs in the priming first expansion is selected from the range of about 1.5×10^6 APCs/cm^2 to about 3.5×10^6 APCs/cm^2, and the number of APCs in the rapid second expansion is selected from the range of about 3.5×10^6 APCs/cm^2 to about 6.0×10^6 APCs/cm^2.

[001429] In some embodiments, the number of APCs in the priming first expansion is selected from the range of about 2.0×10^6 APCs/cm^2 to about 3.0×10^6 APCs/cm^2, and the number of APCs in the rapid second expansion is selected from the range of about 4.0×10^6 APCs/cm^2 to about 5.5×10^6 APCs/cm^2.

B. Optional Cell Medium Components

1. Anti-CD3 Antibodies

[00759] In some embodiments, the culture media used in expansion methods described herein (including those referred to as REP, see for example, Figures 1 and 8 (in particular, *e.g.*, Figure 8B)) include an anti-CD3 antibody. An anti-CD3 antibody in combination with IL-2 induces T cell activation and cell division in the TIL population. This effect can be seen with full length antibodies as well as Fab and F(ab')2 fragments, with the former being generally preferred; see, *e.g.,* Tsoukas *et al.*, *J. Immunol.* **1985,** *135,* 1719, hereby incorporated by reference in its entirety.

[00760] As will be appreciated by those in the art, there are a number of suitable anti-human CD3 antibodies that find use in the invention, including anti-human CD3 polyclonal and monoclonal antibodies from various mammals, including, but not limited to, murine, human, primate, rat, and canine antibodies. In particular embodiments, the OKT3 anti-CD3 antibody muromonab is used (commercially available from Ortho-McNeil, Raritan, NJ or Miltenyi Biotech, Auburn, CA). *See*, Table 1.

[00761] As will be appreciated by those in the art, there are a number of suitable anti-human CD3 antibodies that find use in the invention, including anti-human CD3 polyclonal and monoclonal antibodies from various mammals, including, but not limited to, murine, human, primate, rat, and canine antibodies. In some embodiments, the OKT3 anti-CD3 antibody muromonab is used (commercially available from Ortho-McNeil, Raritan, NJ or Miltenyi Biotech, Auburn, CA).

2. 4-1BB (CD137) Agonists

[00762] In some embodiments, the cell culture medium of the priming first expansion and/or the rapid second expansion comprises a TNFRSF agonist. In some embodiments, the TNFRSF agonist is a 4-1BB (CD137) agonist. The 4-1BB agonist may be any 4-1BB binding molecule known in the art. The 4-1BB binding molecule may be a monoclonal antibody or fusion protein capable of binding to human or mammalian 4-1BB. The 4-1BB agonists or 4-1BB binding molecules may comprise an immunoglobulin heavy chain of any isotype (*e.g.*, IgG, IgE, IgM, IgD, IgA, and IgY), class (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. The 4-1BB agonist or 4-1BB binding molecule may have both a heavy and a light chain. As used herein, the term binding molecule also includes antibodies (including full length antibodies), monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), human, humanized or chimeric antibodies, and antibody fragments, *e.g.*, Fab fragments, F(ab′) fragments, fragments produced by a Fab expression library, epitope-binding fragments of any of the above, and engineered forms of antibodies, *e.g.*, scFv molecules, that bind to

4-1BB. In some embodiments, the 4-1BB agonist is an antigen binding protein that is a fully human antibody. In some embodiments, the 4-1BB agonist is an antigen binding protein that is a humanized antibody. In some embodiments, 4-1BB agonists for use in the presently disclosed methods and compositions include anti-4-1BB antibodies, human anti-4-1BB antibodies, mouse anti-4-1BB antibodies, mammalian anti-4-1BB antibodies, monoclonal anti-4-1BB antibodies, polyclonal anti-4-1BB antibodies, chimeric anti-4-1BB antibodies, anti-4-1BB adnectins, anti-4-1BB domain antibodies, single chain anti-4-1BB fragments, heavy chain anti-4-1BB fragments, light chain anti-4-1BB fragments, anti-4-1BB fusion proteins, and fragments, derivatives, conjugates, variants, or biosimilars thereof. Agonistic anti-4-1BB antibodies are known to induce strong immune responses. Lee, *et al.*, *PLOS One* **2013**, *8,* e69677. In some embodiments, the 4-1BB agonist is an agonistic, anti-4-1BB humanized or fully human monoclonal antibody (*i.e.*, an antibody derived from a single cell line). In some embodiments, the 4-1BB agonist is EU-101 (Eutilex Co. Ltd.), utomilumab, or urelumab, or a fragment, derivative, conjugate, variant, or biosimilar thereof. In some embodiments, the 4-1BB agonist is utomilumab or urelumab, or a fragment, derivative, conjugate, variant, or biosimilar thereof.

[00763] In some embodiments, the 4-1BB agonist or 4-1BB binding molecule may also be a fusion protein. In some embodiments, a multimeric 4-1BB agonist, such as a trimeric or hexameric 4-1BB agonist (with three or six ligand binding domains), may induce superior receptor (4-1BBL) clustering and internal cellular signaling complex formation compared to an agonistic monoclonal antibody, which typically possesses two ligand binding domains. Trimeric (trivalent) or hexameric (or hexavalent) or greater fusion proteins comprising three TNFRSF binding domains and IgG1-Fc and optionally further linking two or more of these fusion proteins are described, *e.g.*, in Gieffers, *et al.*, *Mol. Cancer Therapeutics* **2013,** *12,* 2735-47.

[00764] Agonistic 4-1BB antibodies and fusion proteins are known to induce strong immune responses. In some embodiments, the 4-1BB agonist is a monoclonal antibody or fusion protein that binds specifically to 4-1BB antigen in a manner sufficient to reduce toxicity. In some embodiments, the 4-1BB agonist is an agonistic 4-1BB monoclonal antibody or fusion protein that abrogates antibody-dependent cellular toxicity (ADCC), for example NK cell cytotoxicity. In some embodiments, the 4-1BB agonist is an agonistic 4-1BB monoclonal antibody or fusion protein that abrogates antibody-dependent cell phagocytosis (ADCP). In some embodiments, the 4-1BB agonist is an agonistic 4-1BB monoclonal antibody or fusion protein that abrogates complement-dependent cytotoxicity (CDC). In some embodiments, the 4-1BB agonist is an agonistic 4-1BB monoclonal antibody or fusion protein which abrogates Fc region functionality.

[00765] In some embodiments, the 4-1BB agonists are characterized by binding to human 4-1BB (SEQ ID NO:9) with high affinity and agonistic activity. In some embodiments, the 4-1BB agonist is

a binding molecule that binds to human 4-1BB (SEQ ID NO:40). In some embodiments, the 4-1BB agonist is a binding molecule that binds to murine 4-1BB (SEQ ID NO:41). The amino acid sequences of 4-1BB antigen to which a 4-1BB agonist or binding molecule binds are summarized in Table 5.

TABLE 5. Amino acid sequences of 4-1BB antigens.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:40 human 4-1BB, Tumor necrosis factor receptor superfamily, member 9 (Homo sapiens)	MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP NSFSSAGGQR 60 TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCKQGQ ELTKKGCKDC 120 CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE 180 PGHSPQIISF FLALTSTALL FLLFFLTLRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG 240 CSCRFPEEEE GGCEL 255
SEQ ID NO:41 murine 4-1BB, Tumor necrosis factor receptor superfamily, member 9 (Mus musculus)	MGNNCYNVVV IVLLLVGCEK VGAVQNSCDN CQPGTFCRKY NPVCKSCPPS TFSSIGGQPN 60 CNICRVCAGY FRFKKFCSST HNAECECIEG FHCLGPQCTR CEKDCRPGQE LTKQGCKTCS 120 LGTFNDQNGT GVCRPWTNCS LDGRSVLKTG TTEKDVVCGP PVVSFSPSTT ISVTPEGGPG 180 GHSLQVLTLF LALTSALLLA LIFITLLFSV LKWIRKKFPH IFKQPFKKTT GAAQEEDACS 240 CRCPQEEEGG GGGYEL 256

[00766] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds human or murine 4-1BB with a K_D of about 100 pM or lower, binds human or murine 4-1BB with a K_D of about 90 pM or lower, binds human or murine 4-1BB with a K_D of about 80 pM or lower, binds human or murine 4-1BB with a K_D of about 70 pM or lower, binds human or murine 4-1BB with a K_D of about 60 pM or lower, binds human or murine 4-1BB with a K_D of about 50 pM or lower, binds human or murine 4-1BB with a K_D of about 40 pM or lower, or binds human or murine 4-1BB with a K_D of about 30 pM or lower.

[00767] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human or murine 4-1BB with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human or murine 4-1BB with a k_{assoc} of about 8×10^5 1/M·s or faster, binds to human or murine 4-1BB with a k_{assoc} of about 8.5×10^5 1/M·s or faster, binds to human or murine 4-1BB with a k_{assoc} of about 9×10^5 1/M·s or faster, binds to human or murine 4-1BB with a k_{assoc} of about 9.5×10^5 1/M·s or faster, or binds to human or murine 4-1BB with a k_{assoc} of about 1×10^6 1/M·s or faster.

[00768] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with a k_{dissoc} of about 2×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.1×10^{-5} 1/s or slower , binds to human or murine 4-1BB with a k_{dissoc} of about 2.2×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.3×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.4×10^{-5} 1/s or

slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.5×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.6×10^{-5} 1/s or slower or binds to human or murine 4-1BB with a k_{dissoc} of about 2.7×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.8×10^{-5} 1/s or slower, binds to human or murine 4-1BB with a k_{dissoc} of about 2.9×10^{-5} 1/s or slower, or binds to human or murine 4-1BB with a k_{dissoc} of about 3×10^{-5} 1/s or slower.

[00769] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with an IC_{50} of about 10 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 9 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 8 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 7 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 6 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 5 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 4 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 3 nM or lower, binds to human or murine 4-1BB with an IC_{50} of about 2 nM or lower, or binds to human or murine 4-1BB with an IC_{50} of about 1 nM or lower.

[00770] In some embodiments, the 4-1BB agonist is utomilumab, also known as PF-05082566 or MOR-7480, or a fragment, derivative, variant, or biosimilar thereof. Utomilumab is available from Pfizer, Inc. Utomilumab is an immunoglobulin G2-lambda, anti-[*Homo sapiens* TNFRSF9 (tumor necrosis factor receptor (TNFR) superfamily member 9, 4-1BB, T cell antigen ILA, CD137)], *Homo sapiens* (fully human) monoclonal antibody. The amino acid sequences of utomilumab are set forth in Table 6. Utomilumab comprises glycosylation sites at Asn59 and Asn292; heavy chain intrachain disulfide bridges at positions 22-96 (V_H-V_L), 143-199 (C_H1-C_L), 256-316 (C_H2) and 362-420 (C_H3); light chain intrachain disulfide bridges at positions 22'-87' (V_H-V_L) and 136'-195' (C_H1-C_L); interchain heavy chain-heavy chain disulfide bridges at IgG2A isoform positions 218-218, 219-219, 222-222, and 225-225, at IgG2A/B isoform positions 218-130, 219-219, 222-222, and 225-225, and at IgG2B isoform positions 219-130 (2), 222-222, and 225-225; and interchain heavy chain-light chain disulfide bridges at IgG2A isoform positions 130-213' (2), IgG2A/B isoform positions 218-213' and 130-213', and at IgG2B isoform positions 218-213' (2). The preparation and properties of utomilumab and its variants and fragments are described in U.S. Patent Nos. 8,821,867; 8,337,850; and 9,468,678, and International Patent Application Publication No. WO 2012/032433 A1, the disclosures of each of which are incorporated by reference herein. Preclinical characteristics of utomilumab are described in Fisher, *et al.*, *Cancer Immunolog. & Immunother.* **2012,** *61,* 1721-33. Current clinical trials of utomilumab in a variety of hematological and solid tumor indications include U.S. National Institutes of Health clinicaltrials.gov identifiers NCT02444793, NCT01307267, NCT02315066, and NCT02554812.

[00771] In some embodiments, a 4-1BB agonist comprises a heavy chain given by SEQ ID NO:42 and a light chain given by SEQ ID NO:43. In some embodiments, a 4-1BB agonist comprises heavy and light chains having the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:42 and SEQ ID NO:43, respectively.

[00772] In some embodiments, the 4-1BB agonist comprises the heavy and light chain CDRs or variable regions (VRs) of utomilumab. In some embodiments, the 4-1BB agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:44, and the 4-1BB agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:45, and conservative amino acid substitutions thereof. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively. In some embodiments, a 4-1BB agonist comprises an scFv antibody comprising V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45.

[00773] In some embodiments, a 4-1BB agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:46, SEQ ID NO:47, and SEQ ID NO:48, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:49, SEQ ID NO:50, and SEQ ID NO:51, respectively, and conservative amino acid substitutions thereof..

[00774] In some embodiments, the 4-1BB agonist is a 4-1BB agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to utomilumab. In some embodiments, the biosimilar monoclonal antibody comprises an 4-1BB antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is utomilumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a 4-1BB agonist antibody authorized or submitted for authorization, wherein the 4-1BB agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is utomilumab. The 4-1BB agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is utomilumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is utomilumab.

TABLE 6. Amino acid sequences for 4-1BB agonist antibodies related to utomilumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:42 heavy chain for utomilumab	EVQLVQSGAE VKKPGESLRI SCKGSGYSFS TYWISWVRQM PGKGLEWMGK IYPGDSYTNY	60
	SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARGY GIFDYWGQGT LVTVSSASTK	120
	GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS	180
	LSSVVTVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP	240
	KPKDTLMISR TPEVTCVVVD VSHEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV	300
	LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL	360
	TCLVKGFYPS DIAVEWESNG QPENNYKTTP PMLDSDGSFF LYSKLTVDKS RWQQGNVFSC	420
	SVMHEALHNH YTQKSLSLSP G	441
SEQ ID NO:43 light chain for utomilumab	SYELTQPPSV SVSPGQTASI TCSGDNIGDQ YAHWYQQKPG QSPVLVIYQD KNRPSGIPER	60
	FSGSNSGNTA TLTISGTQAM DEADYYCATY TGFGSLAVFG GGTKLTVLGQ PKAAPSVTLF	120
	PPSSEELQAN KATLVCLISD FYPGAVTVAW KADSSPVKAG VETTTPSKQS NNKYAASSYL	180

	SLTPEQWKSH RSYSCQVTHE GSTVEKTVAP TECS	214
SEQ ID NO:44 heavy chain variable region for utomilumab	EVQLVQSGAE VKKPGESLRI SCKGSGYSFS TYWISWVRQM PGKGLEWMG KIYPGDSYTN YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCARG YGIFDYWGQ GTLVTVSS	60 118
SEQ ID NO:45 light chain variable region for utomilumab	SYELTQPPSV SVSPGQTASI TCSGDNIGDQ YAHWYQQKPG QSPVLVIYQD KNRPSGIPER FSGSNSGNTA TLTISGTQAM DEADYYCATY TGFGSLAVFG GGTKLTVL	60 108
SEQ ID NO:46 heavy chain CDR1 for utomilumab	STYWIS	6
SEQ ID NO:47 heavy chain CDR2 for utomilumab	KIYPGDSYTN YSPSFQG	17
SEQ ID NO:48 heavy chain CDR3 for utomilumab	RGYGIFDY	8
SEQ ID NO:49 light chain CDR1 for utomilumab	SGDNIGDQYA H	11
SEQ ID NO:50 light chain CDR2 for utomilumab	QDKNRPS	7
SEQ ID NO:51 light chain CDR3 for utomilumab	ATYTGFGSLA V	11

[00775] In some embodiments, the 4-1BB agonist is the monoclonal antibody urelumab, also known as BMS-663513 and 20H4.9.h4a, or a fragment, derivative, variant, or biosimilar thereof. Urelumab is available from Bristol-Myers Squibb, Inc., and Creative Biolabs, Inc. Urelumab is an immunoglobulin G4-kappa, anti-[*Homo sapiens* TNFRSF9 (tumor necrosis factor receptor superfamily member 9, 4-1BB, T cell antigen ILA, CD137)], *Homo sapiens* (fully human) monoclonal antibody. The amino acid sequences of urelumab are set forth in Table 7. Urelumab comprises N-glycosylation sites at positions 298 (and 298''); heavy chain intrachain disulfide bridges at positions 22-95 (V_H-V_L), 148-204 (C_H1-C_L), 262-322 (C_H2) and 368-426 (C_H3) (and at positions 22''-95'', 148''-204'', 262''-322'', and 368''-426''); light chain intrachain disulfide bridges at positions 23'-88' (V_H-V_L) and 136'-196' (C_H1-C_L) (and at positions 23'''-88''' and 136'''-196'''); interchain heavy chain-heavy chain disulfide bridges at positions 227-227'' and 230-230''; and interchain heavy chain-light chain disulfide bridges at 135-216' and 135''-216'''. The preparation and properties of urelumab and its variants and fragments are described in U.S. Patent Nos. 7,288,638 and 8,962,804, the disclosures of which are incorporated by reference herein. The preclinical and clinical characteristics of urelumab are described in Segal, *et al.*, *Clin. Cancer Res.* **2016,** *available at* http:/dx.doi.org/ 10.1158/1078-0432.CCR-16-1272. Current clinical trials of urelumab in a variety of hematological and solid tumor

indications include U.S. National Institutes of Health clinicaltrials.gov identifiers NCT01775631, NCT02110082, NCT02253992, and NCT01471210.

[00776] In some embodiments, a 4-1BB agonist comprises a heavy chain given by SEQ ID NO:52 and a light chain given by SEQ ID NO:53. In some embodiments, a 4-1BB agonist comprises heavy and light chains having the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively. In some embodiments, a 4-1BB agonist comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:52 and SEQ ID NO:53, respectively.

[00777] In some embodiments, the 4-1BB agonist comprises the heavy and light chain CDRs or variable regions (VRs) of urelumab. In some embodiments, the 4-1BB agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:54, and the 4-1BB agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:55, and conservative amino acid substitutions thereof. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively. In some embodiments, a 4-1BB agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively. In some embodiments, a 4-1BB agonist comprises an scFv antibody comprising V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55.

[00778] In some embodiments, a 4-1BB agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and

CDR3 domains having the sequences set forth in SEQ ID NO:59, SEQ ID NO:60, and SEQ ID NO:61, respectively, and conservative amino acid substitutions thereof.

[00779] In some embodiments, the 4-1BB agonist is a 4-1BB agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to urelumab. In some embodiments, the biosimilar monoclonal antibody comprises an 4-1BB antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is urelumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a 4-1BB agonist antibody authorized or submitted for authorization, wherein the 4-1BB agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is urelumab. The 4-1BB agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is urelumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is urelumab.

TABLE 7: Amino acid sequences for 4-1BB agonist antibodies related to urelumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:52 heavy chain for urelumab	QVQLQQWGAG LLKPSETLSL TCAVYGGSFS GYYWSWIRQS PEKGLEWIGE INHGGYVTYN 60 PSLESRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARDYG PGNYDWYFDL WGRGTLVTVS 120 SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS 180 SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS 240 VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300 YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT 360 KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE 420 GNVFSCSVME EALHNHYTQK SLSLSLGK 448
SEQ ID NO:53 light chain for urelumab	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA 60 RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPALTF CGGTKVEIKR TVAAPSVFIF 120 PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST 180 LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC 216
SEQ ID NO:54 variable heavy chain for urelumab	MKHLWFFLLL VAAPRWVLSQ VQLQQWGAGL LKPSETLSLT CAVYGGSFSG YYWSWIRQSP 60 EKGLEWIGEI NHGGYVTYNP SLESRVTISV DTSKNQFSLK LSSVTAADTA VYYCARDYGP 120

SEQ ID NO:55 variable light chain for urelumab	MEAPAQLLFL LLLWLPDTTG EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ	60 110
SEQ ID NO:56 heavy chain CDR1 for urelumab	GYYWS	5
SEQ ID NO:57 heavy chain CDR2 for urelumab	EINHGGYVTY NPSLES	16
SEQ ID NO:58 heavy chain CDR3 for urelumab	DYGPGNYDWY FDL	13
SEQ ID NO:59 light chain CDR1 for urelumab	RASQSVSSYL A	11
SEQ ID NO:60 light chain CDR2 for urelumab	DASNRAT	7
SEQ ID NO:61 light chain CDR3 for urelumab	QQRSDWPPAL T	11

[00780] In some embodiments, the 4-1BB agonist is selected from the group consisting of 1D8, 3Elor, 4B4 (BioLegend 309809), H4-1BB-M127 (BD Pharmingen 552532), BBK2 (Thermo Fisher MS621PABX), 145501 (Leinco Technologies B591), the antibody produced by cell line deposited as ATCC No. HB-11248 and disclosed in U.S. Patent No. 6,974,863, 5F4 (BioLegend 31 1503), C65-485 (BD Pharmingen 559446), antibodies disclosed in U.S. Patent Application Publication No. US 2005/0095244, antibodies disclosed in U.S. Patent No. 7,288,638 (such as 20H4.9-IgGl (BMS-663031)), antibodies disclosed in U.S. Patent No. 6,887,673 (such as 4E9 or BMS-554271), antibodies disclosed in U.S. Patent No. 7,214,493, antibodies disclosed in U.S. Patent No. 6,303,121, antibodies disclosed in U.S. Patent No. 6,569,997, antibodies disclosed in U.S. Patent No. 6,905,685 (such as 4E9 or BMS-554271), antibodies disclosed in U.S. Patent No. 6,362,325 (such as 1D8 or BMS-469492; 3H3 or BMS-469497; or 3El), antibodies disclosed in U.S. Patent No. 6,974,863 (such as 53A2); antibodies disclosed in U.S. Patent No. 6,210,669 (such as 1D8, 3B8, or 3El), antibodies described in U.S. Patent No. 5,928,893, antibodies disclosed in U.S. Patent No. 6,303,121, antibodies disclosed in U.S. Patent No. 6,569,997, antibodies disclosed in International Patent Application Publication Nos. WO 2012/177788, WO 2015/119923, and WO 2010/042433, and fragments, derivatives, conjugates, variants, or biosimilars thereof, wherein the disclosure of each of the foregoing patents or patent application publications is incorporated by reference here.

[00781] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic fusion protein described in International Patent Application Publication Nos. WO 2008/025516 A1, WO 2009/007120 A1, WO 2010/003766 A1, WO 2010/010051 A1, and WO 2010/078966 A1; U.S. Patent Application Publication Nos. US 2011/0027218 A1, US 2015/0126709 A1, US 2011/0111494 A1, US 2015/0110734 A1, and US 2015/0126710 A1; and U.S. Patent Nos. 9,359,420, 9,340,599, 8,921,519, and 8,450,460, the disclosures of which are incorporated by reference herein.

[00782] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic fusion protein as depicted in Structure I-A (C-terminal Fc-antibody fragment fusion protein) or Structure I-B (N-terminal Fc-antibody fragment fusion protein), or a fragment, derivative, conjugate, variant, or biosimilar thereof (*see*, Figure 18). In structures I-A and I-B, the cylinders refer to individual polypeptide binding domains. Structures I-A and I-B comprise three linearly-linked TNFRSF binding domains derived from *e.g.*, 4-1BBL (4-1BB ligand, CD137 ligand (CD137L), or tumor necrosis factor superfamily member 9 (TNFSF9)) or an antibody that binds 4-1BB, which fold to form a trivalent protein, which is then linked to a second triavelent protein through IgG1-Fc (including C_H3 and C_H2 domains) is then used to link two of the trivalent proteins together through disulfide bonds (small elongated ovals), stabilizing the structure and providing an agonists capable of bringing together the intracellular signaling domains of the six receptors and signaling proteins to form a signaling complex. The TNFRSF binding domains denoted as cylinders may be scFv domains comprising, *e.g.*, a V_H and a V_L chain connected by a linker that may comprise hydrophilic residues and Gly and Ser sequences for flexibility, as well as Glu and Lys for solubility. Any scFv domain design may be used, such as those described in de Marco, *Microbial Cell Factories*, **2011,** *10,* 44; Ahmad, *et al.*, *Clin. & Dev. Immunol.* **2012,** 980250; Monnier, *et al.*, *Antibodies,* **2013,** *2,* 193-208; or in references incorporated elsewhere herein. Fusion protein structures of this form are described in U.S. Patent Nos. 9,359,420, 9,340,599, 8,921,519, and 8,450,460, the disclosures of which are incorporated by reference herein.

[00783] Amino acid sequences for the other polypeptide domains of structure I-A given in Figure 18 are found in Table 8. The Fc domain preferably comprises a complete constant domain (amino acids 17-230 of SEQ ID NO:62) the complete hinge domain (amino acids 1-16 of SEQ ID NO:62) or a portion of the hinge domain (*e.g.*, amino acids 4-16 of SEQ ID NO:62). Preferred linkers for connecting a C-terminal Fc-antibody may be selected from the embodiments given in SEQ ID NO:63 to SEQ ID NO:72, including linkers suitable for fusion of additional polypeptides.

TABLE 8: Amino acid sequences for TNFRSF agonist fusion proteins, including 4-1BB agonist fusion proteins, with C-terminal Fc-antibody fragment fusion protein design (structure I-A).

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:62 Fc domain	KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK	60 120 180 230
SEQ ID NO:63 linker	GGPGSSKSCD KTHTCPPCPA PE	22
SEQ ID NO:64 linker	GGSGSSKSCD KTHTCPPCPA PE	22

SEQ ID NO:65 linker	GGPGSSSSSS SKSCDKTHTC PPCPAPE	27
SEQ ID NO:66 linker	GGSGSSSSSS SKSCDKTHTC PPCPAPE	27
SEQ ID NO:67 linker	GGPGSSSSSS SSSKSCDKTH TCPPCPAPE	29
SEQ ID NO:68 linker	GGSGSSSSSS SSSKSCDKTH TCPPCPAPE	29
SEQ ID NO:69 linker	GGPGSSGSGS SDKTHTCPPC PAPE	24
SEQ ID NO:70 linker	GGPGSSGSGS DKTHTCPPCP APE	23
SEQ ID NO:71 linker	GGPSSSGSDK THTCPPCPAP E	21
SEQ ID NO:72 linker	GGSSSSSSSS GSDKTHTCPP CPAPE	25

[00784] Amino acid sequences for the other polypeptide domains of structure I-B given in Figure 18 are found in Table 9. If an Fc antibody fragment is fused to the N-terminus of an TNRFSF fusion protein as in structure I-B, the sequence of the Fc module is preferably that shown in SEQ ID NO:73, and the linker sequences are preferably selected from those embodiments set forth in SED ID NO:74 to SEQ ID NO:76.

TABLE 9: Amino acid sequences for TNFRSF agonist fusion proteins, including 4-1BB agonist fusion proteins, with N-terminal Fc-antibody fragment fusion protein design (structure I-B).

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:73 Fc domain	METDTLLLWV LLLWVPAGNG DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG	60 120 180 240 246
SEQ ID NO:74 linker	SGSGSGSGSG S	11
SEQ ID NO:75 linker	SSSSSSGSGS GS	12
SEQ ID NO:76 linker	SSSSSSGSGS GSGSGS	16

[00785] In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains selected from the group consisting of a variable heavy chain and variable light chain of utomilumab, a variable heavy chain and variable light chain of urelumab, a variable heavy chain and variable light chain of utomilumab, a variable heavy chain and variable light chain selected from the variable heavy chains and variable light chains described in

Table 5, any combination of a variable heavy chain and variable light chain of the foregoing, and fragments, derivatives, conjugates, variants, and biosimilars thereof.

[00786] In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains comprising a 4-1BBL sequence. In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains comprising a sequence according to SEQ ID NO:77. In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains comprising a soluble 4-1BBL sequence. In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains comprising a sequence according to SEQ ID NO:78.

[00787] In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:43 and SEQ ID NO:44, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, a 4-1BB agonist fusion protein according to structures I-A or I-B comprises one or more 4-1BB binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the V_H and V_L sequences given in Table 10, wherein the V_H and V_L domains are connected by a linker.

TABLE 10: Additional polypeptide domains useful as 4-1BB binding domains in fusion proteins or as scFv 4-1BB agonist antibodies.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:77 4-1BBL	MEYASDASLD PEAPWPPAPR ARACRVLPWA LVAGLLLLLL LAAACAVFLA CPWAVSGARA	60
	SPGSAASPRL REGPELSPDD PAGLLDLRQG MFAQLVAQNV LLIDGPLSWY SDPGLAGVSL	120
	TGGLSYKEDT KELVVAKAGV YYVFFQLELR RVVAGEGSGS VSLALHLQPL RSAAGAAALA	180
	LTVDLPPASS EARNSAFGFQ GRLLHLSAGQ RLGVHLHTEA RARHAWQLTQ GATVLGLFRV	240
	TPEIPAGLPS PRSE	254
SEQ ID NO:78 4-1BBL soluble domain	LRQGMFAQLV AQNVLLIDGP LSWYSDPGLA GVSLTGGLSY KEDTKELVVA KAGVYYVFFQ	60
	LELRRVVAGE GSGSVSLALH LQPLRSAAGA AALALTVDLP PASSEARNSA FGFQGRLLHL	120
	SAGQRLGVHL HTEARARHAW QLTQGATVLG LFRVTPEIPA GLPSPRSE	168
SEQ ID NO:79 variable heavy chain for 434-1-1 version 1	QVQLQQPGAE LVKPGASVKL SCKASGYTFS SYWMHWVKQR PGQVLEWIGE INPGNGHTNY	60
	NEKFKSKATL TVDKSSSTAY MQLSSLTSED SAVYYCARSF TTARGFAYWG QGTLVTVS	118

SEQ ID NO:80 variable light chain for 4B4-1-1 version 1	DIVMTQSPAT QSVTPGDRVS LSCRASQTIS DYLHWYQQKS HESPRLLIKY ASQSISGIPS RFSGSGSGSD FTLSINSVEP EDVGVYYCQD GHSFPPTFGG GTKLEIK	60 107
SEQ ID NO:81 variable heavy chain for 4B4-1-1 version 2	QVQLQQPGAE LVKPGASVKL SCKASGYTFS SYWMHWVKQR PGQVLEWIGE INPGNGHTNY NEKFKSKATL TVDKSSSTAY MQLSSLTSED SAVYYCARSF TTARGFAYWG QGTLVTVSA	60 119
SEQ ID NO:82 variable light chain for 4B4-1-1 version 2	DIVMTQSPAT QSVTPGDRVS LSCRASQTIS DYLHWYQQKS HESPRLLIKY ASQSISGIPS RFSGSGSGSD FTLSINSVEP EDVGVYYCQD GHSFPPTFGG GTKLEIKR	60 108
SEQ ID NO:83 variable heavy chain for H39E3-2	MDWTWRILFL VAAATGAHSE VQLVESGGGL VQPGGSLRLS CAASGFTFSD YWMSWVRQAP GKGLEWVADI KNDGSYTNYA PSLTNRFTIS RDNAKNSLYL QMNSLRAEDT AVYYCARELT	60 120
SEQ ID NO:84 variable light chain for H39E3-2	MEAPAQLLFL LLLWLPDTTG DIVMTQSPDS LAVSLGERAT INCKSSQSLL SSGNQKNYL WYQQKPGQPP KLLIYYASTR QSGVPDRFSG SGSGTDFTLT ISSLQAEDVA	60 110

[00788] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic single-chain fusion polypeptide comprising (i) a first soluble 4-1BB binding domain, (ii) a first peptide linker, (iii) a second soluble 4-1BB binding domain, (iv) a second peptide linker, and (v) a third soluble 4-1BB binding domain, further comprising an additional domain at the N-terminal and/or C-terminal end, and wherein the additional domain is a Fab or Fc fragment domain. In some embodiments, the 4-1BB agonist is a 4-1BB agonistic single-chain fusion polypeptide comprising (i) a first soluble 4-1BB binding domain, (ii) a first peptide linker, (iii) a second soluble 4-1BB binding domain, (iv) a second peptide linker, and (v) a third soluble 4-1BB binding domain, further comprising an additional domain at the N-terminal and/or C-terminal end, wherein the additional domain is a Fab or Fc fragment domain, wherein each of the soluble 4-1BB domains lacks a stalk region (which contributes to trimerisation and provides a certain distance to the cell membrane, but is not part of the 4-1BB binding domain) and the first and the second peptide linkers independently have a length of 3-8 amino acids.

[00789] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic single-chain fusion polypeptide comprising (i) a first soluble tumor necrosis factor (TNF) superfamily cytokine domain, (ii) a first peptide linker, (iii) a second soluble TNF superfamily cytokine domain, (iv) a second peptide linker, and (v) a third soluble TNF superfamily cytokine domain, wherein each of the soluble TNF superfamily cytokine domains lacks a stalk region and the first and the second peptide linkers independently have a length of 3-8 amino acids, and wherein each TNF superfamily cytokine domain is a 4-1BB binding domain.

[00790] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic scFv antibody comprising any of the foregoing V_H domains linked to any of the foregoing V_L domains.

[00791] In some embodiments, the 4-1BB agonist is BPS Bioscience 4-1BB agonist antibody catalog no. 79097-2, commercially available from BPS Bioscience, San Diego, CA, USA. In some embodiments, the 4-1BB agonist is Creative Biolabs 4-1BB agonist antibody catalog no. MOM-18179, commercially available from Creative Biolabs, Shirley, NY, USA.

3. OX40 (CD134) Agonists

[00792] In some embodiments, the TNFRSF agonist is an OX40 (CD134) agonist. The OX40 agonist may be any OX40 binding molecule known in the art. The OX40 binding molecule may be a monoclonal antibody or fusion protein capable of binding to human or mammalian OX40. The OX40 agonists or OX40 binding molecules may comprise an immunoglobulin heavy chain of any isotype (*e.g.*, IgG, IgE, IgM, IgD, IgA, and IgY), class (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. The OX40 agonist or OX40 binding molecule may have both a heavy and a light chain. As used herein, the term binding molecule also includes antibodies (including full length antibodies), monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), human, humanized or chimeric antibodies, and antibody fragments, *e.g.*, Fab fragments, F(ab′) fragments, fragments produced by a Fab expression library, epitope-binding fragments of any of the above, and engineered forms of antibodies, *e.g.*, scFv molecules, that bind to OX40. In some embodiments, the OX40 agonist is an antigen binding protein that is a fully human antibody. In some embodiments, the OX40 agonist is an antigen binding protein that is a humanized antibody. In some embodiments, OX40 agonists for use in the presently disclosed methods and compositions include anti-OX40 antibodies, human anti-OX40 antibodies, mouse anti-OX40 antibodies, mammalian anti-OX40 antibodies, monoclonal anti-OX40 antibodies, polyclonal anti-OX40 antibodies, chimeric anti-OX40 antibodies, anti-OX40 adnectins, anti-OX40 domain antibodies, single chain anti-OX40 fragments, heavy chain anti-OX40 fragments, light chain anti-OX40 fragments, anti-OX40 fusion proteins, and fragments, derivatives, conjugates, variants, or biosimilars thereof. In some embodiments, the OX40 agonist is an agonistic, anti-OX40 humanized or fully human monoclonal antibody (*i.e.*, an antibody derived from a single cell line).

[00793] In some embodiments, the OX40 agonist or OX40 binding molecule may also be a fusion protein. OX40 fusion proteins comprising an Fc domain fused to OX40L are described, for example, in Sadun, *et al.*, *J. Immunother.* **2009,** *182,* 1481-89. In some embodiments, a multimeric OX40 agonist, such as a trimeric or hexameric OX40 agonist (with three or six ligand binding domains), may induce superior receptor (OX40L) clustering and internal cellular signaling complex formation compared to an agonistic monoclonal antibody, which typically possesses two ligand binding domains. Trimeric (trivalent) or hexameric (or hexavalent) or greater fusion proteins comprising three

TNFRSF binding domains and IgG1-Fc and optionally further linking two or more of these fusion proteins are described, *e.g.*, in Gieffers, *et al.*, *Mol. Cancer Therapeutics* **2013,** *12,* 2735-47.

[00794] Agonistic OX40 antibodies and fusion proteins are known to induce strong immune responses. Curti, *et al.*, *Cancer Res.* **2013**, *73,* 7189-98. In some embodiments, the OX40 agonist is a monoclonal antibody or fusion protein that binds specifically to OX40 antigen in a manner sufficient to reduce toxicity. In some embodiments, the OX40 agonist is an agonistic OX40 monoclonal antibody or fusion protein that abrogates antibody-dependent cellular toxicity (ADCC), for example NK cell cytotoxicity. In some embodiments, the OX40 agonist is an agonistic OX40 monoclonal antibody or fusion protein that abrogates antibody-dependent cell phagocytosis (ADCP). In some embodiments, the OX40 agonist is an agonistic OX40 monoclonal antibody or fusion protein that abrogates complement-dependent cytotoxicity (CDC). In some embodiments, the OX40 agonist is an agonistic OX40 monoclonal antibody or fusion protein which abrogates Fc region functionality.

[00795] In some embodiments, the OX40 agonists are characterized by binding to human OX40 (SEQ ID NO:85) with high affinity and agonistic activity. In some embodiments, the OX40 agonist is a binding molecule that binds to human OX40 (SEQ ID NO:85). In some embodiments, the OX40 agonist is a binding molecule that binds to murine OX40 (SEQ ID NO:86). The amino acid sequences of OX40 antigen to which an OX40 agonist or binding molecule binds are summarized in Table 11.

TABLE 11: Amino acid sequences of OX40 antigens.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:85 human OX40 (Homo sapiens)	MCVGARRLGR GPCAALLLLG LGLSTVTGLH CVGDTYPSND RCCHECRPGN GMVSRCSRSQ	60
	NTVCRPCGPG FYNDVVSSKP CKPCTWCNLR SGSERKQLCT ATQDTVCRCR AGTQPLDSYK	120
	PGVDCAPCPP GHFSPGDNQA CKPWTNCTLA GKHTLQPASN SSDAICEDRD PPATQPQETQ	180
	GPPARPITVQ PTEAWPRTSQ GPSTRPVEVP GGRAVAAILG LGLVLGLLGP LAILLALYLL	240
	RRDQRLPPDA HKPPGGGSFR TPIQEEQADA HSTLAKI	277
SEQ ID NO:86 murine OX40 (Mus musculus)	MYVWVQQPTA LLLLGLTLGV TARRLNCVKH TYPSGHKCCR ECQPGHGMVS RCDHTRDTLC	60
	HPCETGFYNE AVNYDTCKQC TQCNHRSGSE LKQNCTPTQD TVCRCRPGTQ PRQDSGYKLG	120
	VDCVPCPPGH FSPGNNQACK PWTNCTLSGK QTRHPASDSL DAVCEDRSLL ATLLWETQRP	180
	TFRPTTVQST TVWPRTSELP SPPTLVTPEG PAFAVLLGLG LGLLAPLTVL LALYLLRKAW	240
	RLPNTPKPCW GNSFRTPIQE EHTDAHFTLA KI	272

[00796] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds human or murine OX40 with a K_D of about 100 pM or lower, binds human or murine OX40 with a K_D of about 90 pM or lower, binds human or murine OX40 with a K_D of about 80 pM or lower, binds human or murine OX40 with a K_D of about 70 pM or lower, binds human or murine OX40 with a K_D of about 60 pM or lower, binds human or murine OX40 with a K_D of about

50 pM or lower, binds human or murine OX40 with a K_D of about 40 pM or lower, or binds human or murine OX40 with a K_D of about 30 pM or lower.

[00797] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds to human or murine OX40 with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human or murine OX40 with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human or murine OX40 with a k_{assoc} of about 8×10^5 1/M·s or faster, binds to human or murine OX40 with a k_{assoc} of about 8.5×10^5 1/M·s or faster, binds to human or murine OX40 with a k_{assoc} of about 9×10^5 1/M·s or faster, binds to human or murine OX40 with a k_{assoc} of about 9.5×10^5 1/M·s or faster, or binds to human or murine OX40 with a k_{assoc} of about 1×10^6 1/M·s or faster.

[00798] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds to human or murine OX40 with a k_{dissoc} of about 2×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.1×10^{-5} 1/s or slower , binds to human or murine OX40 with a k_{dissoc} of about 2.2×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.3×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.4×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.5×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.6×10^{-5} 1/s or slower or binds to human or murine OX40 with a k_{dissoc} of about 2.7×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.8×10^{-5} 1/s or slower, binds to human or murine OX40 with a k_{dissoc} of about 2.9×10^{-5} 1/s or slower, or binds to human or murine OX40 with a k_{dissoc} of about 3×10^{-5} 1/s or slower.

[00799] In some embodiments, the compositions, processes and methods described include OX40 agonist that binds to human or murine OX40 with an IC_{50} of about 10 nM or lower, binds to human or murine OX40 with an IC_{50} of about 9 nM or lower, binds to human or murine OX40 with an IC_{50} of about 8 nM or lower, binds to human or murine OX40 with an IC_{50} of about 7 nM or lower, binds to human or murine OX40 with an IC_{50} of about 6 nM or lower, binds to human or murine OX40 with an IC_{50} of about 5 nM or lower, binds to human or murine OX40 with an IC_{50} of about 4 nM or lower, binds to human or murine OX40 with an IC_{50} of about 3 nM or lower, binds to human or murine OX40 with an IC_{50} of about 2 nM or lower, or binds to human or murine OX40 with an IC_{50} of about 1 nM or lower.

[00800] In some embodiments, the OX40 agonist is tavolixizumab, also known as MEDI0562 or MEDI-0562. Tavolixizumab is available from the MedImmune subsidiary of AstraZeneca, Inc. Tavolixizumab is immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF4 (tumor necrosis factor receptor (TNFR) superfamily member 4, OX40, CD134)], humanized and chimeric monoclonal antibody. The amino acid sequences of tavolixizumab are set forth in Table 12. Tavolixizumab comprises N-glycosylation sites at positions 301 and 301'', with fucosylated complex bi-antennary

CHO-type glycans; heavy chain intrachain disulfide bridges at positions 22-95 (V_H-V_L), 148-204 (C_H1-C_L), 265-325 (C_H2) and 371-429 (C_H3) (and at positions 22''-95'', 148''-204'', 265''-325'', and 371''-429''); light chain intrachain disulfide bridges at positions 23'-88' (V_H-V_L) and 134'-194' (C_H1-C_L) (and at positions 23'''-88''' and 134'''-194'''); interchain heavy chain-heavy chain disulfide bridges at positions 230-230'' and 233-233''; and interchain heavy chain-light chain disulfide bridges at 224-214' and 224''-214'''. Current clinical trials of tavolixizumab in a variety of solid tumor indications include U.S. National Institutes of Health clinicaltrials.gov identifiers NCT02318394 and NCT02705482.

[00801] In some embodiments, a OX40 agonist comprises a heavy chain given by SEQ ID NO:87 and a light chain given by SEQ ID NO:88. In some embodiments, a OX40 agonist comprises heavy and light chains having the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:87 and SEQ ID NO:88, respectively.

[00802] In some embodiments, the OX40 agonist comprises the heavy and light chain CDRs or variable regions (VRs) of tavolixizumab. In some embodiments, the OX40 agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:89, and the OX40 agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:90, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID

NO:89 and SEQ ID NO:90, respectively. In some embodiments, an OX40 agonist comprises an scFv antibody comprising V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90.

[00803] In some embodiments, a OX40 agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:91, SEQ ID NO:92, and SEQ ID NO:93, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:94, SEQ ID NO:95, and SEQ ID NO:96, respectively, and conservative amino acid substitutions thereof.

[00804] In an embodiment, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to tavolixizumab. In an embodimentIn some embodiments, the biosimilar monoclonal antibody comprises an OX40 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tavolixizumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a OX40 agonist antibody authorized or submitted for authorization, wherein the OX40 agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tavolixizumab. The OX40 agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tavolixizumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tavolixizumab.

TABLE 12: Amino acid sequences for OX40 agonist antibodies related to tavolixizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:87 heavy chain for tavolixizumab	QVQLQESGPG LVKPSQTLSL TCAVYGGSFS SGYWNWIRKH PGKGLEYIGY ISYNGITYHN PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY DYDGGHAMDY WGQGTLVTVS	60 120

	SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS	180
	SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG	240
	GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY	300
	NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRE	360
	EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR	420
	WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K	451
SEQ ID NO:88 light chain for tavolixizumab	DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY TSKLHSGVPS	60
	RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GSALPWTFGQ GTKVEIKRTV AAPSVFIFPP	120
	SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT	180
	LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	214
SEQ ID NO:89 heavy chain variable region for tavolixizumab	QVQLQESGPG LVKPSQTLSL TCAVYGGSFS SGYWNWIRKH PGKGLEYIGY ISYNGITYHN	60
	PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY DYDGGHAMDY WGQGTLVT	118
SEQ ID NO:90 light chain variable region for tavolixizumab	DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY TSKLHSGVPS	60
	RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GSALPWTFGQ GTKVEIKR	108
SEQ ID NO:91 heavy chain CDR1 for tavolixizumab	GSFSSGYWN	9
SEQ ID NO:92 heavy chain CDR2 for tavolixizumab	YIGYISYNGI TYH	13
SEQ ID NO:93 heavy chain CDR3 for tavolixizumab	RYKYDYDGGH AMDY	14
SEQ ID NO:94 light chain CDR1 for tavolixizumab	QDISNYLN	8
SEQ ID NO:95 light chain CDR2 for tavolixizumab	LLIYYTSKLH S	11
SEQ ID NO:96 light chain CDR3 for tavolixizumab	QQGSALPW	8

[00805] In some embodiments, the OX40 agonist is 11D4, which is a fully human antibody available from Pfizer, Inc. The preparation and properties of 11D4 are described in U.S. Patent Nos. 7,960,515; 8,236,930; and 9,028,824, the disclosures of which are incorporated by reference herein. The amino acid sequences of 11D4 are set forth in Table 13.

[00806] In some embodiments, a OX40 agonist comprises a heavy chain given by SEQ ID NO:97 and a light chain given by SEQ ID NO:98. In some embodiments, a OX40 agonist comprises heavy and light chains having the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:97 and SEQ ID NO:98, respectively.

[00807] In some embodiments, the OX40 agonist comprises the heavy and light chain CDRs or variable regions (VRs) of 11D4. In some embodiments, the OX40 agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:99, and the OX40 agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:100, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively.

[00808] In some embodiments, a OX40 agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:101, SEQ ID NO:102, and SEQ ID NO:103, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:104, SEQ ID NO:105, and SEQ ID NO:106, respectively, and conservative amino acid substitutions thereof.

[00809] In some embodiments, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to 11D4. In some embodiments, the biosimilar

monoclonal antibody comprises an OX40 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 11D4. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a OX40 agonist antibody authorized or submitted for authorization, wherein the OX40 agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 11D4. The OX40 agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 11D4. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 11D4.

TABLE 13: Amino acid sequences for OX40 agonist antibodies related to 11D4.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:97 heavy chain for 11D4	EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSY ISSSSSTIDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARES GWYLFDYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSNFGTQTYT CNVDHKPSNT KVDKTVERKC CVECPPCPAP PVAGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTFRVV SVLTVVHQDW LNGKEYKCKV SNKGLPAPIE KTISKTKGQP REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPMLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK	60 120 180 240 300 360 420 444
SEQ ID NO:98 light chain for 11D4	DIQMTQSPSS LSASVGDRVT ITCRASQGIS SWLAWYQQKP EKAPKSLIYA ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPPTFGG GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	60 120 180 214
SEQ ID NO:99 heavy chain variable region for 11D4	EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSY ISSSSSTIDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARES GWYLFDYWGQ GTLVTVSS	60 118
SEQ ID NO:100 light chain variable region for 11D4	DIQMTQSPSS LSASVGDRVT ITCRASQGIS SWLAWYQQKP EKAPKSLIYA ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPPTFGG GTKVEIK	60 107
SEQ ID NO:101 heavy chain CDR1 for 11D4	SYSMN	5
SEQ ID NO:102 heavy chain CDR2 for 11D4	YISSSSSTID YADSVKG	17

SEQ ID NO:103 heavy chain CDR3 for 11D4	ESGWYLFDY	9
SEQ ID NO:104 light chain CDR1 for 11D4	RASQGISSWL A	11
SEQ ID NO:105 light chain CDR2 for 11D4	AASSLQS	7
SEQ ID NO:106 light chain CDR3 for 11D4	QQYNSYPPT	9

[00810] In some embodiments, the OX40 agonist is 18D8, which is a fully human antibody available from Pfizer, Inc. The preparation and properties of 18D8 are described in U.S. Patent Nos. 7,960,515; 8,236,930; and 9,028,824, the disclosures of which are incorporated by reference herein. The amino acid sequences of 18D8 are set forth in Table 14.

[00811] In some embodiments, a OX40 agonist comprises a heavy chain given by SEQ ID NO:107 and a light chain given by SEQ ID NO:108. In some embodiments, a OX40 agonist comprises heavy and light chains having the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively. In some embodiments, a OX40 agonist comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:107 and SEQ ID NO:108, respectively.

[00812] In some embodiments, the OX40 agonist comprises the heavy and light chain CDRs or variable regions (VRs) of 18D8. In some embodiments, the OX40 agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:109, and the OX40 agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:110, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:109 and SEQ ID NO:110, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:109 and SEQ ID NO:110, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:109 and SEQ ID NO:110, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences

shown in SEQ ID NO:109 and SEQ ID NO:110, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:109 and SEQ ID NO:110, respectively.

[00813] In some embodiments, a OX40 agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:111, SEQ ID NO:112, and SEQ ID NO:113, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:114, SEQ ID NO:115, and SEQ ID NO:116, respectively, and conservative amino acid substitutions thereof.

[00814] In some embodiments, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to 18D8. In some embodiments, the biosimilar monoclonal antibody comprises an OX40 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 18D8. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a OX40 agonist antibody authorized or submitted for authorization, wherein the OX40 agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 18D8. The OX40 agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 18D8. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is 18D8.

TABLE 14: Amino acid sequences for OX40 agonist antibodies related to 18D8.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:107 heavy chain for 18D8	EVQLVESGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG ISWNSGSIGY 60 ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKDQ STADYYFYYG MDVWGQGTTV 120 TVSSASTKGP SVFPLAPCSR STSESTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV 180

	LQSSGLYSLS SVVTVPSSNF GTQTYTCNVD HKPSNTKVDK TVERKCCVEC PPCPAPPVAG	240
	PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVQFNW YVDGVEVHNA KTKPREEQFN	300
	STFRVVSVLT VVHQDWLNGK EYKCKVSNKG LPAPIEKTIS KTKGQPREPQ VYTLPPSREE	360
	MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPM LDSDGSFFLY SKLTVDKSRW	420
	QQGNVFSCSV MHEALHNHYT QKSLSLSPGK	450
SEQ ID NO:108 light chain for 18D8	EIVVTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA	60
	RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPTFGQG TKVEIKRTVA APSVFIFPPS	120
	DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL	180
	SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC	213
SEQ ID NO:109 heavy chain variable region for 18D8	EVQLVESGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG ISWNSGSIGY	60
	ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKDQ STADYYFYYG MDVWGQGTTV	120
	TVSS	124
SEQ ID NO:110 light chain variable region for 18D8	EIVVTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA	60
	RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPTFGQG TKVEIK	106
SEQ ID NO:111 heavy chain CDR1 for 18D8	DYAMH	5
SEQ ID NO:112 heavy chain CDR2 for 18D8	GISWNSGSIG YADSVKG	17
SEQ ID NO:113 heavy chain CDR3 for 18D8	DQSTADYYFY YGMDV	15
SEQ ID NO:114 light chain CDR1 for 18D8	RASQSVSSYL A	11
SEQ ID NO:115 light chain CDR2 for 18D8	DASNRAT	7
SEQ ID NO:116 light chain CDR3 for 18D8	QQRSNWPT	8

[00815] In some embodiments, the OX40 agonist is Hu119-122, which is a humanized antibody available from GlaxoSmithKline plc. The preparation and properties of Hu119-122 are described in U.S. Patent Nos. 9,006,399 and 9,163,085, and in International Patent Publication No. WO 2012/027328, the disclosures of which are incorporated by reference herein. The amino acid sequences of Hu119-122 are set forth in Table 15.

[00816] In some embodiments, the OX40 agonist comprises the heavy and light chain CDRs or variable regions (VRs) of Hu119-122. In some embodiments, the OX40 agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:117, and the OX40 agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:118, and conservative amino acid

substitutions thereof. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively.

[00817] In some embodiments, a OX40 agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:122, SEQ ID NO:123, and SEQ ID NO:124, respectively, and conservative amino acid substitutions thereof.

[00818] In some embodiments, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to Hu119-122. In some embodiments, the biosimilar monoclonal antibody comprises an OX40 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu119-122. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a OX40 agonist antibody authorized or submitted for authorization, wherein the OX40 agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu119-122. The OX40 agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu119-122. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or

reference biological product, wherein the reference medicinal product or reference biological product is Hu119-122.

TABLE 15: Amino acid sequences for OX40 agonist antibodies related to Hu119-122.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:117 heavy chain variable region for Hu119-122	EVQLVESGGG LVQPGGSLRL SCAASEYEFP SHDMSWVRQA PGKGLELVAA INSDGGSTYY PDTMERRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARHY DDYYAWFAYW GQGTMVTVSS	60 120
SEQ ID NO:118 light chain variable region for Hu119-122	EIVLTQSPAT LSLSPGERAT LSCRASKSVS TSGYSYMHWY QQKPGQAPRL LIYLASNLES GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRELPL TFGGGTKVEI K	60 111
SEQ ID NO:119 heavy chain CDR1 for Hu119-122	SHDMS	5
SEQ ID NO:120 heavy chain CDR2 for Hu119-122	AINSDGGSTY YPDTMER	17
SEQ ID NO:121 heavy chain CDR3 for Hu119-122	HYDDYYAWFA Y	11
SEQ ID NO:122 light chain CDR1 for Hu119-122	RASKSVSTSG YSYMH	15
SEQ ID NO:123 light chain CDR2 for Hu119-122	LASNLES	7
SEQ ID NO:124 light chain CDR3 for Hu119-122	QHSRELPLT	9

[00819] In some embodiments, the OX40 agonist is Hu106-222, which is a humanized antibody available from GlaxoSmithKline plc. The preparation and properties of Hu106-222 are described in U.S. Patent Nos. 9,006,399 and 9,163,085, and in International Patent Publication No. WO 2012/027328, the disclosures of which are incorporated by reference herein. The amino acid sequences of Hu106-222 are set forth in Table 16.

[00820] In some embodiments, the OX40 agonist comprises the heavy and light chain CDRs or variable regions (VRs) of Hu106-222. In some embodiments, the OX40 agonist heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:125, and the OX40 agonist light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:126, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively. In some embodiments, a OX40 agonist comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively. In some embodiments, a OX40 agonist

comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively.

[00821] In some embodiments, a OX40 agonist comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:127, SEQ ID NO:128, and SEQ ID NO:129, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:130, SEQ ID NO:131, and SEQ ID NO:132, respectively, and conservative amino acid substitutions thereof.

[00822] In some embodiments, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to Hu106-222. In some embodiments, the biosimilar monoclonal antibody comprises an OX40 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu106-222. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is a OX40 agonist antibody authorized or submitted for authorization, wherein the OX40 agonist antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu106-222. The OX40 agonist antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu106-222. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is Hu106-222.

TABLE 16: Amino acid sequences for OX40 agonist antibodies related to Hu106-222.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:125 heavy chain variable region for Hu106-222	QVQLVQSGSE LKKPGASVKV SCKASGYTFT DYSMHWVRQA PGQGLKWMGW INTETGEPTY 60 ADDFKGRFVF SLDTSVSTAY LQISSLKAED TAVYYCANPY YDYVSYYAMD YWGQGTTVTV 120 SS 122

SEQ ID NO:126 light chain variable region for Hu106-222	DIQMTQSPSS LSASVGDRVT ITCKASQDVS TAVAWYQQKP GKAPKLLIYS ASYLYTGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQQ HYSTPRTFGQ GTKLEIK	60 107
SEQ ID NO:127 heavy chain CDR1 for Hu106-222	DYSMH	5
SEQ ID NO:128 heavy chain CDR2 for Hu106-222	WINTETGEPT YADDFKG	17
SEQ ID NO:129 heavy chain CDR3 for Hu106-222	PYYDYVSYYA MDY	13
SEQ ID NO:130 light chain CDR1 for Hu106-222	KASQDVSTAV A	11
SEQ ID NO:131 light chain CDR2 for Hu106-222	SASYLYT	7
SEQ ID NO:132 light chain CDR3 for Hu106-222	QQHYSTPRT	9

[00823] In some embodiments, the OX40 agonist antibody is MEDI6469 (also referred to as 9B12). MEDI6469 is a murine monoclonal antibody. Weinberg, *et al.*, *J. Immunother.* **2006**, *29*, 575-585. In some embodiments the OX40 agonist is an antibody produced by the 9B12 hybridoma, deposited with Biovest Inc. (Malvern, MA, USA), as described in Weinberg, *et al.*, *J. Immunother.* **2006**, *29*, 575-585, the disclosure of which is hereby incorporated by reference in its entirety. In some embodiments, the antibody comprises the CDR sequences of MEDI6469. In some embodiments, the antibody comprises a heavy chain variable region sequence and/or a light chain variable region sequence of MEDI6469.

[00824] In some embodiments, the OX40 agonist is L106 BD (Pharmingen Product #340420). In some embodiments, the OX40 agonist comprises the CDRs of antibody L106 (BD Pharmingen Product #340420). In some embodiments, the OX40 agonist comprises a heavy chain variable region sequence and/or a light chain variable region sequence of antibody L106 (BD Pharmingen Product #340420). In some embodiments, the OX40 agonist is ACT35 (Santa Cruz Biotechnology, Catalog #20073). In some embodiments, the OX40 agonist comprises the CDRs of antibody ACT35 (Santa Cruz Biotechnology, Catalog #20073). In some embodiments, the OX40 agonist comprises a heavy chain variable region sequence and/or a light chain variable region sequence of antibody ACT35 (Santa Cruz Biotechnology, Catalog #20073). In some embodiments, the OX40 agonist is the murine monoclonal antibody anti-mCD134/mOX40 (clone OX86), commercially available from InVivoMAb, BioXcell Inc, West Lebanon, NH.

[00825] In some embodiments, the OX40 agonist is selected from the OX40 agonists described in International Patent Application Publication Nos. WO 95/12673, WO 95/21925, WO 2006/121810, WO 2012/027328, WO 2013/028231, WO 2013/038191, and WO 2014/148895; European Patent Application EP 0672141; U.S. Patent Application Publication Nos. US 2010/136030, US 2014/377284, US 2015/190506, and US 2015/132288 (including clones 20E5 and 12H3); and U.S. Patent Nos. 7,504,101, 7,550,140, 7,622,444, 7,696,175, 7,960,515, 7,961,515, 8,133,983, 9,006,399, and 9,163,085, the disclosure of each of which is incorporated herein by reference in its entirety.

[00826] In some embodiments, the OX40 agonist is an OX40 agonistic fusion protein as depicted in Structure I-A (C-terminal Fc-antibody fragment fusion protein) or Structure I-B (N-terminal Fc-antibody fragment fusion protein), or a fragment, derivative, conjugate, variant, or biosimilar thereof. The properties of structures I-A and I-B are described above and in U.S. Patent Nos. 9,359,420, 9,340,599, 8,921,519, and 8,450,460, the disclosures of which are incorporated by reference herein. Amino acid sequences for the polypeptide domains of structure I-A given in Figure 18 are found in Table 9. The Fc domain preferably comprises a complete constant domain (amino acids 17-230 of SEQ ID NO:62) the complete hinge domain (amino acids 1-16 of SEQ ID NO:62) or a portion of the hinge domain (*e.g.*, amino acids 4-16 of SEQ ID NO:62). Preferred linkers for connecting a C-terminal Fc-antibody may be selected from the embodiments given in SEQ ID NO:63 to SEQ ID NO:72, including linkers suitable for fusion of additional polypeptides. Likewise, amino acid sequences for the polypeptide domains of structure I-B given in Figure 18 are found in Table 9. If an Fc antibody fragment is fused to the N-terminus of an TNRFSF fusion protein as in structure I-B, the sequence of the Fc module is preferably that shown in SEQ ID NO:73, and the linker sequences are preferably selected from those embodiments set forth in SED ID NO:74 to SEQ ID NO:76.

[00827] In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains selected from the group consisting of a variable heavy chain and variable light chain of tavolixizumab, a variable heavy chain and variable light chain of 11D4, a variable heavy chain and variable light chain of 18D8, a variable heavy chain and variable light chain of Hu119-122, a variable heavy chain and variable light chain of Hu106-222, a variable heavy chain and variable light chain selected from the variable heavy chains and variable light chains described in Table 17, any combination of a variable heavy chain and variable light chain of the foregoing, and fragments, derivatives, conjugates, variants, and biosimilars thereof.

[00828] In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains comprising an OX40L sequence. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains comprising a sequence according to SEQ ID NO:133. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or

more OX40 binding domains comprising a soluble OX40L sequence. In some embodiments, a OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains comprising a sequence according to SEQ ID NO:134. In some embodiments, a OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains comprising a sequence according to SEQ ID NO:135.

[00829] In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:109 and SEQ ID NO:110, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:127 and SEQ ID NO:128, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively, wherein the V_H and V_L domains are connected by a linker. In some embodiments, an OX40 agonist fusion protein according to structures I-A or I-B comprises one or more OX40 binding domains that is a scFv domain comprising V_H and V_L regions that are each at least 95% identical to the V_H and V_L sequences given in Table 17, wherein the V_H and V_L domains are connected by a linker.

TABLE 17: Additional polypeptide domains useful as OX40 binding domains in fusion proteins (*e.g.*, structures I-A and I-B) or as scFv OX40 agonist antibodies.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:133 OX40L	MERVQPLEEN VGNAARPRFE RNKLLLVASV IQGLGLLLCF TYICLHFSAL QVSHRYPRIQ SIKVQFTEYK KEKGFILTSQ KEDEIMKVQN NSVIINCDGF YLISLKGYFS QEVNISLHYQ KDEEPLFQLK KVRSVNSLMV ASLTYKDKVY LNVTTDNTSL DDFHVNGGEL ILIHQNPGEF CVL	60 120 180 183
SEQ ID NO:134 OX40L soluble domain	SHRYPRIQSI KVQFTEYKKE KGFILTSQKE DEIMKVQNNS VIINCDGFYL ISLKGYFSQE VNISLHYQKD EEPLFQLKKV RSVNSLMVAS LTYKDKVYLN VTTDNTSLDD FHVNGGELIL IHQNPGEFCV L	60 120 131
SEQ ID NO:135 OX40L soluble	YPRIQSIKVQ FTEYKKEKGF ILTSQKEDEI MKVQNNSVII NCDGFYLISL KGYFSQEVNI SLHYQKDEEP LFQLKKVRSV NSLMVASLTY KDKVYLNVTT DNTSLDDFHV NGGELILIHQ	60 120

domain (alternative)	NPGEFCVL	128
SEQ ID NO:136 variable heavy chain for 008	EVQLVESGGG LVQPGGSLRL SCAASGFTFS NYTMNWVRQA PGKGLEWVSA ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR YSQVHYALDY WGQGTLVTVS	60 120
SEQ ID NO:137 variable light chain for 008	DIVMTQSPDS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKAGQSPQ LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYYNHP TTFGQGTK	60 108
SEQ ID NO:138 variable heavy chain for 011	EVQLVESGGG VVQPGRSLRL SCAASGFTFS DYTMNWVRQA PGKGLEWVSS ISGGSTYYAD SRKGRFTISR DNSKNTLYLQ MNNLRAEDTA VYYCARDRYF RQQNAFDYWG QGTLVTVSSA	60 120
SEQ ID NO:139 variable light chain for 011	DIVMTQSPDS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKAGQSPQ LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYYNHP TTFGQGTK	60 108
SEQ ID NO:140 variable heavy chain for 021	EVQLVESGGG LVQPRGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVAV ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR YITLPNALDY WGQGTLVTVS	60 120
SEQ ID NO:141 variable light chain for 021	DIQMTQSPVS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYKSNP PTFGQGTK	60 108
SEQ ID NO:142 variable heavy chain for 023	EVQLVESGGG LVHPGGSLRL SCAGSGFTFS SYAMHWVRQA PGKGLEWVSA IGTGGGTYYA DSVMGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARYDN VMGLYWFDYW GQGTLVTVSS	60 120
SEQ ID NO:143 variable light chain for 023	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPAFGG GTKVEIKR	60 108
SEQ ID NO:144 heavy chain variable region	EVQLQQSGPE LVKPGASVKM SCKASGYTFT SYVMHWVKQK PGQGLEWIGY INPYNDGTKY NEKFKGKATL TSDKSSSTAY MELSSLTSED SAVYYCANYY GSSLSMDYWG QGTSVTVSS	60 119
SEQ ID NO:145 light chain variable region	DIQMTQTTSS LSASLGDRVT ISCRASQDIS NYLNWYQQKP DGTVKLLIYY TSRLHSGVPS RFSGSGSGTD YSLTISNLEQ EDIATYFCQQ GNTLPWTFGG GTKLEIKR	60 108
SEQ ID NO:146 heavy chain variable region	EVQLQQSGPE LVKPGASVKI SCKTSGYTFK DYTMHWVKQS HGKSLEWIGG IYPNNGGSTY NQNFKDKATL TVDKSSSTAY MEFRSLTSED SAVYYCARMG YHGPHLDFDV WGAGTTVTVS P	60 120 121
SEQ ID NO:147 light chain variable region	DIVMTQSHKF MSTSLGDRVS ITCKASQDVG AAVAWYQQKP GQSPKLLIYW ASTRHTGVPD RFTGGGSGTD FTLTISNVQS EDLTDYFCQQ YINYPLTFGG GTKLEIKR	60 108
SEQ ID NO:148 heavy chain variable region of humanized antibody	QIQLVQSGPE LKKPGETVKI SCKASGYTFT DYSMHWVKQA PGKGLKWMGW INTETGEPTY ADDFKGRFAF SLETSASTAY LQINNLKNED TATYFCANPY YDYVSYYAMD YWGHGTSVTV SS	60 120 122
SEQ ID NO:149 heavy chain variable region of humanized antibody	QVQLVQSGSE LKKPGASVKV SCKASGYTFT DYSMHWVRQA PGQGLKWMGW INTETGEPTY ADDFKGRFVF SLDTSVSTAY LQISSLKAED TAVYYCANPY YDYVSYYAMD YWGQGTTVTV SS	60 120 122
SEQ ID NO:150 light chain variable region of humanized antibody	DIVMTQSHKF MSTSVRDRVS ITCKASQDVS TAVAWYQQKP GQSPKLLIYS ASYLYTGVPD RFTGSGSGTD FTFTISSVQA EDLAVYYCQQ HYSTPRTFGG GTKLEIK	60 107
SEQ ID NO:151 light chain variable region of humanized antibody	DIVMTQSHKF MSTSVRDRVS ITCKASQDVS TAVAWYQQKP GQSPKLLIYS ASYLYTGVPD RFTGSGSGTD FTFTISSVQA EDLAVYYCQQ HYSTPRTFGG GTKLEIK	60 107
SEQ ID NO:152 heavy chain variable region of humanized antibody	EVQLVESGGG LVQPGESLKL SCESNEYEFP SHDMSWVRKT PEKRLELVAA INSDGGSTYY PDTMERRFII SRDNTKKTLY LQMSSLRSED TALYYCARHY DDYYAWFAYW GQGTLVTVSA	60 120
SEQ ID NO:153 heavy chain variable region of humanized antibody	EVQLVESGGG LVQPGGSLRL SCAASEYEFP SHDMSWVRQA PGKGLELVAA INSDGGSTYY PDTMERRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARHY DDYYAWFAYW GQGTMVTVSS	60 120
SEQ ID NO:154 light chain variable region	DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYMHWY QQKPGQPPKL LIYLASNLES GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSRELPL TFGAGTKLEL K	60 111

of humanized antibody		
SEQ ID NO:155 light chain variable region of humanized antibody	EIVLTQSPAT LSLSPGERAT LSCRASKSVS TSGYSYMHWY QQKPGQAPRL LIYLASNLES GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRELPL TFGGGTKVEI K	60 111
SEQ ID NO:156 heavy chain variable region	MYLGLNYVFI VFLLNGVQSE VKLEESGGGL VQPGGSMKLS CAASGFTFSD AWMDWVRQSP EKGLEWVAEI RSKANNHATY YAESVNGRFT ISRDDSKSSV YLQMNSLRAE DTGIYYCTWG EVFYFDYWGQ GTTLTVSS	60 120 138
SEQ ID NO:157 light chain variable region	MRPSIQFLGL LLFWLHGAQC DIQMTQSPSS LSASLGGKVT ITCKSSQDIN KYIAWYQHKP GKGPRLLIHY TSTLQPGIPS RFSGSGSGRD YSFSISNLEP EDIATYYCLQ YDNLLTFGAG TKLELK	60 120 126

[00830] In some embodiments, the OX40 agonist is a OX40 agonistic single-chain fusion polypeptide comprising (i) a first soluble OX40 binding domain, (ii) a first peptide linker, (iii) a second soluble OX40 binding domain, (iv) a second peptide linker, and (v) a third soluble OX40 binding domain, further comprising an additional domain at the N-terminal and/or C-terminal end, and wherein the additional domain is a Fab or Fc fragment domain. In some embodiments, the OX40 agonist is a OX40 agonistic single-chain fusion polypeptide comprising (i) a first soluble OX40 binding domain, (ii) a first peptide linker, (iii) a second soluble OX40 binding domain, (iv) a second peptide linker, and (v) a third soluble OX40 binding domain, further comprising an additional domain at the N-terminal and/or C-terminal end, wherein the additional domain is a Fab or Fc fragment domain wherein each of the soluble OX40 binding domains lacks a stalk region (which contributes to trimerisation and provides a certain distance to the cell membrane, but is not part of the OX40 binding domain) and the first and the second peptide linkers independently have a length of 3-8 amino acids.

[00831] In some embodiments, the OX40 agonist is an OX40 agonistic single-chain fusion polypeptide comprising (i) a first soluble tumor necrosis factor (TNF) superfamily cytokine domain, (ii) a first peptide linker, (iii) a second soluble TNF superfamily cytokine domain, (iv) a second peptide linker, and (v) a third soluble TNF superfamily cytokine domain, wherein each of the soluble TNF superfamily cytokine domains lacks a stalk region and the first and the second peptide linkers independently have a length of 3-8 amino acids, and wherein the TNF superfamily cytokine domain is an OX40 binding domain.

[00832] In some embodiments, the OX40 agonist is MEDI6383. MEDI6383 is an OX40 agonistic fusion protein and can be prepared as described in U.S. Patent No. 6,312,700, the disclosure of which is incorporated by reference herein.

[00833] In some embodiments, the OX40 agonist is an OX40 agonistic scFv antibody comprising any of the foregoing V_H domains linked to any of the foregoing V_L domains.

[00834] In some embodiments, the OX40 agonist is Creative Biolabs OX40 agonist monoclonal antibody MOM-18455, commercially available from Creative Biolabs, Inc., Shirley, NY, USA.

[00835] In some embodiments, the OX40 agonist is OX40 agonistic antibody clone Ber-ACT35 commercially available from BioLegend, Inc., San Diego, CA, USA.

C. Optional Cell Viability Analyses

[00836] Optionally, a cell viability assay can be performed after the priming first expansion (sometimes referred to as the initial bulk expansion), using standard assays known in the art. Thus, in certain embodiments, the method comprises performing a cell viability assay subsequent to the priming first expansion. For example, a trypan blue exclusion assay can be done on a sample of the bulk TILs, which selectively labels dead cells and allows a viability assessment. Other assays for use in testing viability can include but are not limited to the Alamar blue assay; and the MTT assay.

1. Cell Counts, Viability, Flow Cytometry

[00837] In some embodiments, cell counts and/or viability are measured. The expression of markers such as but not limited CD3, CD4, CD8, and CD56, as well as any other disclosed or described herein, can be measured by flow cytometry with antibodies, for example but not limited to those commercially available from BD Bio-sciences (BD Biosciences, San Jose, CA) using a FACSCanto™ flow cytometer (BD Biosciences). The cells can be counted manually using a disposable c-chip hemocytometer (VWR, Batavia, IL) and viability can be assessed using any method known in the art, including but not limited to trypan blue staining. The cell viability can also be assayed based on U.S. Patent Application Publication No. 2018/0282694, incorporated by reference herein in its entirety. Cell viability can also be assayed based on U.S. Patent Application Publication No. 2018/0280436 or International Patent Application Publication No. WO/2018/081473, both of which are incorporate herein in their entireties for all purposes.

[00838] In some cases, the bulk TIL population can be cryopreserved immediately, using the protocols discussed below. Alternatively, the bulk TIL population can be subjected to REP and then cryopreserved as discussed below. Similarly, in the case where genetically modified TILs will be used in therapy, the bulk or REP TIL populations can be subjected to genetic modifications for suitable treatments.

2. Cell Cultures

[00839] In some embodiments, a method for expanding TILs, including those discussed above as well as exemplified in Figures 1 and 8, in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D, may include using about 5,000 mL to about 25,000 mL of cell medium, about 5,000 mL to about 10,000 mL of cell medium, or about 5,800 mL to about 8,700 mL of cell medium. In some embodiments, the

media is a serum free medium. In some embodiments, the media in the priming first expansion is serum free. In some embodiments, the media in the second expansion is serum free. In some embodiments, the media in the priming first expansion and the second expansion (also referred to as rapid second expansion) are both serum free. In some embodiments, expanding the number of TILs uses no more than one type of cell culture medium. Any suitable cell culture medium may be used, *e.g.*, AIM-V cell medium (L-glutamine, 50 μM streptomycin sulfate, and 10 μM gentamicin sulfate) cell culture medium (Invitrogen, Carlsbad CA). In this regard, the inventive methods advantageously reduce the amount of medium and the number of types of medium required to expand the number of TIL. In some embodiments, expanding the number of TIL may comprise feeding the cells no more frequently than every third or fourth day. Expanding the number of cells in a gas permeable container simplifies the procedures necessary to expand the number of cells by reducing the feeding frequency necessary to expand the cells.

[00840] In some embodiments, the cell culture medium in the first and/or second gas permeable container is unfiltered. The use of unfiltered cell medium may simplify the procedures necessary to expand the number of cells. In some embodiments, the cell medium in the first and/or second gas permeable container lacks beta-mercaptoethanol (BME).

[00841] In some embodiments, the duration of the method comprising obtaining a tumor tissue sample from the mammal; culturing the tumor tissue sample in a first gas permeable container containing cell medium including IL-2, 1X antigen-presenting feeder cells, and OKT-3 for a duration of about 1 to 8 days, *e.g.*, about 7 days as a priming first expansion, or about 8 days as a priming first expansion; transferring the TILs to a second gas permeable container and expanding the number of TILs in the second gas permeable container containing cell medium including IL-2, 2X antigen-presenting feeder cells, and OKT-3 for a duration of about 7 to 9 days, *e.g.*, about 7 days, about 8 days, or about 9 days.

[00842] In some embodiments, the duration of the method comprising obtaining a tumor tissue sample from the mammal; culturing the tumor tissue sample in a first gas permeable container containing cell medium including IL-2, 1X antigen-presenting feeder cells, and OKT-3 for a duration of about 1 to 7 days, *e.g.*, about 7 days as a priming first expansion; transferring the TILs to a second gas permeable container and expanding the number of TILs in the second gas permeable container containing cell medium including IL-2, 2X antigen-presenting feeder cells, and OKT-3 for a duration of about 7 to 14 days, or about 7 to 9 days, *e.g.*, about 7 days, about 8 days, or about 9 days, about 10 days, or about 11 days.

[00843] In some embodiments, the duration of the method comprising obtaining a tumor tissue sample from the mammal; culturing the tumor tissue sample in a first gas permeable container

containing cell medium including IL-2, 1X antigen-presenting feeder cells, and OKT-3 for a duration of about 1 to 7 days, *e.g.*, about 7 days, as a priming first expansion; transferring the TILs to a second gas permeable container and expanding the number of TILs in the second gas permeable container containing cell medium including IL-2, 2X antigen-presenting feeder cells, and OKT-3 for a duration of about 7 to 11 days, *e.g.*, about 7 days, about 8 days, about 9 days, about 10, or about 11 days.

[00844] In some embodiments, TILs are expanded in gas-permeable containers. Gas-permeable containers have been used to expand TILs using PBMCs using methods, compositions, and devices known in the art, including those described in U.S. Patent Application Publication No. 2005/0106717 A1, the disclosures of which are incorporated herein by reference. In some embodiments, TILs are expanded in gas-permeable bags. In some embodiments, TILs are expanded using a cell expansion system that expands TILs in gas permeable bags, such as the Xuri Cell Expansion System W25 (GE Healthcare). In some embodiments, TILs are expanded using a cell expansion system that expands TILs in gas permeable bags, such as the WAVE Bioreactor System, also known as the Xuri Cell Expansion System W5 (GE Healthcare). In some embodiments, the cell expansion system includes a gas permeable cell bag with a volume selected from the group consisting of about 100 mL, about 200 mL, about 300 mL, about 400 mL, about 500 mL, about 600 mL, about 700 mL, about 800 mL, about 900 mL, about 1 L, about 2 L, about 3 L, about 4 L, about 5 L, about 6 L, about 7 L, about 8 L, about 9 L, and about 10 L.

[00845] In some embodiments, TILs can be expanded in G-REX flasks (commercially available from Wilson Wolf Manufacturing). Such embodiments allow for cell populations to expand from about $5 \underline{\times} 10^5$ cells/cm^2 to between $10 \underline{\times} 10^6$ and $30 \underline{\times} 10^6$ cells/cm^2. In some embodiments this is without feeding. In some embodiments, this is without feeding so long as medium resides at a height of about 10 cm in the G-REX flask. In some embodiments this is without feeding but with the addition of one or more cytokines. In some embodiments, the cytokine can be added as a bolus without any need to mix the cytokine with the medium. Such containers, devices, and methods are known in the art and have been used to expand TILs, and include those described in U.S. Patent Application Publication No. US 2014/0377739A1, International Publication No. WO 2014/210036 A1, U.S. Patent Application Publication No. us 2013/0115617 A1, International Publication No. WO 2013/188427 A1, U.S. Patent Application Publication No. US 2011/0136228 A1, U.S. Patent No. US 8,809,050 B2, International publication No. WO 2011/072088 A2, U.S. Patent Application Publication No. US 2016/0208216 A1, U.S. Patent Application Publication No. US 2012/0244133 A1, International Publication No. WO 2012/129201 A1, U.S. Patent Application Publication No. US 2013/0102075 A1, U.S. Patent No. US 8,956,860 B2, International Publication No. WO 2013/173835 A1, U.S. Patent Application Publication No. US 2015/0175966 A1, the disclosures of which are

incorporated herein by reference. Such processes are also described in Jin *et al.*, *J. Immunotherapy,* **2012**, 35:283-292.

D. Optional Knockdown or Knockout of Genes in TILs

[00846] In some embodiments, the expanded TILs of the present invention are further manipulated before, during, or after an expansion step, including during closed, sterile manufacturing processes, each as provided herein, in order to alter protein expression in a transient manner. In some embodiments, the transiently altered protein expression is due to transient gene editing. In some embodiments, the expanded TILs of the present invention are treated with transcription factors (TFs) and/or other molecules capable of transiently altering protein expression in the TILs. In some embodiments, the TFs and/or other molecules that are capable of transiently altering protein expression provide for altered expression of tumor antigens and/or an alteration in the number of tumor antigen-specific T cells in a population of TILs.

[00847] In certain embodiments, the method comprises genetically editing a population of TILs. In certain embodiments, the method comprises genetically editing the first population of TILs, the second population of TILs and/or the third population of TILs.

[00848] In some embodiments, the present invention includes genetic editing through nucleotide insertion, such as through ribonucleic acid (RNA) insertion, including insertion of messenger RNA (mRNA) or small (or short) interfering RNA (siRNA), into a population of TILs for promotion of the expression of one or more proteins or inhibition of the expression of one or more proteins, as well as simultaneous combinations of both promotion of one set of proteins with inhibition of another set of proteins.

[00849] In some embodiments, the expanded TILs of the present invention undergo transient alteration of protein expression. In some embodiments, the transient alteration of protein expression occurs in the bulk TIL population prior to first expansion, including, for example in the TIL population obtained from for example, Step A as indicated in Figure 8 (particularly Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the transient alteration of protein expression occurs during the first expansion, including, for example in the TIL population expanded in for example, Step B as indicated in Figure 8 (for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the transient alteration of protein expression occurs after the first expansion, including, for example in the TIL population in transition between the first and second expansion (*e.g.,* the second population of TILs as described herein), the TIL population obtained from for example, Step B and included in Step C as indicated in Figure 8. In some embodiments, the transient alteration of

protein expression occurs in the bulk TIL population prior to second expansion, including, for example in the TIL population obtained from for example, Step C and prior to its expansion in Step D as indicated in Figure 8. In some embodiments, the transient alteration of protein expression occurs during the second expansion, including, for example in the TIL population expanded in for example, Step D as indicated in Figure 8 (*e.g.,* the third population of TILs). In some embodiments, the transient alteration of protein expression occurs after the second expansion, including, for example in the TIL population obtained from the expansion in for example, Step D as indicated in Figure 8.

[00850] In some embodiments, a method of transiently altering protein expression in a population of TILs includes the step of electroporation. Electroporation methods are known in the art and are described, *e.g.*, in Tsong, *Biophys. J.* 1991, *60,* 297-306, and U.S. Patent Application Publication No. 2014/0227237 A1, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of transiently altering protein expression in population of TILs includes the step of calcium phosphate transfection. Calcium phosphate transfection methods (calcium phosphate DNA precipitation, cell surface coating, and endocytosis) are known in the art and are described in Graham and van der Eb, *Virology* 1973, *52,* 456-467; Wigler, *et al.*, *Proc. Natl. Acad. Sci.* 1979, *76,* 1373-1376; and Chen and Okayarea, *Mol. Cell. Biol.* 1987, *7,* 2745-2752; and in U.S. Patent No. 5,593,875, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of transiently altering protein expression in a population of TILs includes the step of liposomal transfection. Liposomal transfection methods, such as methods that employ a 1:1 (w/w) liposome formulation of the cationic lipid *N*-[1-(2,3-dioleyloxy)propyl]-*n,n,n*-trimethylammonium chloride (DOTMA) and dioleoyl phophotidylethanolamine (DOPE) in filtered water, are known in the art and are described in Rose, *et al.*, *Biotechniques* 1991, *10,* 520-525 and Felgner, *et al.*, *Proc. Natl. Acad. Sci. USA*, 1987, *84,* 7413-7417 and in U.S. Patent Nos. 5,279,833; 5,908,635; 6,056,938; 6,110,490; 6,534,484; and 7,687,070, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of transiently altering protein expression in a population of TILs includes the step of transfection using methods described in U.S. Patent Nos. 5,766,902; 6,025,337; 6,410,517; 6,475,994; and 7,189,705; the disclosures of each of which are incorporated by reference herein.

[00851] In some embodiments, transient alteration of protein expression results in an increase in Stem Memory T cells (TSCMs). TSCMs are early progenitors of antigen-experienced central memory T cells. TSCMs generally display the long-term survival, self-renewal, and multipotency abilities that define stem cells, and are generally desirable for the generation of effective TIL products. TSCM have shown enhanced anti-tumor activity compared with other T cell subsets in mouse models of adoptive cell transfer. In some embodiments, transient alteration of protein expression results in a TIL population with a composition comprising a high proportion of TSCM. In some embodiments,

transient alteration of protein expression results in an at least 5%, at least 10%, at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% increase in TSCM percentage. In some embodiments, transient alteration of protein expression results in an at least a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, or 10-fold increase in TSCMs in the TIL population. In some embodiments, transient alteration of protein expression results in a TIL population with at least at least 5%, at least 10%, at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% TSCMs. In some embodiments, transient alteration of protein expression results in a therapeutic TIL population with at least at least 5%, at least 10%, at least 10%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% TSCMs.

[00852] In some embodiments, transient alteration of protein expression results in rejuvenation of antigen-experienced T-cells. In some embodiments, rejuvenation includes, for example, increased proliferation, increased T-cell activation, and/or increased antigen recognition.

[00853] In some embodiments, transient alteration of protein expression alters the expression in a large fraction of the T-cells in order to preserve the tumor-derived TCR repertoire. In some embodiments, transient alteration of protein expression does not alter the tumor-derived TCR repertoire. In some embodiments, transient alteration of protein expression maintains the tumor-derived TCR repertoire.

[00854] In some embodiments, transient alteration of protein results in altered expression of a particular gene. In some embodiments, the transient alteration of protein expression targets a gene including but not limited to PD-1 (also referred to as PDCD1 or CC279), TGFBR2, CCR4/5, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-12, IL-15, IL-21, NOTCH 1/2 ICD, CTLA-4, TIM3, LAG3, TIGIT, TET2, TGFβ, CCR2, CCR4, CCR5, CXCR1, CXCR2, CSCR3, CCL2 (MCP-1), CCL3 (MIP-1α), CCL4 (MIP1-β), CCL5 (RANTES), CXCL1/CXCL8, CCL22, CCL17, CXCL1/CXCL8, VHL, CD44, PIK3CD, SOCS1, thymocyte selection associated high mobility group (HMG) box (TOX), ankyrin repeat domain 11 (ANKRD11), BCL6 co-repressor (BCOR), and/or cAMP protein kinase A (PKA). In some embodiments, the transient alteration of protein expression targets a gene selected from the group consisting of PD-1, TGFBR2, CCR4/5, CTLA-4, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-12, IL-15, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, TET2, TGFβ, CCR2, CCR4, CCR5, CXCR1, CXCR2, CSCR3, CCL2 (MCP-1), CCL3 (MIP-1α), CCL4 (MIP1-β), CCL5 (RANTES), CXCL1/CXCL8, CCL22, CCL17, CXCL1/CXCL8, VHL, CD44, PIK3CD, SOCS1, thymocyte selection associated

high mobility group (HMG) box (TOX), ankyrin repeat domain 11 (ANKRD11), BCL6 co-repressor (BCOR), and/or cAMP protein kinase A (PKA). In some embodiments, the transient alteration of protein expression targets PD-1. In some embodiments, the transient alteration of protein expression targets TGFBR2. In some embodiments, the transient alteration of protein expression targets CCR4/5. In some embodiments, the transient alteration of protein expression targets CTLA-4. In some embodiments, the transient alteration of protein expression targets CBLB. In some embodiments, the transient alteration of protein expression targets CISH. In some embodiments, the transient alteration of protein expression targets CCRs (chimeric co-stimulatory receptors). In some embodiments, the transient alteration of protein expression targets IL-2. In some embodiments, the transient alteration of protein expression targets IL-12. In some embodiments, the transient alteration of protein expression targets IL-15. In some embodiments, the transient alteration of protein expression targets IL-21. In some embodiments, the transient alteration of protein expression targets NOTCH 1/2 ICD. In some embodiments, the transient alteration of protein expression targets TIM3. In some embodiments, the transient alteration of protein expression targets LAG3. In some embodiments, the transient alteration of protein expression targets TIGIT. In some embodiments, the transient alteration of protein expression targets TET2. In some embodiments, the transient alteration of protein expression targets TGFβ. In some embodiments, the transient alteration of protein expression targets CCR1. In some embodiments, the transient alteration of protein expression targets CCR2. In some embodiments, the transient alteration of protein expression targets CCR4. In some embodiments, the transient alteration of protein expression targets CCR5. In some embodiments, the transient alteration of protein expression targets CXCR1. In some embodiments, the transient alteration of protein expression targets CXCR2. In some embodiments, the transient alteration of protein expression targets CSCR3. In some embodiments, the transient alteration of protein expression targets CCL2 (MCP-1). In some embodiments, the transient alteration of protein expression targets CCL3 (MIP-1α). In some embodiments, the transient alteration of protein expression targets CCL4 (MIP1-β). In some embodiments, the transient alteration of protein expression targets CCL5 (RANTES). In some embodiments, the transient alteration of protein expression targets CXCL1. In some embodiments, the transient alteration of protein expression targets CXCL8. In some embodiments, the transient alteration of protein expression targets CCL22. In some embodiments, the transient alteration of protein expression targets CCL17. In some embodiments, the transient alteration of protein expression targets VHL. In some embodiments, the transient alteration of protein expression targets CD44. In some embodiments, the transient alteration of protein expression targets PIK3CD. In some embodiments, the transient alteration of protein expression targets SOCS1. In some embodiments, the transient alteration of protein expression targets thymocyte selection associated high mobility group (HMG) box (TOX). In some embodiments, the transient alteration of protein expression targets ankyrin repeat domain 11 (ANKRD11). In some embodiments, the transient alteration of protein

expression targets BCL6 co-repressor (BCOR). In some embodiments, the transient alteration of protein expression targets cAMP protein kinase A (PKA).

[00855] In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of a chemokine receptor. In some embodiments, the chemokine receptor that is overexpressed by transient protein expression includes a receptor with a ligand that includes but is not limited to CCL2 (MCP-1), CCL3 (MIP-1α), CCL4 (MIP1-β), CCL5 (RANTES), CXCL1, CXCL8, CCL22, and/or CCL17.

[00856] In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of PD-1, CTLA-4, CBLB, CISH, TIM-3, LAG-3, TIGIT, TET2, TGFβR2, and/or TGFβ (including resulting in, for example, TGFβ pathway blockade). In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of PD-1. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of CBLB (CBL-B). In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of CISH. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of TIM-3. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of LAG-3. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of TIGIT. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of TET2. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of TGFβR2. In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of TGFβ.

[00857] In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of chemokine receptors in order to, for example, improve TIL trafficking or movement to the tumor site. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of a CCR (chimeric co-stimulatory receptor). In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of a chemokine receptor selected from the group consisting of CCR1, CCR2, CCR4, CCR5, CXCR1, CXCR2, and/or CSCR3.

[00858] In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of an interleukin. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of an interleukin selected from the group consisting of IL-2, IL-12, IL-15, and/or IL-21.

[00859] In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of NOTCH 1/2 ICD. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of VHL. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of CD44. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of PIK3CD. In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of SOCS1,

[00860] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of cAMP protein kinase A (PKA).

[00861] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of a molecule selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of two molecules selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and one molecule selected from the group consisting of LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1, CTLA-4, LAG-3, CISH, CBLB, TIM3, TIGIT, TET2 and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and one of CTLA-4, LAG3, CISH, CBLB, TIM3, TIGIT, TET2 and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and CTLA-4. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and LAG3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and CISH. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and TIM3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1 and TET2. IIn some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CTLA-4 and LAG3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CTLA-4 and CISH. In some embodiments, the transient alteration of

protein expression results in decreased and/or reduced expression of CTLA-4 and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CTLA-4 and TIM3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CTLA-4 and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CTLA-4 and TET2. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of LAG3 and CISH. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of LAG3 and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of LAG3 and TIM3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of LAG3 and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of LAG3 and TET2. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CISH and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CISH and TIM3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CISH and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CISH and TET2. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CBLB and TIM3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CBLB and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of CBLB and TET2. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and PD-1. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and LAG3. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and CISH. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and TIGIT. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIM3 and TET2.

[00862] In some embodiments, an adhesion molecule selected from the group consisting of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof, is inserted by a gammaretroviral or lentiviral method into the first population of TILs, second population of TILs, or harvested population of TILs (*e.g.*, the expression of the adhesion molecule is increased).

[00863] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of a molecule selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof, and increased and/or enhanced expression of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of a molecule selected from the group consisting of PD-1, CTLA-4, LAG3, TIM3, CISH, CBLB, TIGIT, TET2 and combinations thereof, and increased and/or enhanced expression of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof.

[00864] In some embodiments, there is a reduction in expression of about 5%, about 10%, about 10%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 80%. In some embodiments, there is a reduction in expression of at least about 85%, In some embodiments, there is a reduction in expression of at least about 90%. In some embodiments, there is a reduction in expression of at least about 95%. In some embodiments, there is a reduction in expression of at least about 99%.

[00865] In some embodiments, there is an increase in expression of about 5%, about 10%, about 10%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is an increase in expression of at least about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is an increase in expression of at least about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is an increase in expression of at least about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is an increase in expression of at least about 85%, about 90%, or about 95%. In some embodiments, there is an increase in expression of at least about 80%. In some embodiments, there is an increase in expression of at least about 85%, In some embodiments, there is an increase in expression of at least about 90%. In some embodiments, there is an increase in expression of at least about 95%. In some embodiments, there is an increase in expression of at least about 99%.

[00866] In some embodiments, transient alteration of protein expression is induced by treatment of the TILs with transcription factors (TFs) and/or other molecules capable of transiently altering protein expression in the TILs. In some embodiments, the SQZ vector-free microfluidic platform is employed for intracellular delivery of the transcription factors (TFs) and/or other molecules capable of transiently altering protein expression. Such methods demonstrating the ability to deliver proteins, including transcription factors, to a variety of primary human cells, including T cells (which have been described in U.S. Patent Application Publication Nos. US 2019/0093073 A1, US 2018/0201889 A1, and US 2019/0017072 A1, as well as *Sharei et al.* PNAS 2013, as well as *Sharei et al.* PLOS ONE 2015 and *Greisbeck et al.* J. Immunology vol. 195, 2015) the disclosures of each of which are incorporated herein by reference). Such method can be employed with the present invention in order to expose a population of TILs to transcription factors (TFs) and/or other molecules capable of inducing transient protein expression, wherein said TFs and/or other molecules capable of inducing transient protein expression provide for increased expression of tumor antigens and/or an increase in the number of tumor antigen-specific T cells in the population of TILs, thus resulting in reprogramming of the TIL population and an increase in therapeutic efficacy of the reprogrammed TIL population as compared to a non-reprogrammed TIL population. In some embodiments, the reprogramming results in an increased subpopulation of effector T cells and/or central memory T cells relative to the starting or prior population (*i.e.*, prior to reprogramming) population of TILs, as described herein.

[00867] In some embodiments, the transcription factor (TF) includes but is not limited to TCF-1, NOTCH 1/2 ICD, and/or MYB. In some embodiments, the transcription factor (TF) is TCF-1. In some embodiments, the transcription factor (TF) is NOTCH 1/2 ICD. In some embodiments, the transcription factor (TF) is MYB. In some embodiments, the transcription factor (TF) is administered with induced pluripotent stem cell culture (iPSC), such as the commercially available KNOCKOUT Serum Replacement (Gibco/ThermoFisher), to induce additional TIL reprogramming. In some embodiments, the transcription factor (TF) is administered with an iPSC cocktail to induce additional TIL reprogramming. In some embodiments, the transcription factor (TF) is administered without an iPSC cocktail. In some embodiments, reprogramming results in an increase in the percentage of TSCMs. In some embodiments, reprogramming results in an increase in the percentage of TSCMs by about 5%, about 10%, about 10%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95% TSCMs.

[00868] In some embodiments, a method of transient altering protein expression, as described above, may be combined with a method of genetically modifying a population of TILs includes the step of stable incorporation of genes for production of one or more proteins. In certain embodiments,

the method comprises a step of genetically modifying a population of TILs. In certain embodiments, the method comprises genetically modifying the first population of TILs, the second population of TILs and/or the third population of TILs. In some embodiments, a method of genetically modifying a population of TILs includes the step of retroviral transduction. In some embodiments, a method of genetically modifying a population of TILs includes the step of lentiviral transduction. Lentiviral transduction systems are known in the art and are described, *e.g.*, in Levine, *et al.*, *Proc. Nat'l Acad. Sci.* 2006, *103,* 17372-77; Zufferey, *et al., Nat. Biotechnol.* 1997, *15,* 871-75; Dull, *et al.*, *J. Virology* 1998, *72,* 8463-71, and U.S. Patent No. 6,627,442, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of gamma-retroviral transduction. Gamma-retroviral transduction systems are known in the art and are described, *e.g.*, Cepko and Pear, *Cur. Prot. Mol. Biol.* 1996, 9.9.1-9.9.16, the disclosure of which is incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of transposon-mediated gene transfer. Transposon-mediated gene transfer systems are known in the art and include systems wherein the transposase is provided as DNA expression vector or as an expressible RNA or a protein such that long-term expression of the transposase does not occur in the transgenic cells, for example, a transposase provided as an mRNA (*e.g.*, an mRNA comprising a cap and poly-A tail). Suitable transposon-mediated gene transfer systems, including the salmonid-type Tel-like transposase (SB or Sleeping Beauty transposase), such as SB10, SB11, and SB100x, and engineered enzymes with increased enzymatic activity, are described in, *e.g.*, Hackett, *et al.*, *Mol. Therapy* 2010, *18,* 674-83 and U.S. Patent No. 6,489,458, the disclosures of each of which are incorporated by reference herein.

[00869] In some embodiments, transient alteration of protein expression in TILs is induced by small interfering RNA (siRNA), sometimes known as short interfering RNA or silencing RNA, which is a double stranded RNA molecule, generally 19-25 base pairs in length. siRNA is used in RNA interference (RNAi), where it interferes with expression of specific genes with complementary nucleotide sequences. In some embodiments, transient alteration of protein expression is a reduction in expression. In some embodiments, transient alteration of protein expression in TILs is induced by self-delivering RNA interference (sdRNA), which is a chemically-synthesized asymmetric siRNA duplex with a high percentage of 2'-OH substitutions (typically fluorine or $-OCH_3$) which comprises a 20-nucleotide antisense (guide) strand and a 13 to 15 base sense (passenger) strand conjugated to cholesterol at its 3' end using a tetraethylenglycol (TEG) linker. Small interfering RNA (siRNA), sometimes known as short interfering RNA or silencing RNA, is a double stranded RNA molecule, generally 19-25 base pairs in length. siRNA is used in RNA interference (RNAi), where it interferes with expression of specific genes with complementary nucleotide sequences. sdRNA are covalently and hydrophobically modified RNAi compounds that do not require a delivery vehicle to enter cells. sdRNAs are generally asymmetric chemically modified nucleic acid molecules with minimal double

stranded regions. sdRNA molecules typically contain single stranded regions and double stranded regionsand can contain a variety of chemical modifications within both the single stranded and double stranded regions of the molecule. Additionally, the sdRNA molecules can be attached to a hydrophobic conjugate such as a conventional and advanced sterol-type molecule, as described herein. sdRNAs and associated methods for making such sdRNAs have also been described extensively in, for example,U.S. Patent Application Publication Nos. US 2016/0304873 A1, US 2019/0211337 A1, US 2009/0131360 A1, and US 2019/0048341 A1, and U.S. Patent Nos. 10,633,654 and 10,913,948B2, the disclosures of each of which are incorporated by reference herein.To optimize sdRNA structure, chemistry, targeting position, sequence preferences, and the like, analgorithm has been developed and utilized for sdRNA potency prediction. Based on these analyses, functional sdRNA sequences have been generally defined as having over 70% reduction in expression at 1 μM concentration, with a probability over 40%.

[00870] Double stranded DNA (dsRNA) can be generally used to define any molecule comprising a pair of complementary strands of RNA, generally a sense (passenger) and antisense (guide) strands, and may include single-stranded overhang regions. The term dsRNA, contrasted with siRNA, generally refers to a precursor molecule that includes the sequence of an siRNA molecule which is released from the larger dsRNA molecule by the action of cleavage enzyme systems, including Dicer.

[00871] In some embodiments, the method comprises transient alteration of protein expression in a population of TILs, including TILs modified to express a CCR, comprising the use of self-delivering RNA interference (sdRNA), which is for example, a chemically-synthesized asymmetric siRNA duplex with a high percentage of 2'-OH substitutions (typically fluorine or -OCH_3) which comprises a 20-nucleotide antisense (guide) strand and a 13 to 15 base sense (passenger) strand conjugated to cholesterol at its 3' end using a tetraethylenglycol (TEG) linker. Methods of using siRNA and sdRNA have been described in Khvorova and Watts, *Nat. Biotechnol.* 2017, *35,* 238–248; Byrne, *et al., J. Ocul. Pharmacol. Ther.* 2013, *29,* 855-864; and Ligtenberg, *et al., Mol. Therapy,* 2018, *26,* 1482-93, the disclosures of which are incorporated by reference herein. In some embodiments, delivery of siRNA is accomplished using electroporation or cell membrane disruption (such as the squeeze or SQZ method). In some embodiments, delivery of siRNA or sdRNA to a TIL population is accomplished without use of electroporation, SQZ, or other methods, instead using a 1 to 3 day period in which a TIL population is exposed to siRNA or sdRNA at a concentration of 1 μM/10,000 TILs in medium. In certain embodiments, the method comprises delivery or siRNA or sdRNA to a TILs population comprising exposing the TILs population to siRNA or sdRNA at a concentration of 1 μM/10,000 TILs in medium for a period of between 1 to 3 days. In some embodiments, delivery of siRNA or sdRNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to siRNA or sdRNA at a concentration of 10 μM/10,000 TILs in medium. In

some embodiments, delivery of sdRNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to siRNA or sdRNA at a concentration of 50 μM/10,000 TILs in medium. In some embodiments, delivery of siRNA or sdRNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to siRNA or sdRNA at a concentration of between 0.1 μM/10,000 TILs and 50 μM/10,000 TILs in medium. In some embodiments, delivery of siRNA or sdRNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to siRNA or sdRNA at a concentration of between 0.1 μM/10,000 TILs and 50 μM/10,000 TILs in medium, wherein the exposure to siRNA or sdRNA is performed two, three, four, or five times by addition of fresh siRNA or sdRNA to the media. Other suitable processes are described, for example, in U.S. Patent Application Publication No. US 2011/0039914 A1, US 2013/0131141 A1, and US 2013/0131142 A1, and U.S. Patent No. 9,080,171, the disclosures of which are incorporated by reference herein.

[00872] In some embodiments, siRNA or sdRNA is inserted into a population of TILs during manufacturing. In some embodiments, the sdRNA encodes RNA that interferes with NOTCH 1/2 ICD, PD-1, CTLA-4 TIM-3, LAG-3, TIGIT, TGFβ, TGFBR2, cAMP protein kinase A (PKA), BAFF BR3, CISH, and/or CBLB. In some embodiments, the reduction in expression is determined based on a percentage of gene silencing, for example, as assessed by flow cytometry and/or qPCR. In some embodiments, there is a reduction in expression of about 5%, about 10%, about 10%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 75%, about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 80%, about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 85%, about 90%, or about 95%. In some embodiments, there is a reduction in expression of at least about 80%. In some embodiments, there is a reduction in expression of at least about 85%, In some embodiments, there is a reduction in expression of at least about 90%. In some embodiments, there is a reduction in expression of at least about 95%. In some embodiments, there is a reduction in expression of at least about 99%.

[00873] The self-deliverable RNAi technology based on the chemical modification of siRNAs can be employed with the methods of the present invention to successfully deliver the sdRNAs to the TILs as described herein. The combination of backbone modifications with asymmetric siRNA structure and a hydrophobic ligand (*see*, for example, Ligtenberg, *et al.*, *Mol. Therapy,* **2018**, *26,* 1482-93 and U.S. Patent Application Publication No. 2016/0304873 A1, the disclosures of which are incorporated by reference herein) allow sdRNAs to penetrate cultured mammalian cells without additional

formulations and methods by simple addition to the culture media, capitalizing on the nuclease stability of sdRNAs. This stability allows the support of constant levels of RNAi-mediated reduction of target gene activity simply by maintaining the active concentration of sdRNA in the media. While not being bound by theory, the backbone stabilization of sdRNA provides for extended reduction in gene expression effects which can last for months in non-dividing cells.

[00874] In some embodiments, over 95% transfection efficiency of TILs and a reduction in expression of the target by various specific siRNAs or sdRNAs occurs. In some embodiments, siRNAs or sdRNAs containing several unmodified ribose residues were replaced with fully modified sequences to increase potency and/or the longevity of RNAi effect. In some embodiments, a reduction in expression effect is maintained for 12 hours, 24 hours, 36 hours, 48 hours, 5 days, 6 days, 7 days, or 8 days or more. In some embodiments, the reduction in expression effect decreases at 10 days or more post siRNA or sdRNA treatment of the TILs. In some embodiments, more than 70% reduction in expression of the target expression is maintained. In some embodiments, more than 70% reduction in expression of the target expression is maintained TILs. In some embodiments, a reduction in expression in the PD-1/PD-L1 pathway allows for the TILs to exhibit a more potent in vivo effect, which is in some embodiments, due to the avoidance of the suppressive effects of the PD-1/PD-L1 pathway. In some embodiments, a reduction in expression of PD-1 by siRNA or sdRNA results in an increase TIL proliferation.

[00875] In some embodiments, the sdRNA sequences used in the invention exhibit a 70% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit a 75% reduction in expression of the target gene.
In some embodiments, the sdRNA sequences used in the invention exhibit an 80% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit an 85% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit a 90% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit a 95% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit a 99% reduction in expression of the target gene. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.25 μM to about 4 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.25 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.5 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.75 μM. In some embodiments, the sdRNA

sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.0 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.25 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.5 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.75 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.0 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.25 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.5 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.75 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.0 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.25 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.5 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.75 μM. In some embodiments, the sdRNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 4.0 μM.

[00876] In some emodiments, the siRNA or sdRNA oligonucleotide agents comprise one or more modification to increase stability and/or effectiveness of the therapeutic agent, and to effect efficient delivery of the oligonucleotide to the cells or tissue to be treated. Such modifications can include a 2'-O-methyl modification, a 2'-O-fluro modification, a diphosphorothioate modification, 2' F modified nucleotide, a2'-O-methyl modified and/or a 2'deoxy nucleotide. In some embodiments, the oligonucleotide is modified to include one or more hydrophobic modifications including, for example, sterol, cholesterol, vitamin D, naphtyl, isobutyl, benzyl, indol, tryptophane, and/or phenyl. In asome embodiments, chemically modified nucleotides are combination of phosphorothioates, 2'-O-methyl, 2'deoxy, hydrophobic modifications and phosphorothioates. In some embodiments, the sugars can be modified and modified sugars can include but are not limited to D-ribose, 2'-O-alkyl (including 2'-O-methyl and 2'-0-ethyl), i.e., 2'-alkoxy, 2'-amino, 2'-S-alkyl, 2'-halo (including 2'-fluoro), T-methoxyethoxy, 2'-allyloxy (-$OCH_2CH{=}CH_2$), 2'-propargyl, 2'-propyl, ethynyl, ethenyl, propenyl, and cyano and the like. In some embodiments, the sugar moiety can be a hexose and incorporated into an

oligonucleotide as described in Augustyns, *et al.*, *Nucl. Acids. Res.* **1992**, *18,* 4711, the disclosure of which is incorporated by reference herein.

[00877] In some embodiments, the double-stranded siRNA or sdRNA oligonucleotide of the invention is double-stranded over its entire length, *i.e.*, with no overhanging single-stranded sequence at either end of the molecule, *i.e.*, is blunt-ended. In some embodiments, the individual nucleic acid molecules can be of different lengths. In other words, a double-stranded siRNA or sdRNA oligonucleotide of the invention is not double-stranded over its entire length. For instance, when two separate nucleic acid molecules are used, one of the molecules, *e.g.*, the first molecule comprising an antisense sequence, can be longer than the second molecule hybridizing thereto (leaving a portion of the molecule single-stranded). In some embodiments, when a single nucleic acid molecule is used a portion of the molecule at either end can remain single-stranded.

[00878] In some embodiments, a double-stranded siRNA or sdRNA oligonucleotide of the invention contains mismatches and/or loops or bulges, but is double-stranded over at least about 70% of the length of the oligonucleotide. In some embodiments, a double-stranded oligonucleotide of the invention is double-stranded over at least about 80% of the length of the oligonucleotide. In other embodiments, a double-stranded siRNA or sdRNA oligonucleotide of the invention is double-stranded over at least about 90%-95% of the length of the oligonucleotide. In some embodiments, a double-stranded siRNA or sdRNA oligonucleotide of the invention is double-stranded over at least about 96%-98% of the length of the oligonucleotide. In some embodiments, the double-stranded siRNA or sdRNA oligonucleotide of the invention contains at least or up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 mismatches.

[00879] In some embodiments, the siRNA or sdRNA oligonucleotide can be substantially protected from nucleases *e.g.*, by modifying the 3' or 5' linkages, as described in U.S. Patent. No. 5,849,902, the disclosure of which is incorporated by reference herein). For example, oligonucleotides can be made resistant by the inclusion of a "blocking group." The term "blocking group" as used herein refers to substituents (*e.g.*, other than OH groups) that can be attached to oligonucleotides or nucleomonomers, either as protecting groups or coupling groups for synthesis (*e.g.*, FITC, propyl (CH_2-CH_2-CH_3), glycol (-0-CH_2-CH_2-O-) phosphate ($PO_3^{2"}$), hydrogen phosphonate, or phosphoramidite). "Blocking groups" can also include "end blocking groups" or "exonuclease blocking groups" which protect the 5' and 3' termini of the oligonucleotide, including modified nucleotides and non-nucleotide exonuclease resistant structures.

[00880] In some embodiments, at least a portion of the contiguous polynucleotides within the siRNA or sdRNA are linked by a substitute linkage, *e.g.*, a phosphorothioate linkage.

[00881] In some embodiments, chemical modification can lead to at least a 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, or 500 percent enhancement in cellular uptake of an siRNA or sdRNA. In some embodiments, at least one of the C or U residues includes a hydrophobic modification. In some embodiments, a plurality of Cs and Us contain a hydrophobic modification. In some embodiments, at least 10%, 15%, 20%, 30%, 40%, 50%, 55%, 60% 65%, 70%, 75%, 80%, 85%, 90% or at least 95% of the Cs and Us can contain a hydrophobic modification. In some embodiments, all of the Cs and Us contain a hydrophobic modification.

[00882] In some embodiments, the siRNA or sdRNA molecules exhibit enhanced endosomal release through the incorporation of protonatable amines. In some embodiments, protonatable amines are incorporated in the sense strand (in the part of the molecule which is discarded after RISC loading). In some embodiments, the siRNA or sdRNA compounds of the invention comprise an asymmetric compound comprising a duplex region (required for efficient RISC entry of 10-15 bases long) and single stranded region of 4-12 nucleotides long; with a 13 nucleotide duplex. In some embodiments, a 6 nucleotide single stranded region is employed. In some embodiments, the single stranded region of the siRNA or sdRNA comprises 2-12 phosphorothioate internucleotide linkages (referred to as phosphorothioate modifications). In some embodiments, 6-8 phosphorothioate internucleotide linkages are employed. In some embodiments, the siRNA or sdRNA compounds of the invention also include a unique chemical modification pattern, which provides stability and is compatible with RISC entry.

[00883] The guide strand, for example, may also be modified by any chemical modification which confirms stability without interfering with RISC entry. In some embodiments, the chemical modification pattern in the guide strand includes the majority of C and U nucleotides being 2' F modified and the 5 ' end being phosphorylated.

[00884] In some embodiments, at least 30% of the nucleotides in the siRNA or sdRNA ae modified. In some embodiments, at least 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of the nucleotides in the siRNA or sdRNA are modified. In some embodiments, 100% of the nucleotides in the siRNA or sdRNA are modified.

[00885] In some embodiments, the siRNA or sdRNA molecules have minimal double stranded regions. In some embodiments the region of the molecule that is double stranded ranges from 8-15

nucleotides long. In some embodiments, the region of the molecule that is double stranded is 8, 9, 10, 11, 12, 13, 14 or 15 nucleotides long. In some embodiments the double stranded region is 13 nucleotides long. There can be 100% complementarity between the guide and passenger strands, or there may be one or more mismatches between the guide and passenger strands. In some embodiments, on one end of the double stranded molecule, the molecule is either blunt-ended or has a one-nucleotide overhang. The single stranded region of the molecule is in some embodiments between 4-12 nucleotides long. In some embodiments, the single stranded region can be 4, 5, 6, 7, 8, 9, 10, 11 or 12 nucleotides long. In some embodiments, the single stranded region can also be less than 4 or greater than 12 nucleotides long. In certain embodiments, the single stranded region is 6 or 7 nucleotides long.

[00886] In some embodiments, the siRNA or sdRNA molecules have increased stability. In some instances, a chemically modified siRNA or sdRNA molecule has a half-life in media that is longer than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or more than 24 hours, including any intermediate values. In some embodiments, the siRNA or sdRNA has a half-life in media that is longer than 12 hours.

[00887] In some embodiments, the siRNA or sdRNA is optimized for increased potency and/or reduced toxicity. In some embodiments, nucleotide length of the guide and/or passenger strand, and/or the number of phosphorothioate modifications in the guide and/or passenger strand, can in some aspects influence potency of the RNA molecule, while replacing 2'-fluoro (2'F) modifications with 2'-0-methyl (2'OMe) modifications can in some aspects influence toxicity of the molecule. In some embodiments, reduction in 2'F content of a molecule is predicted to reduce toxicity of the molecule. In some embodiments, the number of phosphorothioate modifications in an RNA molecule can influence the uptake of the molecule into a cell, for example the efficiency of passive uptake of the molecule into a cell. In some embodiments, the siRNA or sdRNA has no 2'F modification and yet are characterized by equal efficacy in cellular uptake and tissue penetration.

[00888] In some embodiments, a guide strand is approximately 18-19 nucleotides in length and has approximately 2-14 phosphate modifications. For example, a guide strand can contain 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or more than 14 nucleotides that are phosphate-modified. The guide strand may contain one or more modifications that confer increased stability without interfering with RISC entry. The phosphate modified nucleotides, such as phosphorothioate modified nucleotides, can be at the 3' end, 5' end or spread throughout the guide strand. In some embodiments, the 3' terminal 10 nucleotides of the guide strand contain 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 phosphorothioate modified nucleotides. The guide strand can also contain 2'F and/or 2'OMe modifications, which can be located throughout the molecule. In some embodiments, the nucleotide in position one of the guide strand (the nucleotide in the most 5' position of the guide strand) is 2'OMe modified and/or phosphorylated. C

and U nucleotides within the guide strand can be 2'F modified. For example, C and U nucleotides in positions 2-10 of a 19 nt guide strand (or corresponding positions in a guide strand of a different length) can be 2'F modified. C and U nucleotides within the guide strand can also be 2'OMe modified. For example, C and U nucleotides in positions 11-18 of a 19 nt guide strand (or corresponding positions in a guide strand of a different length) can be 2'OMe modified. In some embodiments, the nucleotide at the most 3' end of the guide strand is unmodified. In certain embodiments, the majority of Cs and Us within the guide strand are 2'F modified and the 5' end of the guide strand is phosphorylated. In other embodiments, position 1 and the Cs or Us in positions 11-18 are 2'OMe modified and the 5' end of the guide strand is phosphorylated. In other embodiments, position 1 and the Cs or Us in positions 11-18 are 2'OMe modified, the 5' end of the guide strand is phosphorylated, and the Cs or Us in position 2-10 are 2'F modified.

[00889] The self-deliverable RNAi technology provides a method of directly transfecting cells with the RNAi agent (whether siRNA, sdRNA, or other RNAi agents), without the need for additional formulations or techniques. The ability to transfect hard-to-transfect cell lines, high *in vivo* activity, and simplicity of use, are characteristics of the compositions and methods that present significant functional advantages over traditional siRNA-based techniques, and as such, the sdRNA methods are employed in several embodiments related to the methods of reduction in expression of the target gene in the TILs of the present invention. The sdRNA method allows direct delivery of chemically synthesized compounds to a wide range of primary cells and tissues, both *ex-vivo* and *in vivo*. The sdRNAs described in some embodiments of the invention herein are commercially available from Advirna LLC, Worcester, MA, USA.

[00890] The siRNA or sdRNA may be formed as hydrophobically-modified siRNA-antisense oligonucleotide hybrid structures, and are disclosed, for example in Byrne , *et al.*, *J. Ocular Pharmacol. Therapeut.*, 2013, 29, 855-864, the disclosure of which is incorporated by reference herein.

[00891] In some embodiments, the siRNA or sdRNA oligonucleotides can be delivered to the TILs described herein using sterile electroporation. In certain embodiments, the method comprises sterile electroporation of a population of TILs to deliver siRNA or sdRNA oligonucleotides.

[00892] In some embodiments, the oligonucleotides can be delivered to the cells in combination with a transmembrane delivery system. In some embodiments, this transmembrane delivery system comprises lipids, viral vectors, and the like. In some embodiments, the oligonucleotide agent is a self-delivery RNAi agent, that does not require any delivery agents. In certain embodiments, the method comprises use of a transmembrane delivery system to deliver siRNA or sdRNA oligonucleotides to a population of TILs.

[00893] Oligonucleotides and oligonucleotide compositions are contacted with (*e.g.*, brought into contact with, also referred to herein as administered or delivered to) and taken up by TILs described herein, including through passive uptake by TILs. The sdRNA can be added to the TILs as described herein during the first expansion, for example Step B, after the first expansion, for example, during Step C, before or during the second expansion, for example before or during Step D, after Step D and before harvest in Step E, during or after harvest in Step F, before or during final formulation and/or transfer to infusion Bag in Step F, as well as before any optional cryopreservation step in Step F. Moreeover, sdRNA can be added after thawing from any cryopreservation step in Step F. In some embodiments, one or more sdRNAs targeting genes as described herein, including PD-1, LAG-3, TIM-3, CISH, CTLA-4, TIGIT, TET2 and CBLB, may be added to cell culture media comprising TILs and other agents at concentrations selected from the group consisting of 100 nM to 20 mM, 200 nM to 10 mM, 500 nm to 1 mM, 1 μM to 100 μM, and 1 μM to 100 μM. In some embodiments, one or more sdRNAs targeting genes as described herein, including PD-1, LAG-3, TIM-3, CISH, CTLA-4, TIGIT, TET2 and CBLB, may be added to cell culture media comprising TILs and other agents at amounts selected from the group consisting of 0.1 μM sdRNA/10,000 TILs/100 μL media, 0.5 μM sdRNA/10,000 TILs /100 μL media, 0.75 μM sdRNA/10,000 TILs /100 μL media, 1 μM sdRNA/10,000 TILs /100 μL media, 1.25 μM sdRNA/10,000 TILs /100 μL media, 1.5 μM sdRNA/10,000 TILs /100 μL media, 2 μM sdRNA/10,000 TILs /100 μL media, 5 μM sdRNA/10,000 TILs /100 μL media, or 10 μM sdRNA/10,000 TILs /100 μL media. In some embodiments, one or more sdRNAs targeting genes as described herein, including PD-1, LAG-3, TIM-3, CISH, CTLA-4, TIGIT, TET2 and CBLB, may be added to TIL cultures during the pre-REP or REP stages twice a day, once a day, every two days, every three days, every four days, every five days, every six days, or every seven days.

[00894] Oligonucleotide compositions of the invention, including siRNA or sdRNA, can be contacted with TILs as described herein during the expansion process, for example by dissolving sdRNA at high concentrations in cell culture media and allowing sufficient time for passive uptake to occur. In certain embodiments, the method of the present invention comprises contacting a population of TILs with an oligonucleotide composition as described herein. In certain embodiments, the method comprises dissolving an oligonucleotide *e.g.* sdRNA in a cell culture media and contacting the cell culture media with a population of TILs. The TILs may be a first population, a second population and/or a third population as described herein.

[00895] In some embodiments, delivery of oligonucleotides into cells can be enhanced by suitable art recognized methods including calcium phosphate, DMSO, glycerol or dextran, electroporation, or by transfection, *e.g.*, using cationic, anionic, or neutral lipid compositions or liposomes using methods known in the art, such as those methods described in U.S. Patent Nos. 4,897,355; 5,459,127;

5,631,237; 5,955,365; 5,976,567; 10,087,464; and 10,155,945; and Bergan, *et al.*, *Nucl. Acids Res.* 1993, *21,* 3567, the disclosures of each of which are incorporated by reference herein.

[00896] In some embodiments, more than one siRNA or sdRNA is used to reduce expression of a target gene. In some embodiments, one or more of PD-1, TIM-3, CBLB, LAG3, CTLA-4, TIGIT, TET2 and/or CISH targeting siRNA or sdRNAs are used together. In some embodiments, a PD-1 siRNA or sdRNA is used with one or more of TIM-3, CBLB, LAG3, CTLA-4, TIGIT, TET2 and/or CISH in order to reduce expression of more than one gene target. In some embodiments, a LAG3 siRNA or sdRNA is used in combination with a CISH targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, a TIGIT siRNA or sdRNA is used in combination with a PD-1 targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, a CISH siRNA or sdRNA is used in combination with a PD-1 targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, a CTLA-4 siRNA or sdRNA is used in combination with a PD-1 targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, a LAG-3 siRNA or sdRNA is used in combination with a PD-1 targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, a CBL-B siRNA or sdRNA is used in combination with a PD-1 targeting siRNA or sdRNA to reduce gene expression of both targets. In some embodiments, the siRNA or sdRNAs targeting one or more of PD-1, TIM-3, CBLB, LAG3, CTLA-4, TIGIT, TET2 and/or CISH herein are commercially available from Advirna LLC, Worcester, MA, USA or multiple other vendors.

[00897] In some embodiments, the siRNA or sdRNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the siRNA or sdRNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, one siRNA or sdRNA targets PD-1 and another siRNA or sdRNA targets a gene selected from the group consisting of LAG3, TIM3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the siRNA or sdRNA targets a gene selected from PD-1, LAG-3, CISH, CBLB, TIM3, CTLA-4, TIGIT, TET2 and combinations thereof. In some embodiments, the siRNA or sdRNA targets a gene selected from PD-1 and one of LAG3, CISH, CBLB, TIM3, CTLA-4, TIGIT, TET2 and combinations thereof. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets LAG3. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets CISH. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets CBLB. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets TIM3. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets CTLA-4. In some embodiments, one siRNA or sdRNA targets PD-1

and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets PD-1 and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets CISH. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets CBLB. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets TIM3. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets CTLA-4. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets LAG3 and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets CISH and one siRNA or sdRNA targets CBLB. In some embodiments, one siRNA or sdRNA targets CISH and one siRNA or sdRNA targets TIM3. In some embodiments, one siRNA or sdRNA targets CISH and one siRNA or sdRNA targets CTLA-4. In some embodiments, one siRNA or sdRNA targets CISH and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets CISH and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets CBLB and one siRNA or sdRNA targets TIM3. In some embodiments, one siRNA or sdRNA targets CBLB and one siRNA or sdRNA targets CTLA-4. In some embodiments, one siRNA or sdRNA targets CBLB and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets CBLB and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets PD-1. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets LAG3. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets CISH. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets CBLB. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets CTLA-4. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets TIM3 and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets CTLA-4 and one siRNA or sdRNA targets TIGIT. In some embodiments, one siRNA or sdRNA targets CTLA-4 and one siRNA or sdRNA targets TET2. In some embodiments, one siRNA or sdRNA targets TIGIT and one siRNA or sdRNA targets TET2.

[00898] As discussed herein, embodiments of the present invention provide tumor infiltrating lymphocytes (TILs) that have been genetically modified via gene-editing to enhance their therapeutic effect. Embodiments of the present invention embrace genetic editing through nucleotide insertion (RNA or DNA) into a population of TILs for both promotion of the expression of one or more proteins and inhibition of the expression of one or more proteins, as well as combinations thereof. Embodiments of the present invention also provide methods for expanding TILs into a therapeutic population, wherein the methods comprise gene-editing the TILs. There are several gene-editing technologies that may be used to genetically modify a population of TILs, which are suitable for use in accordance with the present invention. Such methods include the methods described below as well

as the viral and transposon methods described elsewhere herein. In some embodiments, a method of genetically modifying a TIL, MIL, or PBL to express a CCR may also include a modification to suppress the expression of a gene either via stable knockout of such a gene or transient knockdown of such a gene.

[00899] In some embodiments, the method comprises a method of genetically modifying a population of TILs in a first population, a second population and/or a third population as described herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of stable incorporation of genes for production or inhibition (*e.g.*, silencing) of one ore more proteins. In some embodiments, a method of genetically modifying a population of TILs includes the step of electroporation. Electroporation methods are known in the art and are described, *e.g.*, in Tsong, *Biophys. J.* 1991, *60,* 297-306, and U.S. Patent Application Publication No. 2014/0227237 A1, the disclosures of each of which are incorporated by reference herein. Other electroporation methods known in the art, such as those described in U.S. Patent Nos. 5,019,034; 5,128,257; 5,137,817; 5,173,158; 5,232,856; 5,273,525; 5,304,120; 5,318,514; 6,010,613 and 6,078,490, the disclosures of which are incorporated by reference herein, may be used. In some embodiments, the electroporation method is a sterile electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of the at least three pulses differ from each other in pulse amplitude. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein at least two of

the at least three pulses differ from each other in pulse width. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to alter, manipulate, or cause defined and controlled, permanent or temporary changes in the TILs, comprising the step of applying a sequence of at least three single, operator-controlled, independently programmed, DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to the TILs, wherein a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses. In some embodiments, the electroporation method is a pulsed electroporation method comprising the steps of treating TILs with pulsed electrical fields to induce pore formation in the TILs, comprising the step of applying a sequence of at least three DC electrical pulses, having field strengths equal to or greater than 100 V/cm, to TILs, wherein the sequence of at least three DC electrical pulses has one, two, or three of the following characteristics: (1) at least two of the at least three pulses differ from each other in pulse amplitude; (2) at least two of the at least three pulses differ from each other in pulse width; and (3) a first pulse interval for a first set of two of the at least three pulses is different from a second pulse interval for a second set of two of the at least three pulses, such that induced pores are sustained for a relatively long period of time, and such that viability of the TILs is maintained. In some embodiments, a method of genetically modifying a population of TILs includes the step of calcium phosphate transfection. Calcium phosphate transfection methods (calcium phosphate DNA precipitation, cell surface coating, and endocytosis) are known in the art and are described in Graham and van der Eb, *Virology* 1973, *52,* 456-467; Wigler, *et al.*, *Proc. Natl. Acad. Sci.* 1979, *76,* 1373-1376; and Chen and Okayarea, *Mol. Cell. Biol.* 1987, *7,* 2745-2752; and in U.S. Patent No. 5,593,875, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of liposomal transfection. Liposomal transfection methods, such as methods that employ a 1:1 (w/w) liposome formulation of the cationic lipid *N*-[1-(2,3-dioleyloxy)propyl]-*n,n,n*-trimethylammonium chloride (DOTMA) and dioleoyl phophotidylethanolamine (DOPE) in filtered water, are known in the art and are described in Rose, *et al.*, *Biotechniques* 1991, *10,* 520-525 and Felgner, *et al.*, *Proc. Natl. Acad. Sci. USA*, 1987, *84,* 7413-7417 and in U.S. Patent Nos. 5,279,833; 5,908,635; 6,056,938; 6,110,490; 6,534,484; and 7,687,070, the disclosures of each of which are incorporated by reference herein. In some embodiments, a method of genetically modifying a population of TILs includes the step of transfection using methods described in U.S. Patent Nos. 5,766,902; 6,025,337; 6,410,517; 6,475,994; and 7,189,705; the disclosures of each of which are incorporated by reference herein. The TILs may be a first population, a second population and/or a third population of TILs as described herein.

[00900] According to an embodiment, the gene-editing process may comprise the use of a programmable nuclease that mediates the generation of a double-strand or single-strand break at one or more immune checkpoint genes. Such programmable nucleases enable precise genome editing by

introducing breaks at specific genomic loci, *i.e.,* they rely on the recognition of a specific DNA sequence within the genome to target a nuclease domain to this location and mediate the generation of a double-strand break at the target sequence. A double-strand break in the DNA subsequently recruits endogenous repair machinery to the break site to mediate genome editing by either non-homologous end-joining (NHEJ) or homology-directed repair (HDR). Thus, the repair of the break can result in the introduction of insertion/deletion mutations that disrupt (*e.g.*, silence, repress, or enhance) the target gene product.

[00901] Major classes of nucleases that have been developed to enable site-specific genomic editing include zinc finger nucleases (ZFNs), transcription activator-like nucleases (TALENs), and CRISPR-associated nucleases (*e.g.*, CRISPR/Cas9). These nuclease systems can be broadly classified into two categories based on their mode of DNA recognition: ZFNs and TALENs achieve specific DNA binding via protein-DNA interactions, whereas CRISPR systems, such as Cas9, are targeted to specific DNA sequences by a short RNA guide molecule that base-pairs directly with the target DNA and by protein-DNA interactions. *See, e.g.,* Cox *et al.*, *Nature Medicine,* 2015, Vol. 21, No. 2.

[00902] Non-limiting examples of gene-editing methods that may be used in accordance with TIL expansion methods of the present invention include CRISPR methods, TALE methods, and ZFN methods, which are described in more detail below. According to an embodiment, a method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, Gen 3) or as described in U.S. Patent Application Publication Nos. US 2020/0299644 A1 and US 2020/0121719 A1 and U.S. Patent No. 10,925,900, the disclosures of which are incorporated by reference herein, wherein the method further comprises gene-editing at least a portion of the TILs by one or more of a CRISPR method, a TALE method or a ZFN method, in order to generate TILs that can provide an enhanced therapeutic effect. According to an embodiment, gene-edited TILs can be evaluated for an improved therapeutic effect by comparing them to non-modified TILs *in vitro, e.g.,* by evaluating *in vitro* effector function, cytokine profiles, etc. compared to unmodified TILs. In certain embodiments, the method comprises gene editing a population of TILs using CRISPR, TALE and/ or ZFN methods.

[00903] In some embodiments of the present invention, electroporation is used for delivery of a gene editing system, such as CRISPR, TALEN, and ZFN systems. In some embodiments of the present invention, the electroporation system is a flow electroporation system. An example of a suitable flow electroporation system suitable for use with some embodiments of the present invention is the commercially-available MaxCyte STX system. There are several alternative commercially-available electroporation instruments which may be suitable for use with the present invention, such as the AgilePulse system or ECM 830 available from BTX-Harvard Apparatus, Cellaxess Elektra (Cellectricon), Nucleofector (Lonza/Amaxa), GenePulser MXcell (BIORAD), iPorator-96 (Primax) or

siPORTer96 (Ambion). In some embodiments of the present invention, the electroporation system forms a closed, sterile system with the remainder of the TIL expansion method. In some embodiments of the present invention, the electroporation system is a pulsed electroporation system as described herein, and forms a closed, sterile system with the remainder of the TIL expansion method.

[00904] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, Gen 2) or as described in U.S. Patent Application Publication Nos. US 2020/0299644 A1 and US 2020/0121719 A1 and U.S. Patent No. 10,925,900, the disclosures of which are incorporated by reference herein, wherein the method further comprises gene-editing at least a portion of the TILs by a CRISPR method (*e.g.*, CRISPR/Cas9 or CRISPR/Cpf1). According to particular embodiments, the use of a CRISPR method during the TIL expansion process causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs. Alternatively, the use of a CRISPR method during the TIL expansion process causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs.

[00905] CRISPR stands for "clustered regularly interspaced short palindromic repeats." A method of using a CRISPR system for gene editing is also referred to herein as a CRISPR method. There are three types of CRISPR systems which incorporate RNAs and Cas proteins, and which may be used in accordance with the present invention: Types I, II, and III. The Type II CRISPR (exemplified by Cas9) is one of the most well-characterized systems.

[00906] CRISPR technology was adapted from the natural defense mechanisms of bacteria and archaea (the domain of single-celled microorganisms). These organisms use CRISPR-derived RNA and various Cas proteins, including Cas9, to foil attacks by viruses and other foreign bodies by chopping up and destroying the DNA of a foreign invader. A CRISPR is a specialized region of DNA with two distinct characteristics: the presence of nucleotide repeats and spacers. Repeated sequences of nucleotides are distributed throughout a CRISPR region with short segments of foreign DNA (spacers) interspersed among the repeated sequences. In the type II CRISPR/Cas system, spacers are integrated within the CRISPR genomic loci and transcribed and processed into short CRISPR RNA (crRNA). These crRNAs anneal to trans-activating crRNAs (tracrRNAs) and direct sequence-specific cleavage and silencing of pathogenic DNA by Cas proteins. Target recognition by the Cas9 protein requires a "seed" sequence within the crRNA and a conserved dinucleotide-containing protospacer adjacent motif (PAM) sequence upstream of the crRNA-binding region. The CRISPR/Cas system can thereby be retargeted to cleave virtually any DNA sequence by redesigning the crRNA. The crRNA and tracrRNA in the native system can be simplified into a single guide RNA (sgRNA) of approximately 100 nucleotides for use in genetic engineering. The CRISPR/Cas system is directly portable to human cells by co-delivery of plasmids expressing the Cas9 endo-nuclease and the

necessary crRNA components. Different variants of Cas proteins may be used to reduce targeting limitations (*e.g.*, orthologs of Cas9, such as Cpf1).

[00907] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a CRISPR method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00908] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a CRISPR method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL12, IL-15, IL-18 and IL-21.

[00909] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a CRISPR method, and which may be used in accordance with embodiments of the present invention, are described in U.S. Patent Nos. 8,697,359; 8,993,233; 8,795,965; 8,771,945; 8,889,356; 8,865,406; 8,999,641; 8,945,839; 8,932,814; 8,871,445; 8,906,616; and 8,895,308, the disclosures of each of which are incorporated by reference herein. Resources for carrying out CRISPR methods, such as plasmids for expressing CRISPR/Cas9 and CRISPR/Cpf1, are commercially available from companies such as GenScript.

[00910] In some embodiments, genetic modifications of populations of TILs, as described herein, may be performed using the CRISPR/Cpf1 system as described in U.S. Patent No. US 9790490, the disclosure of which is incorporated by reference herein.

[00911] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein (*e.g.*, Gen 2) or as described in U.S. Patent Application Publication Nos. US 2020/0299644 A1 and US 2020/0121719 A1 and U.S. Patent No. 10,925,900, the disclosures of which are incorporated by reference herein, wherein the method further comprises gene-editing at least a portion of the TILs by a TALE method. According to particular embodiments, the use of a TALE method during the TIL expansion process causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs. Alternatively, the use of a TALE method during the TIL expansion process causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs.

[00912] TALE stands for transcription activator-like effector "" proteins, which include transcription activator-like effector nucleases (TALENs""). A method of using a TALE system for gene editing may also be referred to herein as a TALE method. TALEs are naturally occurring proteins from the plant pathogenic bacteria genus *Xanthomonas*, and contain DNA-binding domains composed of a series of 33–35-amino-acid repeat domains that each recognizes a single base pair. TALE specificity is determined by two hypervariable amino acids that are known as the repeat-variable di-residues (RVDs). Modular TALE repeats are linked together to recognize contiguous DNA sequences. A specific RVD in the DNA-binding domain recognizes a base in the target locus, providing a structural feature to assemble predictable DNA-binding domains. The DNA binding domains of a TALE are fused to the catalytic domain of a type IIS FokI endonuclease to make a targetable TALE nuclease. To induce site-specific mutation, two individual TALEN arms, separated by a 14-20 base pair spacer region, bring FokI monomers in close proximity to dimerize and produce a targeted double-strand break.

[00913] Several large, systematic studies utilizing various assembly methods have indicated that TALE repeats can be combined to recognize virtually any user-defined sequence. Custom-designed TALE arrays are also commercially available through Cellectis Bioresearch (Paris, France), Transposagen Biopharmaceuticals (Lexington, KY, USA), and Life Technologies (Grand Island, NY, USA). TALE and TALEN methods suitable for use in the present invention are described in U.S. Patent Application Publication Nos. US 2011/0201118 A1; US 2013/0117869 A1; US 2013/0315884 A1; US 2015/0203871 A1 and US 2016/0120906 A1, the disclosures of each of which are incorporated by reference herein.

[00914] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a TALE method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00915] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a TALE method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL12, IL-15, IL-18 and IL-21.

[00916] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a TALE method, and which may be used in accordance with embodiments of the

present invention, are described in U.S. Patent No. 8,586,526, which is incorporated by reference herein.

[00917] A method for expanding TILs into a therapeutic population may be carried out in accordance with any embodiment of the methods described herein or as described in U.S. Patent Application Publication Nos. US 2020/0299644 A1 and US 2020/0121719 A1 and U.S. Patent No. 10,925,900, the disclosures of which are incorporated by reference herein, wherein the method further comprises gene-editing at least a portion of the TILs by a zinc finger or zinc finger nuclease method. According to particular embodiments, the use of a zinc finger method during the TIL expansion process causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs. Alternatively, the use of a zinc finger method during the TIL expansion process causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs.

[00918] An individual zinc finger contains approximately 30 amino acids in a conserved ββα configuration. Several amino acids on the surface of the α-helix typically contact 3 bp in the major groove of DNA, with varying levels of selectivity. Zinc fingers have two protein domains. The first domain is the DNA binding domain, which includes eukaryotic transcription factors and contain the zinc finger. The second domain is the nuclease domain, which includes the FokI restriction enzyme and is responsible for the catalytic cleavage of DNA.

[00919] The DNA-binding domains of individual ZFNs typically contain between three and six individual zinc finger repeats and can each recognize between 9 and 18 base pairs. If the zinc finger domains are specific for their intended target site then even a pair of 3-finger ZFNs that recognize a total of 18 base pairs can, in theory, target a single locus in a mammalian genome. One method to generate new zinc-finger arrays is to combine smaller zinc-finger "modules" of known specificity. The most common modular assembly process involves combining three separate zinc fingers that can each recognize a 3 base pair DNA sequence to generate a 3-finger array that can recognize a 9 base pair target site. Alternatively, selection-based approaches, such as oligomerized pool engineering (OPEN) can be used to select for new zinc-finger arrays from randomized libraries that take into consideration context-dependent interactions between neighboring fingers. Engineered zinc fingers are available commercially from Sangamo Biosciences (Richmond, CA, USA) and Sigma–Aldrich (St. Louis, MO, USA).

[00920] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a zinc finger method include PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8,

CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

[00921] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a zinc finger method include CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL12, IL-15, IL-18 and IL-21.

[00922] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a zinc finger method, which may be used in accordance with embodiments of the present invention, are described in U.S. Patent Nos. 6,534,261, 6,607,882, 6,746,838, 6,794,136, 6,824,978, 6,866,997, 6,933,113, 6,979,539, 7,013,219, 7,030,215, 7,220,719, 7,241,573, 7,241,574, 7,585,849, 7,595,376, 6,903,185, and 6,479,626, each of which are incorporated by reference herein.

[00923] Other examples of systems, methods, and compositions for altering the expression of a target gene sequence by a zinc finger method, which may be used in accordance with embodiments of the present invention, are described in Beane, *et al.*, *Mol. Therapy*, 2015, *23*, 1380-1390, the disclosure of which is incorporated by reference herein.

[00924] In some embodiments, the TILs are optionally genetically engineered to include additional functionalities, including, but not limited to, a high-affinity TCR, *e.g.*, a TCR targeted at a tumor-associated antigen such as MAGE-1, HER2, or NY-ESO-1, or a chimeric antigen receptor (CAR) which binds to a tumor-associated cell surface molecule (*e.g.*, mesothelin) or lineage-restricted cell surface molecule (*e.g.*, CD19). In some embodiments, the method comprises genetically engineering a population of TILs to include a high-affinity TCR, *e.g.*, a TCR targeted at a tumor-associated antigen such as MAGE-1, HER2, or NY-ESO-1, or a chimeric antigen receptor (CAR) which binds to a tumor-associated cell surface molecule (*e.g.*, mesothelin) or lineage-restricted cell surface molecule (*e.g.*, CD19). Aptly, the population of TILs may be a first population, a second population and/or a third population as described herein.

E. Closed Systems for TIL Manufacturing

[00925] The present invention provides for the use of closed systems during the TIL culturing process. Such closed systems allow for preventing and/or reducing microbial contamination, allow for the use of fewer flasks, and allow for cost reductions. In some embodiments, the closed system uses two containers.

[00926] Such closed systems are well-known in the art and can be found, for example, at http://www.fda.gov/cber/guidelines.htm and

https://www.fda.gov/BiologicsBloodVaccines/GuidanceComplianceRegulatoryInformation/Guidances/Blood/ucm076779.htm.

[00927] Sterile connecting devices (STCDs) produce sterile welds between two pieces of compatible tubing. This procedure permits sterile connection of a variety of containers and tube diameters. In some embodiments, the closed systems include luer lock and heat sealed systems as described in the Examples. In some embodiments, the closed system is accessed via syringes under sterile conditions in order to maintain the sterility and closed nature of the system. In some embodiments, a closed system as described in Example 21 is employed. In some embodiments, the TILs are formulated into a final product formulation container according to the methods described herein in the Examples"".

[00928] In some embodiments, the closed system uses one container from the time the tumor fragments are obtained until the TILs are ready for administration to the patient or cryopreserving. In some embodiments when two containers are used, the first container is a closed G-container and the population of TILs is centrifuged and transferred to an infusion bag without opening the first closed G-container. In some embodiments, when two containers are used, the infusion bag is a HypoThermosol-containing infusion bag. A closed system or closed TIL cell culture system is characterized in that once the tumor sample and/or tumor fragments have been added, the system is tightly sealed from the outside to form a closed environment free from the invasion of bacteria, fungi, and/or any other microbial contamination.

[00929] In some embodiments, the reduction in microbial contamination is between about 5% and about 100%. In some embodiments, the reduction in microbial contamination is between about 5% and about 95%. In some embodiments, the reduction in microbial contamination is between about 5% and about 90%. In some embodiments, the reduction in microbial contamination is between about 10% and about 90%. In some embodiments, the reduction in microbial contamination is between about 15% and about 85%. In some embodiments, the reduction in microbial contamination is about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 98%, about 99%, or about 100%.

[00930] The closed system allows for TIL growth in the absence and/or with a significant reduction in microbial contamination.

[00931] Moreover, pH, carbon dioxide partial pressure and oxygen partial pressure of the TIL cell culture environment each vary as the cells are cultured. Consequently, even though a medium appropriate for cell culture is circulated, the closed environment still needs to be constantly maintained as an optimal environment for TIL proliferation. To this end, it is desirable that the

physical factors of pH, carbon dioxide partial pressure and oxygen partial pressure within the culture liquid of the closed environment be monitored by means of a sensor, the signal whereof is used to control a gas exchanger installed at the inlet of the culture environment, and the that gas partial pressure of the closed environment be adjusted in real time according to changes in the culture liquid so as to optimize the cell culture environment. In some embodiments, the present invention provides a closed cell culture system which incorporates at the inlet to the closed environment a gas exchanger equipped with a monitoring device which measures the pH, carbon dioxide partial pressure and oxygen partial pressure of the closed environment, and optimizes the cell culture environment by automatically adjusting gas concentrations based on signals from the monitoring device.

[00932] In some embodiments, the pressure within the closed environment is continuously or intermittently controlled. That is, the pressure in the closed environment can be varied by means of a pressure maintenance device for example, thus ensuring that the space is suitable for growth of TILs in a positive pressure state, or promoting exudation of fluid in a negative pressure state and thus promoting cell proliferation. By applying negative pressure intermittently, moreover, it is possible to uniformly and efficiently replace the circulating liquid in the closed environment by means of a temporary shrinkage in the volume of the closed environment.

[00933] In some embodiments, optimal culture components for proliferation of the TILs can be substituted or added, and including factors such as IL-2 and/or OKT3, as well as combination, can be added.

F. Optional Cryopreservation of TILs

[00934] Either the bulk TIL population (for example the second population of TILs) or the expanded population of TILs (for example the third population of TILs) can be optionally cryopreserved. In some embodiments, cryopreservation occurs on the therapeutic TIL population. In some embodiments, cryopreservation occurs on the TILs harvested after the second expansion. In some embodiments, cryopreservation occurs on the TILs in exemplary Step F of Figures 1 and/or 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the TILs are cryopreserved in the infusion bag. In some embodiments, the TILs are cryopreserved prior to placement in an infusion bag. In some embodiments, the TILs are cryopreserved and not placed in an infusion bag. In some embodiments, cryopreservation is performed using a cryopreservation medium. In some embodiments, the cryopreservation media contains dimethylsulfoxide (DMSO). This is generally accomplished by putting the TIL population into a freezing solution, *e.g.* 85% complement inactivated AB serum and 15% dimethyl sulfoxide (DMSO). The cells in solution are placed into

cryogenic vials and stored for 24 hours at -80 °C, with optional transfer to gaseous nitrogen freezers for cryopreservation. See, Sadeghi, *et al., Acta Oncologica* **2013,** *52,* 978-986.

[00935] When appropriate, the cells are removed from the freezer and thawed in a 37 °C water bath until approximately 4/5 of the solution is thawed. The cells are generally resuspended in complete media and optionally washed one or more times. In some embodiments, the thawed TILs can be counted and assessed for viability as is known in the art.

[00936] In some embodiments, a population of TILs is cryopreserved using CS10 cryopreservation media (CryoStor 10, BioLife Solutions). In some embodiments, a population of TILs is cryopreserved using a cryopreservation media containing dimethylsulfoxide (DMSO). In some embodiments, a population of TILs is cryopreserved using a 1:1 (vol:vol) ratio of CS10 and cell culture media. In some embodiments, a population of TILs is cryopreserved using about a 1:1 (vol:vol) ratio of CS10 and cell culture media, further comprising additional IL-2.

[00937] As discussed above, and exemplified in Steps A through E as provided in Figures 1 and/or 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), cryopreservation can occur at numerous points throughout the TIL expansion process. In some embodiments, the expanded population of TILs after the first expansion (as provided for example, according to Step B or the expanded population of TILs after the one or more second expansions according to Step D of Figures 1 or 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) can be cryopreserved. Cryopreservation can be generally accomplished by placing the TIL population into a freezing solution, *e.g.*, 85% complement inactivated AB serum and 15% dimethyl sulfoxide (DMSO). The cells in solution are placed into cryogenic vials and stored for 24 hours at -80 °C, with optional transfer to gaseous nitrogen freezers for cryopreservation. See Sadeghi, *et al., Acta Oncologica* **2013,** *52,* 978-986. In some embodiments, the TILs are cryopreserved in 5% DMSO. In some embodiments, the TILs are cryopreserved in cell culture media plus 5% DMSO. In some embodiments, the TILs are cryopreserved according to the methods provided in Example 6.

[00938] When appropriate, the cells are removed from the freezer and thawed in a 37 °C water bath until approximately 4/5 of the solution is thawed. The cells are generally resuspended in complete media and optionally washed one or more times. In some embodiments, the thawed TILs can be counted and assessed for viability as is known in the art.

[00939] In some cases, the Step B from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) TIL population can be cryopreserved immediately, using the protocols discussed below.

Alternatively, the bulk TIL population can be subjected to Step C and Step D from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and then cryopreserved after Step D from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). Similarly, in the case where genetically modified TILs will be used in therapy, the Step B or Step D from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) TIL populations can be subjected to genetic modifications for suitable treatments.

G. Phenotypic Characteristics of Expanded TILs

[001430] In some embodiment, the TILs are analyzed for expression of numerous phenotype markers after expansion, including those described herein and in the Examples. In some embodiments, expression of one or more phenotypic markers is examined. In some embodiments, the phenotypic characteristics of the TILs are analyzed after the first expansion in Step B from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the phenotypic characteristics of the TILs are analyzed during the transition in Step C from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the phenotypic characteristics of the TILs are analyzed during the transition according to Step C from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and after cryopreservation. In some embodiments, the phenotypic characteristics of the TILs are analyzed after the second expansion according to Step D from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the phenotypic characteristics of the TILs are analyzed after two or more expansions according to Step D from Figures 1 or 8, (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001431] In some embodiments, the marker is selected from the group consisting of CD8 and CD28. In some embodiments, expression of CD8 is examined. In some embodiments, expression of CD28 is examined. In some embodiments, the expression of CD8 and/or CD28 is higher on TILs produced according the current invention process, as compared to other processes (*e.g.*, the Gen 3 process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as

compared to the 2A process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the expression of CD8 is higher on TILs produced according the current invention process, as compared to other processes (*e.g.*, the Gen 3 process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8B), as compared to the 2A process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the expression of CD28 is higher on TILs produced according the current invention process, as compared to other processes (*e.g.*, the Gen 3 process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as compared to the 2A process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A)). In some embodiments, high CD28 expression is indicative of a younger, more presisitent TIL phenotype. In some embodiments, expression of one or more regulatory markers is measured.

[001432] In some embodiments, no selection of the first population of TILs, second population of TILs, third population of TILs, or harvested TIL population based on CD8 and/or CD28 expression is performed during any of the steps for the method for expanding tumor infiltrating lymphocytes (TILs) described herein.

[001433] In some embodiments, the percentage of central memory cells is higher on TILs produced according the current invention process, as compared to other processes (*e.g.*, the Gen 3 process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), as compared to the 2A process as provided for example in Figure 8 (in particular, *e.g.*, Figure 8A)). In some embodiments the memory marker for central memory cells is selected from the group consisting of CCR7 and CD62L.

[001434] In some embodiments, the CD4+ and/or CD8+ TIL Memory subsets can be divided into different memory subsets. In some embodiments, the CD4+ and/or CD8+ TILs comprise the naïve (CD45RA+CD62L+) TILs. In some embodiments, the CD4+ and/or CD8+ TILs comprise the central memory (CM; CD45RA-CD62L+) TILs. In some embodiments, the CD4+ and/or CD8+ TILs comprise the effector memory (EM; CD45RA-CD62L-) TILs. In some embodiments, the CD4+ and/or CD8+ TILs comprise the, RA+ effector memory/effector (TEMRA/TEFF; CD45RA+CD62L+) TILs.

[001435] In some embodiments, the TILs express one more markers selected from the group consisting of granzyme B, perforin, and granulysin. In some embodiments, the TILs express

granzyme B. In some embodiments, the TILs express perforin. In some embodiments, the TILs express granulysin.

[001436] In some embodiments, restimulated TILs can also be evaluated for cytokine release, using cytokine release assays. In some embodiments, TILs can be evaluated for interferon-γ (IFN-γ) secretion. In some embodiments, the IFN-γ secretion is measured by an ELISA assay. In some embodiments, the IFN-γ secretion is measured by an ELISA assay after the rapid second expansion step, after Step D as provided in for example, Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, TIL health is measured by IFN-gamma (IFN-γ) secretion. In some embodiments, IFN-γ secretion is indicative of active TILs. In some embodiments, a potency assay for IFN-γ production is employed. IFN-γ production is another measure of cytotoxic potential. IFN-γ production can be measured by determining the levels of the cytokine IFN-γ in the media of TIL stimulated with antibodies to CD3, CD28, and CD137/4-1BB. IFN-γ levels in media from these stimulated TIL can be determined using by measuring IFN-γ release. In some embodiments, an increase in IFN-γ production in for example Step D in the Gen 3 process as provided in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) TILs as compared to for example Step D in the 2A process as provided in Figure 8 (in particular, *e.g.*, Figure 8A) is indicative of an increase in cytotoxic potential of the Step D TILs. In some embodiments, IFN-γ secretion is increased one-fold, two-fold, three-fold, four-fold, or five-fold or more. In some embodiments, IFN-γ secretion is increased one-fold. In some embodiments, IFN-γ secretion is increased two-fold. In some embodiments, IFN-γ secretion is increased three-fold. In some embodiments, IFN-γ secretion is increased four-fold. In some embodiments, IFN-γ secretion is increased five-fold. In some embodiments, IFN-γ is measured using a Quantikine ELISA kit. In some embodiments, IFN-γ is measured in TILs *ex vivo*. In some embodiments, IFN-γ is measured in TILs *ex vivo*, including TILs produced by the methods of the present invention, including, for example Figure 8B methods.

[001437] In some embodiments, TILs capable of at least one-fold, two-fold, three-fold, four-fold, or five-fold or more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least one-fold more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least two-fold more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure

8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least three-fold more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least four-fold more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least five-fold more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001438] In some embodiments, TILs capable of at least 100 pg/mL to about 1000 pg/mL or more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL, at least 250 pg/mL, at least 300 pg/mL, at least 350 pg/mL, at least 400 pg/mL, at least 450 pg/mL, at least 500 pg/mL, at least 550 pg/mL, at least 600 pg/mL, at least 650 pg/mL, at least 700 pg/mL, at least 750 pg/mL, at least 800 pg/mL, at least 850 pg/mL, at least 900 pg/mL, at least 950 pg/mL, or at least 1000 pg/mL or more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 300 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 400 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 500 pg/mL IFN-γ secretion are

TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 600 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 700 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 800 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 900 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 1000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 2000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 3000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 4000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 5000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 6000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 7000 pg/mL IFN-γ secretion are TILs produced by the

expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 8000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 9000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 10,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 15,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 20,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 25,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 30,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 35,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 40,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 45,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 50,000 pg/mL IFN-γ secretion are TILs produced by the expansion methods of the present

invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001439] In some embodiments, TILs capable of at least 100 pg/mL/5e5 cells to about 1000 pg/mL/5e5 cells or more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL/5e5 cells, at least 250 pg/mL/5e5 cells, at least 300 pg/mL/5e5 cells, at least 350 pg/mL/5e5 cells, at least 400 pg/mL/5e5 cells, at least 450 pg/mL/5e5 cells, at least 500 pg/mL/5e5 cells, at least 550 pg/mL/5e5 cells, at least 600 pg/mL/5e5 cells, at least 650 pg/mL/5e5 cells, at least 700 pg/mL/5e5 cells, at least 750 pg/mL/5e5 cells, at least 800 pg/mL/5e5 cells, at least 850 pg/mL/5e5 cells, at least 900 pg/mL/5e5 cells, at least 950 pg/mL/5e5 cells, or at least 1000 pg/mL/5e5 cells or more IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 200 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 300 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 400 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 500 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 600 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 700 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for

example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 800 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 900 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 1000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 2000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 3000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 4000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 5000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 6000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 7000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 8000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 9000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by

the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 10,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 15,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 20,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 25,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 30,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 35,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 40,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 45,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 50,000 pg/mL/5e5 cells IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001440] The diverse antigen receptors of T and B lymphocytes are produced by somatic recombination of a limited, but large number of gene segments. These gene segments: V (variable), D (diversity), J (joining), and C (constant), determine the binding specificity and downstream

applications of immunoglobulins and T-cell receptors (TCRs). The present invention provides a method for generating TILs which exhibit and increase the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity. In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity as compared to freshly harvested TILs and/or TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the TILs obtained by the present method exhibit an increase in the T-cell repertoire diversity as compared to freshly harvested TILs and/or TILs prepared using methods referred to as Gen 2, as exemplified in Figure 8 (in particular, *e.g.*, Figure 8A). In some embodiments, the TILs obtained in the first expansion exhibit an increase in the T-cell repertoire diversity. In some embodiments, the increase in diversity is an increase in the immunoglobulin diversity and/or the T-cell receptor diversity. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin heavy chain. In some embodiments, the diversity is in the immunoglobulin is in the immunoglobulin light chain. In some embodiments, the diversity is in the T-cell receptor. In some embodiments, the diversity is in one of the T-cell receptors selected from the group consisting of alpha, beta, gamma, and delta receptors. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha and/or beta. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) alpha. In some embodiments, there is an increase in the expression of T-cell receptor (TCR) beta. In some embodiments, there is an increase in the expression of TCRαβ (*i.e.*, TCRα/β). In some embodiments, the process as described herein (*e.g.*, the Gen 3 process) shows higher clonal diversity as compared to other processes, for example the process referred to as the Gen 2 based on the number of unique peptide CDRs within the sample.

[001441] In some embodiments, the activation and exhaustion of TILs can be determined by examining one or more markers. In some embodiments, the activation and exhaustion can be determined using multicolor flow cytometry. In some embodiments, the activation and exhaustion of markers include but not limited to one or more markers selected from the group consisting of CD3, PD-1, 2B4/CD244, CD8, CD25, BTLA, KLRG, TIM-3, CD194/CCR4, CD4, TIGIT, CD183, CD69, CD95, CD127, CD103, and/or LAG-3). In some embodiments, the activation and exhaustion of markers include but not limited to one or more markers selected from the group consisting of BTLA, CTLA-4, ICOS, Ki67, LAG-3, PD-1, TIGIT, and/or TIM-3. In some embodiments, the activation and exhaustion of markers include but not limited to one or more markers selected from the group consisting of BTLA, CTLA-4, ICOS, Ki67, LAG-3, CD103+/CD69+, CD103+/CD69-, PD-1, TIGIT, and/or TIM-3. In some embodiments, the T-cell markers (including activation and exhaustion markers) can be determined and/or analyzed to examine T-cell activation, inhibition, or function. In

some embodiments, the T-cell markers can include but are not limited to one or more markers selected from the group consisting of TIGIT, CD3, FoxP3, Tim-3, PD-1, CD103, CTLA-4, LAG-3, BTLA-4, ICOS, Ki67, CD8, CD25, CD45, CD4, and/or CD59.

[001442] In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs to 300000 pg/10^6 TILs or more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs greater than 5000 pg/10^6 TILs, greater than 7000 pg/10^6 TILs, greater than 9000 pg/10^6 TILs, greater than 11000 pg/10^6 TILs, greater than 13000 pg/10^6 TILs, greater than 15000 pg/10^6 TILs, greater than 17000 pg/10^6 TILs, greater than 19000 pg/10^6 TILs, greater than 20000 pg/10^6 TILs, greater than 40000 pg/10^6 TILs, greater than 60000 pg/10^6 TILs, greater than 80000 pg/10^6 TILs, greater than 100000 pg/10^6 TILs, greater than 120000 pg/10^6 TILs, greater than 140000 pg/10^6 TILs, greater than 160000 pg/10^6 TILs, greater than 180000 pg/10^6 TILs, greater than 200000 pg/10^6 TILs, greater than 220000 pg/10^6 TILs, greater than 240000 pg/10^6 TILs, greater than 260000 pg/10^6 TILs, greater than 280000 pg/10^6 TILs, greater than 300000 pg/10^6 TILsor more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 5000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 7000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 9000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 11000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 13000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion

methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 15000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 17000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 19000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 20000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 40000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 60000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 80000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 100000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 120000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 140000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 160000 pg/10^6 TILs

Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 180000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 200000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 220000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 240000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 260000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 280000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 300000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs to 300000 pg/10^6 TILs or more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs greater than 5000 pg/10^6 TILs, greater than 7000 pg/10^6 TILs, greater than 9000 pg/10^6 TILs, greater than 11000 pg/10^6 TILs, greater than 13000 pg/10^6 TILs, greater than 15000 pg/10^6 TILs, greater than 17000 pg/10^6 TILs, greater than 19000 pg/10^6 TILs, greater than 20000 pg/10^6 TILs, greater than 40000 pg/10^6 TILs, greater than 60000 pg/10^6 TILs, greater than 80000 pg/10^6 TILs, greater than 100000 pg/10^6 TILs, greater than 120000 pg/10^6 TILs, greater than 140000 pg/10^6 TILs, greater than 160000 pg/10^6 TILs, greater than 180000 pg/10^6 TILs,

greater than 200000 pg/10^6 TILs, greater than 220000 pg/10^6 TILs, greater than 240000 pg/10^6 TILs, greater than 260000 pg/10^6 TILs, greater than 280000 pg/10^6 TILs, greater than 300000 pg/10^6 TILsor more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 5000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 7000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 9000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 11000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 13000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 15000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 17000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 19000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 20000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion

methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 40000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 60000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 80000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 100000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 120000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 140000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 160000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 180000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 200000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 220000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 240000 pg/10^6 TILs

Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 260000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 280000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 300000 pg/10^6 TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D.

[001443] In some embodiments, TILs that exhibit greater than 1000 pg/mL to 300000 pg/mL or more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 1000 pg/mL, greater than 2000 pg/mL, greater than 3000 pg/mL, greater than 4000 pg/mL, greater than 5000 pg/mL, greater than 6000 pg/mL, greater than 7000 pg/mL, greater than 8000 pg/mL, greater than 9000 pg/mL, greater than 10000 pg/mL, greater than 20000 pg/mL, greater than 30000 pg/mL, greater than 40000 pg/mL, greater than 50000 pg/mL, greater than 60000 pg/mL, greater than 70000 pg/mL, greater than 80000 pg/mL, greater than 90000 pg/mL, greater than 100000 pg/mL or more Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 1000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 2000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 3000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 4000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for

example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 5000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 6000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 7000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 8000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 9000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 10000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 20000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 30000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 40000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 50000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 60000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or

Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 70000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 80000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 90000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 100000 pg/mL Granzyme B are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 120000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 140000 pg/mL Granzyme B are TILs Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 160000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 180000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 200000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 220000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 240000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or

Figure 48D. In some embodiments, TILs that exhibit greater than 260000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 280000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D. In some embodiments, TILs that exhibit greater than 300000 pg/mL Granzyme B secretion are TILs produced by the expansion methods of the present invention, including for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D.

[001444] In some embodiments, the expansion methods of the present invention produce an expanded population of TILs that exhibits increased Granzyme B secretion in vitro including for example TILs as provided in Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D, as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least one-fold to fifty-fold or more as compared to non-expanded population of TILs. In some embodiments, IFN-γ secretion is increased by at least one-fold, at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least six-fold, at least seven-fold, at least eight-fold, at least nine-fold, at least ten-fold, at least twenty-fold, at least thirty-fold, at least forty-fold, at least fifty-fold or more as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least one-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least two-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least three-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least four-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least five-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least six-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least seven-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least eight-fold as compared to non-expanded population of TILs. In some

embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least nine-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least ten-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least twenty-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least thirty-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least forty-fold as compared to non-expanded population of TILs. In some embodiments, Granzyme B secretion of the expanded population of TILs of the present invention is increased by at least fifty-fold as compared to non-expanded population of TILs.

[001445] In some embodiments, TILs capable of at least one-fold, two-fold, three-fold, four-fold, or five-fold or more lower levels of TNF-α (*i.e.*, TNF-alpha) secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least one-fold lower levels of TNF-α secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least two-fold lower levels of TNF-α secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least three-fold lower levels of TNF-α secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least four-fold lower levels of TNF-α secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least five-fold lower levels of TNF-α secretion as compared to IFN-γ secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001446] In some embodiments, TILs capable of at least 200 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α (*i.e.*, TNF-alpha) secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 500 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 1000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 2000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 3000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 4000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 5000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 6000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 7000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 8000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present

invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, TILs capable of at least 9000 pg/mL/5e5 cells to about 10,000 pg/mL/5e5 cells or more TNF-α secretion are TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001447] In some embodiments, IFN-γ and granzyme B levels are measured to determine the phenotypic characteristics of the TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, IFN-γ and TNF-α levels are measured to determine the phenotypic characteristics of the TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, granzyme B and TNF-α levels are measured to determine the phenotypic characteristics of the TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods. In some embodiments, IFN-γ, granzyme B and TNF-α levels are measured to determine the phenotypic characteristics of the TILs produced by the expansion methods of the present invention, including, for example Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D methods.

[001448] In some embodiments, the phenotypic characterization is examined after cryopreservation.

H. Additional Process Embodiments

[001449] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising: (a) obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments; (b) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and OKT-3, wherein the priming first expansion is performed for about 1 to 7 days or about about 1 to 8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs; (c) performing a rapid second expansion by contacting the second population of TILs with a cell culture medium comprising IL-2, OKT-3 and exogenous antigen presenting cells (APCs) to produce a third population of TILs, wherein the rapid second expansion is performed for about 1 to 11 days or about 1 to 10 days to obtain the third population of TILs, wherein the third

population of TILs is a therapeutic population of TILs; and (d) harvesting the therapeutic population of TILs obtained from step (c). In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, or about 2 to 4 days, and then (2) effecting the transfer of the second population of TILs from the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, wherein in the second container the second population of TILs from the small scale culture is cultured in a larger scale culture for a period of about 4 to 7 days, or about 4 to 8 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the second population of TILs from the first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days, or about about 4 to 8 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, or about 2 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 4 to 7 days, or about 4 to 8 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 5 to 7 days.

[001450] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising: (a) obtaining a first population

of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments; (b) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and OKT-3, wherein the priming first expansion is performed for about 1 to 8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs; (c) performing a rapid second expansion by contacting the second population of TILs with a cell culture medium comprising IL-2, OKT-3 and exogenous antigen presenting cells (APCs) to produce a third population of TILs, wherein the rapid second expansion is performed for about 1 to 8 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs; and (d) harvesting the therapeutic population of TILs obtained from step (c). In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (2) effecting the transfer of the second population of TILs from the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, wherein in the second container the second population of TILs from the small scale culture is cultured in a larger scale culture for a period of about 4 to 8 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the second population of TILs from the first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 6 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 4 to 6 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS

container, for a period of about 3 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 4 to 5 days.

[001451] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising: (a) obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments; (b) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 and OKT-3, wherein the priming first expansion is performed for about 1 to 7 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs; (c) performing a rapid second expansion by contacting the second population of TILs with a cell culture medium comprising IL-2, OKT-3 and exogenous antigen presenting cells (APCs) to produce a third population of TILs, wherein the rapid second expansion is performed for about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs; and (d) harvesting the therapeutic population of TILs obtained from step (c). In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (2) effecting the transfer of the second population of TILs from the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, wherein in the second container the second population of TILs from the small scale culture is cultured in a larger scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the second population of TILs from the first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small

scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (1) performing the rapid second expansion by culturing the second population of TILs in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 4 days, and then (2) effecting the transfer and apportioning of the second population of TILs from the first small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the second population of TILs transferred from the small scale culture to such second container is cultured in a larger scale culture for a period of about 5 days.

[001452] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by contacting the first population of TILs with a culture medium which further comprises exogenous antigen-presenting cells (APCs), wherein the number of APCs in the culture medium in step (c) is greater than the number of APCs in the culture medium in step (b).

[001453] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the culture medium is supplemented with additional exogenous APCs.

[001454] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 20:1.

[001455] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 10:1.

[001456] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 9:1.

[001457] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 8:1.

[001458] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 7:1.

[001459] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 6:1.

[001460] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 5:1.

[001461] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 4:1.

[001462] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 3:1.

[001463] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.9:1.

[001464] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.8:1.

[001465] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.7:1.

[001466] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.6:1.

[001467] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.5:1.

[001468] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.4:1.

[001469] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.3:1.

[001470] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.2:1.

[001471] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2.1:1.

[001472] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 1.1:1 to at or about 2:1.

[001473] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 10:1.

[001474] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 5:1.

[001475] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 4:1.

[001476] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 3:1.

[001477] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.9:1.

[001478] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.8:1.

[001479] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.7:1.

[001480] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.6:1.

[001481] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.5:1.

[001482] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.4:1.

[001483] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.3:1.

[001484] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.2:1.

[001485] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is selected from a range of from at or about 2:1 to at or about 2.1:1.

[001486] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is at or about 2:1.

[001487] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of number of APCs added in the rapid second expansion to the number of APCs added in step (b) is at or about 1.1:1, 1.2:1, 1.3:1, 1.4:1, 1.5:1, 1.6:1, 1.7:1, 1.8:1, 1.9:1, 2:1, 2.1:1, 2.2:1, 2.3:1, 2.4:1, 2.5:1, 2.6:1, 2.7:1, 2.8:1, 2.9:1, 3:1, 3.1:1, 3.2:1, 3.3:1, 3.4:1, 3.5:1, 3.6:1, 3.7:1, 3.8:1, 3.9:1, 4:1, 4.1:1, 4.2:1, 4.3:1, 4.4:1, 4.5:1, 4.6:1, 4.7:1, 4.8:1, 4.9:1, or 5:1.

[001488] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of APCs added in the primary first expansion is at or about 1×10^8, 1.1×10^8, 1.2×10^8, 1.3×10^8, 1.4×10^8, 1.5×10^8, 1.6×10^8, 1.7×10^8, 1.8×10^8, 1.9×10^8, 2×10^8, 2.1×10^8, 2.2×10^8, 2.3×10^8, 2.4×10^8, 2.5×10^8, 2.6×10^8, 2.7×10^8, 2.8×10^8,

2.9×10^8, 3×10^8, 3.1×10^8, 3.2×10^8, 3.3×10^8, 3.4×10^8 or 3.5×10^8 APCs, and such that the number of APCs added in the rapid second expansion is at or about 3.5×10^8, 3.6×10^8, 3.7×10^8, 3.8×10^8, 3.9×10^8, 4×10^8, 4.1×10^8, 4.2×10^8, 4.3×10^8, 4.4×10^8, 4.5×10^8, 4.6×10^8, 4.7×10^8, 4.8×10^8, 4.9×10^8, 5×10^8, 5.1×10^8, 5.2×10^8, 5.3×10^8, 5.4×10^8, 5.5×10^8, 5.6×10^8, 5.7×10^8, 5.8×10^8, 5.9×10^8, 6×10^8, 6.1×10^8, 6.2×10^8, 6.3×10^8, 6.4×10^8, 6.5×10^8, 6.6×10^8, 6.7×10^8, 6.8×10^8, 6.9×10^8, 7×10^8, 7.1×10^8, 7.2×10^8, 7.3×10^8, 7.4×10^8, 7.5×10^8, 7.6×10^8, 7.7×10^8, 7.8×10^8, 7.9×10^8, 8×10^8, 8.1×10^8, 8.2×10^8, 8.3×10^8, 8.4×10^8, 8.5×10^8, 8.6×10^8, 8.7×10^8, 8.8×10^8, 8.9×10^8, 9×10^8, 9.1×10^8, 9.2×10^8, 9.3×10^8, 9.4×10^8, 9.5×10^8, 9.6×10^8, 9.7×10^8, 9.8×10^8, 9.9×10^8 or 1×10^9 APCs.

[001489] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of APCs added in the primary first expansion is selected from the range of at or about 1×10^8 APCs to at or about 3.5×10^8 APCs, and wherein the number of APCs added in the rapid second expansion is selected from the range of at or about 3.5×10^8 APCs to at or about 1×10^9 APCs.

[001490] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of APCs added in the primary first expansion is selected from the range of at or about 1.5×10^8 APCs to at or about 3×10^8 APCs, and wherein the number of APCs added in the rapid second expansion is selected from the range of at or about 4×10^8 APCs to at or about 7.5×10^8 APCs.

[001491] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of APCs added in the primary first expansion is selected from the range of at or about 2×10^8 APCs to at or about 2.5×10^8 APCs, and wherein the number of APCs added in the rapid second expansion is selected from the range of at or about 4.5×10^8 APCs to at or about 5.5×10^8 APCs.

[001492] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that at or about 2.5×10^8 APCs are added to the primary first expansion and at or about 5×10^8 APCs are added to the rapid second expansion.

[001493] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the antigen-presenting cells are peripheral blood mononuclear cells (PBMCs).

[001494] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple tumor fragments are distributed into a plurality of separate containers, in each of which separate containers the first population of TILs is obtained in step (a), the second population of TILs is obtained in step (b), and the third population of

TILs is obtained in step (c), and the therapeutic populations of TILs from the plurality of containers in step (c) are combined to yield the harvested TIL population from step (d).

[001495] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple tumors are evenly distributed into the plurality of separate containers.

[001496] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises at least two separate containers.

[001497] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises from two to twenty separate containers.

[001498] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises from two to fifteen separate containers.

[001499] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises from two to ten separate containers.

[001500] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises from two to five separate containers.

[001501] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the plurality of separate containers comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 separate containers.

[001502] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that for each container in which the priming first expansion is performed on a first population of TILs in step (b) the rapid second expansion in step (c) is performed in the same container on the second population of TILs produced from such first population of TILs.

[001503] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each of the separate containers comprises a first gas-permeable surface area.

[001504] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple tumor fragments are distributed in a single container.

[001505] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the single container comprises a first gas-permeable surface area.

[001506] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about one cell layer to at or about three cell layers.

[001507] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1.5 cell layers to at or about 2.5 cell layers.

[001508] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 2 cell layers.

[001509] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 or 3 cell layers.

[001510] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 3 cell layers to at or about 10 cell layers.

[001511] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 4 cell layers to at or about 8 cell layers.

[001512] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 3, 4, 5, 6, 7, 8, 9 or 10 cell layers.

[001513] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9 or 8 cell layers.

[001514] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the priming first expansion is performed in a first container comprising a first gas-permeable surface area and in step (c) the rapid second expansion is performed in a second container comprising a second gas-permeable surface area.

[001515] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second container is larger than the first container.

[001516] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about one cell layer to at or about three cell layers.

[001517] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1.5 cell layers to at or about 2.5 cell layers.

[001518] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 2 cell layers.

[001519] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 or 3 cell layers.

[001520] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the second gas-permeable surface area at an average thickness of at or about 3 cell layers to at or about 10 cell layers.

[001521] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the second gas-permeable surface area at an average thickness of at or about 4 cell layers to at or about 8 cell layers.

[001522] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the second gas-permeable surface area at an average thickness of at or about 3, 4, 5, 6, 7, 8, 9 or 10 cell layers.

[001523] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable modified such that in step (c) the APCs are layered onto the second gas-permeable surface area at an average thickness of at or about 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9 or 8 cell layers.

[001524] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the priming first expansion is performed in a first container comprising a first gas-permeable surface area and in step (c) the rapid second expansion is performed in the first container.

[001525] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about one cell layer to at or about three cell layers.

[001526] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1.5 cell layers to at or about 2.5 cell layers.

[001527] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 2 cell layers.

[001528] In other embodiments, the invention provides the method described any of the preceding paragraphs as applicable above modified such that in step (b) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 or 3 cell layers.

[001529] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 3 cell layers to at or about 10 cell layers.

[001530] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 4 cell layers to at or about 8 cell layers.

[001531] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 3, 4, 5, 6, 7, 8, 9 or 10 cell layers.

[001532] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (c) the APCs are layered onto the first gas-permeable surface area at an average thickness of at or about 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9 or 8 cell layers.

[001533] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:10.

[001534] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:9.

[001535] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step

(b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:8.

[001536] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:7.

[001537] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:6.

[001538] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:5.

[001539] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:4.

[001540] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of

APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:3.

[001541] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.1 to at or about 1:2.

[001542] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.2 to at or about 1:8.

[001543] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.3 to at or about 1:7.

[001544] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.4 to at or about 1:6.

[001545] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-

presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.5 to at or about 1:5.

[001546] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.6 to at or about 1:4.

[001547] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.7 to at or about 1:3.5.

[001548] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.8 to at or about 1:3.

[001549] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:1.9 to at or about 1:2.5.

[001550] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed

by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from the range of at or about 1:2.

[001551] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the primary first expansion is performed by supplementing the cell culture medium of the first population of TILs with additional antigen-presenting cells (APCs), wherein the number of APCs added in step (c) is greater than the number of APCs added in step (b), and wherein the ratio of the average number of layers of APCs layered in step (b) to the average number of layers of APCs layered in step (c) is selected from at or about 1:1.1, 1:1.2, 1:1.3, 1:1.4, 1:1.5, 1:1.6, 1:1.7, 1:1.8, 1:1.9, 1:2, 1:2.1, 1:2.2, 1:2.3, 1:2.4, 1:2.5, 1:2.6, 1:2.7, 1:2.8, 1:2.9, 1:3, 1:3.1, 1:3.2, 1:3.3, 1:3.4, 1:3.5, 1:3.6, 1:3.7, 1:3.8, 1:3.9, 1:4, 1:4.1, 1:4.2, 1:4.3, 1:4.4, 1:4.5, 1:4.6, 1:4.7, 1:4.8, 1:4.9, 1:5, 1:5.1, 1:5.2, 1:5.3, 1:5.4, 1:5.5, 1:5.6, 1:5.7, 1:5.8, 1:5.9, 1:6, 1:6.1, 1:6.2, 1:6.3, 1:6.4, 1:6.5, 1:6.6, 1:6.7, 1:6.8, 1:6.9, 1:7, 1:7.1, 1:7.2, 1:7.3, 1:7.4, 1:7.5, 1:7.6, 1:7.7, 1:7.8, 1:7.9, 1:8, 1:8.1, 1:8.2, 1:8.3, 1:8.4, 1:8.5, 1:8.6, 1:8.7, 1:8.8, 1:8.9, 1:9, 1:9.1, 1:9.2, 1:9.3, 1:9.4, 1:9.5, 1:9.6, 1:9.7, 1:9.8, 1:9.9 or 1:10.

[001552] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of TILs in the second population of TILs to the number of TILs in the first population of TILs is at or about 1.5:1 to at or about 100:1.

[001553] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of TILs in the second population of TILs to the number of TILs in the first population of TILs is at or about 50:1.

[001554] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of TILs in the second population of TILs to the number of TILs in the first population of TILs is at or about 25:1.

[001555] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of TILs in the second population of TILs to the number of TILs in the first population of TILs is at or about 20:1.

[001556] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of TILs in the second population of TILs to the number of TILs in the first population of TILs is at or about 10:1.

[001557] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second population of TILs is at least at or about 50-fold greater in number than the first population of TILs.

[001558] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second population of TILs is at least at or about 1-, 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 11-, 12-, 13-, 14-, 15-, 16-, 17-, 18-, 19-, 20-, 21-, 22-, 23-, 24-, 25-, 26-, 27-, 28-, 29-, 30-, 31-, 32-, 33-, 34-, 35-, 36-, 37-, 38-, 39-, 40-, 41-, 42-, 43-, 44-, 45-, 46-, 47-, 48-, 49- or 50-fold greater in number than the first population of TILs.

[001559] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that at or about 2 days or at or about 3 days after the commencement of the second period in step (c), the cell culture medium is supplemented with additional IL-2.

[001560] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified to further comprise the step of cryopreserving the harvested TIL population in step (d) using a cryopreservation process.

[001561] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified to comprise performing after step (d) the additional step of (e) transferring the harvested TIL population from step (d) to an infusion bag that optionally contains HypoThermosol.

[001562] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified to comprise the step of cryopreserving the infusion bag comprising the harvested TIL population in step (e) using a cryopreservation process.

[001563] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the cryopreservation process is performed using a 1:1 ratio of harvested TIL population to cryopreservation media.

[001564] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the antigen-presenting cells are peripheral blood mononuclear cells (PBMCs).

[001565] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the PBMCs are irradiated and allogeneic.

[001566] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the total number of APCs added to the cell culture in step (b) is 2.5×10^8.

[001567] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the total number of APCs added to the cell culture in step (c) is 5×10^8.

[001568] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the APCs are PBMCs.

[001569] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the PBMCs are irradiated and allogeneic.

[001570] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the antigen-presenting cells are artificial antigen-presenting cells.

[001571] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the harvesting in step (d) is performed using a membrane-based cell processing system.

[001572] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the harvesting in step (d) is performed using a LOVO cell processing system.

[001573] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 5 to at or about 60 fragments per container in step (b).

[001574] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 10 to at or about 60 fragments per container in step (b).

[001575] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 15 to at or about 60 fragments per container in step (b).

[001576] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 20 to at or about 60 fragments per container in step (b).

[001577] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 25 to at or about 60 fragments per container in step (b).

[001578] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 30 to at or about 60 fragments per container in step (b).

[001579] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 35 to at or about 60 fragments per container in step (b).

[001580] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 40 to at or about 60 fragments per container in step (b).

[001581] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 45 to at or about 60 fragments per container in step (b).

[001582] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 50 to at or about 60 fragments per container in step (b).

[001583] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 or 60 fragment(s) per container in step (b).

[001584] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 27 mm^3.

[001585] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 20 mm^3 to at or about 50 mm^3.

[001586] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 21 mm^3 to at or about 30 mm^3.

[001587] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 22 mm^3 to at or about 29.5 mm^3.

[001588] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 23 mm^3 to at or about 29 mm^3.

[001589] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 24 mm^3 to at or about 28.5 mm^3.

[001590] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 25 mm^3 to at or about 28 mm^3.

[001591] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 26.5 mm^3 to at or about 27.5 mm^3.

[001592] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each fragment has a volume of at or about 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 mm^3.

[001593] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 30 to at or about 60 fragments with a total volume of at or about 1300 mm^3 to at or about 1500 mm^3.

[001594] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 50 fragments with a total volume of at or about 1350 mm^3.

[001595] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the multiple fragments comprise at or about 50 fragments with a total mass of at or about 1 gram to at or about 1.5 grams.

[001596] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the cell culture medium is provided in a container that is a G-container or a Xuri cellbag.

[001597] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the IL-2 concentration in the cell culture medium is about 10,000 IU/mL to about 5,000 IU/mL.

[001598] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the IL-2 concentration in the cell culture medium is about 6,000 IU/mL.

[001599] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the cryopreservation media comprises dimethlysulfoxide (DMSO).

[001600] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the cryopreservation media comprises 7% to 10% DMSO.

[001601] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first period in step (b) is performed within a period of at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days.

[001602] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second period in step (c) is performed within a period of at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days or 11 days.

[001603] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first period in step (b) and the second period in step (c) are each individually performed within a period of at or about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days.

[001604] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first period in step (b) and the second period in step (c) are each individually performed within a period of at or about 5 days, 6 days, or 7 days.

[001605] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first period in step (b) and the second period in step (c) are each individually performed within a period of at or about 7 days.

[001606] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 14 days to at or about 18 days.

[001607] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 15 days to at or about 18 days.

[001608] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 16 days to at or about 18 days.

[001609] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 17 days to at or about 18 days.

[001610] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 14 days to at or about 17 days.

[001611] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 15 days to at or about 17 days.

[001612] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 16 days to at or about 17 days.

[001613] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 14 days to at or about 16 days.

[001614] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 15 days to at or about 16 days.

[001615] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 14 days.

[001616] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 15 days.

[001617] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 16 days.

[001618] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 17 days.

[001619] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 18 days.

[001620] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 14 days or less.

[001621] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 15 days or less.

[001622] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 16 days or less.

[001623] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that steps (a) through (d) are performed in a total of at or about 18 days or less.

[001624] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs harvested in step (d) comprises sufficient TILs for a therapeutically effective dosage of the TILs.

[001625] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of TILs sufficient for a therapeutically effective dosage is from at or about 2.3×10^{10} to at or about 13.7×10^{10}.

[001626] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the third population of TILs in step (c) provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality.

[001627] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the third population of TILs in step (c) provides for at least a one-fold to five-fold or more interferon-gamma production as compared to TILs prepared by a process longer than 16 days.

[001628] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the third population of TILs in step (c) provides for at least a one-fold to five-fold or more interferon-gamma production as compared to TILs prepared by a process longer than 17 days.

[001629] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the third population of TILs in step (c) provides for at least a one-fold to five-fold or more interferon-gamma production as compared to TILs prepared by a process longer than 18 days.

[001630] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the effector T cells and/or central memory T cells obtained from the third population of TILs step (c) exhibit increased CD8 and CD28 expression relative to effector T cells and/or central memory T cells obtained from the second population of cells step (b).

[001631] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each container recited in the method is a closed container.

[001632] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each container recited in the method is a G-container.

[001633] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each container recited in the method is a GREX-10.

[001634] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each container recited in the method is a GREX-100.

[001635] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that each container recited in the method is a GREX-500.

[001636] In other embodiments, the invention provides the therapeutic population of tumor infiltrating lymphocytes (TILs) made by the method described in any of the preceding paragraphs as applicable above.

[001637] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process in which the first expansion of TILs is performed without any added antigen-presenting cells (APCs) or OKT3.

[001638] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process in which the first expansion of TILs is performed without any added antigen-presenting cells (APCs).

[001639] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process in which the first expansion of TILs is performed without any added OKT3.

[001640] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process in which the first expansion of TILs is performed with no added antigen-presenting cells (APCs) and no added OKT3.

[001641] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process by a process longer than 16 days.

[001642] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process by a process longer than 17 days.

[001643] In other embodiments, the invention provides a therapeutic population of tumor infiltrating lymphocytes (TILs) prepared from tumor tissue of a patient, wherein the therapeutic population of

TILs provides for increased efficacy, increased interferon-gamma production, and/or increased polyclonality compared to TILs prepared by a process by a process longer than 18 days.

[001644] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above that provides for increased interferon-gamma production.

[001645] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above that provides for increased polyclonality.

[001646] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above that provides for increased efficacy.

[001647] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least one-fold more interferon-gamma production as compared to TILs prepared by a process longer than 16 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least one-fold more interferon-gamma production as compared to TILs prepared by a process longer than 17 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least one-fold more interferon-gamma production as compared to TILs prepared by a process longer than 18 days. In other embodiments, the TILs are rendered capable of the at least one-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001648] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least two-fold more interferon-gamma production as compared to TILs prepared by a process longer than 16 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least two-fold more interferon-gamma production as compared to TILs prepared by a process longer than 17 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is

capable of at least two-fold more interferon-gamma production as compared to TILs prepared by a process longer than 18 days. In other embodiments, the TILs are rendered capable of the at least two-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001649] In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least three-fold more interferon-gamma production as compared to TILs prepared by a process longer than 16 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least three-fold more interferon-gamma production as compared to TILs prepared by a process longer than 17 days. In other embodiments, the invention provides for the therapeutic population of TILs described in any of the preceding paragraphs as applicable above modified such that the therapeutic population of TILs is capable of at least three-fold more interferon-gamma production as compared to TILs prepared by a process longer than 18 days. In other embodiments, the TILs are rendered capable of the at least three-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001650] In other embodiments, the invention provides for a therapeutic population of tumor infiltrating lymphocytes (TILs) that is capable of at least one-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added antigen-presenting cells (APCs). In other embodiments, the TILs are rendered capable of the at least one-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001651] In other embodiments, the invention provides for a therapeutic population of tumor infiltrating lymphocytes (TILs) that is capable of at least one-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added OKT3. In other embodiments, the TILs are rendered capable of the at least one-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in

Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001652] In other embodiments, the invention provides for a therapeutic population of TILs that is capable of at least two-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added APCs. In other embodiments, the TILs are rendered capable of the at least two-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001653] In other embodiments, the invention provides for a therapeutic population of TILs that is capable of at least two-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added OKT3. In other embodiments, the TILs are rendered capable of the at least two-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001654] In other embodiments, the invention provides for a therapeutic population of TILs that is capable of at least three-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added APCs. In other embodiments, the TILs are rendered capable of the at least one-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001655] In other embodiments, the invention provides for a therapeutic population of TILs that is capable of at least three-fold more interferon-gamma production as compared to TILs prepared by a process in which the first expansion of TILs is performed without any added OKT3. In other embodiments, the TILs are rendered capable of the at least three-fold more interferon-gamma production due to the expansion process described herein, for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 8 (in particular, *e.g.,* Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

[001656] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the tumor fragments are small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates.

[001657] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the tumor fragments are core biopsies.

[001658] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the tumor fragments are fine needle aspirates.

[001659] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the tumor fragments are small biopsies (including, for example, a punch biopsy).

[001660] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the tumor fragments are core needle biopsies.

[001661] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from one or more small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising IL-2 for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion for a period of about 8 days, and (iv) the method comprises performing the rapid second expansion for a period of about 11 days. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001662] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from one or more small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising IL-2 for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion for a period of about 8 days, and (iv) the method comprises performing the rapid second expansion by culturing the culture of the second population of TILs for about 5 days, splitting the culture into up to 5 subcultures and culturing the subcultures for about 6 days. In some of the foregoing embodiments, the up to 5

subcultures are each cultured in a container that is the same size or larger than the container in which the culture of the second population of TILs is commenced in the rapid second expansion. In some of the foregoing embodiments, the culture of the second population of TILs is equally divided amongst the up to 5 subcultures. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001663] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 20 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject.

[001664] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 10 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject.

[001665] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject.

[001666] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the subject.

[001667] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from 1 to about 10 core biopsies of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising IL-2 for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion step by culturing the first population of TILs in a culture medium comprising IL-2, OKT-3 and antigen presenting cells (APCs) for a period of about 8 days to obtain the second population of TILs, and (iv) the method comprises performing the rapid second expansion step by culturing the second population of TILs in a culture medium comprising IL-2, OKT-3 and APCs for a period of about 11 days. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001668] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 20 core biopsies of tumor tissue from the subject.

[001669] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 10 core biopsies of tumor tissue from the subject.

[001670] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 core biopsies of tumor tissue from the subject.

[001671] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 core biopsies of tumor tissue from the subject.

[001672] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 20 fine needle aspirates of tumor tissue from the subject.

[001673] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 10 fine needle aspirates of tumor tissue from the subject.

[001674] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 fine needle aspirates of tumor tissue from the subject.

[001675] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 fine needle aspirates of tumor tissue from the subject.

[001676] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 20 core needle biopsies of tumor tissue from the subject.

[001677] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 10 core needle biopsies of tumor tissue from the subject.

[001678] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 core needle biopsies of tumor tissue from the subject.

[001679] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 core needle biopsies of tumor tissue from the subject.

[001680] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 20 small biopsies (including, for example, a punch biopsy) of tumor tissue from the subject.

[001681] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1 to about 10 small biopsies (including, for example, a punch biopsy) of tumor tissue from the subject.

[001682] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 small biopsies (including, for example, a punch biopsy) of tumor tissue from the subject.

[001683] In other embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of TILs is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 small biopsies (including, for example, a punch biopsy) of tumor tissue from the subject.

[001684] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from 1 to about 10 core biopsies of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising IL-2 for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion step by culturing the first population of TILs in a culture medium comprising IL-2, OKT-3 and antigen presenting cells (APCs) for a period of about 8 days to obtain the second population of TILs, and (iv) the method comprises performing the rapid second expansion step by culturing the second population of TILs in a

culture medium comprising IL-2, OKT-3 and APCs for a period of about 11 days. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001685] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from 1 to about 10 core biopsies of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising IL-2 for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion step by culturing the first population of TILs in a culture medium comprising IL-2, OKT-3 and antigen presenting cells (APCs) for a period of about 8 days to obtain the second population of TILs, and (iv) the method comprises performing the rapid second expansion by culturing the culture of the second population of TILs in a culture medium comprising IL-2, OKT-3 and APCs for about 5 days, splitting the culture into up to 5 subcultures and culturing each of the subcultures in a culture medium comprising IL-2 for about 6 days. In some of the foregoing embodiments, the up to 5 subcultures are each cultured in a container that is the same size or larger than the container in which the culture of the second population of TILs is commenced in the rapid second expansion. In some of the foregoing embodiments, the culture of the second population of TILs is equally divided amongst the up to 5 subcultures. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001686] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that (i) the method comprises obtaining the first population of TILs from 1 to about 10 core biopsies of tumor tissue from the subject, (ii) the method comprises performing the step of culturing the first population of TILs in a cell culture medium comprising 6000 IU IL-2/mL in 0.5 L of CM1 culture medium in a G-REX 100M flask for a period of about 3 days prior to performing the step of the priming first expansion, (iii) the method comprises performing the priming first expansion by adding 0.5 L of CM1 culture medium containing 6000 IU/mL IL-2, 30 ng/mL OKT-3, and about 10^8 feeder cells and culturing for a period of about 8 days, and (iv) the method comprises performing the rapid second expansion by (a) transferring the second population of TILs to a G-REX 500MCS flask containing 5 L of CM2 culture medium with 3000 IU/mL IL-2, 30 ng/mL OKT-3, and $5x10^9$ feeder cells and culturing for about 5 days (b) splitting the culture into up to 5 subcultures by transferring 10^9 TILs into each of up to 5 G-REX 500MCS flasks containing 5 L of AIM-V medium with 3000 IU/mL IL-2, and culturing the subcultures for about 6 days. In some of the foregoing embodiments, the steps of the method are completed in about 22 days.

[001687] In some embodiments, the invention provides a method of expanding T cells comprising: (a) performing a priming first expansion of a first population of T cells obtained from a donor by culturing the first population of T cells to effect growth and to prime an activation of the first population of T cells; (b) after the activation of the first population of T cells primed in step (a) begins to decay, performing a rapid second expansion of the first population of T cells by culturing the first population of T cells to effect growth and to boost the activation of the first population of T cells to obtain a second population of T cells; and (c) harvesting the second population of T cells. In some embodiments, the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer of the first population of T cells from the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, and culturing the first population of T cells from the small scale culture in a larger scale culture in the second container for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the first population of T cells from first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 4 to 7 days. In some embodiments, the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second

container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 5 days.

[001688] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid second expansion is split into a plurality of steps to achieve a scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (b) effecting the transfer of the first population of T cells from the small scale culture to a second container larger than the first container, *e.g.*, a G-REX 500MCS container, and culturing the first population of T cells from the small scale culture in a larger scale culture in the second container for a period of about 5 to 7 days.

[001689] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a first small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the first small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are equal in size to the first container, wherein in each second container the portion of the first population of T cells from first small scale culture transferred to such second container is cultured in a second small scale culture for a period of about 5 to 7 days.

[001690] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 2 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 5 to 7 days.

[001691] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a

G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 5 to 6 days.

[001692] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 5 days.

[001693] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale culture transferred to such second container is cultured in a larger scale culture for a period of about 6 days.

[001694] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the step of rapid expansion is split into a plurality of steps to achieve a scaling out and scaling up of the culture by: (a) performing the rapid second expansion by culturing the first population of T cells in a small scale culture in a first container, *e.g.*, a G-REX 100MCS container, for a period of about 3 to 4 days, and then (b) effecting the transfer and apportioning of the first population of T cells from the small scale culture into and amongst 2, 3 or 4 second containers that are larger in size than the first container, *e.g.*, G-REX 500MCS containers, wherein in each second container the portion of the first population of T cells from the small scale

culture transferred to such second container is cultured in a larger scale culture for a period of about 7 days.

[001695] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion of step (a) is performed during a period of up to 7 days.

[001696] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the rapid second expansion of step (b) is performed during a period of up to 8 days.

[001697] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the rapid second expansion of step (b) is performed during a period of up to 9 days.

[001698] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the rapid second expansion of step (b) is performed during a period of up to 10 days.

[001699] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the rapid second expansion of step (b) is performed during a period of up to 11 days.

[001700] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed during a period of 7 days and the rapid second expansion of step (b) is performed during a period of up to 9 days.

[001701] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed during a period of 7 days and the rapid second expansion of step (b) is performed during a period of up to 10 days.

[001702] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed during a period of 7 days or 8 days and the rapid second expansion of step (b) is performed during a period of up to 9 days.

[001703] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed

during a period of 7 days or 8 days and the rapid second expansion of step (b) is performed during a period of up to 10 days.

[001704] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed during a period of 8 days and the rapid second expansion of step (b) is performed during a period of up to 9 days.

[001705] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the priming first expansion in step (a) is performed during a period of 8 days and the rapid second expansion of step (b) is performed during a period of up to 8 days.

[001706] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of T cells is cultured in a first culture medium comprising OKT-3 and IL-2.

[001707] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first culture medium comprises 4-1BB agonist, OKT-3 and IL-2.

[001708] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first culture medium comprises OKT-3, IL-2 and antigen-presenting cells (APCs).

[001709] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first culture medium comprises 4-1BB agonist, OKT-3, IL-2 and antigen-presenting cells (APCs).

[001710] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the first population of T cells is cultured in a second culture medium comprising OKT-3, IL-2 and antigen-presenting cells (APCs).

[001711] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second culture medium comprises 4-1BB agonist, OKT-3, IL-2 and antigen-presenting cells (APCs).

[001712] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of T cells is cultured in a first culture medium in a container comprising a first gas-permeable surface, wherein the first culture medium comprises OKT-3, IL-2 and a first population of antigen-presenting cells (APCs),

wherein the first population of APCs is exogenous to the donor of the first population of T cells and the first population of APCs is layered onto the first gas-permeable surface, wherein in step (b) the first population of T cells is cultured in a second culture medium in the container, wherein the second culture medium comprises OKT-3, IL-2 and a second population of APCs, wherein the second population of APCs is exogenous to the donor of the first population of T cells and the second population of APCs is layered onto the first gas-permeable surface, and wherein the second population of APCs is greater than the first population of APCs.

[001713] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of T cells is cultured in a first culture medium in a container comprising a first gas-permeable surface, wherein the first culture medium comprises 4-1BB agonist, OKT-3, IL-2 and a first population of antigen-presenting cells (APCs), wherein the first population of APCs is exogenous to the donor of the first population of T cells and the first population of APCs is layered onto the first gas-permeable surface, wherein in step (b) the first population of T cells is cultured in a second culture medium in the container, wherein the second culture medium comprises OKT-3, IL-2 and a second population of APCs, wherein the second population of APCs is exogenous to the donor of the first population of T cells and the second population of APCs is layered onto the first gas-permeable surface, and wherein the second population of APCs is greater than the first population of APCs.

[001714] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of T cells is cultured in a first culture medium in a container comprising a first gas-permeable surface, wherein the first culture medium comprises OKT-3, IL-2 and a first population of antigen-presenting cells (APCs), wherein the first population of APCs is exogenous to the donor of the first population of T cells and the first population of APCs is layered onto the first gas-permeable surface, wherein in step (b) the first population of T cells is cultured in a second culture medium in the container, wherein the second culture medium comprises 4-1BB agonist, OKT-3, IL-2 and a second population of APCs, wherein the second population of APCs is exogenous to the donor of the first population of T cells and the second population of APCs is layered onto the first gas-permeable surface, and wherein the second population of APCs is greater than the first population of APCs.

[001715] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of T cells is cultured in a first culture medium in a container comprising a first gas-permeable surface, wherein the first culture medium comprises 4-1BB agonist, OKT-3, IL-2 and a first population of antigen-presenting cells (APCs), wherein the first population of APCs is exogenous to the donor of the first population of T cells and the first population of APCs is layered onto the first gas-permeable surface, wherein in

step (b) the first population of T cells is cultured in a second culture medium in the container, wherein the second culture medium comprises 4-1BB agonist, OKT-3, IL-2 and a second population of APCs, wherein the second population of APCs is exogenous to the donor of the first population of T cells and the second population of APCs is layered onto the first gas-permeable surface, and wherein the second population of APCs is greater than the first population of APCs.

[001716] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the number of APCs in the second population of APCs to the number of APCs in the first population of APCs is about 2:1.

[001717] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the number of APCs in the first population of APCs is about 2.5×10^8 and the number of APCs in the second population of APCs is about 5×10^8.

[001718] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is layered onto the first gas-permeable surface at an average thickness of 2 layers of APCs.

[001719] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the second population of APCs is layered onto the first gas-permeable surface at an average thickness selected from the range of 4 to 8 layers of APCs.

[001720] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the ratio of the average number of layers of APCs layered onto the first gas-permeable surface in step (b) to the average number of layers of APCs layered onto the first gas-permeable surface in step (a) is 2:1.

[001721] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 1.0×10^6 APCs/cm^2 to at or about 4.5×10^6 APCs/cm^2.

[001722] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 1.5×10^6 APCs/cm^2 to at or about 3.5×10^6 APCs/cm^2.

[001723] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded

on the first gas permeable surface at a density selected from the range of at or about 2.0×10^6 APCs/cm^2 to at or about 3.0×10^6 APCs/cm^2.

[001724] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density of at or about 2.0×10^6 APCs/cm^2.

[001725] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 2.5×10^6 APCs/cm^2 to at or about 7.5×10^6 APCs/cm^2.

[001726] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 3.5×10^6 APCs/cm^2 to at or about 6.0×10^6 APCs/cm^2.

[001727] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 4.0×10^6 APCs/cm^2 to at or about 5.5×10^6 APCs/cm^2.

[001728] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (b) the second population of APCs is seeded on the first gas permeable surface at a density of at or about 4.0×10^6 APCs/cm^2.

[001729] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 1.0×10^6 APCs/cm^2 to at or about 4.5×10^6 APCs/cm^2 and in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 2.5×10^6 APCs/cm^2 to at or about 7.5×10^6 APCs/cm^2.

[001730] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 1.5×10^6 APCs/cm^2 to at or about 3.5×10^6 APCs/cm^2 and in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 3.5×10^6 APCs/cm^2 to at or about 6.0×10^6 APCs/cm^2.

[001731] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 2.0×10^6 APCs/cm^2 to at or about 3.0×10^6 APCs/cm^2 and in step (b) the second population of APCs is seeded on the first gas permeable surface at a density selected from the range of at or about 4.0×10^6 APCs/cm^2 to at or about 5.5×10^6 APCs/cm^2.

[001732] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that in step (a) the first population of APCs is seeded on the first gas permeable surface at a density of at or about 2.0×10^6 APCs/cm^2 and in step (b) the second population of APCs is seeded on the first gas permeable surface at a density of at or about 4.0×10^6 APCs/cm^2.

[001733] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the APCs are peripheral blood mononuclear cells (PBMCs).

[001734] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the PBMCs are irradiated and exogenous to the donor of the first population of T cells.

[001735] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the T cells are tumor infiltrating lymphocytes (TILs).

[001736] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the T cells are marrow infiltrating lymphocytes (MILs).

[001737] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the T cells are peripheral blood lymphocytes (PBLs).

[001738] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained by separation from the whole blood of the donor.

[001739] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained by separation from the apheresis product of the donor.

[001740] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is separated from the whole blood or apheresis product of the donor by positive or negative selection of a T cell phenotype.

[001741] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the T cell phenotype is CD3+ and CD45+.

[001742] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that before performing the priming first expansion of the first population of T cells the T cells are separated from NK cells. In some embodiments, the T cells are separated from NK cells in the first population of T cells by removal of CD3- CD56+ cells from the first population of T cells. In some embodiments, the CD3- CD56+ cells are removed from the first population of T cells by subjecting the first population of T cells to cell sorting using a gating strategy that removes the CD3- CD56+ cell fraction and recovers the negative fraction. In some embodiments, the foregoing method is utilized for the expansion of T cells in a first population of T cells characterized by a high percentage of NK cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in a first population of T cells characterized by a high percentage of CD3- CD56+ cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue characterized by the present of a high number of NK cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue characterized by a high number of CD3- CD56+ cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue obtained from a patient suffering from a tumor characterized by the presence of a high number of NK cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue obtained from a patient suffering from a tumor characterized by the presence of a high number of CD3- CD56+ cells. In some embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue obtained from a patient suffering from ovarian cancer.

[001743] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that at or about $1x10^7$ T cells from the first population of T cells are seeded in a container to initiate the primary first expansion culture in such container.

[001744] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is distributed into a plurality of containers, and in each container at or about $1x10^7$ T cells from the first population of T cells are seeded to initiate the primary first expansion culture in such container.

[001745] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the second population of T cells harvested in step (c) is a therapeutic population of TILs.

[001746] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from one or more small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the donor.

[001747] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 20 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the donor.

[001748] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 10 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the donor.

[001749] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the donor.

[001750] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 small biopsies (including, for example, a punch biopsy), core biopsies, core needle biopsies or fine needle aspirates of tumor tissue from the donor.

[001751] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from one or more core biopsies of tumor tissue from the donor.

[001752] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 20 core biopsies of tumor tissue from the donor.

[001753] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 10 core biopsies of tumor tissue from the donor.

[001754] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 core biopsies of tumor tissue from the donor.

[001755] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 core biopsies of tumor tissue from the donor.

[001756] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from one or more fine needle aspirates of tumor tissue from the donor.

[001757] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 20 fine needle aspirates of tumor tissue from the donor.

[001758] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 10 fine needle aspirates of tumor tissue from the donor.

[001759] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 fine needle aspirates of tumor tissue from the donor.

[001760] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 fine needle aspirates of tumor tissue from the donor.

[001761] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from one or more small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001762] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 20 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001763] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 10 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001764] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001765] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001766] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from one or more core needle biopsies of tumor tissue from the donor.

[001767] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 20 core needle biopsies of tumor tissue from the donor.

[001768] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1 to 10 core needle biopsies of tumor tissue from the donor.

[001769] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 core needle biopsies of tumor tissue from the donor.

[001770] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that the first population of T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 core needle biopsies of tumor tissue from the donor.

[001771] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising: i) obtaining and/or

receiving a first population of TILs from a tumor sample obtained from one or more small biopsies, core biopsies, or needle biopsies of a tumor in a subject by culturing the tumor sample in a first cell culture medium comprising IL-2 for about 3 days; (ii) performing a priming first expansion by culturing the first population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 7 or 8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs; (iii) performing a rapid second expansion by supplementing the second cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (ii), wherein the rapid second expansion is performed for a second period of about 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area; (iv) harvesting the therapeutic population of TILs obtained from step (iii); and (v) transferring the harvested TIL population from step (iv) to an infusion bag.

[001772] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising: (i) obtaining and/or receiving a first population of TILs from a tumor sample obtained from one or more small biopsies, core biopsies, or needle biopsies of a tumor in a subject by culturing the tumor sample in a first cell culture medium comprising IL-2 for about 3 days; (ii) performing a priming first expansion by culturing the first population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed for first period of about 7 or 8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs; (iii) performing a rapid second expansion by contacting the second population of TILs with a third cell culture medium comprising IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the rapid second expansion is performed for a second period of about 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs; and (iv) harvesting the therapeutic population of TILs obtained from step (iii).

[001773] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that after day 5 of the second period the culture is split into 2 or more subcultures, and each subculture is supplemented with an additional quantity of the third culture medium and cultured for about 6 days.

[001774] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that after day 5 of the second period the culture is split into 2 or more subcultures, and each subculture is supplemented with a fourth culture medium comprising IL-2 and cultured for about 6 days.

[001775] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that after day 5 of the second period the culture is split into up to 5 subcultures.

[001776] In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that all steps in the method are completed in about 24 days. In some embodiments, the invention provides the method described in any of the preceding paragraphs as applicable above modified such that all steps in the method are completed in about 22 days.

[001777] In some embodiments, the invention provides a method of expanding T cells comprising: (i) performing a priming first expansion of a first population of T cells from a tumor sample obtained from one or more small biopsies, core biopsies, or needle biopsies of a tumor in a donor by culturing the first population of T cells to effect growth and to prime an activation of the first population of T cells; (ii) after the activation of the first population of T cells primed in step (a) begins to decay, performing a rapid second expansion of the first population of T cells by culturing the first population of T cells to effect growth and to boost the activation of the first population of T cells to obtain a second population of T cells; and (iv) harvesting the second population of T cells. In some embodiments, the tumor sample is obtained from a plurality of core biopsies. In some embodiments, the plurality of core biopsies is selected from the group consisting of 2, 3, 4, 5, 6, 7, 8, 9 and 10 core biopsies.

[001778] In some embodiments, the invention the method described in any of the preceding paragraphs as applicable above modified such that T cells or TILs are obtained from tumor digests. In some embodiments, tumor digests are generated by incubating the tumor in enzyme media, for example but not limited to RPMI 1640, 2mM GlutaMAX, 10 mg/mL gentamicin, 30 U/mL DNase, and 1.0 mg/mL collagenase, followed by mechanical dissociation (GentleMACS, Miltenyi Biotec, Auburn, CA). In some embodiments, the tumor is placed in a tumor dissociating enzyme mixture including one or more dissociating (digesting) enzymes such as, but not limited to, collagenase (including any blend or type of collagenase), Accutase™, Accumax™, hyaluronidase, neutral protease (dispase), chymotrypsin, chymopapain, trypsin, caseinase, elastase, papain, protease type XIV (pronase), deoxyribonuclease I (DNase), trypsin inhibitor, any other dissociating or proteolytic enzyme, and any combination thereof. In other embodiments, the tumor is placed in a tumor

dissociating enzyme mixture including collagenase (including any blend or type of collagenase), neutral protease (dispase) and deoxyribonuclease I (DNase).

VIII. Immunomodulatory Agent Associated Tumor Infiltrating Lymphocytes

[00676] Provided herein are modified tumor infiltrating lymphocytes (TIL) that include one or more immunomodulatory agents associated with the TIL cell surface. In some embodiments, the subject modified TILs exhibit enhanced in vivo survival, proliferation and/or anti-tumor effects in a patient recipient.

[00677] The immunomodulatory agent can be attached to the TIL disclosed herein (*e.g.* therapeutics TILs provided herein) using any suitable method. In some embodiments the one or more immunomodulatory agents are part of an immunomodulatory fusion protein that is attached to the TIL cell surface. In some embodiments, the one or more immunomodulatory agents are included as part of nanoparticles that are associated with the TIL cell surfaces. The immunomodulatory agents can be any immunomodulatory agent that promotes TIL survival proliferation, and/or anti-tumor effects in a patient recipient. In some embodiments, the immunomodulatory agent is a cytokine (*e.g.*, an interleukin). In exemplary embodiments, the TILs include IL-12, IL-15, and/or IL-21.

[00678] Any suitable TIL population can be modified to produce the subject compositions, including TILs produced using the manufacturing processes described herein. In some embodiments, the modified TILs are derived from TILs produced during any of the steps of the Process 2A method disclosure herein (see, *e.g.*, FIGs 2-6). In exemplary embodiments, the modified TILs are derived from TILs produced during any of the steps of the GEN 3 method disclosure herein (see, *e.g.*, FIG. 7). In some embodiments, the TILs are PD-1 positive TILs that are derived from the methods disclosed herein.

[00679] Aspects of the subject modified TILs are further detailed herein.

A. Immunomodulatory Fusion Proteins

[00680] In some embodiments, the modified TILs provided herein includes an immunomodulatory fusion protein that includes an immunomodulatory agent (*e.g.*, a cytokine) linked to a moiety that facilitates the tethering of the immunomodulatory agent to surface of the TILs. In some embodiments, the fusion protein includes a cell membrane anchor moiety (a transmembrane domain). In certain embodiments, the fusion protein includes a TIL surface antigen binding moiety that binds to a TIL surface antigen. Aspects of these fusion proteins are further discussed in detail below.

1. MEMBRANE ANCHORED IMMUNOMODULATORY FUSION PROTEINS

[00681] In some embodiments, the modified TILs provided herein include a membrane anchored immunomodulatory fusion protein. The membrane anchored immunomodulatory fusion protein includes one or more of the immunomodulatory agents (*e.g.*, a cytokine) linked to a cell membrane anchor moiety. In such embodiments, the membrane anchored immunomodulatory agent is tethered to the TIL surface membrane via the cell membrane anchor moiety, thus allowing the immunomodulatory agent to exert its effects in a targeted manner.

[00682] The immunomodulatory agent can be any suitable immunomodulatory agent including, for example, any of the immunomodulatory agents provided herein. In some embodiments, the immunomodulatory agent is an interleukin that promotes an anti-tumor response. In some embodiments, the immunomodulatory agent is a cytokine. In particular embodiments, the immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, IL-21, or a CD40 agonist (e.g., CD40L or agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. In certain embodiments, two or more different a membrane anchored immunomodulatory fusion proteins are expressed on a TIL surface. In exemplary embodiments, a TIL includes 2, 3, 4, 5, 6, 7, 8, 9 or 10 different membrane anchored immunomodulatory fusion proteins.

[00683] The immunomodulatory agent is linked to a cell membrane anchor moiety that allows the tethering of the immunomodulatory agent to the TIL cell surface. Suitable cell membrane anchor moieties include, for example, transmembrane domains of endogenous TIL cell surface proteins and fragments thereof. Exemplary transmembrane domains that can be used in the subject fusion proteins, include for example, B7-1, B7-2, and CD8a transmembrane domains and fragments thereof. In some embodiments, the cell membrane anchor moiety further includes a transmembrane and intracellular domain of an endogenous TIL cell surface protein or fragment thereof. In some embodiments, the cell membrane anchor moiety is a B7-1, B7-2 or CD8a transmembrane-intracellular domain or fragment thereof. In certain embodiments, the cell membrane anchor moiety is a CD8a transmembrane domain having the amino acid sequence of IYIWAPLAGTCGVLLLSLVIT (SEQ ID NO:238). In certain embodiments, the cell membrane anchor moiety is a B7-1 transmembrane-intracellular domain having the amino acid sequence of LLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:239). In certain embodiments, the cell membrane anchor moiety is a non-peptide cell membrane anchor moiety. In exemplary embodiments, the non-peptide cell membrane anchor moiety is a glycophosphatidylinositol (GPI) anchor. GPI anchors have a structure that includes a phosphoethanolamine linker, glycan core, and phospholipid tail. In some embodiments, the glycan core is modified with one or more side chains. In some embodiments, the glycan core is modified with one or more of the following side chains: a phosphoethanolamine group, mannose, galactose, sialic acid, or other sugars.

[00684] The membrane anchored immunomodulatory fusion protein include linkers that allow for the linkage of components of the membrane anchored immunomodulatory fusion protein (e.g. an immunomodulatory agent to a cell membrane anchor moiety). Suitable linkers include linkers that are at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 amino acid residues in length. In some embodiments, the linker is 5-10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 45-50, 50-60 amino acids in length. Suitable linkers include, but are not limited: a cleavable linker, a non-cleavable linker, a peptide linker, a flexible linker, a rigid linker, a helical linker, or a non-helical linker. In some embodiments, the linker is a peptide linker that optionally comprises Gly and Ser. In certain embodiments, the peptide linker utilize a glycine-serine polymer, including for example (GS)n (SEQ ID NO:240), (GSGGS)n (SEQ ID NO:241), (GGGS)n (SEQ ID NO:242), (GGGGS)n (SEQ ID NO:243), (GGGGGS)n (SEQ ID NO:244), and (GGGGGGS)n (SEQ ID NO:245), where n is an integer of at least one (and generally from 3 to 10). Additional linkers that can be used with the present compositions and methods are described in U.S. Patent Publication Nos. US 2006/0074008, US 20050238649, and US 2006/0024317, each of which is incorporated by reference herein in its entirety, and particularly in pertinent parts related to linkers. In some embodiments, the peptide linker is SGGGGSGGGGSGGGGSGGGGSGGGSLQ (SEQ ID NO:246).

[00685] In some embodiments, the linker is a cleavable linker. In exemplary embodiments, the cleavable linker allows for the release of the immunomodulatory agent into the tumor microenvironment. Cleavable linkers are also useful in embodiments, wherein two membrane anchored immunomodulatory fusion proteins are co-expressed in the same TIL (see, e.g., Figure 51 and Tables 58 and 59 below).

[00686] TABLE 58. Membrane anchored IL-15 and IL-21 fusion protein DNA sequences

Construct	DNA sequence
teIL-15	atggactggacttggatactctttctggtcgctgccgccacacgggtgcactctaattgggtcaacgtgatcagcgacctgaagaagatc gaggacctgatccagagcatgcacatcgacgccacactgtacaccgagtccgatgtgcaccctagctgcaaagtgaccgccatgaagt gctttctgctggaactgcaagtgatcagcctggaaagcggcgacgccagcatccacgataccgtggaaaatctgatcatcctggccaac aacagcctgtccagcaacggcaatgtgaccgagagcggctgcaaagagtgcgaggaactggaagaaaagaacatcaaagagtttct gcagagcttcgtccacatcgtgcagatgttcatcaacacctcatcaggtggcggtggaagcggaggtggcggtagtggcggcggagg ctcaggcggcggaggttccggcggaggatctcttcagctcctgccatcttgggctatcaccctgattagtgtgaatgggatctttgtcatct gttgtctcacgtactgtttcgctccccggtgcagagagagaagcgcaacgaaagactgcggagagaaagcgtcagacccgtg (SEQ ID NO:296)

te IL - 21	atggattggacctggattctgttcctggtggccgctgccacaagagtgcatagccagggccaagaccggcacatgatccggatgagac agctgatcgacatcgtggaccagctgaagaactacgtgaacgacctggtgcctgagttcctgcctgctcctgaggacgtggaaacaaat tgcgagtggtccgccttcagctgcttccagaaggcccagctgaaaagcgccaacaccggcaacaacgagcggatcatcaacgtgtcc atcaagaagctgaagcggaagcctcctagcaccaatgccggaagaaggcagaagcacagactgacctgtcctagctgcgacagcta cgagaagaagcctccaaaagagttcctggaacggttcaagagcctgctgcagaagatgatccaccagcacctgagcagcagaaccc acggctctgaagattctagcggaggcggaggaagtggtggcggaggttctggtggcggtggatcaggcggtggcggatctggcggc ggaggcagtggcggaggtggaagcggtggtggtggctctggcggaggcggtagcggcggaggcggatctcttcaattgctgcctag ctgggccatcacactgatctccgtgaacggcatcttcgtgatctgctgcctgacctactgcttcgcccctagatgcagagagcggagaag aaacgagcggctgagaagagaatctgtgcggcctgtt (SEQ ID NO:297)
te IL - 15 /I L 21	atggattggacctggattctgttcctggtggccgctgccacaagagtgcatagccagggccaagaccggcacatgatccggatgagac agctgatcgacatcgtggaccagctgaagaactacgtgaacgacctggtgcctgagttcctgcctgctcctgaggacgtggaaacaaat tgcgagtggtccgccttcagctgcttccagaaggcccagctgaaaagcgccaacaccggcaacaacgagcggatcatcaacgtgtcc atcaagaagctgaagcggaagcctcctagcaccaatgccggaagaaggcagaagcacagactgacctgtcctagctgcgacagcta cgagaagaagcctccaaaagagttcctggaacggttcaagagcctgctgcagaagatgatccaccagcacctgagcagcagaaccc acggctctgaagattctagcggaggcggaggaagtggtggcggaggttctggtggcggtggatcaggcggtggcggatctggcggc ggaggcagtggcggaggtggaagcggtggtggtggctctggcggaggcggtagcggcggaggcggatctcttcaattgctgcctag ctgggccatcacactgatctccgtgaacggcatcttcgtgatctgctgcctgacctactgcttcgcccctagatgcagagagcggagaag aaacgagcggctgagaagagaatctgtgcggcctgttagagccaagagatctggaagcggcgccaccaactttagcctgctgaaaca ggctggcgacgtggaagagaaccctggacctatggactggacttggatactctttctggtcgctgccgccacacgggtgcactctaatt gggtcaacgtgatcagcgacctgaagaagatcgaggacctgatccagagcatgcacatcgacgccacactgtacaccgagtccgatg tgcaccctagctgcaaagtgaccgccatgaagtgctttctgctggaactgcaagtgatcagcctggaaagcggcgacgccagcatcca cgataccgtggaaaatctgatcatcctggccaacaacagcctgtccagcaacggcaatgtgaccgagagcggctgcaaagagtgcga ggaactggaagaaaagaacatcaaagagtttctgcagagcttcgtccacatcgtgcagatgttcatcaacacctcatcaggtggcggtg gaagcggaggtggcggtagtggcggcggaggctcaggcggcggaggttccggcggaggatctcttcagctcctgccatcttgggct atcaccctgattagtgtgaatgggatctttgtcatctgttgtctcacgtactgtttcgctccccggtgcagagagagaaggcgcaacgaaa gactgcggagagaaagcgtcagacccgtg (SEQ ID NO:298)

[00687] Table 59. Membrane anchored IL-12, IL-15 and IL-21 DNA sequences (with NFAT Promoter)

Construct	DNA sequence
NFAT- Te-IL12 DNA seq	tcgaggtcgacggtatcgataagcttgatatcgaattaggaggaaaaactgtttcatacagaaggcgtcaattag gaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcc catcgaattaggaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggc gtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcccgggacattttgacacccccataatattt ttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactctctttaatcactactcacagtaacct caactcctggccaccATGGATTGGACCTGGATTCTGTTCCTCGTGGCCGCCG CTACCCGCGTGCACTCCATCTGGGAGCTGAAGAAAGACGTGTACGT GGTGGAATTGGATTGGTACCCCGACGCCCCAGGCGAGATGGTGGTT CTGACTTGCGACACGCCGGAGGAGGACGGCATCACCTGGACGCTG GACCAGAGCAGCGAAGTGCTGGGCTCTGGTAAGACCTTAACCATCC AGGTCAAGGAGTTCGGTGATGCAGGACAGTACACGTGTCACAAGG GCGGGGAGGTCTTGTCCCATAGCCTGCTGCTCCTGCACAAGAAGGA AGACGGCATCTGGTCTACGGATATCCTTAAAGACCAGAAGGAGCC CAAGAACAAAACCTTCCTGCGATGCGAGGCTAAGAATTACTCCGG GCGCTTTACCTGTTGGTGGCTCACAACCATCTCGACCGACCTGACC TTCTCCGTGAAGTCTTCCAGGGGATCTTCTGATCCGCAAGGCGTTA CCTGCGGGGCCGCTACCCTGTCGGCTGAGCGCGTCCGTGGTGACAA

	CAAGGAGTACGAGTACTCGGTGGAATGCCAGGAGGACAGCGCCTG CCCAGCGGCCGAAGAGTCCTTGCCCATCGAGGTGATGGTGGACGCT GTACACAAGCTCAAGTACGAGAACTACACCTCCTCCTTCTTTATAC GCGACATCATCAAGCCTGACCCCCCTAAAAACCTGCAGCTGAAGCC CCTTAAAAACTCTCGACAGGTCGAGGTATCCTGGGAGTACCCCGAC ACCTGGTCTACTCCTCATTCGTATTTCAGCCTGACCTTCTGCGTGCA GGTGCAGGGCAAGTCCAAGCGCGAGAAGAAGGACCGCGTGTTCAC CGACAAAACCAGCGCGACTGTCATTTGTCGGAAGAACGCGAGCAT CTCCGTACGGGCACAGGATCGCTATTACTCCAGCAGTTGGTCAGAG TGGGCTTCGGTTCCGTGTTCTGGAGGAGGTGGCGGCGGCTCACGCA ACCTGCCCGTGGCGACGCCGGACCCGGGTATGTTTCCTTGTCTGCA CCACTCTCAGAACTTGCTCCGTGCCGTCTCGAATATGCTGCAGAAG GCCCGCCAGACTCTGGAGTTCTATCCATGCACTAGTGAGGAGATCG ATCATGAGGACATCACCAAGGACAAGACATCCACCGTGGAGGCTT GTCTGCCGCTGGAGTTGACAAAGAACGAGAGCTGCCTCAATAGCC GCGAGACTTCCTTCATCACCAACGGCTCCTGCCTCGCGAGCCGTAA GACCTCCTTTATGATGGCGCTGTGCCTGTCAAGTATCTACGAAGAT CTGAAAATGTATCAGGTGGAGTTCAAAACTATGAACGCAAAACTCC TGATGGATCCCAAGCGCCAAATTTTCTTGGACCAGAACATGCTTGC CGTGATCGACGAGCTGATGCAGGCCCTGAACTTCAACTCCGAGACC GTCCCTCAGAAGTCGTCTCTGGAGGAACCCGACTTTTACAAGACAA AGATCAAGCTGTGCATCCTGCTACACGCGTTCCGCATTCGGGCCGT GACCATTGACCGCGTGATGTCCTACCTGAATGCCTCGTCCGGCGGG GGGGGCTCCGGTGGGGGCGGCTCTGGCGGAGGCGGCTCAGGTGGC GGCGGCTCCGGCGGAGGTTCGCTTCAGCTTCTGCCCAGTTGGGCAA TCACTCTGATTTCCGTCAACGGAATCTTCGTCATCTGCTGCCTGACC TACTGCTTTGCTCCCAGATGTAGAGAGCGCCGCCGCAACGAGCGCC TGCGTCGTGAGAGCGTGAGGCCTGTGTGA (SEQ ID NO:299)
NFAT-Te-IL15 DNA seq	tcgaggtcgacggtatcgataagcttgatatcgaattaggaggaaaaactgtttcatacagaaggcgtcaattag gaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcc catcgaattaggaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggc gtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcccgggacattttgacacccccataatattt ttccagaattaacagtataaattgcatcttgttcaagagttccctatcactctctttaatcactactcacagtaacct caactcctggccaccATGGACTGGACTTGGATACTCTTTCTGGTCGCTGCCG CCACACGGGTGCACTCTAATTGGGTCAACGTGATCAGCGACCTGAA GAAGATCGAGGACCTGATCCAGAGCATGCACATCGACGCCACACT GTACACCGAGTCCGATGTGCACCCTAGCTGCAAAGTGACCGCCATG AAGTGCTTTCTGCTGGAACTGCAAGTGATCAGCCTGGAAAGCGGCG ACGCCAGCATCCACGATACCGTGGAAAATCTGATCATCCTGGCCAA CAACAGCCTGTCCAGCAACGGCAATGTGACCGAGAGCGGCTGCAA AGAGTGCGAGGAACTGGAAGAAAAGAACATCAAAGAGTTTCTGCA GAGCTTCGTCCACATCGTGCAGATGTTCATCAACACCTCATCAGGT GGCGGTGGAAGCGGAGGTGGCGGTAGTGGCGGCGGAGGCTCAGGC GGCGGAGGTTCCGGCGGAGGATCTCTTCAGCTCCTGCCATCTTGGG CTATCACCCTGATTAGTGTGAATGGGATCTTTGTCATCTGTTGTCTC ACGTACTGTTTCGCTCCCCGGTGCAGAGAGAGAAGGCGCAACGAA AGACTGCGGAGAGAAAGCGTCAGACCCGTGTGA (SEQ ID NO:300)

NFAT-TeIL21 DNA seq	tcgaggtcgacggtatcgataagcttgatatcgaattaggaggaaaaactgtttcatacagaaggcgtcaattag gaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcc catcgaattaggaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggc gtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcccgggacattttgacacccccataatattt ttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactctctttaatcactactcacagtaacct caactcctggccaccATGGATTGGACCTGGATTCTGTTCCTGGTGGCCGCTG CCACAAGAGTGCATAGCCAGGGCCAAGACCGGCACATGATCCGGA TGAGACAGCTGATCGACATCGTGGACCAGCTGAAGAACTACGTGA ACGACCTGGTGCCTGAGTTCCTGCCTGCTCCTGAGGACGTGGAAAC AAATTGCGAGTGGTCCGCCTTCAGCTGCTTCCAGAAGGCCCAGCTG AAAAGCGCCAACACCGGCAACAACGAGCGGATCATCAACGTGTCC ATCAAGAAGCTGAAGCGGAAGCCTCCTAGCACCAATGCCGGAAGA AGGCAGAAGCACAGACTGACCTGTCCTAGCTGCGACAGCTACGAG AAGAAGCCTCCAAAAGAGTTCCTGGAACGGTTCAAGAGCCTGCTG CAGAAGATGATCCACCAGCACCTGAGCAGCAGAACCCACGGCTCT GAAGATTCTAGCGGAGGCGGAGGAAGTGGTGGCGGAGGTTCTGGT GGCGGTGGATCAGGCGGTGGCGGATCTGGCGGCGGAGGCAGTGGC GGAGGTGGAAGCGGTGGTGGTGGCTCTGGCGGAGGCGGTAGCGGC GGAGGCGGATCTCTTCAATTGCTGCCTAGCTGGGCCATCACACTGA TCTCCGTGAACGGCATCTTCGTGATCTGCTGCCTGACCTACTGCTTC GCCCCTAGATGCAGAGAGCGGAGAAGAAACGAGCGGCTGAGAAG AGAATCTGTGCGGCCTGTTTAA (SEQ ID NO:301)
NFAT-TeIL15-IL21 DNA seq	tcgaggtcgacggtatcgataagcttgatatcgaattaggaggaaaaactgtttcatacagaaggcgtcaattag gaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcc catcgaattaggaggaaaaactgtttcatacagaaggcgtcaattaggaggaaaaactgtttcatacagaaggc gtcaattaggaggaaaaactgtttcatacagaaggcgtcaattggtcccgggacattttgacacccccataatattt ttccagaattaacagtataaattgcatctcttgttcaagagttccctatcactctctttaatcactactcacagtaacct caactcctggccaccATGGATTGGACCTGGATTCTGTTCCTGGTGGCCGCTG CCACAAGAGTGCATAGCCAGGGCCAAGACCGGCACATGATCCGGA TGAGACAGCTGATCGACATCGTGGACCAGCTGAAGAACTACGTGA ACGACCTGGTGCCTGAGTTCCTGCCTGCTCCTGAGGACGTGGAAAC AAATTGCGAGTGGTCCGCCTTCAGCTGCTTCCAGAAGGCCCAGCTG AAAAGCGCCAACACCGGCAACAACGAGCGGATCATCAACGTGTCC ATCAAGAAGCTGAAGCGGAAGCCTCCTAGCACCAATGCCGGAAGA AGGCAGAAGCACAGACTGACCTGTCCTAGCTGCGACAGCTACGAG AAGAAGCCTCCAAAAGAGTTCCTGGAACGGTTCAAGAGCCTGCTG CAGAAGATGATCCACCAGCACCTGAGCAGCAGAACCCACGGCTCT GAAGATTCTAGCGGAGGCGGAGGAAGTGGTGGCGGAGGTTCTGGT GGCGGTGGATCAGGCGGTGGCGGATCTGGCGGCGGAGGCAGTGGC GGAGGTGGAAGCGGTGGTGGTGGCTCTGGCGGAGGCGGTAGCGGC GGAGGCGGATCTCTTCAATTGCTGCCTAGCTGGGCCATCACACTGA TCTCCGTGAACGGCATCTTCGTGATCTGCTGCCTGACCTACTGCTTC GCCCCTAGATGCAGAGAGCGGAGAAGAAACGAGCGGCTGAGAAG AGAATCTGTGCGGCCTGTTAGAGCCAAGAGATCTGGAAGCGGCGC CACCAACTTTAGCCTGCTGAAACAGGCTGGCGACGTGGAAGAGAA CCCTGGACCTATGGACTGGACTTGGATACTCTTTCTGGTCGCTGCCG CCACACGGGTGCACTCTAATTGGGTCAACGTGATCAGCGACCTGAA GAAGATCGAGGACCTGATCCAGAGCATGCACATCGACGCCACACT GTACACCGAGTCCGATGTGCACCCTAGCTGCAAAGTGACCGCCATG

	AAGTGCTTTCTGCTGGAACTGCAAGTGATCAGCCTGGAAAGCGGCG ACGCCAGCATCCACGATACCGTGGAAAATCTGATCATCCTGGCCAA CAACAGCCTGTCCAGCAACGGCAATGTGACCGAGAGCGGCTGCAA AGAGTGCGAGGAACTGGAAGAAAAGAACATCAAAGAGTTTCTGCA GAGCTTCGTCCACATCGTGCAGATGTTCATCAACACCTCATCAGGT GGCGGTGGAAGCGGAGGTGGCGGTAGTGGCGGCGGAGGCTCAGGC GGCGGAGGTTCCGGCGGAGGATCTCTTCAGCTCCTGCCATCTTGGG CTATCACCCTGATTAGTGTGAATGGGATCTTTGTCATCTGTTGTCTC ACGTACTGTTTCGCTCCCCGGTGCAGAGAGAGAAGGCGCAACGAA AGACTGCGGAGAGAAAGCGTCAGACCCGTGTAA (SEQ ID NO:302)

[00688] In exemplary embodiments, the linker is a self-cleaving 2A peptide. See, *e.g.*, Liu et al., Sci. Rep. 7(1):2193 (2017), which is incorporated by reference in relevant parts relating to 2A peptides. 2A peptides are viral oligopeptides that mediate cleavage of polypeptides during translation in eukaryotic cells. In some embodiments, the 2A peptide includes a C-terminus having the amino acid sequence GDVEXiNPGP (SEQ ID NO:247), wherein Xi is any naturally occurring amino acid residue. In certain embodiments, the 2A peptide is a porcine teschovirus-1 2A peptide (GSGATNFSLLKQAGDVEENPGP, SEQ ID NO:248). In some embodiments, the 2A peptide is an equine rhinitis A virus 2A peptide (GSGQCTNYALLKLAGDVESNPGP, SEQ ID NO:249). In certain embodiments, the 2A peptide is a foot-and-mouth disease virus 2A peptide: (GSGEGRGSLLTCGDVEENPGP, SEQ ID NO:250). In some embodiments, the cleavable linker includes a furin-cleavable sequence. Exemplary furin-cleavable sequences are described for example, Duckert et al., Protein Engineering, Design & Selection 17(1):107-112 (2004), and US Patent No. 8,871,906, each of which is incorporated herein by reference, particularly in relevant parts relating to furin-cleavable sequences. In some embodiments, the linker includes a 2A peptide and a furin-cleavable sequence. In exemplary embodiments, the furin-cleavable 2A peptide includes the amino acid sequence RAKRSGSGATNFSLLKQAGDVEENPGP (SEQ ID NO:251).

[00689] In some embodiments, the immunomodulatory agents are attached in the membrane anchored immunomodulatory fusion protein by a degradable linker (*e.g.*, a disulfide linker) such that under physiological conditions, the linker degrades, thereby releasing the immunomodulatory agent. In some embodiments, the immunomodulatory agents are reversibly linked to functional groups through a degradable linker such that under physiological conditions, the linker degrades and releases the immunomodulatory agent. Suitable degradable linkers include, but are not limited to: a protease sensitive linker that is sensitive to one or more enzymes present in biological media such as proteases

in a tumor microenvironment such a matrix metalloproteases present in a tumor microenvironment or in inflamed tissue (*e.g.* matrix metalloproteinase 2 (MMP2) or matrix metalloproteinase 9 (MMP9)).

[00690] In other embodiments, the components of the membrane anchored immunomodulatory fusion protein are linked by an enzyme-sensitive linker. Exemplary cleavable linker include those that are recognized by one of the following enzymes: metalloprotease MMP-1, MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, plasmin, PSA, PSMA, CATHEPSIN D, CATHEPSIN K, CATHEPSIN S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. See, *e.g.*, US Patent Nos. 8,541,203 and 8,580,244, each of which is incorporated by reference in its entirety and in pertinent parts related to cleavable linkers.

[00691] In certain embodiments, the membrane anchored immunomodulatory fusion protein includes a signal peptide that facilitates the translocation of the fusion protein to the TIL cell membrane. Any suitable signal peptide that facilities the localization of the fusion protein to the TIL cell membrane can be used. In some embodiments, the signal peptide does not interfere with the bioactivity of the immunomodulatory agent. Exemplary signal peptide sequences include, but are not limited to: human granulocyte-macrophage colony-stimulating factor (GM-CSF) receptor signal sequence, human prolactin signal sequence, and human IgE signal sequence. In certain embodiments, the fusion protein includes a human IgE signal sequence. In exemplary embodiments, the human IgE signal sequence has the amino acid sequence MDWTWILFLVAAATRVHS (SEQ ID NO:252). In some embodiments, the human IgE signal sequence includes the amino acid sequence NIKGSPWKGSLLLLLVSNLLLCQSVAP (SEQ ID NO:253). In some embodiments, the signal peptide sequence is an IL-2 signal sequence having the amino acid sequence MYRMQLLSCIALSLALVTNS (SEQ ID NO:254).

[00692] In some embodiments, the membrane anchored immunomodulatory fusion protein is according to the formula, from N- to C-terminus:

[00693] S-IA-L-C,

[00694] wherein S is a signal peptide, IA is an immunomodulatory agent, L is a linker and C is a cell membrane anchor moiety.

[00695] In some embodiments, the signal peptide S is any one of SEQ ID NOs:252-254. In some emboidments, the cell membrane anchor moiety is SEQ ID NO:277. In exemplary embodiments, the immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, IL-21, or a CD40 agonist (e.g., CD40L or an anti-CD40 scFv as described herein). In some embodimnets, C is a B7-1 trnasmembrane-intracellular domain (e.g., SEQ ID NO:239). Exemplary membrane anchored immunomodulatory fusion proteins according to the above formula are depicted in Figures 51 and 52.

[00696] In some embodiments, the TIL includes two or more different membrane anchored immunomodulatory fusion proteins according to the formula, from N- to C-terminus: S-IA-L-C, wherein each of the different membrane anchored immunomodulatory fusion proteins includes a different immunomodulatory agent. In some embodiments, the two or more different immunomodulatory agents are selected from the group consisting of: IL-12 and IL-15, IL-15 and IL-18, CD40L and IL-15, IL-15 and IL-21, and IL-2 and IL-12.

[00697] In some embodiments that includes two membrane anchored immunomodulatory fusion proteins, the membrane anchored immunomodulatory fusion proteins are arranged according to the formula, from N- to C-terminus:

[00698] S1-IA1-L1-C1-L2-S2-IA2-L3-C2,

[00699] wherein S1 and S2 are each a signal peptide, IA1 and IA2 are each an immunomodulatory agent, L1-L3 are each a linker, and C1 and C2 are each a cell membrane anchor moiety. In some embodiments, IA1 and IA2 are the same immunomodulatory agent. In certain embodiments, IA1 and IA2 are different immunomodulatory agents. Suitable immunomodulatory agents including any of those described herein. In some embodiments, IA1 and IA2 are independently selected from IL-2, IL-12, IL-15, IL-18, IL-21, a CD40 agonist (e.g., CD40L or an agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. In some embodiments, IA1 and IA2 are selected from the group consisting of: IL-12 and IL-15, IL-15 and IL-18, CD40L and IL-15, IL-15 and IL-21, and IL-2 and IL-12. In some embodiments, one or more of L1-L3 is a cleavable linker. In some embodiments two or more of L1-L3 are different linkers. In exemplary embodiments L2 is a cleavable linker. In some embodiments, L2 is furin cleavable P2A linker (e.g., SEQ ID NO:251). In some embodiments, C1 and C2 are independently transmembrane domains and/or transmembrane-intracellular domains. In certain embodiments C1 and C2 are the same. In exemplary embodiments, C1 and C2 are each a B7-1 transmembrane-intracellular domain (e.g., SEQ ID NO:239). In exemplary embodiments, C1 and C2 are different. Exemplary constructs that include two membrane anchored immunomodulatory fusion proteins according to the above formula are depicted in Figure 51, and Tables 58 and 59.

[00700] Modified TILs that include cell membrane anchored immunomodulatory fusion proteins associated with their surfaces can be made by genetically modifying a populations of TILs to include a nucleic acid encoding the fusion protein. Any suitable genetic modification method can be used to produce such modified TILs including, for example, CRISPR, TALE, and zinc finger method described herein.

[00701] Any suitable population of TILs can be genetically modified to make the subject modified TIL compositions. In some embodiments, a population TILs produced during any of the

steps of the Process 2A method disclosure herein (see, *e.g.*, FIGs 2-6) is genetically modified to produce the subject modified TILs. In exemplary embodiments, a population TILs produced during any of the steps of the GEN 3 method disclosure herein (see, *e.g.*, FIG. 7) is genetically modified to produce the subject modified TILs. In exemplary embodiments, TILs produced from the second step in the Process 2A method and/or the rapid expansion step in the GEN 3 method provided herein are genetically modified to produce the subject modified TILs. In some embodiments, PD-1 positive TILs that have been preselected using the methods described herein are genetically modified to produce the subject modified TILs.

[00702] Any suitable population of TILs can be transiently modified to make the subject transiently modified TIL compositions. In some embodiments, a population of TILs produced during any of the steps of the Process 2A method disclosure herein (see, *e.g.*, FIGS. 2-6) is transfected with nucleic acid encoding a cell membrane anchored immunomodulatory fusion protein to transiently express the cell membrane anchored immunomodulatory fusion protein in the subject transiently modified TILs. In exemplary embodiments, a population of TILs produced during any of the steps of the GEN 3 method disclosure herein (see, *e.g.*, FIG. 7) is transfected with nucleic acid encoding a cell membrane anchored immunomodulatory fusion protein to transiently express the cell membrane anchored immunomodulatory fusion protein in the subject transiently modified TILs. In exemplary embodiments, TILs produced from the first expansion step in the Process 2A method and/or the priming expansion step in the GEN 3 method provided herein are transfected with nucleic acid encoding a cell membrane anchored immunomodulatory fusion protein to transiently express the cell membrane anchored immunomodulatory fusion protein in the subject transiently modified TILs. In exemplary embodiments, TILs produced from the second expansion step in the Process 2A method and/or the rapid expansion step in the GEN 3 method provided herein are transfected with nucleic acid encoding a cell membrane anchored immunomodulatory fusion protein to transiently express the cell membrane anchored immunomodulatory fusion protein in the subject transiently modified TILs. In some embodiments, PD-1 positive TILs that have been preselected using the methods described herein are transfected with nucleic acid encoding a cell membrane anchored immunomodulatory fusion protein to transiently express the cell membrane anchored immunomodulatory fusion protein in the subject transiently modified TILs.

[00703] Also provided herein are nucleic acids encoding the membrane anchored immunomodulatory fusion proteins, expression vectors that include such nucleic acids, and host cells that include the nucleic acids or expression vectors. Any suitable promoter can be used for the expression of the membrane anchored immunomodulatory fusion protein. In exemplary embodiments, the promoter is an inducible promoter. Exemplary nucleic acids that encode for

exemplary membrane anchored immunomodulatory fusion proteins and components of such fusion proteins are depicted in Figures 51 and 52, and Tables 58 and 59.

[00704] In some embodiments, the nucleic acids encoding the membrane anchored immunomodulatory fusion protein is mRNA. In exemplary embodiments, the mRNA includes one or more modifications that improves intracellular stability and/or translation efficiency of the mRNA. In some embodiments, the mRNA includes a 5' cap or cap analog that improves mRNA half-life. Exemplary cap structures, include, but are not limited to ARCA, mCAP, m^7GpppN (cap 0), m^7GpppNm (cap 1), and m^7GpppNmpNm (cap 2) caps. In some embodiments, the 5' cap is according ot the formula: $^{m7}Gppp[N_{2'Ome}]_n[N]_m$ wherein ^{m7}G is N7-methylated guanosine or any guanosine analog, N is any natural, modified or unnatural nucleoside, "n" can be any integer from 0 to 4 and "m" can be an integer from 1 to 9. Exemplary 5' caps are disclosed in US Patent No. 10,703,789 and WO2017053297, which are incorporated by reference in their entirety, and specifically for disclosures relating to 5' caps and cap analogs.

[00705] In some embodiments, the nucleic acids encoding the membrane anchored immunomodulatory fusion protein is mRNA further includes a 3' untranslated region (UTR) or modified UTR. 3′ UTRs are known to have stretches of adenosines and uridines. These AU rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU rich elements (AREs) can be separated into three classes (Chen et al, 1995): Class I AREs contain several dispersed copies of an AUUUA motif within U-rich regions. C-Myc and MyoD contain class I AREs. Class II AREs possess two or more overlapping UUAUUUA(U/A)(U/A) nonamers. Molecules containing this type of AREs include GM-CSF and TNF-a. Class III ARES are less well defined. These U rich regions do not contain an AUUUA motif. c-Jun and Myogenin are two well-studied examples of this class. Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3′ UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message in vivo.

[00706] Introduction, removal or modification of 3′ UTR AU rich elements (AREs) can be used to modulate the stability of the nucleic acids described herein . When engineering specific nucleic acids, one or more copies of an ARE can be introduced to make polynucleotides of the invention less stable and thereby curtail translation and decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein. Transfection experiments can be conducted in relevant cell lines, using nucleic acids, and protein production can be assayed at various time points post-transfection. For example, cells can be transfected with different ARE-engineering

molecules and by using an ELISA kit to the relevant protein and assaying protein produced at 6 hour, 12 hour, 24 hour, 48 hour, and 7 days post-transfection.

[00707] In some embodiments, the nucleic acid encoding the membrane anchored immunomodulatory fusion proteins is operably linked to a nuclear factor of activated T-cells (NFAT) promoter or a functional portion or functional variant thereof. "NFAT promoter" as used herein means one or more NFAT responsive elements linked to a minimal promoter of any gene expressed by T-cells. Preferably, the minimal promoter of a gene expressed by T-cells is a minimal human IL-2 promoter. The NFAT responsive elements may comprise, e.g., NFATl, NFAT2, NFAT3, and/or NFAT4 responsive elements. The NFAT promoter (or functional portion or functional variant thereof) may comprise any number of binding motifs, e.g., at least two, at least three, at least four, at least five, or at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or up to twelve binding motifs.

TABLE 4 – NFAT Promoter Related Sequences.

Description	Amino Acid Sequence
6X NFAT IL-2 minimal promoter	TCGAGGTCGACGGTATCGATAAGCTTGA TATCGAATTAGGAGGAAAAACTGTTTCA TACAGAAGGCGTCAATTAGGAGGAAAA ACTGTTTCATACAGAAGGCGTCAATTAG GAGGAAAAACTGTTTCATACAGAAGGCG TCAATTGGTCCCATCGAATTAGGAGGAA AAACTGTTTCATACAGAAGGCGTCAATT AGGAGGAAAAACTGTTTCATACAGAAG GCGTCAATTAGGAGGAAAAACTGTTTCA TACAGAAGGCGTCAATTGGTCCCGGGAC ATTTTGACACCCCCATAATATTTTTCCAG AATTAACAGTATAAATTGCATCTCTTGTT CAAGAGTTCCCTATCACTCTCTTTAATCA CTACTCACAGTAACCTCAACTCCTGGCC ACC (SEQ ID NO: 255)
NFAT responsive element	GGAGGAAAAACTGTTTCATACAGAAGGC GT (SEQ ID NO: 256)
Human IL-2 Promoter	CATTTTGACACCCCCATAATATTTTTCCA GAATTAACAGTATAAATTGCATCTCTTG TTCAAGAGTTCCCTATCACTCTCTTTAAT CACTACTCACAGTAACCTCAACTCCTG (SEQ ID NO:257)

[00708] In a preferred embodiment, the NFAT promoter comprises six NFAT binding motifs. See, e.g., US Patent No. 8,556,882, which is incorporated by reference in its entirety and particularly for pertinent parts relating to NFAT promoters. In some embodiments, the NFAT promoter system controls expression of an immunomodulatory fusion protein that includes any of the immunomodulatory agents described herein. In certain embodiments, the immunomodulatory agent is selected from: IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., CD40L or agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. Exemplary nucleic acids encoding exemplary subject membrane anchored immunomodulatory fusion proteins operably linked to a NFAT promoter are depicted in Table 59. In some embodiments, the NFAT promoter system controls expression of an immunomodulatory fusion protein that includes IL-15. In some embodiments, the NFAT promoter system controls expression of an immunomodulatory fusion protein that includes IL-21. In some embodiments, the NFAT promoter system controls expression of an immunomodulatory fusion protein that includes IL-15 and IL-21.

[00709] In some embodiments, the invention provides TILs genetically modified to comprise DNA encoding an immunomodulatory fusion protein operably linked to the NFAT promoter. In some embodiments, the NFAT promoter controls expression of DNA encoding an immunomodulatory fusion protein that includes any of the immunomodulatory agents described herein. In certain embodiments, the immunomodulatory agent is selected from: IL-2, IL-12, IL-15, IL-18, IL-21, and a CD40 agonist (e.g., CD40L or agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. In some embodiments, the NFAT promoter controls expression of DNA encoding an immunomodulatory fusion protein that includes IL-15. In some embodiments, the NFAT promoter controls expression of DNA encoding an immunomodulatory fusion protein that includes IL-21. In some embodiments, the NFAT promoter controls expression of DNA encoding an immunomodulatory fusion protein that includes IL-15 and IL-21.

[00710] In some embodiments, the invention provides TILs genetically modified to comprise DNA encoding an immunomodulatory fusion protein operably linked to the NFAT promoter, wherein the immunomodulatory fusion protein is arranged according to the formula, from N- to C-terminus:

[00711] S1-IA1-L1-C1-L2-S2-IA2-L3-C2,

[00712] wherein S1 and S2 are each a signal peptide, IA1 and IA2 are each an immunomodulatory agent, L1-L3 are each a linker, and C1 and C2 are each a cell membrane anchor moiety. In some embodiments, IA1 and IA2 are the same immunomodulatory agent. In certain embodiments, IA1 and IA2 are different immunomodulatory agents. Suitable immunomodulatory agents including any of those described herein. In some embodiments, IA1 and IA2 are

independently selected from IL-2, IL-12, IL-15, IL-18, IL-21, a CD40 agonist (e.g., CD40L or an agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. In some embodiments, IA1 and IA2 are selected from the group consisting of: IL-12 and IL-15, IL-15 and IL-18, CD40L and IL-15, IL-15 and IL-21, and IL-2 and IL-12. In some embodiments, IA1 and IA2 are independently selected from IL-15 and IL-21. In some embodiments, IA1 is IL-15 and IA2 is IL-21. In some embodiments, IA1 is IL-21 and IA2 is IL-15. In some embodiments, one or more of L1-L3 is a cleavable linker. In some embodiments two or more of L1-L3 are different linkers. In exemplary embodiments L2 is a cleavable linker. In some embodiments, L2 is furin cleavable P2A linker (e.g., SEQ ID NO:251). In some embodiments, C1 and C2 are independently transmembrane domains and/or transmembrane-intracellular domains. In certain embodiments C1 and C2 are the same. In exemplary embodiments, C1 and C2 are each a B7-1 transmembrane-intracellular domain (e.g., SEQ ID NO:239). In exemplary embodiments, C1 and C2 are different. Exemplary constructs that include two membrane anchored immunomodulatory fusion proteins according to the above formula are depicted in Figure 51.

[00713] Nucleic acids encoding the subject membrane anchored immunomodulatory fusion proteins may be introduced into a population of TILs to produce transiently modified or genetically modified TILs that express the membrane anchored immunomodulatory fusion proteins using any suitable method. In some embodiments, nucleic acids encoding the membrane anchored immunomodulatory fusion proteins are introduced into a population of TILs using a microfluidic platform. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. See, e.g., International Patent Application Publication Nos. WO 2013/059343A1, WO 2017/008063A1, or WO 2017/123663A1, or U.S. Patent Application Publication Nos. US 2014/0287509A1, US 2018/0201889A1, or US 2018/0245089A1, all of which are incorporated by reference herein in their entireties, and particularly for disclosures of microfluidic platforms for nucleic acid delivery. In the SQZ platform, the cell membranes of the cells for modification (e.g., TILs) are temporarily disrupted by microfluidic constriction, thereby allowing the delivery of nucleic acids encoding the membrane anchored immunomodulatory fusion proteins into the cells.

[00714] In some embodiments, the nucleic acid encoding the membrane anchored immunomodulatory fusion protein is mRNA and the microfluidic platform (e.g., SQZ vector-free microfluidic platform) is used to deliver the mRNA into TILs to produce transiently modified TILs. In some embodiments, the nucleic acid encoding the membrane anchored immunomodulatory fusion protein is DNA and the microfluidic platform (e.g., SQZ vector-free microfluidic platform) is used to deliver the DNA into TILs to produce stable genetically-modified TILs. The microfluidic platform (e.g., SQZ vector-free microfluidic platform) may be used to deliver the nucleic acid to any population of TILs produced during any steps of the Process 2A method disclosure herein (see, *e.g.*,

FIGS. 2-6) or GEN 3 method disclosure herein (see, *e.g.*, FIG. 7) to produce the modified TILs. In some embodiments, the membrane anchored immunomodulatory fusion protein includes an IL-2, an IL-12, an IL-15, an IL-18, an IL-21, a CD40 agonist (e.g., CD40L or agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or any combination thereof.

[00715] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-15. In some embodiments, the second immunomodulatory agent is IL-2, IL-12, IL-18, IL-21, CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00716] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is CD40L. In some embodiments, the second immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, IL-21, a CD40 agonist (e.g., CD40L or an agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof.

[00717] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-12. In some embodiments, the second immunomodulatory agent is IL-2, IL-15, IL-18, IL-21, CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00718] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-18. In some embodiments, the second immunomodulatory agent is IL-2, IL-12, IL-15, IL-21, CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00719] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-21. In some embodiments, the second immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00720] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first

immunomodulatory agents is IL-2. In some embodiments, the second immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, IL-21, CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00721] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-2 and the second immunomodulatory agent is IL-12.

[00722] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-2 and the second immunomodulatory agent is IL-15.

[00723] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-2 and the second immunomodulatory agent is IL-18.

[00724] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-2 and the second immunomodulatory agent is IL-21.

[00725] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-2 and the second immunomodulatory agent is CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00726] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-12 and the second immunomodulatory agent is IL-15.

[00727] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-12 and the second immunomodulatory agent is IL-18.

[00728] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different

immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-12 and the second immunomodulatory agent is IL-21.

[00729] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-12 and the second immunomodulatory agent is CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00730] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-15 and the second immunomodulatory agent is IL-18.

[00731] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-15 and the second immunomodulatory agent is IL-21.

[00732] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-15 and the second immunomodulatory agent is CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00733] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-18 and the second immunomodulatory agent is IL-21.

[00734] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-18 and the second immunomodulatory agent is CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00735] In exemplary embodiments, the modified TILs provided herein include two membrane anchored immunomodulatory fusion proteins that each include a different immunomodulatory agent (i.e., a first and second immunomodulatory agent), wherein the first immunomodulatory agents is IL-21 and the second immunomodulatory agent is CD40L or an anti-CD40 binding domain (e.g., an anti-CD40 scFv).

[00736] Additional membrane anchored immunomodulatory fusion proteins that can be included in the modified TILs provided herein are described in WO 2019/157130 A1, which is incorporated by reference in its entirety, particularly in relevant parts related to membrane anchored immunomodulatory fusion proteins.

[00737] Exemplary membrane anchored immunomodulatory fusion proteins to be included in the modified TILs provided herein are depicted in Figures 51 and 52, and Tables 58 and 59.

[00738] In some embodiments, the nucleic acid encoding any of the membrane anchored immunomodulatory fusion proteins described above is operably linked to an NFAT promoter or a functional portion or functional variant thereof.

2. IMMUNOMODULATORY AGENT-TIL ANTIGEN BINDING DOMAIN FUSION PROTEINS

[00739] In some embodiments, the modified TILs provided herein include immunomodulatory fusion proteins, wherein such fusion proteins include one or more immunomodulatory agents linked to a TIL antigen binding domain (ABD). In some embodiments, the one or more immunomodulatory agents is tethered to the TIL surface membrane upon TIL ABD binding to a TIL surface antigen.

[00740] The TIL antigen binding domain includes an antibody variable heavy domain (VH) and variable light domain (VL). In some embodiments, the TIL antigen binding domain is a full length antibody that includes a heavy chain according to the formula: VH-CH1-hinge-CH2-CH3 and a light chain according to the formula: VL-CL, wherein VH is a variable heavy domain; CH1, CH2, CH3 are heavy chain constant domains, VL is a variable light domain and CL is a light chain constant domain. In some embodiments, the TIL antigen binding domain is antibody fragment. In certain embodiments, TIL antigen binding domain is a Fab, Fab′ , F(ab′)2, F(ab)2, variable fragment (Fv), domain antibody (dAb), or single chain variable fragment (scFv).

[00741] The TIL antigen binding domain can bind to any suitable TIL antigen that allows for the attachment of the immunomodulatory agent-TIL ABD fusion protein to the surface of the TIL. In exemplary embodiments, the TIL antigen binding domain is capable of binding to a TIL surface antigen. TIL surface antigens include, but are not limited to D16, CD45, CD4, CD8, CD3, CD11a, CD11b, CD11c, CD18, LFA-1, CD25, CD127, CD56, CD19, CD20, CD22, HLA-DR, CD197, CD38, CD27, CD137, OX40, GITR, CD56, CD196, CXCR3, CXCR4, CXCR5, CD84, CD229, CCR1, CCR5, CCR4, CCR6, CCR8, and/or CCR10. In some embodiments, the ABD binds to CD45. In particular embodiments, the ABD binds to a CD45 isoform selected from CD45RA, CD45RB, CD45RC or CD45Rβ. In particular embodiments, the ABD binds to a CD45 expressed primary on T cells.

[00742] In certain embodiments, the ABD binds to a checkpoint inhibitor. Exemplary checkpoint inhibitors include, but are not limited to PD-1, PD-L1, LAG-3, TIM-3 and CTLA-4 (see, *e.g.*, Qin et al., Molecular Cancer 18:155 (2019)). In some embodiments, the ABD binds to a checkpoint inhibitor expressed on an immune effector cell (*e.g.*, a T cell or NK cell). Exemplary anti-PD-1 antibodies are disclosed, for example, in US Patent Nos. US 7,695,715, US 7,332,582, US 9,205,148, US 8,686,119, US 8,735,553, US 7,488,802, US 8,927,697, US 8,993,731, and US 9,102,727, which are incorporated by reference in their entireties, particularly in pertinent parts relating to anti-PD-1 antibodies. Exemplary anti PD-L1 antibodies are disclosed in US Patent Nos. US 8,217,149, US 8,779,108, US 8,168,179, US 8,552,154, US 8,460,927, and US 9,175,082, which are incorporated by reference in their entireties, particularly in pertinent parts relating to anti-PD-L1 antibodies. Exemplary anti-LAG-3 antibodies are disclosed in US Patent Nos. US 9,244,059, US 9,244,059, US 9,505,839, which are incorporated by reference in their entireties, particularly in pertinent parts relating to anti-LAG-3 antibodies. Exemplary TIM-3 antibodies are disclosed in WO 2016/161270, US 8,841,418, and US 9,163,087, which are incorporated by reference in their entireties, particularly in pertinent parts relating to anti-TIM-3 antibodies. Exemplary CTLA-4 antibodies are disclosed in US 6,984,720 and US 7,411,057, which are incorporated by reference in their entireties, particularly in pertinent parts relating to anti-CTLA-4 antibodies.

[00743] In some embodiments, the ABD is an anti-CD45 antibody or a fragment thereof. In certain embodiments, the anti-CD45 antibody is a human anti-CD45 antibody, a humanized anti-CD45 antibody, or a chimeric anti-CD45 antibody. In exemplary embodiments, the ABD includes the vhCDR1-3 and vlCDR1-3 of anti-CD45 antibody BC8 (see US20170326259, incorporated by reference herein, particularly in relevant parts relating to anti-CD45 antibody sequences). In some embodiments, the ABD includes the variable heavy domain and variable domain of anti-CD45 antibody BC8. In some embodiments, the ABD includes the vhCDR1-3 and vlCDR1-3 or VH and VL of one of the following anti-CD45 antibodies: 10G10, UCHL1, 9.4, 4B2, or GAP8.3 (see Spertini et al., Immunology 113(4):441-452 (2004), Buzzi et al., Cancer Research 52:4027-4035 (1992)).

[00744] The immunomodulatory fusion proteins can be any suitable immunomodulatory agent including, for example, any of the immunomodulatory agents provided herein. In some embodiments, the immunomodulatory agent is an interleukin that promotes an anti-tumor response. In some embodiments, the immunomodulatory agent is a cytokine. In particular embodiments, the immunomodulatory agent is IL-2, IL-12, IL-15, IL-21 or a bioactive variant thereof. In certain embodiments, the fusion protein includes more than one immunomodulatory agents. In exemplary embodiments, the fusion protein includes 2, 3, 4, 5, 6, 7, 8, 9 or 10 different immunomodulatory agents.

[00745] The TIL antigen binding domain is attached to the immunomodulatory agent using any suitable linker. Suitable linkers include, but are not limited: a cleavable linker, a non-cleavable linker, a peptide linker, a flexible linker, a rigid linker, a helical linker, or a non-helical linker. In some embodiments, the linker is a peptide linker that optionally comprises Gly and Ser. Suitable linkers include linkers that are at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 amino acid residues in length. In some embodiments, the linker is 5-10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 45-50, or 50-60 amino acids in length. In certain embodiments, the peptide linker is a $(GGGS)_n$ or $(GGGGS)_n$ linker, wherein n indicates the number of repeats of the motif and is an integer selected from 1-10. In some embodiments, the linker is an antibody hinge domain or a fragment thereof. In certain embodiments, the linker is a human immunoglobulin (Ig) hinge domain (*e.g.*, an IgG1, IgG2, IgG3, IgG4, IgD, IgE, IgM or IgA hinge) or a fragment thereof. In some embodiments, the immunomodulatory agent is directly coupled to the TIL without a linker.

[00746] The immunomodulatory agent can be attached to the TIL antigen binding domain at a suitable position that does not impede binding of the fusion protein to a TIL. In some embodiments wherein the antigen binding domain is a full length antibody, the immunomodulatory agent is attached to the C-terminus or N-terminus of either the heavy chain or light chain. In some embodiments wherein the antigen binding domain is an scFv, the immunomodulatory agent is attached to the C-terminus or N-terminus of the variable heavy domain or variable light domain. In some embodiments wherein the antigen binding domain is an Fab, the immunomodulatory agent is attached to the C-terminus or N-terminus of the variable heavy domain or variable light domain. In some embodiments wherein the antigen binding domain is an Fab', the immunomodulatory agent is attached to the C-terminus or N-terminus of the variable heavy domain or variable light domain. In some embodiments wherein the antigen binding domain is an Fab'_2, the immunomodulatory agent is attached to the C-terminus or N-terminus of the variable heavy domain or variable light domain.

[00747] In some embodiments wherein the fusion protein includes two or more immunomodulatory agents, the immunomodulatory agents are attached to each other using any of the linkers described herein. In some embodiments, the two or more immunomodulatory agents are attached to different locations of the antigen binding domain. For example, in some embodiments wherein the TIL antigen binding domain is a full length antibody, the two or more immunomodulatory agents are attached at (i) different locations on the heavy chain (ii) different locations on the light chain or (iii) different locations on the heavy chain and/or light chain.

[00748] The subject immunomodulatory agent-TIL antigen binding domain fusion proteins can be made using any suitable method. In one aspect, provided herein are nucleic acids that encode the subject fusion proteins, expression vectors that include such nucleic acids, and host cells that

include the expression vectors. Host cells that include the expression vectors encoding the subject fusion proteins are cultured under conditions for the expression of the fusion proteins and the fusion proteins are subsequently isolated and purified. In some embodiments, the purified fusion proteins are then incubated with a population of TILs under conditions that allow for the binding of the fusion protein to the TILs.

[00749] In some embodiments, the subject immunomodulatory agent-TIL antigen binding domain fusion proteins are attached to TILs produced during any of the steps of the Process 2A method disclosure herein (see, *e.g.*, FIGs 2-6). In exemplary embodiments, the fusion proteins are attached to TILs produced during any of the steps of the GEN 3 method disclosure herein (see, *e.g.*, FIG. 7). In exemplary embodiments, the fusion proteins are attached to TILs produced from the first expansion step in the Process 2A method and/or the priming expansion step in the GEN 3 method provided herein. In exemplary embodiments, the fusion proteins are attached to TILs produced from the second expansion step in the Process 2A method and/or the rapid expansion step in the GEN 3 method provided herein. In some embodiments, the TILs are PD-1 positive TILs that have been preselected using the methods described herein.

[00750] Nucleic acids encoding the subject the subject immunomodulatory agent-TIL antigen binding domain fusion proteins may be introduced into a population of TILs to produce transiently modified or genetically modified TILs that express the subject immunomodulatory agent-TIL antigen binding domain fusion proteins using any suitable method. In some embodiments, nucleic acids encoding the subject immunomodulatory agent-TIL antigen binding domain fusion proteins are introduced into a population of TILs using a microfluidic platform. In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform. See, e.g., International Patent Application Publication Nos. WO 2013/059343A1, WO 2017/008063A1, or WO 2017/123663A1, or U.S. Patent Application Publication Nos. US 2014/0287509A1, US 2018/0201889A1, or US 2018/0245089A1, all of which are incorporated by reference herein in their entireties, and particularly for disclosures of microfluidic platforms for nucleic acid delivery. In the SQZ platform, the cell membranes of the cells for modification (e.g., TILs) are temporarily disrupted by microfluidic constriction, thereby allowing the delivery of nucleic acids encoding the immunomodulatory agent-TIL antigen binding domain fusion protein into the cells.

[00751] In some embodiments, the nucleic acid encoding the subject immunomodulatory agent-TIL antigen binding domain fusion protein is mRNA and the microfluidic platform (e.g., SQZ vector-free microfluidic platform) is used to deliver the mRNA into TILs to produce transiently modified TILs. In some embodiments, the nucleic acid encoding the subject immunomodulatory agent-TIL antigen binding domain fusion protein is DNA and the microfluidic platform (e.g., SQZ vector-free microfluidic platform) is used to deliver the nucleic acid into TILs to produce stable

genetically-modified TILs. The microfluidic platform (e.g., SQZ vector-free microfluidic platform) may be used to deliver the nucleic acid to any population of TILs produced during any steps of the Process 2A method disclosure herein (see, *e.g.*, FIGS. 2-6) or GEN 3 method disclosure herein (see, *e.g.*, FIG. 7) to produce the modified TILs. In some embodiments, the membrane anchored immunomodulatory fusion protein comprises an IL-2, an IL-12, an IL-15, an IL-21 or combinations thereof (e.g., IL-15 and IL-21).

[00752] Exemplary immunomodulatory agent-TIL antigen binding domain fusion proteins useful for the compositions and methods provided herein are further described, for example, in US Patent Application Publication No. 20200330514, which is incorporated by reference in its entirety and in pertinent parts related to immunomodulatory agent-TIL antigen binding domain fusion proteins.

I. Nanoparticle Compositions

[00753] In some embodiments, the subject modified TILs provided herein include one or more nanoparticles, and those nanoparticles include one or more immunomodulatory agents. In some embodiments, the nanoparticles provided herein include a plurality of two or more proteins that are coupled to each other and/or a second component of the particle (*e.g.*, reversibly linked through a degradable linker). In some embodiments, the proteins of the nanoparticles are present in a polymer or silica. In certain embodiments, the nanoparticle includes a nanoshell. The nanoparticles provided herein include one or more immunomodulatory agent. In some embodiments, the immunomodulatory agent is IL-2, IL-12, IL-15, IL-18, IL-21, a CD40 agonist (e.g., CD40L or agonistic anti-CD40 binding domain (e.g., an anti-CD40 scFv)) or a bioactive variant thereof. Nanoparticles are attached to the surface of the TIL using any suitable technique described herein.

[00754] Exemplary nanoparticles of use in the subject modified TILs provided herein include without limitation a liposome, a protein nanogel, a nucleotide nanogel, a polymer nanoparticle, or a solid nanoparticle. In some embodiments, the nanoparticle includes a liposome. In exemplary embodiments, the nanoparticle includes an immunomodulatory agent nanogel. In particular embodiments, the nanoparticle is an immunomodulatory agent nanogel with a plurality of immunomodulatory agents (*e.g.*, cytokines) covalently linked to each other. In some embodiments, the nanoparticle includes at least one polymer, cationic polymer, or cationic block co-polymer on the nanoparticle surface. Exemplary nanoparticles that can be used in the compositions provided herein are disclosed, for example, in US Patent Nos. 9,283,184 and 9,603,944, each of which is incorporated by reference in its entirety and in pertinent parts related to nanoparticles.

[00755] The immunomodulatory agent can be any suitable immunomodulatory agent including, for example, any of the immunomodulatory agents provided herein. In some embodiments,

the immunomodulatory agent is an interleukin that promotes an anti-tumor response. In some embodiments, the immunomodulatory agent is a cytokine. In particular embodiments, the immunomodulatory agent is IL-2, IL-12, IL-15, IL-21 or a bioactive variant thereof. In certain embodiments, the fusion protein includes more than one immunomodulatory agents. In exemplary embodiments, the fusion protein includes 2, 3, 4, 5, 6, 7, 8, 9 or 10 different immunomodulatory agents.

[00756] In some embodiments, the nanoparticle includes proteins that are covalently cross-linked to each other and/or a second component (*e.g.*, a degradable linker). In some embodiments, the nanoparticle includes immunomodulatory agents that are reversibly linked through a degradable linker to a function group or polymer, or "reversibly modified." In some embodiments, the nanoparticle is a nanogel that includes a plurality of immunomodulatory agents cross-linked to each other through a degradable linker (see US Patent No. 9,603,944). In exemplary embodiments, the protein of the nanogel are cross-linked to a polymer (*e.g.*, polyethylene glycol (PEG)). In some embodiments, the polymers are cross-linked to the nanogel surface.

[00757] In some embodiments, the immunomodulatory agents of the nanoparticles are reversibly linked to each other through a degradable linker (*e.g.*, a disulfide linker) such that under physiological conditions, the linker degrades, thereby releasing the immunomodulatory agent. In some embodiments, the immunomodulatory agents of the nanoparticles are reversibly linked to functional groups through a degradable linker such that under physiological conditions, the linker degrades and releases the immunomodulatory agent. Suitable degradable linkers include, but are not limited to: two N-hydroxysuccinimide (NHS) ester groups joined together by a flexible disulfide-containing linker that is sensitive to a reductive physiological environment; a hydrolysable linker that is sensitive to an acidic physiological environment (pH < 7, for example, a pH of 4-5, 5-6, or 6- to less than 7, *e.g.*, 6.9), or a protease sensitive linker that is sensitive to one or more enzymes present in biological media such as proteases in a tumor microenvironment such a matrix metalloproteases present in a tumor microenvironment or in inflamed tissue (*e.g.* matrix metalloproteinase 2 (MMP2) or matrix metalloproteinase 9 (MMP9)). A crosslinker sensitive to a reductive physiological environment is, for example, a crosslinker with disulfide containing linker that will react with amine groups on proteins by the presence of NHS groups which cross-link the proteins into high density protein nanogels. In some embodiments, the degradable cross-linker includes Bis[2-(N-succinimidyl-oxycarbonyloxy)ethyl] disulfide.

[00758] In some embodiments, the degradable linker includes at least one N-hydroxysuccinimide ester. In some embodiments, the degradable linker is a redox responsive linker. In some embodiments, the redox responsive linker includes a disulfide bond. In some embodiments, the degradable linkers provided herein include at least one Nhydroxysuccinimide ester, which is

capable of reacting with proteins at neutral pH (*e.g.*, about 6 to about 8, or about 7) without substantially denaturing the protein. In some embodiments, the degradable linkers are "redox responsive" linkers, meaning that they degrade in the presence of a reducing agent (*e.g.*, glutathione, GSH) under physiological conditions (*e.g.*, 20-40 °C and/or pH 4-8), thereby releasing intact protein from the compound to which it is reversibly linked. In some embodiments, the protein of the nanoparticles are linked to the degradable linker through a terminal or internal-NH_2 functional group (*e.g.*, a side chain of a lysine).

[00759] In other embodiments, the proteins of the nanoparticle are linked by an enzyme-sensitive linker. Exemplary cleavable linker include those that are recognized by one of the following enzymes: metalloprotease MMP-1, MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, plasmin, PSA, PSMA, CATHEPSIN D, CATHEPSIN K, CATHEPSIN S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. See, *e.g.*, US Patent Nos. 8,541,203 and 8,580,244, each of which is incorporated by reference in its entirety and in pertinent parts related to cleavable linkers.

[00760] In some embodiments, the nanoparticles are nanogels that include a monodispersed plurality of immunomodulatory agents (*e.g.*, cytokines). In some embodiments, the immunomodulatory agents of the nanogels are cross-linked to polymer. In certain embodiments, the polymer is cross-linked to the surface of the nanogel. In particular embodiments, the nanogel includes: a) one more immunomodulatory agents reversibly and covalently cross-linked to each other through a degradable linker; and b) polymers cross-linked to surface exposed proteins of the nanogels. Such nanogels can be made by contacting the one or more immunomodulatory agents with a degradable linker under conditions that permit reversible covalent crosslinking of the immunomodulatory agents to each other through the degradable linker to form a plurality of immunomodulatory agent nanogels. Subsequently, the immunomodulatory agent nanogels are contacted with a polymer (*e.g.*, polyethylene glycol) under conditions that permit crosslinking of the polymer to the immunomodulatory agents of the immunomodulatory agent nanogels, thereby producing a plurality of immunomodulatory agent-polymer nanogels.

[00761] In some embodiments, the nanoparticles include one or more polymers. Exemplary polymers include, but are not limited to: aliphatic polyesters, poly (lactic acid) (PLA), poly (glycolic acid) (PGA), co-polymers of lactic acid and glycolic acid (PLGA), polycarprolactone (PCL), polyanhydrides, poly(ortho)esters, polyurethanes, poly(butyric acid), poly(valeric acid), and poly(lactide-co-caprolactone), and natural polymers such as alginate and other polysaccharides including dextran and cellulose, collagen, chemical derivatives thereof, including substitutions, additions of chemical groups such as for example alkyl, alkylene, hydroxylations, oxidations, and

other modifications routinely made by those skilled in the art), albumin and other hydrophilic proteins, zein and other prolamines and hydrophobic proteins, copolymers and mixtures thereof. In some embodiments, the immunomodulatory agents of the nanoparticles are linked to hydrophilic polymers. Exemplary hydrophilic polymers include, but are not limited to: polyethylene glycol (PEG), polyethylene glycol-b-poly lysine (PEG-PLL), and/or polyethylene glycol-b-poly arginine (PEG-PArg).

[00762] In some embodiments, the nanoparticle (*e.g.*, nanogel) includes one or more polycations on its surface. Exemplary polycations for use in the subject nanoparticles include, but are not limited to, polylysine (poly-L-lysine and/or poly-D-lysine), poly(argininate glyceryl succinate) (PAGS, an arginine-based polymer), polyethyleneimine, polyhistidine, polyarginine, protamine sulfate, polyethylene glycol-b-polylysine (PEG-PLL), and polyethylene glycol-g-polylysine.

[00763] In some embodiments, the nanoparticle is associated with the TIL surface by electrostatic attraction to the TIL. In certain embodiments, the nanoparticle includes a ligand that has affinity for a surface molecule of the TIL (*e.g.*, a surface protein, carbohydrate and/or lipid).

[00764] In particular embodiments, the nanoparticle includes an antigen binding domain that binds a TIL surface antigen as described herein. In some embodiments, the antigen binding domain is an antibody or fragment thereof. In exemplary embodiments, the TIL surface antigen is CD45, LFA-1, CD 11a (integrin alpha- L), CD 18 (integrin beta-2), CD11b, CD11c, CD25, CD8, or CD4. In exemplary embodiments, the antigen binding domain (ABD) is an anti-CD45 antibody or a fragment thereof. In certain embodiments, the anti-CD45 antibody is a human anti-CD45 antibody, a humanized anti-CD45 antibody, or a chimeric anti-CD45 antibody. In exemplary embodiments, the ABD includes the vhCDR1-3 and vlCDR1-3 of anti-CD45 antibody BC8 (see US20170326259, incorporated by reference herein, particularly in relevant parts relating to anti-CD45 antibody sequences). In some embodiments, the ABD includes the variable heavy domain and variable domain of anti-CD45 antibody BC8. In some embodiments, the ABD includes the vhCDR1-3 and vlCDR1-3 or VH and VL of one of the following anti-CD45 antibodies: 10G10, UCHL1, 9.4, 4B2, or GAP8.3 (see Spertini et al., Immunology 113(4):441-452 (2004), Buzzi et al., Cancer Research 52:4027-4035 (1992)). In such embodiments, the nanoparticles are attached to the surface of a population of TILs by incubating the TILs in the presence of the nanoparticles under conditions wherein the nanoparticles bind to the surface of the TILs.

[00765] In some embodiments, the nanoparticle is associated with the TIL cell surface by electrostatic attraction. In some embodiments the nanoparticle is covalently conjugated to the TIL. In other embodiments, the nanoparticle is not covalently conjugated to the TIL.

[00766] In some embodiments, the subject nanoparticles are attached to TILs produced during any of the steps of the Process 2A method disclosure herein (see, *e.g.*, FIGs 2-6). In exemplary embodiments, the subject nanoparticles are attached to TILs produced during any of the steps of the GEN 3 method disclosure herein (see, *e.g.*, FIG. 7). In exemplary embodiments, the subject nanoparticles are attached to TILs produced from the first expansion step in the Process 2A method and/or the priming expansion step in the GEN 3 method provided herein. In exemplary embodiments, the subject nanoparticles are attached to TILs produced from the second expansion step in the Process 2A method and/or the rapid expansion step in the GEN 3 method provided herein. In some embodiments, the TILs are PD-1 positive TILs that have been preselected using the methods described herein.

[00767] Additional suitable nanoparticles for use in the modified TILs provided herein are disclosed in US Patent Application Publication No. US20200131239 and WO2020205808, each of which is incorporated by reference in its entirety and in relevant parts related to nanoparticles.

B. Immunomodulatory Agents

[00768] The modified TILs provided herein include one or more immunomodulatory agents attached to its surface. The immunomodulatory agents can be incorporated into any of the immunomodulatory fusion proteins described herein, including, for example, the membrane anchored immunomodulatory fusion proteins described herein. Any suitable immunomodulatory agent can be included in the subject modified TIL. In some embodiments, the immunomodulatory agent enhances TIL survival and/or anti-tumor activity once transferred to a patient. Exemplary immunomodulatory agents include, for example, cytokines. In some embodiments, the modified TIL includes one or more of the following cytokines: IL-2, IL-7, IL-12, IL-15, IL-18, IL-21, IL-23, IL-27, IL-4, IL-1α, IL-1β, IL-5, IFNγ, TNF α (TNFa), IFNα, IFNβ, GM-CSF, or GCSF or a biologically active variant thereof. In some embodiments, the immunomodulatory agent is a costimulatory molecule. In particular embodiments, the costimulatory molecule is one of the following: OX40, CD28, GITR, VISTA, CD40, CD3, or an agonist of CD137. In some embodiments, the immunomodulatory agent is a CD40 agonist (e.g., CD40L or an agonistic CD40 binding domain). Exemplary immunomodulatory agents are discussed in detailed further below.

1. IL-15

[00769] In some embodiments, the modified TILs provided herein include an IL-15. In exemplary embodiments, the IL-15 is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00770] As used herein, "interleukin 15", "IL-15" and "IL15" all refer to an interleukin that binds to and signals through a complex composed of an IL-15 specific receptor alpha chain (IL-15Rα), an IL-2/IL-15 receptor beta chain (CD122) and the common gamma chain (gamma-C, CD132) (e.g., Genbank Accession numbers: NM_00000585, NP_000576 and NP_751915 (human); and NM_001254747 and NP_001241676 (mouse)). IL-15 has been shown to stimulate T cell proliferation inside tumors. IL-15 also is able to extend the survivability of effector memory CD8+ T cells and is critical for the development of NK cells. Therefore, without being bound by any particular theory of operation, it is believed that modified TILs associated with an IL-15s described herein exhibit enhanced survival and/or anti-tumor effects.

[00771] IL-15 has a short half-life of less than 40 minutes in vivo. Modifications to IL-15 monomer can improve its in vivo pharmacokinetics in the treatment of cancers. These modifications have generally centered on improving the trans-presentation of IL-15 with the alpha subunit of IL-15 receptor, IL-15Rα. Such modifications include: 1) pre-association of IL-15 and its soluble receptor a-subunit-Fc fusion to form IL-15: IL-15Rα-Fc complex (see, *e.g.*, Rubinstein et al., Proc Natl Acad Sci U.S.A. 103:9166–71 (2006)); 2) expression of the superagonist IL-15-sIL-15Rα-sushi protein (see, *e.g.*, Bessard et al., Molecular cancer therapeutics 8: 2736-45 (2009)); and 3) pre-association of human IL-15 mutant IL-15N72D with IL-15Rα-Fc sushi-Fc fusion complex (see, *e.g.*, Zhu et al., Journal of Immunology 183: 3598-6007 (2009)).

[00772] In some embodiments, the IL-15 associated with the modified TIL is a full length IL-15, a fragment or a variant of IL-15. In some embodiments, the IL-15 is a human IL-15 or a variant human IL-15. In exemplary embodiments, the IL-15 is a biological active human IL-15 variant. In some embodiments, the IL-15 includes a 1, 2, 3,4 ,5 ,6 7, 8, 9, or 10 mutations as compared to a wild-type IL-15. In certain embodiments, the IL-15 includes an N72D mutation relative to a wild type human IL-15. In some embodiments, the variant IL-15 exhibits IL-15Rα binding activity.

[00773] In some embodiments, the immunomodulatory agent includes an IL-15 and an extracellular domain of an IL-15Rα. In certain embodiments, the immunomodulatory agent includes an IL-15 and an IL-15Rα fused to an Fc domain (IL-15Rα-Fc)

TABLE 5 – IL-15 Related Sequences.

Description	Amino Acid Sequence
Human IL-15 (N72D mutant)	NWVNVISDLKKIEDLIQSMHIDATLYTESD VHPSCKVTAMKCFLLELQVISLESGDASIH DTVENLIILANDSLSSNGNVTESGCKECEE LEEKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 258)

Human IL-15R-alpha-Su/Fc domain	ITCPPPMSVEHADIWVKSYSLYSRERYICN SGFKRKAGTSSLTECVLNKATNVAHWTTP SLKCIREPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK (SEQ ID NO: 259)
Human IL-15R-alpha-Su (65aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICN SGFKRKAGTSSLTECVLNKATNVAHWTTP SLKCIR (SEQ ID NO: 260)
Human IL-15 isoform 2	MVLGTIDLCSCFSAGLPKTEANWVNVISD LKKIEDLIQSMHIDATLYTESDVHPSCKVT AMKCFLLELQVISLESGDASIHDTVENLIIL ANNSLSSNGNVTESGCKECEELEEKNIKEF LQSFVHIVQMFINTS (SEQ ID NO: 261)
Human IL-15 isoform 1	MRISKPHLRSISIQCYLCLLLNSHFLTEAGI HVFILGCFSAGLPKTEANWVNVISDLKKIE DLIQSMHIDATLYTESDVHPSCKVTAMKC FLLELQVISLESGDASIHDTVENLIILANNS LSSNGNVTESGCKECEELEEKNIKEFLQSF VHIVQMFINTS (SEQ ID NO: 262)
Human IL-15 (without signal peptide)	NWVNVISDLKKIEDLIQSMHIDATLYTESD VHPSCKVTAMKCFLLELQVISLESGDASIH DTVENLIILANNSLSSNGNVTESGCKECEE LEEKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 263)
Human IL-15R-alpha (85 aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICN SGFKRKAGTSSLTECVLNKATNVAHWTTP SLKCIRDPALVHQRPAPPSTVTTAGV (SEQ ID NO: 264)

Human IL-15R-alpha (182aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICN SGFKRKAGTSSLTECVLNKATNVAHWTTP SLKCIRDPALVHQRPAPPSTVTTAGVTPQP ESLSPSGKEPAASSPSSNNTAATTAAIVPGS QLMPSKSPSTGTTEISSHESSHGTPSQTTAK NWELTASASHQPPGVYPQGHSDTTVAIST ST (SEQ ID NO: 265)
Human IL-15R-alpha	MAPRRARGCRTLGLPALLLLLLLRPPATR GITCPPPMSVEHADIWVKSYSLYSRERYIC NSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIRDPALVHQRPAPPSTVTTAGVTP QPESLSPSGKEPAASSPSSNNTAATTAAIVP GSQLMPSKSPSTGTTEISSHESSHGTPSQTT AKNWELTA SASHQPPGVYPQGHSDTTVAISTSTVLLCG LSAVSLLACYLKSRQTPPLASVEMEAMEA LPVTWGTSSRDEDLENCSHHL (SEQ ID NO: 266)

[00774] In some embodiments the immunostimulatory protein is a superagonist IL-15 (IL-15SA) that includes a complex of human IL-15 and soluble human IL-15Rα. The combination of human IL-15 with soluble human IL-15Rα forms an IL-15 SA complex that possesses greater biological activity than human IL-15 alone. Soluble human IL-15Rα, as well as truncated versions of the extracellular domain, has been described in the art (Wei et al., 2001 J of Immunol. 167: 277-282). The amino acid sequence of human IL-15Rα is set forth in SEQ ID NO: 266. In some embodiments, the IL-15SA includes a complex of human IL-15 and soluble human. IL-15Rα comprising all or a portion of the extracellular domain, without the transmembrane or cytoplasmic domain. In some embodiments, the IL-15SA includes a complex of human IL-15 and soluble human IL-15Rα that includes the full extracellular domain or a truncated form of the extracellular domain which retains IL-15 binding activity.

[00775] In some embodiments, the IL-15SA includes a complex of human IL-15 and soluble human IL-15Rα that includes a truncated form of the extracellular domain which retains IL-15 binding activity. In some embodiments, the soluble human IL-15Rα includes amino acids 1-60, 1-61, 1-62, 1-63, 1-64 or 1-65 of human IL-15Rα. In some embodiments, the soluble human IL-15Rα

includes amino acids 1-80, 1-81, 1-82, 1-83, 1-84 or 1-85 of human IL-15Rα. In some embodiments, the soluble human IL-15Rα includes amino acids 1-180, 1-181, or 1-182 of human IL-15Rα.

[00776] In some embodiments, the immunomodulatory agent is an IL-15SA comprising a complex of human IL-15 and soluble human IL-15Rα comprising a truncated form of the extracellular domain which retains IL-15 binding activity and comprises a Sushi domain. The Sushi domain of IL-15Rα is described in the art as approximately 60 amino acids in length and comprises 4 cysteines. (Wei et al., 2001). Truncated forms of soluble human IL-15Rα which retain IL-15 activity and comprise a Sushi domain are useful in IL-15SA of the present disclosure.

[00777] In some embodiments, the immunomodulatory agent includes a complex comprising soluble human IL-15Rα expressed as a fusion protein, such as an Fc fusion as described herein (*e.g.*, human IgG1 Fc), with IL-15. In some embodiments, IL-15SA comprises a dimeric human IL-15RαFc fusion protein (*e.g.*, human IgG1 Fc) complexed with two human IL-15 molecules.

[00778] In some embodiments, the immunomodulatory agent is an IL-15SA cytokine complex that includes an IL-15 molecule comprising an amino acid sequence set forth in SEQ ID NO: 258, SEQ ID NO: 261, SEQ ID NO:262, or SEQ ID NO:263. In some embodiments, an IL-15SA cytokine complex comprises a soluble IL-15Rα molecule comprising a sequence of SEQ ID NO:260, SEQ ID NO: 264 or SEQ ID NO:265.

[00779] In some embodiments, the immunomodulatory agent is an IL-15SA cytokine complex that includes a dimeric IL-15RαFc fusion protein complexed with two IL-15 molecules. In some embodiments, IL-15-SA comprises a dimeric IL-15RαSu (Sushi domain)/Fc (SEQ ID NO:259) and two IL-15N72D (SEQ ID NO:258) molecules (also known as ALT-803), as described in US20140134128, incorporated herein by reference. In some embodiments, the IL-15SA comprises a dimeric IL-15RαSu/Fc molecule (SEQ ID NO: 259) and two IL-15 molecules (SEQ ID NO: 261). In some embodiments, the IL-15SA comprises a dimeric IL-15RαSu/Fc molecule (SEQ ID NO: 259) and two IL-15 molecules (SEQ ID NO:262). In some embodiments, the IL-15SA comprises a dimeric IL-15RαSu/Fc molecule (SEQ ID NO:259) and two IL-15 molecules (SEQ ID NO:263).

[00780] In some embodiments, the IL-15SA includes a dimeric IL-15RαSu/Fc molecule (SEQ ID NO:259) and two IL-15 molecules having amino acid sequences selected from SEQ ID NO: 258, 258, 262, and 263.

[00781] In some embodiments, the IL-15SA includes a soluble IL-15Rα molecule (SEQ ID NO:260) and two IL-15 molecules (SEQ ID NO:258). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:260) and two IL-15 molecules (SEQ ID NO:261). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:260) and two IL-15

molecules (SEQ ID NO:262). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:260) and two IL-15 molecules (SEQ ID NO:263).

[00782] In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:264) and two IL-15 molecules (SEQ ID NO:258). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:264) and two IL-15 molecules (SEQ ID NO:261). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:264) and two IL-15 molecules (SEQ ID NO:262). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:264) and two IL-15 molecules (SEQ ID NO:261).

[00783] In some embodiments, the IL-15SA includes a soluble IL-15Rα molecule (SEQ ID NO:265) and two IL-15 molecules (SEQ ID NO:258). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:265) and two IL-15 molecules (SEQ ID NO:261). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:265) and two IL-15 molecules (SEQ ID NO:262). In some embodiments, the IL-15SA comprises a soluble IL-15Rα molecule (SEQ ID NO:265) and two IL-15 molecules (SEQ ID NO:263).

[00784] In some embodiments, the IL-15SA comprises a dimeric IL-15RαSu/Fc (SEQ ID NO:269) molecule and two IL-15 molecules (SEQ ID NO:262). In some embodiments, the IL-15SA includes a dimeric IL-15RαSu/Fc (SEQ ID NO:259) molecule and two IL-15 molecules (SEQ ID NO:263).

[00785] In some embodiments, the IL-15SA includes SEQ ID NO:259 and SEQ ID NO:260. In some embodiments IL-15SA comprises SEQ ID NO:261 or SEQ ID NO:262. In some embodiments the IL-15SA comprises SEQ ID NO:261 and SEQ ID NO:259. In some embodiments the IL-15SA comprises SEQ ID NO:262 and SEQ ID NO:259. In some embodiments the IL-15SA comprises SEQ ID NO:263 and SEQ ID NO:259. In some embodiments, the IL-15SA comprises SEQ ID NO:261 and SEQ ID NO:260. In some embodiments the IL-15SA comprises SEQ ID NO:262 and SEQ ID NO:260.

[00786] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-15 or a bioactive variant thereof. Exemplary fusion proteins that include IL-15 are depicted in Figures 51 and 52, and Tables 58 and 59.

[00787] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes an IL-15, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein. Exemplary NFAT promoter-driven constructs for expression of immunomodulatory fusion proteins that include IL-15 are depicted in Table 59.

2. IL-12

[00788] In some embodiments, the modified TIL is associated with an IL-12 or a variant thereof. In exemplary embodiments, the IL-12 is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00789] As used herein, "interleukin 12", "IL-12" and "IL12" all refer to an interleukin that is a heterodimeric cytokine encoded by the IL-12A and IL-12B genes (Genbank Accession numbers: NM_000882 (IL-12A) and NM_002187 (IL-12B)). IL-12 is composed of a bundle of four alpha helices and is involved in the differentiation of native T cells into TH1 cells. It is encoded by two separate genes, IL-12A (p35) and IL-12B (p40). The active heterodimer (referred to as 'p70'), and a homodimer of p40 are formed following protein synthesis. IL-12 binds to the IL-12 receptor, which is a heterodimeric receptor formed by IL-12R-β1 and IL-12R-β2. IL-12 is known as a T cell-stimulating factor that can stimulate the growth and function of T cells. In particular, IL-12 can stimulate the production of interferon gamma (IFN-γ), and tumor necrosis factor-alpha (TNF-α) from T cells and natural killer (NK) cells and reduce IL-4 mediated suppression of IFN-γ. IL-12 can further mediate enhancement of the cytotoxic activity of NK cells and CD8+ cytotoxic T lymphocytes. Moreover, IL-12 can also have anti-angiogenic activity by increasing production of interferon gamma, which in turn increases the production of the chemokine inducible protein-10 (IP-10 or CXCL10). IP-10 then mediates this anti-angiogenic effect. Thus, without being bound by any particular theory of operation, it is believed that IL-12 can increase the survivability and/or anti-tumor effects of the TIL compositions provided herein.

[00790] In some embodiments, the IL-12 associated with the modified TIL is a full length IL-12, a fragment or a variant of IL-12. In some embodiments, the IL-12 is a human IL-12 or a variant human IL-12. In exemplary embodiments, the IL-12 is a biological active human IL-12 variant. In some embodiments, the IL-12 includes a 1, 2, 3,4 ,5 ,6 7, 8, 9, or 10 mutations as compared to a wild-type IL-12.

[00791] In some embodiments, the IL-12 included in the modified TIL compositions include an IL-12 p35 subunit or a variant thereof. In some embodiments, the IL-12 p35 subunit is a human IL-12 p35 subunit. In some embodiments, the IL-12 p35 subunit has the amino acid sequence In certain embodiments, the IL-12 included in the modified TIL compositions include an IL-12 p40 subunit or a variant thereof. In certain embodiments, the IL-12 is a single chain IL-12 polypeptide comprising an IL-12 p35 subunit attached to an IL-12 p40 subunit. Such IL-12 single chain polypeptides advantageously retain one or more of the biological activities of wildtype IL-12. In some embodiments, the single chain IL-12 polypeptide described herein is according to the formula, from N-terminus to C-terminus, (p40)-(L)-(p35), wherein "p40" is an IL-12 p40 subunit, "p35" is IL-12 p35 subunit and L is a linker. In other embodiments, the single chain IL-12 is according to the

formula from N-terminus to C-terminus, (p35)-(L)-(p40). Any suitable linker can be used in the single chain IL-12 polypeptide including those described herein. Suitable linkers can include, for example, linkers having the amino acid sequence $(GGGGS)_x$ wherein x is an integer from 1-10. Other suitable linkers include, for example, the amino acid sequence GGGGGGS. Exemplary single chain IL-12 linkers than can be used with the subject single chain IL-12 polypeptides are also described in Lieschke et al., *Nature Biotechnology* 15: 35-40 (1997), which is incorporated herein in its entirety by reference and particularly for its teaching of IL-12 polypeptide linkers. In an exemplary embodiment, the single chain IL-12 polypeptide is a single chain human IL-12 polypeptide (*i.e.*, it includes a human p35 and p40 IL-12 subunit).

TABLE 6 – IL-12 Related Sequences.

Description	Amino Acid Sequence
Human IL-12 p35 subunit	RNLPVATPDPGMFPCLHHSQNLLRAVSNM LQKARQTLEFYPCTSEEIDHEDITKDKTST VEACLPLELTKNESCLNSRETSFITNGSCLA SRKTSFMMALCLSSIYEDLKMYQVEFKTM NAKLLMDPKRQIFLDQNMLAVIDELMQA LNFNSETVPQKSSLEEPDFYKTKIKLCILLH AFRIRAVTIDRVMSYLNAS (SEQ ID NO:267)
Human IL-12 p40 subunit	IWELKKDVYVVELDWYPDAPGEMVVLTC DTPEEDGITWTLDQSSEVLGSGKTLTIQVK EFGDAGQYTCHKGGEVLSHSLLLLHKKED GIWSTDILKDQKEPKNKTFLRCEAKNYSG RFTCWWLTTISTDLTFSVKSSRGSSDPQGV TCGAATLSAERVRGDNKEYEYSVECQEDS ACPAAEESLPIEVMVDAVHKLKYENYTSS FFIRDIIKPDPPKNLQLKPLKNSRQVEVSWE YPDTWSTPHSYFSLTFCVQVQGKSKREKK DRVFTDKTSATVICRKNASISVRAQDRYYS SSWSEWASVPCS (SEQ ID NO:268)

[00792] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-12 or a bioactive variant thereof.

[00793] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes an IL-12, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein. See, e.g., US Patent No. 8,556,882, which is incorporated by reference in its entirety and particularly for pertinent parts relating to NFAT

promoters for IL-12 expression. Exemplary fusion proteins that include IL-12 are depicted in Figures 51 and 52, and Table 58.

3. IL-18

[00794] In some embodiments, the modified TIL is associated with an IL-18 or a variant thereof. In exemplary embodiments, the IL-18 is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00795] As used herein, "interleukin 18", "IL-18," "IL18," "IGIF," "IL-1g," "interferon-gamma inducing factor," and "IL1F4," all refer to an interleukin that is a heterodimeric cytokine encoded by the IL-18 gene (e.g., Genbank Accession numbers: NM_001243211, NM_001562 and NM_001386420). IL-18, structurally similar to IL-1β, is a member of IL-1 superfamily of cytokines. This cytokine, which is expressed by many human lymphoid and nonlymphoid cells, has an important role in inflammatory processes. IL-18 in combination with IL-12 can activate cytotoxic T cells (CTLs), as well as natural killer (NK) cells, to produce IFN-γ and, therefore, contributes to tumor immunity. Thus, without being bound by any particular theory of operation, it is believed that IL-18 can enhance the anti-tumor effects of the TIL compositions provided herein.

[00796] In some embodiments, the IL-18 associated with the modified TIL is a full length IL-18, a fragment or a variant of IL-18. In some embodiments, the IL-18 is a human IL-18 or a variant human IL-18. In exemplary embodiments, the IL-18 is a biological active human IL-18 variant. In some embodiments, the IL-18 includes 1, 2, 3,4 ,5 ,6 7, 8, 9, or 10 mutations as compared to a wild-type IL-18. In some embodiments, the variant IL-18 has the amino acid sequence:

TABLE 7 – IL-18 Related Sequences.

Description	Amino Acid Sequence
Human IL-18	YFGKLESKLSVIRNLNDQVLFIDQGNRPLF EDMTDSDCRDNAPRTIFIISMYKDSQPRGM AVTISVKCEKISTLSCENKIISFKEMNPPDNI KDTKSDIIFFQRSVPGHDNKMQFESSSYEG YFLACEKERDLFKLILKKEDELGDRSIMFT VQNED (SEQ ID NO: 269)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLF EDMTDSDCRDNAPRTIFIISKYSDSRARGL AVTISVKCEKISTLSCENKIISFKEMNPPDNI KDTKSDIIFFARVPGHGRKTQFESSSYEGY FLACEKERDLFKLILKKEDELGDRSIMFTV QNED (SEQ ID NO: 270)

[00797] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-18 or a bioactive variant thereof. Exemplary fusion proteins that include IL-18 are depicted in Figure 51.

[00798] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes an IL-18, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein. Exemplary NFAT promoter-driven constructs for expression of immunomodulatory fusion proteins that include IL-21 are depicted in Table 59.

4. IL-21

[00799] In some embodiments, the modified TIL is associated with an IL-21 or a variant thereof. In exemplary embodiments, the IL-21 is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00800] In certain embodiments, the cytokine-ABD includes an IL-21 molecule or fragment thereof. As used herein, "interleukin 21" "IL-21", and "IL21" (e.g., Genbank Accession numbers: NM_001207006 and NP_001193935 (human); and NM_0001291041 and NP_001277970 (mouse)) all refer to a member of a cytokine that binds to IL-21 receptor and has potent regulatory effects on cells of the immune system, including natural killer (NK) cells and cytotoxic cells and binds to IL-21

receptor that can destroy virally infected or cancerous cells. Thus, without being bound by any particular theory of operation, it is believed that IL-21 can increase the survivability and/or anti-tumor effects of the TIL compositions provided herein.

[00801] In some embodiments, the IL-21 is a human IL-21. In some embodiments, the IL-21 associated with the modified TIL is a full length IL-21, a fragment or a variant of IL-21. In some embodiments, the IL-21 is a human IL-21 or a variant human IL-21. In exemplary embodiments, the IL-21 is a biological active human IL-21 variant. In some embodiments, the IL-21 includes a 1, 2, 3,4 ,5 ,6 7, 8, 9, or 10 mutations as compared to a wild-type IL-21.

TABLE 8 – IL-21 Related Sequences.

Description	Amino Acid Sequence
Human IL-21	QGQDRHMIRMRQLIDIVDQLKNYVNDLVP EFLPAPEDVETNCEWSAFSCFQKAQLKSA NTGNNERIINVSIKKLKRKPPSTNAGRRQK HRLTCPSCDSYEKKPPKEFLERFKSLLQKM IHQHLSSRTHGSEDS (SEQ ID NO:271)

[00802] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes an IL-21 or a bioactive variant thereof. Exemplary fusion proteins that include IL-21 are depicted in Figures 51 and 52, and Tables 58 and 59.

[00803] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes an IL-21, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein.

5. IL-2

[00804] In some embodiments, the modified TIL is associated with an IL-2 or a variant thereof. In exemplary embodiments, the IL-2 is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00805] In certain embodiments, the cytokine-ABD includes an IL-2 molecule or fragment thereof. As used herein, "interleukin 2" "IL-2", "IL2," and "TCGF" (e.g., Genbank Accession numbers: NM_000586 and NP_000577 (human) all refer to a member of a cytokine that binds to IL-2 receptor. IL-2 enhances activation-induced cell death (AICD). IL-2 also promotes the differentiation

of T cells into effector T cells and into memory T cells when the initial T cell is also stimulated by an antigen, thus helping the body fight off infections. Together with other polarizing cytokines, IL-2 stimulates naive CD4+ T cell differentiation into Th1 and Th2 lymphocytes and impedes differentiation into Th17 and follicular Th lymphocytes.. IL-2 also increases the cell killing activity of both natural killer cells and cytotoxic T cells. Thus, without being bound by any particular theory of operation, it is believed that IL-2 can increase the survivability and/or anti-tumor effects of the TIL compositions provided herein.

[00806] In some embodiments, the IL-2 is a human IL-2. In some embodiments, the IL-2 associated with the modified TIL is a full length IL-2, a fragment or a variant of IL-2. In some embodiments, the IL-2 is a human IL-2 or a variant human IL-2. In exemplary embodiments, the IL-2 is a biological active human IL-2 variant. In some embodiments, the IL-2 includes a 1, 2, 3,4 ,5 ,6 7, 8, 9, or 10 mutations as compared to a wild-type IL-2.

TABLE 9 – IL-2 Related Sequences.

Description	Amino Acid Sequence
Human IL-2	MYRMQLLSCIALSLALVTNSAPTSSSTKKT QLQLEHLLLDLQMILNGINNYKNPKLTRM LTFKFYMPKKATELKHLQCLEEELKPLEE VLNLAQSKNFHLRPRDLISNINVIVLELKG SETTFMCEYADETATIVEFLNRWITFCQSII STLT (SEQ ID NO:272)

[00807] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-2 or a bioactive variant thereof. Exemplary fusion proteins that include IL-2 are depicted in Figures 51 and 52.

[00808] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes an IL-2, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein.

6. CD40 AGONISTS

[00809] In some embodiments, the modified TIL is associated with CD40 agonist. In exemplary embodiments, the CD40 agonist is included as part of an immunomodulatory fusion protein as described herein (e.g., a membrane anchored immunomodulatory fusion protein).

[00810] Cluster of differentiation 40, CD40, is a costimulatory protein found on antigen-presenting cells (APCs) and is required for APC activation. The binding of CD40L (CD154) on T helper cells to CD40 activates antigen presenting cells (e.g., dendritic cells) and induces a variety of downstream effects. Without being by any particular theory of operation, it is believed that the addition of one or more immunomodulatory agents that activate CD40 on antigen presenting cells (i.e., CD40 agonists) can enhance the anti-tumor effects of the TIL compositions provided herein. CD40 agonists, include, for example, CD40L and antibody or antibody fragments thereof (e.g., an scFv) that agonistically binds CD40. In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a CD40L or a bioactive variant thereof. In some embodiments, the TIL composition includes an immunomodulatory fusion protein that includes an agonistic anti-CD40 binding domain (e.g., an scFv). Exemplary CD40 agonist sequences are depicted in the table below.

[00811] CD40 agonist activity can be measured using any suitable method known in the art. Ligation of CD40 on DC, for example, induces increased surface expression of costimulatory and MHC molecules, production of proinflammatory cytokines, and enhanced T cell triggering. CD40 ligation on resting B cells increases antigen-presenting function and proliferation. In exemplary embodiments, the CD40 agonist is capable of activating human dendritic cells.

[00812] In some embodiments, the TIL composition includes an agonistic anti-CD40 binding domain having the VH and VL sequences of an anti-CD40 scFv depicted in Table 10 or a bioactive variant thereof. In some embodiments, the anti-CD40 binding domain includes a VH sequence that is at least about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to the VH sequence depicted in Table 10. In some embodiments, the agonistic anti-CD40 binding domain includes a VH sequence that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions as compared to the VH sequence depicted in Table 10. In some embodiments, the anti-CD40 binding domain includes a VL sequence that is at least about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to the VL sequence depicted in Table 10. In some embodiments, the anti-CD40 binding domain includes a VL sequence that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions as compared to the VL sequence depicted in Table 10. In exemplary embodiments, the anti-CD40 binding domain is an anti-CD40 scFv selected from SEQ ID NOs:276, 279, 282, and 285 in Table 10.

[00813] In some embodiments, the anti-CD40 binding domain is a variant of an anti-CD40 scFv in Table 10 that is capable of binding to human CD40. In exemplary embodiments, the variant anti-CD40 scFv is least about 75%, 80%, 85%, 90%, 95%, or 99% identical to an anti-CD40 scFv selected from SEQ ID NOs:276, 279, 282, and 285 in Table 10.

[00814] Assessment of CD40 binding domain binding can be measured using any suitable assay known in the art, including, but not limited to: a Biacore, surface plasmon resonance (SPR) and/or BLI (biolayer interferometry, e.g., Octet assay) assay.

[00815] Additional CD40 binding domains (VH and VLs) that are useful as immunomodulatory agents include those described in US Patent Nos. US 6,838,261, US 6,843,989, US 7,338,660, US 8,7778,345, which are incorporated by reference herein, particularly with respect to teachings of anti-CD40 antibodies and VH, VL and CDR sequences.

[00816] In some embodiments, the CD40 agonist is a CD40 ligand (CD40L). In exemplary embodiments, the CD40L is human CD40L (SEQ ID NO:270). In some embodiments, the CD40L is a variant of a human CD40L that is at least about 75%, 80%, 85%, 90%, 95%, or 99% identical to SEQ ID NO:253. In some embodiments, the CD40L is a variant of a human CD40L that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions as compared to SEQ ID NO:273.

[00817] Exemplary fusion proteins that include CD40 agonists are depicted in Figures 51 and 52.

[00818] In exemplary embodiments the TIL compositions provided herein includes a nucleic acid encoding an immunomodulatory fusion protein that includes a CD40 agonist, wherein the nucleic acid is operably linked to a NFAT promoter, as described herein.

TABLE 10 – CD40 Agonist Related Sequences.

Description	Amino Acid Sequence
Human CD40L	MIETYNQTSPRSAATGLPISMKIFMYLLTV FLITQMIGSALFAVYLHRRLDKIEDERNLH EDFVFMKTIQRCNTGERSLSLLNCEEIKSQ FEGFVKDIMLNKEETKKENSFEMQKGDQN PQIAAHVISEASSKTTSVLQWAEKGYYTM SNNLVTLENGKQLTVKRQGLYYIYAQVTF CSNREASSQAPFIASLCLKSPGRFERILLRA ANTHSSAKPCGQQSIHLGGVFELQPGASVF VNVTDPSQVSHGTGFTSFGLLKL (SEQ ID NO: 273)
Anti-human CD40 VH (Sotigalimab)	QVQLVESGGGVVQPGRSLRLSCAASGFSF SSTYVCWVRQAPGKGLEWIACIYTGDGTN YSASWAKGRFTISKDSSKNTVYLQMNSLR AEDTAVYFCARPDITYGFAINFWGPGTLV TVSS (SEQ ID NO: 274)

Anti-human CD40 VL (Sotigalimab)	DIQMTQSPSSLSASVGDRVTIKCQASQSISS RLAWYQQKPGKPPKLLIYRASTLASGVPS RFSGSGSGTDFTLTISSLQPEDVATYYCQC TGYGISWPIGGGTKVEIK (SEQ ID NO: 275)
Anti-human CD40 scFv (Sotigalimab)	QVQLVESGGGVVQPGRSLRLSCAASGFSF SSTYVCWVRQAPGKGLEWIACIYTGDGTN YSASWAKGRFTISKDSSKNTVYLQMNSLR AEDTAVYFCARPDITYGFAINFWGPGTLV TVSSGGGGSGGGGSGGGGSGGGGSDIQM TQSPSSLSASVGDRVTIKCQASQSISSRLA WYQQKPGKPPKLLIYRASTLASGVPSRFSG SGSGTDFTLTISSLQPEDVATYYCQCTGYG ISWPIGGGTKVEIK (SEQ ID NO: 276)
Anti-human CD40 VH (Dacetuzumab)	QLVESGGGLVQPGGSLRLSCAASGYSFTG YYIHWVRQAPGKGLEWVARVIPNAGGTS YNQKFKGRFTLSVDNSKNTAYLQMNSLR AEDTAVYYCAREGIYWWGQGTLVTVSS (SEQ ID NO: 277)
Anti-human CD40 VL (Dacetuzumab)	DIQMTQSPSSLSASVGDRVTITCRSSQSLV HSNGNTFLHWYQQKPGKAPKLLIYTVSNR FSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YFCSQTTHVPWTFGQGTKVEIK (SEQ ID NO: 278)
Anti-human CD40 scFv (Dacetuzumab)	QLVESGGGLVQPGGSLRLSCAASGYSFTG YYIHWVRQAPGKGLEWVARVIPNAGGTS YNQKFKGRFTLSVDNSKNTAYLQMNSLR AEDTAVYYCAREGIYWWGQGTLVTVSSG GGGSGGGGSGGGGSGGGGSDIQMTQSPSS LSASVGDRVTITCRSSQSLVHSNGNTFLH WYQQKPGKAPKLLIYTVSNRFSGVPSRFS GSGSGTDFTLTISSLQPEDFATYFCSQTTHV PWTFGQGTKVEIK (SEQ ID NO: 279)
Anti-CD40 VH (Lucatutuzumab)	QVQLVESGGGVVQPGRSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVAVISYEESN RYHADSVKGRFTISRDNSKITLYLQMNSLR TEDTAVYYCARDGGIAAPGPDYWGQGTL VTVSS (SEQ ID NO: 280)

Anti-CD40 VL (Lucatutuzumab)	DIVMTQSPLSLTVTPGEPASISCRSSQSLLY SNGYNYLDWYLQKPGQSPQVLISLGSNRA SGVPDRFSGSGSGTDFTLKISRVEAEDVGV YYCMQARQTPFTFGPGTKVDIR (SEQ ID NO: 281)
Anti-CD40 scFv (Lucatutuzumab)	QVQLVESGGGVVQPGRSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVAVISYEESN RYHADSVKGRFTISRDNSKITLYLQMNSLR TEDTAVYYCARDGGIAAPGPDYWGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSDIV MTQSPLSLTVTPGEPASISCRSSQSLLYSNG YNYLDWYLQKPGQSPQVLISLGSNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYC MQARQTPFTFGPGTKVDIR (SEQ ID NO: 282)
Anti-CD40 VH (Selicrelumab)	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGWINPDS GGTNYAQKFQGRVTMTRDTSISTAYMEL NRLRSDDTAVYYCARDQPLGYCTNGVCS YFDYWGQGTLVTVSS (SEQ ID NO: 283)
Anti-CD40 VL (Selicrelumab)	DIQMTQSPSSVSASVGDRVTITCRASQGIY SWLAWYQQKPGKAPNLLIYTASTLQSGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQ ANIFPLTFGGGTKVEIK (SEQ ID NO: 284)
Anti-CD40 scFv (Selicrelumab)	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGWINPDS GGTNYAQKFQGRVTMTRDTSISTAYMEL NRLRSDDTAVYYCARDQPLGYCTNGVCS YFDYWGQGTLVTVSSGGGGSGGGGSGGG GSGGGGSDIQMTQSPSSVSASVGDRVTITC RASQGIYSWLAWYQQKPGKAPNLLIYTAS TLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQANIFPLTFGGGTKVEIK (SEQ ID NO: 285)

IX. Pharmaceutical Compositions, Dosages, and Dosing Regimens

[001779] In some embodiments, TILs, MILs, or PBLs expanded and/or genetically modified (including TILs, MILs, or PBLs genetically-modified to express a CCR) using the methods of the present disclosure are administered to a patient as a pharmaceutical composition. In some embodiments, the pharmaceutical composition is a suspension of TILs in a sterile buffer. TILs expanded using PBMCs of the present disclosure may be administered by any suitable route as known in the art. In some embodiments, the T-cells are administered as a single intra-arterial or intravenous infusion, which preferably lasts approximately 30 to 60 minutes. Other suitable routes of administration include intraperitoneal, intrathecal, and intralymphatic administration.

[001780] Any suitable dose of TILs can be administered. In some embodiments, from about 2.3×10^{10} to about 13.7×10^{10} TILs are administered, with an average of around 7.8×10^{10} TILs, particularly if the cancer is NSCLC or melanoma. In some embodiments, from about 2.3×1010 to about 13.7×1010 TILs are administered, with an average of around 7.8×1010 TILs, particularly if the cancer is metastatic NSCLC or metastatic melanoma. In some embodiments, about 1.2×10^{10} to about 4.3×10^{10} of TILs are administered. In some embodiments, about 3×10^{10} to about 12×10^{10} TILs are administered. In some embodiments, about 4×10^{10} to about 10×10^{10} TILs are administered. In some embodiments, about 5×10^{10} to about 8×10^{10} TILs are administered. In some embodiments, about 6×10^{10} to about 8×10^{10} TILs are administered. In some embodiments, about 7×10^{10} to about 8×10^{10} TILs are administered. In some embodiments, the therapeutically effective dosage is about 2.3×10^{10} to about 13.7×10^{10}. In some embodiments, the therapeutically effective dosage is about 7.8×10^{10} TILs, particularly of the cancer is melanoma. In some embodiments, the therapeutically effective dosage is about 7.8×1010 TILs, particularly of the cancer is metastatic melanoma. In some embodiments, the therapeutically effective dosage is about 7.8×1010 TILs, particularly of the cancer is NSCLC. In some embodiments, the therapeutically effective dosage is about 7.8×1010 TILs, particularly of the cancer is metastatic NSCLC. In some embodiments, the therapeutically effective dosage is about 1.2×10^{10} to about 4.3×10^{10} of TILs. In some embodiments, the therapeutically effective dosage is about 3×10^{10} to about 12×10^{10} TILs. In some embodiments, the therapeutically effective dosage is about 4×10^{10} to about 10×10^{10} TILs. In some embodiments, the therapeutically effective dosage is about 5×10^{10} to about 8×10^{10} TILs. In some embodiments, the therapeutically effective dosage is about 6×10^{10} to about 8×10^{10} TILs. In some embodiments, the therapeutically effective dosage is about 7×10^{10} to about 8×10^{10} TILs.

[001781] In some embodiments, the number of the TILs provided in the pharmaceutical compositions of the invention is about 1×10^{6}, 2×10^{6}, 3×10^{6}, 4×10^{6}, 5×10^{6}, 6×10^{6}, 7×10^{6}, 8×10^{6}, 9×10^{6}, 1×10^{7}, 2×10^{7}, 3×10^{7}, 4×10^{7}, 5×10^{7}, 6×10^{7}, 7×10^{7}, 8×10^{7}, 9×10^{7}, 1×10^{8}, 2×10^{8}, 3×10^{8}, 4×10^{8}, 5×10^{8}, 6×10^{8}, 7×10^{8}, 8×10^{8}, 9×10^{8}, 1×10^{9}, 2×10^{9}, 3×10^{9}, 4×10^{9}, 5×10^{9}, 6×10^{9}, 7×10^{9}, 8×10^{9}, 9×10^{9}, 1×10^{10}, 2×10^{10},

3×10^{10}, 4×10^{10}, 5×10^{10}, 6×10^{10}, 7×10^{10}, 8×10^{10}, 9×10^{10}, 1×10^{11}, 2×10^{11}, 3×10^{11}, 4×10^{11}, 5×10^{11}, 6×10^{11}, 7×10^{11}, 8×10^{11}, 9×10^{11}, 1×10^{12}, 2×10^{12}, 3×10^{12}, 4×10^{12}, 5×10^{12}, 6×10^{12}, 7×10^{12}, 8×10^{12}, 9×10^{12}, 1×10^{13}, 2×10^{13}, 3×10^{13}, 4×10^{13}, 5×10^{13}, 6×10^{13}, 7×10^{13}, 8×10^{13}, and 9×10^{13}. In some embodiments, the number of the TILs provided in the pharmaceutical compositions of the invention is in the range of 1×10^{6} to 5×10^{6}, 5×10^{6} to 1×10^{7}, 1×10^{7} to 5×10^{7}, 5×10^{7} to 1×10^{8}, 1×10^{8} to 5×10^{8}, 5×10^{8} to 1×10^{9}, 1×10^{9} to 5×10^{9}, 5×10^{9} to 1×10^{10}, 1×10^{10} to 5×10^{10}, 5×10^{10} to 1×10^{11}, 5×10^{11} to 1×10^{12}, 1×10^{12} to 5×10^{12}, and 5×10^{12} to 1×10^{13}.

[001782] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is less than, for example, 100%, 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1%, 0.09%, 0.08%, 0.07%, 0.06%, 0.05%, 0.04%, 0.03%, 0.02%, 0.01%, 0.009%, 0.008%, 0.007%, 0.006%, 0.005%, 0.004%, 0.003%, 0.002%, 0.001%, 0.0009%, 0.0008%, 0.0007%, 0.0006%, 0.0005%, 0.0004%, 0.0003%, 0.0002% or 0.0001% w/w, w/v or v/v of the pharmaceutical composition.

[001783] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is greater than 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 19.75%, 19.50%, 19.25% 19%, 18.75%, 18.50%, 18.25% 18%, 17.75%, 17.50%, 17.25% 17%, 16.75%, 16.50%, 16.25% 16%, 15.75%, 15.50%, 15.25% 15%, 14.75%, 14.50%, 14.25% 14%, 13.75%, 13.50%, 13.25% 13%, 12.75%, 12.50%, 12.25% 12%, 11.75%, 11.50%, 11.25% 11%, 10.75%, 10.50%, 10.25% 10%, 9.75%, 9.50%, 9.25% 9%, 8.75%, 8.50%, 8.25% 8%, 7.75%, 7.50%, 7.25% 7%, 6.75%, 6.50%, 6.25% 6%, 5.75%, 5.50%, 5.25% 5%, 4.75%, 4.50%, 4.25%, 4%, 3.75%, 3.50%, 3.25%, 3%, 2.75%, 2.50%, 2.25%, 2%, 1.75%, 1.50%, 125%, 1%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1%, 0.09%, 0.08%, 0.07%, 0.06%, 0.05%, 0.04%, 0.03%, 0.02%, 0.01%, 0.009%, 0.008%, 0.007%, 0.006%, 0.005%, 0.004%, 0.003%, 0.002%, 0.001%, 0.0009%, 0.0008%, 0.0007%, 0.0006%, 0.0005%, 0.0004%, 0.0003%, 0.0002% or 0.0001% w/w, w/v, or v/v of the pharmaceutical composition.

[001784] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is in the range from about 0.0001% to about 50%, about 0.001% to about 40%, about 0.01% to about 30%, about 0.02% to about 29%, about 0.03% to about 28%, about 0.04% to about 27%, about 0.05% to about 26%, about 0.06% to about 25%, about 0.07% to about 24%, about 0.08% to about 23%, about 0.09% to about 22%, about 0.1% to about 21%, about 0.2% to about 20%, about 0.3% to about 19%, about 0.4% to about 18%, about 0.5% to about 17%, about 0.6% to about 16%, about 0.7% to about 15%, about 0.8% to about 14%, about 0.9% to about 12% or about 1% to about 10% w/w, w/v or v/v of the pharmaceutical composition.

[001785] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is in the range from about 0.001% to about 10%, about 0.01% to about 5%, about 0.02% to about 4.5%, about 0.03% to about 4%, about 0.04% to about 3.5%, about 0.05% to about 3%, about 0.06% to about 2.5%, about 0.07% to about 2%, about 0.08% to about 1.5%, about 0.09% to about 1%, about 0.1% to about 0.9% w/w, w/v or v/v of the pharmaceutical composition.

[001786] In some embodiments, the amount of the TILs provided in the pharmaceutical compositions of the invention is equal to or less than 10 g, 9.5 g, 9.0 g, 8.5 g, 8.0 g, 7.5 g, 7.0 g, 6.5 g, 6.0 g, 5.5 g, 5.0 g, 4.5 g, 4.0 g, 3.5 g, 3.0 g, 2.5 g, 2.0 g, 1.5 g, 1.0 g, 0.95 g, 0.9 g, 0.85 g, 0.8 g, 0.75 g, 0.7 g, 0.65 g, 0.6 g, 0.55 g, 0.5 g, 0.45 g, 0.4 g, 0.35 g, 0.3 g, 0.25 g, 0.2 g, 0.15 g, 0.1 g, 0.09 g, 0.08 g, 0.07 g, 0.06 g, 0.05 g, 0.04 g, 0.03 g, 0.02 g, 0.01 g, 0.009 g, 0.008 g, 0.007 g, 0.006 g, 0.005 g, 0.004 g, 0.003 g, 0.002 g, 0.001 g, 0.0009 g, 0.0008 g, 0.0007 g, 0.0006 g, 0.0005 g, 0.0004 g, 0.0003 g, 0.0002 g, or 0.0001 g.

[001787] In some embodiments, the amount of the TILs provided in the pharmaceutical compositions of the invention is more than 0.0001 g, 0.0002 g, 0.0003 g, 0.0004 g, 0.0005 g, 0.0006 g, 0.0007 g, 0.0008 g, 0.0009 g, 0.001 g, 0.0015 g, 0.002 g, 0.0025 g, 0.003 g, 0.0035 g, 0.004 g, 0.0045 g, 0.005 g, 0.0055 g, 0.006 g, 0.0065 g, 0.007 g, 0.0075 g, 0.008 g, 0.0085 g, 0.009 g, 0.0095 g, 0.01 g, 0.015 g, 0.02 g, 0.025 g, 0.03 g, 0.035 g, 0.04 g, 0.045 g, 0.05 g, 0.055 g, 0.06 g, 0.065 g, 0.07 g, 0.075 g, 0.08 g, 0.085 g, 0.09 g, 0.095 g, 0.1 g, 0.15 g, 0.2 g, 0.25 g, 0.3 g, 0.35 g, 0.4 g, 0.45 g, 0.5 g, 0.55 g, 0.6 g, 0.65 g, 0.7 g, 0.75 g, 0.8 g, 0.85 g, 0.9 g, 0.95 g, 1 g, 1.5 g, 2 g, 2.5, 3 g, 3.5, 4 g, 4.5 g, 5 g, 5.5 g, 6 g, 6.5 g, 7 g, 7.5 g, 8 g, 8.5 g, 9 g, 9.5 g, or 10 g.

[001788] The TILs provided in the pharmaceutical compositions of the invention are effective over a wide dosage range. The exact dosage will depend upon the route of administration, the form in which the compound is administered, the gender and age of the subject to be treated, the body weight of the subject to be treated, and the preference and experience of the attending physician. The clinically-established dosages of the TILs may also be used if appropriate. The amounts of the pharmaceutical compositions administered using the methods herein, such as the dosages of TILs, will be dependent on the human or mammal being treated, the severity of the disorder or condition, the rate of administration, the disposition of the active pharmaceutical ingredients and the discretion of the prescribing physician.

[001789] In some embodiments, TILs may be administered in a single dose. Such administration may be by injection, *e.g.*, intravenous injection. In some embodiments, TILs may be administered in multiple doses. Dosing may be once, twice, three times, four times, five times, six times, or more than six times per year. Dosing may be once a month, once every two weeks, once a week, or once every other day. Administration of TILs may continue as long as necessary.

[001790] In some embodiments, an effective dosage of TILs is about 1×10^6, 2×10^6, 3×10^6, 4×10^6, 5×10^6, 6×10^6, 7×10^6, 8×10^6, 9×10^6, 1×10^7, 2×10^7, 3×10^7, 4×10^7, 5×10^7, 6×10^7, 7×10^7, 8×10^7, 9×10^7, 1×10^8, 2×10^8, 3×10^8, 4×10^8, 5×10^8, 6×10^8, 7×10^8, 8×10^8, 9×10^8, 1×10^9, 2×10^9, 3×10^9, 4×10^9, 5×10^9, 6×10^9, 7×10^9, 8×10^9, 9×10^9, 1×10^{10}, 2×10^{10}, 3×10^{10}, 4×10^{10}, 5×10^{10}, 6×10^{10}, 7×10^{10}, 8×10^{10}, 9×10^{10}, 1×10^{11}, 2×10^{11}, 3×10^{11}, 4×10^{11}, 5×10^{11}, 6×10^{11}, 7×10^{11}, 8×10^{11}, 9×10^{11}, 1×10^{12}, 2×10^{12}, 3×10^{12}, 4×10^{12}, 5×10^{12}, 6×10^{12}, 7×10^{12}, 8×10^{12}, 9×10^{12}, 1×10^{13}, 2×10^{13}, 3×10^{13}, 4×10^{13}, 5×10^{13}, 6×10^{13}, 7×10^{13}, 8×10^{13}, and 9×10^{13}. In some embodiments, an effective dosage of TILs is in the range of 1×10^6 to 5×10^6, 5×10^6 to 1×10^7, 1×10^7 to 5×10^7, 5×10^7 to 1×10^8, 1×10^8 to 5×10^8, 5×10^8 to 1×10^9, 1×10^9 to 5×10^9, 5×10^9 to 1×10^{10}, 1×10^{10} to 5×10^{10}, 5×10^{10} to 1×10^{11}, 5×10^{11} to 1×10^{12}, 1×10^{12} to 5×10^{12}, and 5×10^{12} to 1×10^{13}.

[001791] In some embodiments, an effective dosage of TILs is in the range of about 0.01 mg/kg to about 4.3 mg/kg, about 0.15 mg/kg to about 3.6 mg/kg, about 0.3 mg/kg to about 3.2 mg/kg, about 0.35 mg/kg to about 2.85 mg/kg, about 0.15 mg/kg to about 2.85 mg/kg, about 0.3 mg to about 2.15 mg/kg, about 0.45 mg/kg to about 1.7 mg/kg, about 0.15 mg/kg to about 1.3 mg/kg, about 0.3 mg/kg to about 1.15 mg/kg, about 0.45 mg/kg to about 1 mg/kg, about 0.55 mg/kg to about 0.85 mg/kg, about 0.65 mg/kg to about 0.8 mg/kg, about 0.7 mg/kg to about 0.75 mg/kg, about 0.7 mg/kg to about 2.15 mg/kg, about 0.85 mg/kg to about 2 mg/kg, about 1 mg/kg to about 1.85 mg/kg, about 1.15 mg/kg to about 1.7 mg/kg, about 1.3 mg/kg mg to about 1.6 mg/kg, about 1.35 mg/kg to about 1.5 mg/kg, about 2.15 mg/kg to about 3.6 mg/kg, about 2.3 mg/kg to about 3.4 mg/kg, about 2.4 mg/kg to about 3.3 mg/kg, about 2.6 mg/kg to about 3.15 mg/kg, about 2.7 mg/kg to about 3 mg/kg, about 2.8 mg/kg to about 3 mg/kg, or about 2.85 mg/kg to about 2.95 mg/kg.

[001792] In some embodiments, an effective dosage of TILs is in the range of about 1 mg to about 500 mg, about 10 mg to about 300 mg, about 20 mg to about 250 mg, about 25 mg to about 200 mg, about 1 mg to about 50 mg, about 5 mg to about 45 mg, about 10 mg to about 40 mg, about 15 mg to about 35 mg, about 20 mg to about 30 mg, about 23 mg to about 28 mg, about 50 mg to about 150 mg, about 60 mg to about 140 mg, about 70 mg to about 130 mg, about 80 mg to about 120 mg, about 90 mg to about 110 mg, or about 95 mg to about 105 mg, about 98 mg to about 102 mg, about 150 mg to about 250 mg, about 160 mg to about 240 mg, about 170 mg to about 230 mg, about 180 mg to about 220 mg, about 190 mg to about 210 mg, about 195 mg to about 205 mg, or about 198 to about 207 mg.

[001793] An effective amount of the TILs may be administered in either single or multiple doses by any of the accepted modes of administration of agents having similar utilities, including intranasal and transdermal routes, by intra-arterial injection, intravenously, intraperitoneally, parenterally, intramuscularly, subcutaneously, topically, by transplantation, or by inhalation.

[001794] In some embodiments, the invention provides an infusion bag comprising the therapeutic population of TILs described in any of the preceding paragraphs above.

[001795] In some embodiments, the invention provides a tumor infiltrating lymphocyte (TIL) composition comprising the therapeutic population of TILs described in any of the preceding paragraphs above and a pharmaceutically acceptable carrier.

[001796] In some embodiments, the invention provides an infusion bag comprising the TIL composition described in any of the preceding paragraphs above.

[001797] In some embodiments, the invention provides a cryopreserved preparation of the therapeutic population of TILs described in any of the preceding paragraphs above.

[001798] In some embodiments, the invention provides a tumor infiltrating lymphocyte (TIL) composition comprising the therapeutic population of TILs described in any of the preceding paragraphs above and a cryopreservation media.

[001799] In some embodiments, the invention provides the TIL composition described in any of the preceding paragraphs above modified such that the cryopreservation media contains DMSO.

[001800] In some embodiments, the invention provides the TIL composition described in any of the preceding paragraphs above modified such that the cryopreservation media contains 7-10% DMSO.

[001801] In some embodiments, the invention provides a cryopreserved preparation of the TIL composition described in any of the preceding paragraphs above.

[001802] In some embodiments, TILs expanded using the methods of the present disclosure are administered to a patient as a pharmaceutical composition. In some embodiments, the pharmaceutical composition is a suspension of TILs in a sterile buffer. TILs expanded using PBMCs of the present disclosure may be administered by any suitable route as known in the art. In some embodiments, the T-cells are administered as a single intra-arterial or intravenous infusion, which preferably lasts approximately 30 to 60 minutes. Other suitable routes of administration include intraperitoneal, intrathecal, and intralymphatic administration.

[001803] Any suitable dose of TILs can be administered. In some embodiments, from about 2.3×10^{10} to about 13.7×10^{10} TILs are administered, with an average of around 7.8×10^{10} TILs, particularly if the cancer is NSCLC. In some embodiments, about 1.2×10^{10} to about 4.3×10^{10} of TILs are administered. In some embodiments, about 3×10^{10} to about 12×10^{10} TILs are administered. In some embodiments, about 4×10^{10} to about 10×10^{10} TILs are administered. In some embodiments, about 5×10^{10} to about 8×10^{10} TILs are administered. In some embodiments, about 6×10^{10} to about 8×10^{10} TILs are administered. In some embodiments, about 7×10^{10} to about 8×10^{10} TILs are administered. In some

embodiments, therapeutically effective dosage is about 2.3×10^{10} to about 13.7×10^{10}. In some embodiments, therapeutically effective dosage is about 7.8×10^{10} TILs, particularly of the cancer is NSCLC. In some embodiments, therapeutically effective dosage is about 1.2×10^{10} to about 4.3×10^{10} of TILs. In some embodiments, therapeutically effective dosage is about 3×10^{10} to about 12×10^{10} TILs. In some embodiments, therapeutically effective dosage is about 4×10^{10} to about 10×10^{10} TILs. In some embodiments, therapeutically effective dosage is about 5×10^{10} to about 8×10^{10} TILs. In some embodiments, therapeutically effective dosage is about 6×10^{10} to about 8×10^{10} TILs. In some embodiments, therapeutically effective dosage is about 7×10^{10} to about 8×10^{10} TILs.

[001804] In some embodiments, the number of the TILs provided in the pharmaceutical compositions of the invention is about 1×10^{6}, 2×10^{6}, 3×10^{6}, 4×10^{6}, 5×10^{6}, 6×10^{6}, 7×10^{6}, 8×10^{6}, 9×10^{6}, 1×10^{7}, 2×10^{7}, 3×10^{7}, 4×10^{7}, 5×10^{7}, 6×10^{7}, 7×10^{7}, 8×10^{7}, 9×10^{7}, 1×10^{8}, 2×10^{8}, 3×10^{8}, 4×10^{8}, 5×10^{8}, 6×10^{8}, 7×10^{8}, 8×10^{8}, 9×10^{8}, 1×10^{9}, 2×10^{9}, 3×10^{9}, 4×10^{9}, 5×10^{9}, 6×10^{9}, 7×10^{9}, 8×10^{9}, 9×10^{9}, 1×10^{10}, 2×10^{10}, 3×10^{10}, 4×10^{10}, 5×10^{10}, 6×10^{10}, 7×10^{10}, 8×10^{10}, 9×10^{10}, 1×10^{11}, 2×10^{11}, 3×10^{11}, 4×10^{11}, 5×10^{11}, 6×10^{11}, 7×10^{11}, 8×10^{11}, 9×10^{11}, 1×10^{12}, 2×10^{12}, 3×10^{12}, 4×10^{12}, 5×10^{12}, 6×10^{12}, 7×10^{12}, 8×10^{12}, 9×10^{12}, 1×10^{13}, 2×10^{13}, 3×10^{13}, 4×10^{13}, 5×10^{13}, 6×10^{13}, 7×10^{13}, 8×10^{13}, and 9×10^{13}. In some embodiments, the number of the TILs provided in the pharmaceutical compositions of the invention is in the range of 1×10^{6} to 5×10^{6}, 5×10^{6} to 1×10^{7}, 1×10^{7} to 5×10^{7}, 5×10^{7} to 1×10^{8}, 1×10^{8} to 5×10^{8}, 5×10^{8} to 1×10^{9}, 1×10^{9} to 5×10^{9}, 5×10^{9} to 1×10^{10}, 1×10^{10} to 5×10^{10}, 5×10^{10} to 1×10^{11}, 5×10^{11} to 1×10^{12}, 1×10^{12} to 5×10^{12}, and 5×10^{12} to 1×10^{13}.

[001805] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is less than, for example, 100%, 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1%, 0.09%, 0.08%, 0.07%, 0.06%, 0.05%, 0.04%, 0.03%, 0.02%, 0.01%, 0.009%, 0.008%, 0.007%, 0.006%, 0.005%, 0.004%, 0.003%, 0.002%, 0.001%, 0.0009%, 0.0008%, 0.0007%, 0.0006%, 0.0005%, 0.0004%, 0.0003%, 0.0002% or 0.0001% w/w, w/v or v/v of the pharmaceutical composition.

[001806] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is greater than 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 19.75%, 19.50%, 19.25% 19%, 18.75%, 18.50%, 18.25% 18%, 17.75%, 17.50%, 17.25% 17%, 16.75%, 16.50%, 16.25% 16%, 15.75%, 15.50%, 15.25% 15%, 14.75%, 14.50%, 14.25% 14%, 13.75%, 13.50%, 13.25% 13%, 12.75%, 12.50%, 12.25% 12%, 11.75%, 11.50%, 11.25% 11%, 10.75%, 10.50%, 10.25% 10%, 9.75%, 9.50%, 9.25% 9%, 8.75%, 8.50%, 8.25% 8%, 7.75%, 7.50%, 7.25% 7%, 6.75%, 6.50%, 6.25% 6%, 5.75%, 5.50%, 5.25% 5%, 4.75%, 4.50%, 4.25%, 4%, 3.75%, 3.50%, 3.25%, 3%, 2.75%, 2.50%, 2.25%, 2%, 1.75%, 1.50%, 125%, 1%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1%, 0.09%, 0.08%, 0.07%, 0.06%, 0.05%, 0.04%, 0.03%, 0.02%, 0.01%, 0.009%, 0.008%, 0.007%,

0.006%, 0.005%, 0.004%, 0.003%, 0.002%, 0.001%, 0.0009%, 0.0008%, 0.0007%, 0.0006%, 0.0005%, 0.0004%, 0.0003%, 0.0002% or 0.0001% w/w, w/v, or v/v of the pharmaceutical composition.

[001807] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is in the range from about 0.0001% to about 50%, about 0.001% to about 40%, about 0.01% to about 30%, about 0.02% to about 29%, about 0.03% to about 28%, about 0.04% to about 27%, about 0.05% to about 26%, about 0.06% to about 25%, about 0.07% to about 24%, about 0.08% to about 23%, about 0.09% to about 22%, about 0.1% to about 21%, about 0.2% to about 20%, about 0.3% to about 19%, about 0.4% to about 18%, about 0.5% to about 17%, about 0.6% to about 16%, about 0.7% to about 15%, about 0.8% to about 14%, about 0.9% to about 12% or about 1% to about 10% w/w, w/v or v/v of the pharmaceutical composition.

[001808] In some embodiments, the concentration of the TILs provided in the pharmaceutical compositions of the invention is in the range from about 0.001% to about 10%, about 0.01% to about 5%, about 0.02% to about 4.5%, about 0.03% to about 4%, about 0.04% to about 3.5%, about 0.05% to about 3%, about 0.06% to about 2.5%, about 0.07% to about 2%, about 0.08% to about 1.5%, about 0.09% to about 1%, about 0.1% to about 0.9% w/w, w/v or v/v of the pharmaceutical composition.

[001809] In some embodiments, the amount of the TILs provided in the pharmaceutical compositions of the invention is equal to or less than 10 g, 9.5 g, 9.0 g, 8.5 g, 8.0 g, 7.5 g, 7.0 g, 6.5 g, 6.0 g, 5.5 g, 5.0 g, 4.5 g, 4.0 g, 3.5 g, 3.0 g, 2.5 g, 2.0 g, 1.5 g, 1.0 g, 0.95 g, 0.9 g, 0.85 g, 0.8 g, 0.75 g, 0.7 g, 0.65 g, 0.6 g, 0.55 g, 0.5 g, 0.45 g, 0.4 g, 0.35 g, 0.3 g, 0.25 g, 0.2 g, 0.15 g, 0.1 g, 0.09 g, 0.08 g, 0.07 g, 0.06 g, 0.05 g, 0.04 g, 0.03 g, 0.02 g, 0.01 g, 0.009 g, 0.008 g, 0.007 g, 0.006 g, 0.005 g, 0.004 g, 0.003 g, 0.002 g, 0.001 g, 0.0009 g, 0.0008 g, 0.0007 g, 0.0006 g, 0.0005 g, 0.0004 g, 0.0003 g, 0.0002 g, or 0.0001 g.

[001810] In some embodiments, the amount of the TILs provided in the pharmaceutical compositions of the invention is more than 0.0001 g, 0.0002 g, 0.0003 g, 0.0004 g, 0.0005 g, 0.0006 g, 0.0007 g, 0.0008 g, 0.0009 g, 0.001 g, 0.0015 g, 0.002 g, 0.0025 g, 0.003 g, 0.0035 g, 0.004 g, 0.0045 g, 0.005 g, 0.0055 g, 0.006 g, 0.0065 g, 0.007 g, 0.0075 g, 0.008 g, 0.0085 g, 0.009 g, 0.0095 g, 0.01 g, 0.015 g, 0.02 g, 0.025 g, 0.03 g, 0.035 g, 0.04 g, 0.045 g, 0.05 g, 0.055 g, 0.06 g, 0.065 g, 0.07 g, 0.075 g, 0.08 g, 0.085 g, 0.09 g, 0.095 g, 0.1 g, 0.15 g, 0.2 g, 0.25 g, 0.3 g, 0.35 g, 0.4 g, 0.45 g, 0.5 g, 0.55 g, 0.6 g, 0.65 g, 0.7 g, 0.75 g, 0.8 g, 0.85 g, 0.9 g, 0.95 g, 1 g, 1.5 g, 2 g, 2.5, 3 g, 3.5, 4 g, 4.5 g, 5 g, 5.5 g, 6 g, 6.5 g, 7 g, 7.5 g, 8 g, 8.5 g, 9 g, 9.5 g, or 10 g.

[001811] The TILs provided in the pharmaceutical compositions of the invention are effective over a wide dosage range. The exact dosage will depend upon the route of administration, the form in which the compound is administered, the gender and age of the subject to be treated, the body weight of the

subject to be treated, and the preference and experience of the attending physician. The clinically-established dosages of the TILs may also be used if appropriate. The amounts of the pharmaceutical compositions administered using the methods herein, such as the dosages of TILs, will be dependent on the human or mammal being treated, the severity of the disorder or condition, the rate of administration, the disposition of the active pharmaceutical ingredients and the discretion of the prescribing physician.

[001812] In some embodiments, TILs may be administered in a single dose. Such administration may be by injection, *e.g.*, intravenous injection. In some embodiments, TILs may be administered in multiple doses. Dosing may be once, twice, three times, four times, five times, six times, or more than six times per year. Dosing may be once a month, once every two weeks, once a week, or once every other day. Administration of TILs may continue as long as necessary.

[001813] In some embodiments, an effective dosage of TILs is about 1×10^6, 2×10^6, 3×10^6, 4×10^6, 5×10^6, 6×10^6, 7×10^6, 8×10^6, 9×10^6, 1×10^7, 2×10^7, 3×10^7, 4×10^7, 5×10^7, 6×10^7, 7×10^7, 8×10^7, 9×10^7, 1×10^8, 2×10^8, 3×10^8, 4×10^8, 5×10^8, 6×10^8, 7×10^8, 8×10^8, 9×10^8, 1×10^9, 2×10^9, 3×10^9, 4×10^9, 5×10^9, 6×10^9, 7×10^9, 8×10^9, 9×10^9, 1×10^{10}, 2×10^{10}, 3×10^{10}, 4×10^{10}, 5×10^{10}, 6×10^{10}, 7×10^{10}, 8×10^{10}, 9×10^{10}, 1×10^{11}, 2×10^{11}, 3×10^{11}, 4×10^{11}, 5×10^{11}, 6×10^{11}, 7×10^{11}, 8×10^{11}, 9×10^{11}, 1×10^{12}, 2×10^{12}, 3×10^{12}, 4×10^{12}, 5×10^{12}, 6×10^{12}, 7×10^{12}, 8×10^{12}, 9×10^{12}, 1×10^{13}, 2×10^{13}, 3×10^{13}, 4×10^{13}, 5×10^{13}, 6×10^{13}, 7×10^{13}, 8×10^{13}, and 9×10^{13}. In some embodiments, an effective dosage of TILs is in the range of 1×10^6 to 5×10^6, 5×10^6 to 1×10^7, 1×10^7 to 5×10^7, 5×10^7 to 1×10^8, 1×10^8 to 5×10^8, 5×10^8 to 1×10^9, 1×10^9 to 5×10^9, 5×10^9 to 1×10^{10}, 1×10^{10} to 5×10^{10}, 5×10^{10} to 1×10^{11}, 5×10^{11} to 1×10^{12}, 1×10^{12} to 5×10^{12}, and 5×10^{12} to 1×10^{13}.

[001814] In some embodiments, an effective dosage of TILs is in the range of about 0.01 mg/kg to about 4.3 mg/kg, about 0.15 mg/kg to about 3.6 mg/kg, about 0.3 mg/kg to about 3.2 mg/kg, about 0.35 mg/kg to about 2.85 mg/kg, about 0.15 mg/kg to about 2.85 mg/kg, about 0.3 mg to about 2.15 mg/kg, about 0.45 mg/kg to about 1.7 mg/kg, about 0.15 mg/kg to about 1.3 mg/kg, about 0.3 mg/kg to about 1.15 mg/kg, about 0.45 mg/kg to about 1 mg/kg, about 0.55 mg/kg to about 0.85 mg/kg, about 0.65 mg/kg to about 0.8 mg/kg, about 0.7 mg/kg to about 0.75 mg/kg, about 0.7 mg/kg to about 2.15 mg/kg, about 0.85 mg/kg to about 2 mg/kg, about 1 mg/kg to about 1.85 mg/kg, about 1.15 mg/kg to about 1.7 mg/kg, about 1.3 mg/kg mg to about 1.6 mg/kg, about 1.35 mg/kg to about 1.5 mg/kg, about 2.15 mg/kg to about 3.6 mg/kg, about 2.3 mg/kg to about 3.4 mg/kg, about 2.4 mg/kg to about 3.3 mg/kg, about 2.6 mg/kg to about 3.15 mg/kg, about 2.7 mg/kg to about 3 mg/kg, about 2.8 mg/kg to about 3 mg/kg, or about 2.85 mg/kg to about 2.95 mg/kg.

[001815] In some embodiments, an effective dosage of TILs is in the range of about 1 mg to about 500 mg, about 10 mg to about 300 mg, about 20 mg to about 250 mg, about 25 mg to about 200 mg,

about 1 mg to about 50 mg, about 5 mg to about 45 mg, about 10 mg to about 40 mg, about 15 mg to about 35 mg, about 20 mg to about 30 mg, about 23 mg to about 28 mg, about 50 mg to about 150 mg, about 60 mg to about 140 mg, about 70 mg to about 130 mg, about 80 mg to about 120 mg, about 90 mg to about 110 mg, or about 95 mg to about 105 mg, about 98 mg to about 102 mg, about 150 mg to about 250 mg, about 160 mg to about 240 mg, about 170 mg to about 230 mg, about 180 mg to about 220 mg, about 190 mg to about 210 mg, about 195 mg to about 205 mg, or about 198 to about 207 mg.

[001816] An effective amount of the TILs may be administered in either single or multiple doses by any of the accepted modes of administration of agents having similar utilities, including intranasal and transdermal routes, by intra-arterial injection, intravenously, intraperitoneally, parenterally, intramuscularly, subcutaneously, topically, by transplantation, or by inhalation.

X. Methods of Treating Patients

[001817] Methods of treatment begin with the initial TIL collection and culture of TILs. Such methods have been both described in the art by, for example, Jin *et al., J. Immunotherapy*, **2012**, 35(3):283-292, incorporated by reference herein in its entirety. Embodiments of methods of treatment are described throughout the sections below, including the Examples.

[001818] The expanded TILs produced according the methods described herein, including for example as described in Steps A through F above or according to Steps A through F above (also as shown, for example, in Figure 1 and/or Figure 8) find particular use in the treatment of patients with cancer (for example, as described in Goff, et al., *J. Clinical Oncology*, **2016**, 34(20):2389-239, as well as the supplemental content; incorporated by reference herein in its entirety. In some embodiments, TIL were grown from resected deposits of metastatic melanoma as previously described (*see*, Dudley, et al., *J Immunother.*, **2003**, 26:332-342; incorporated by reference herein in its entirety). Fresh tumor can be dissected under sterile conditions. A representative sample can be collected for formal pathologic analysis. Single fragments of 2 mm^3 to 3 mm^3 may be used. In some embodiments, 5, 10, 15, 20, 25 or 30 samples per patient are obtained. In some embodiments, 20, 25, or 30 samples per patient are obtained. In some embodiments, 20, 22, 24, 26, or 28 samples per patient are obtained. In some embodiments, 24 samples per patient are obtained. Samples can be placed in individual wells of a 24-well plate, maintained in growth media with high-dose IL-2 (6,000 IU/mL), and monitored for destruction of tumor and/or proliferation of TIL. Any tumor with viable cells remaining after processing can be enzymatically digested into a single cell suspension and cryopreserved, as described herein.

[001819] In some embodiments, successfully grown TIL can be sampled for phenotype analysis (CD3, CD4, CD8, and CD56) and tested against autologous tumor when available. TIL can be

considered reactive if overnight coculture yielded interferon-gamma (IFN-γ) levels > 200 pg/mL and twice background. (Goff, et al., *J Immunother.*, **2010**, 33:840-847; incorporated by reference herein in its entirety). In some embodiments, cultures with evidence of autologous reactivity or sufficient growth patterns can be selected for a second expansion (for example, a second expansion as provided in according to Step D of Figure 1 and/or Figure 8), including second expansions that are sometimes referred to as rapid expansion (REP). In some embodiments, expanded TILs with high autologous reactivity (for example, high proliferation during a second expansion), are selected for an additional second expansion. In some embodiments, TILs with high autologous reactivity (for example, high proliferation during second expansion as provided in Step D of Figure 1 and/or Figure 8), are selected for an additional second expansion according to Step D of Figure 1 and/or Figure 8.

[001820] Cell phenotypes of cryopreserved samples of infusion bag TIL can be analyzed by flow cytometry (*e.g.,* FlowJo) for surface markers CD3, CD4, CD8, CCR7, and CD45RA (BD BioSciences), as well as by any of the methods described herein. Serum cytokines were measured by using standard enzyme-linked immunosorbent assay techniques. A rise in serum IFN-g was defined as >100 pg/mL and greater than 4 3 baseline levels.

[001821] In some embodiments, the TILs produced by the methods provided herein, for example those exemplified in Figure 1 and/or Figure 8, provide for a surprising improvement in clinical efficacy of the TILs. In some embodiments, the TILs produced by the methods provided herein, for example those exemplified in Figure 1 and/or Figure 8, exhibit increased clinical efficacy as compared to TILs produced by methods other than those described herein, including for example, methods other than those exemplified in Figure 1 and/or Figure 8. In some embodiments, the methods other than those described herein include methods referred to as process 1C and/or Generation 1 (Gen 1). In some embodiments, the increased efficacy is measured by DCR, ORR, and/or other clinical responses. In some embodiments, the TILs produced by the methods provided herein, for example those exemplified in Figure 1, exhibit a similar time to response and safety profile compared to TILs produced by methods other than those described herein, including for example, methods other than those exemplified in Figure 1 and/or Figure 8.

[001822] In some embodiments, IFN-gamma (IFN-γ) is indicative of treatment efficacy and/or increased clinical efficacy. In some embodiments, IFN-γ in the blood of subjects treated with TILs is indicative of active TILs. In some embodiments, a potency assay for IFN-γ production is employed. IFN-γ production is another measure of cytotoxic potential. IFN-γ production can be measured by determining the levels of the cytokine IFN-γ in the blood, serum, or TILs *ex vivo* of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8. In some embodiments, an increase in IFN-γ is indicative of treatment efficacy in a patient treated with the TILs produced by the methods of the present invention. In some

embodiments, IFN-γ is increased one-fold, two-fold, three-fold, four-fold, or five-fold or more as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ secretion is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ secretion is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ secretion is increased three-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ secretion is increased four-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ secretion is increased five-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, IFN-γ is measured using a Quantikine ELISA kit. In some embodiments, IFN-γ is measured in TILs *ex vivo* of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8. In some embodiments, IFN-γ is measured in blood of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8. In some embodiments, IFN-γ is measured in TILs serum of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8. In some embodiments, IFN-gamma (IFN-γ) is indicative of treatment efficacy and/or increased clinical efficacy in the treatment of cancer

[001823] In some embodiments, in the TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8 IFN-gamma (IFN-γ) is indicative of treatment efficacy and/or increased clinical efficacy. In some embodiments, IFN-γ in the blood of subjects treated with TILs is indicative of active TILs. In some embodiments, a potency assay for IFN-γ production is employed. IFN-γ production is another measure of cytotoxic potential. IFN-γ production can be measured by determining the levels of the cytokine IFN-γ in the blood, serum, or TILs *ex vivo* of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8. In some embodiments, an increase in IFN-γ is indicative of treatment efficacy in a patient treated with the TILs produced by the

methods of the present invention. In some embodiments, IFN-γ is increased one-fold, two-fold, three-fold, four-fold, or five-fold or more IFN-γ as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8.

[001824] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8, exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 1 and/or Figure 8, including for example, methods referred to as process 1C methods. In some embodiments, significantly improved polyclonality and/or increased polyclonality is indicative of treatment efficacy and/or increased clinical efficacy. In some embodiments, polyclonality refers to the T-cell repertoire diversity. In some embodiments, an increase in polyclonality can be indicative of treatment efficacy with regard to administration of the TILs produced by the methods of the present invention. In some embodiments, polyclonality is increased one-fold, two-fold, ten-fold, 100-fold, 500-fold, or 1000-fold as compared to TILs prepared using methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased ten-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased 100-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased 500-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8. In some embodiments, polyclonality is increased 1000-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1 and/or Figure 8.

[001825] Measures of efficacy can include the disease control rate (DCR) as well as overall response rate (ORR), as known in the art as well as described herein.

[001826] In some embodiments, the invention includes a method of treating NSCLC with a population of TILs, wherein a patient is pre-treated with non-myeloablative chemotherapy prior to an infusion of TILs according to the present disclosure. In some embodiments, the non-myeloablative chemotherapy is cyclophosphamide 60 mg/kg/d for 2 days (days 27 and 26 prior to TIL infusion) and fludarabine 25 mg/m2/d for 5 days (days 27 to 23 prior to TIL infusion). In some embodiments, the non-myeloablative chemotherapy is cyclophosphamide 60 mg/kg/d for 2 days (days 27 and 26 prior to TIL infusion) and fludarabine 25 mg/m2/d for 3 days (days 27 to 25 prior to TIL infusion). In some embodiments, the non-myeloablative chemotherapy is cyclophosphamide 60 mg/kg/d for 2 days (days 27 and 26 prior to TIL infusion) followed by fludarabine 25 mg/m2/d for 3 days (days 25 to 23 prior to TIL infusion). In some embodiments, after non-myeloablative chemotherapy and TIL infusion (at day 0) according to the present disclosure, the patient receives an intravenous infusion of IL-2 intravenously at 720,000 IU/kg every 8 hours to physiologic tolerance.

[001827] Efficacy of the compounds and combinations of compounds described herein in treating, preventing and/or managing the indicated diseases or disorders can be tested using various models known in the art, which provide guidance for treatment of human disease. For example, models for determining efficacy of treatments for lung cancer are described, *e.g.*, in Meuwissen, et al., Genes & Development, 2005, 19, 643-664. Models for determining efficacy of treatments for lung cancer are described, *e.g.*, in Kim, Clin. Exp. Otorhinolaryngol. 2009, 2, 55-60; and Sano, Head Neck Oncol. 2009, 1, 32.

[001828] In some embodiments, IFN-gamma (IFN-γ) is indicative of treatment efficacy for NSCLC treatment. In some embodiments, IFN-γ in the blood of subjects treated with TILs is indicative of active TILs. In some embodiments, a potency assay for IFN-γ production is employed. IFN-γ production is another measure of cytotoxic potential. IFN-γ production can be measured by determining the levels of the cytokine IFN-γ in the blood of a subject treated with TILs prepared by the methods of the present invention, including those as described for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, the TILs obtained by the present method provide for increased IFN-γ in the blood of subjects treated with the TILs of the present method as compared subjects treated with TILs prepared using methods referred to as the Gen 3 process, as exemplified Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D) and throughout this application. In some embodiments, an increase in IFN-γ is indicative of treatment efficacy in a patient treated with the TILs produced by the methods of the present invention. In some embodiments, IFN-γ is increased one-fold, two-fold, three-fold, four-fold, or five-fold or more as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using

other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ secretion is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ secretion is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ secretion is increased three-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ secretion is increased four-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ secretion is increased five-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, IFN-γ is measured using a Quantikine ELISA kit. In some embodiments, IFN-γ is measured using a Quantikine ELISA kit. In some embodiments, IFN-γ is measured in TILs ex vivo from a patient treated with the TILs produced by the methods of the present invention. In some embodiments, IFN-γ is measured in blood in a patient treated with the TILs produced by the methods of the present invention. In some embodiments, IFN-γ is measured in serum in a patient treated with the TILs produced by the methods of the present invention.

[001829] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D and/or Figure 8E and/or Figure 8F and/or Figure 8G), exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 8 (in

particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D), such as for example, methods referred to as process 1C methods. In some embodiments, significantly improved polyclonality and/or increased polyclonality is indicative of treatment efficacy and/or increased clinical efficacy for cancer treatment. In some embodiments, polyclonality refers to the T-cell repertoire diversity. In some embodiments, an increase in polyclonality can be indicative of treatment efficacy with regard to administration of the TILs produced by the methods of the present invention. In some embodiments, polyclonality is increased one-fold, two-fold, ten-fold, 100-fold, 500-fold, or 1000-fold as compared to TILs prepared using methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased ten-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased 100-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased 500-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D). In some embodiments, polyclonality is increased 1000-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including, for example, methods other than those

embodied in Figure 8 (in particular, *e.g.*, Figure 8A and/or Figure 8B and/or Figure 8C and/or Figure 8D and/or Figure 48A and/or Figure 48B and/or Figure 48C and/or Figure 48D).

A. Methods of Treating Cancers

[001830] The compositions and methods described herein can be used in a method for treating diseases. In some embodiments, they are for use in treating hyperproliferative disorders, such as cancer, in an adult patient or in a pediatric patient. They may also be used in treating other disorders as described herein and in the following paragraphs.

[001831] In some embodiments, the hyperproliferative disorder is cancer. In some embodiments, the hyperproliferative disorder is a solid tumor cancer. In some embodiments, the solid tumor cancer is selected from the group consisting of anal cancer, bladder cancer, breast cancer (including triple-negative breast cancer), bone cancer, cancer caused by human papilloma virus (HPV), central nervous system associated cancer (including ependymoma, medulloblastoma, neuroblastoma, pineoblastoma, and primitive neuroectodermal tumor), cervical cancer (including squamous cell cervical cancer, adenosquamous cervical cancer, and cervical adenocarcinoma), colon cancer, colorectal cancer, endometrial cancer, esophageal cancer, esophagogastric junction cancer, gastric cancer, gastrointestinal cancer, gastrointestinal stromal tumor, glioblastoma, glioma, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC), hypopharynx cancer, larynx cancer, nasopharynx cancer, oropharynx cancer, and pharynx cancer), kidney cancer, liver cancer, lung cancer (including non-small-cell lung cancer (NSCLC), metastatic NSCLC, and small-cell lung cancer), melanoma (including uveal melanoma, choroidal melanoma, ciliary body melanoma, iris melanoma, or metastatic melanoma), mesothelioma (including malignant pleural mesothelioma), ovarian cancer, pancreatic cancer (including pancreatic ductal adenocarcinoma), penile cancer, rectal cancer, renal cancer, renal cell carcinoma, sarcoma (including Ewing sarcoma, osteosarcoma, rhabdomyosarcoma, and other bone and soft tissue sarcomas), thyroid cancer (including anaplastic thyroid cancer), uterine cancer, and vaginal cancer.

[001832] In some embodiments, the hyperproliferative disorder is a hematological malignancy. In some embodiments, the hematological malignancy is selected from the group consisting of chronic lymphocytic leukemia, acute lymphoblastic leukemia, diffuse large B cell lymphoma, non-Hodgkin's lymphoma, Hodgkin's lymphoma, follicular lymphoma, mantle cell lymphoma, and multiple myeloma. In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is a hematological malignancy. In some embodiments, the present invention includes a method of treating a patient with a cancer using TILs, MILs, or PBLs modified to downregulate one or more of PD-1, CTLA-4, LAG-3, CISH and CBL-B, wherein the cancer is a hematological malignancy. In some embodiments, the present invention includes a method of treating

a patient with a cancer using MILs or PBLs modified to downregulate one or more of PD-1, CTLA-4, LAG-3, CISH and CBL-BRs, wherein the cancer is a hematological malignancy.

[001833] In some embodiments, the cancer is one of the foregoing cancers, including solid tumor cancers and hematological malignancies, that is relapsed or refractory to treatment with at least one prior therapy, including chemotherapy, radiation therapy, or immunotherapy. In some embodiments, the cancer is one of the foregoing cancers that is relapsed or refractory to treatment with at least two prior therapies, including chemotherapy, radiation therapy, and/or immunotherapy. In some embodiments, the cancer is one of the foregoing cancers that is relapsed or refractory to treatment with at least three prior therapies, including chemotherapy, radiation therapy, and/or immunotherapy.

[001834] In some embodiments, the cancer is a microsatellite instability-high (MSI-H) or a mismatch repair deficient (dMMR) cancer. MSI-H and dMMR cancers and testing therefore have been described in Kawakami, *et al., Curr. Treat. Options Oncol.* **2015,** *16,* 30, the disclosures of which are incorporated by reference herein.

[001835] In some embodiments, the present invention includes a method of treating a patient with a cancer using TILs, MILs, or PBLs modified downregulate one or more of PD-1, CTLA-4, LAG-3, CISH, TIGIT and CBL-B, wherein the patient is a human. In some embodiments, the present invention includes a method of treating a patient with a cancer using TILs, MILs, or PBLs modified to downregulate one or more of PD-1, CTLA-4, LAG-3, CISH, TIGIT and CBL-B, wherein the patient is a non-human. In some embodiments, the present invention includes a method of treating a patient with a cancer using TILs, MILs, or PBLs modified to downregulate one or more of PD-1, CTLA-4, LAG-3, CISH, TIGIT and CBL-B, wherein the patient is a companion animal.

[001836] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is refractory to treatment with a BRAF inhibitor and/or a MEK inhibitor. In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is refractory to treatment with a BRAF inhibitor selected from the group consisting of vemurafenib, dabrafenib, encorafenib, sorafenib, and pharmaceutically acceptable salts or solvates thereof. In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is refractory to treatment with a MEK inhibitor selected from the group consisting of trametinib, cobimetinib, binimetinib, selumetinib, pimasertinib, refametinib, and pharmaceutically acceptable salts or solvates thereof. In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is refractory to treatment with a BRAF inhibitor selected from the group consisting of vemurafenib, dabrafenib, encorafenib, sorafenib, and pharmaceutically acceptable salts or solvates thereof, and a MEK inhibitor selected from the group consisting of trametinib, cobimetinib, binimetinib, selumetinib, pimasertinib, refametinib, and pharmaceutically acceptable salts or solvates thereof.

[001837] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is a pediatric cancer.

[001838] In some embodiments, the present invention includes a method of treating a patient with a cancer wherein the cancer is uveal melanoma.

[001839] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the uveal melanoma is choroidal melanoma, ciliary body melanoma, or iris melanoma.

[001840] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the pediatric cancer is a neuroblastoma.

[001841] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the pediatric cancer is a sarcoma.

[001842] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the sarcoma is osteosarcoma.

[001843] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the sarcoma is a soft tissue sarcoma.

[001844] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the soft tissue sarcoma is rhabdomyosarcoma, Ewing sarcoma, or primitive neuroectodermal tumor (PNET).

[0002] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the pediatric cancer is a central nervous system (CNS) associated cancer. In some embodiments, the pediatric cancer is refractory to treatment with chemotherapy. In some embodiments, the pediatric cancer is refractory to treatment with radiation therapy. In some embodiments, the pediatric cancer is refractory to treatment with dinutuximab.

[001845] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the CNS associated cancer is medulloblastoma, pineoblastoma, glioma, ependymoma, or glioblastoma.

[001846] The compositions and methods described herein can be used in a method for treating cancer, wherein the cancer is refractory or resistant to prior treatment with an anti-PD-1 or anti-PD-L1 antibody. In some embodiments, the patient is a primary refractory patient to an anti-PD-1 or anti-PD-L1 antibody. In some embodiments, the patient shows no prior response to an anti-PD-1 or anti-PD-L1 antibody. In some embodiments, the patient shows a prior response to an anti-PD-1 or anti-PD-L1 antibody, follow by progression of the patient's cancer. In some embodiments, the cancer is refractory

to an anti-CTLA-4 antibody and/or an anti-PD-1 or anti-PD-L1 antibody in combination with at least one chemotherapeutic agent. In some embodiments, the prior chemotherapeutic agent is carboplatin, paclitaxel, pemetrexed, and/or cisplatin. In some prior embodiments, the chemotherapeutic agent(s) is a platinum doublet chemotherapeutic agent. In some embodiments, the platinum doublet therapy comprises a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel). In some embodiments, the platinum doublet chemotherapeutic agent is in combination with pemetrexed.

[001847] In some embodiments, the NSCLC is PD-L1 negative and/or is from a patient with a cancer that expresses PD-L1 with a tumor proportion score (TPS) of < 1%, as described elsewhere herein.

[001848] In some embodiments, the NSCLC is refractory to a combination therapy comprising an anti-PD-1 or the anti-PD-L1 antibody and a platinum doublet therapy, wherein the platinum doublet therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

[001849] In some embodiments, the NSCLC is refractory to a combination therapy comprising an anti-PD-1 or the anti-PD-L1 antibody, pemetrexed, and a platinum doublet therapy, wherein the platinum doublet therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

[001850] In some embodiments, the NSCLC has been treated with an anti-PD-1 antibody. In some embodiments, the NSCLC has been treated with an anti-PD-L1 antibody. In some embodiments, the NSCLC patient is treatment naïve. In some embodiments, the NSCLC has not been treated with an anti-PD-1 antibody. In some embodiments, the NSCLC has not been treated with an anti-PD-L1 antibody. In some embodiments, the NSCLC has been previously treated with a chemotherapeutic agent. In some embodiments, the NSCLC has been previously treated with a chemotherapeutic agent but is no longer being treated with the chemotherapeutic agent. In some embodiments, the NSCLC patient is anti-PD-1/PD-L1 naïve. In some embodiments, the NSCLC patient has low expression of PD-L1. In some embodiments, the NSCLC patient has treatment naïve NSCLC or is post-

chemotherapeutic treatment but anti-PD-1/PD-L1 naïve. In some embodiments, the NSCLC patient is treatment naïve or post-chemotherapeutic treatment but anti-PD-1/PD-L1 naïve and has low expression of PD-L1. In some embodiments, the NSCLC patient has bulky disease at baseline. In some embodiments, the subject has bulky disease at baseline and has low expression of PD-L1. In some embodiments, the NSCLC patient has no detectable expression of PD-L1. In some embodiments, the NSCLC patient is treatment naïve or post-chemotherapeutic treatment but anti-PD-1/PD-L1 naïve and has no detectable expression of PD-L1. In some embodiments, the patient has bulky disease at baseline and has no detectable expression of PD-L1. In some embodiments, the NSCLC patient has treatment naïve NSCLC or post chemotherapy (*e.g.*, post chemotherapeutic agent) but anti-PD-1/PD-L1 naïve who have low expression of PD-L1 and/or have bulky disease at baseline. In some embodiments, bulky disease is indicated where the maximal tumor diameter is greater than 7 cm measured in either the transverse or coronal plane. In some embodiments, bulky disease is indicated when there are swollen lymph nodes with a short-axis diameter of 20 mm or greater. In some embodiments, the chemotherapeutic includes a standard of care therapeutic for NSCLC.

[001851] In some embodiments, PD-L1 expression is determined by the tumor proportion score. In some embodiments, the subject with a refractory NSCLC tumor has a $< 1\%$ tumor proportion score (TPS). In some embodiments, the subject with a refractory NSCLC tumor has a $\geq 1\%$ TPS. In some embodiments, subject with the refractory NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to said anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, subject with the refractory NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to said anti-PD-L1 antibody treatment.

[001852] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1, Figure 36, or Figure 8, exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 1, Figure 36, or Figure 8, such as for example, methods referred to as process 1C methods. In some embodiments, significantly improved polyclonality and/or increased polyclonality is indicative of treatment efficacy and/or increased clinical efficacy for cancer treatment. In some embodiments, polyclonality refers to the T-cell repertoire diversity. In some embodiments, an increase in polyclonality can be indicative of treatment efficacy with regard to administration of the TILs produced by the methods of the present invention. In some embodiments, polyclonality is increased one-fold, two-fold, ten-fold, 100-fold, 500-fold, or 1000-fold as compared to TILs prepared using methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein

including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased ten-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased 100-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased 500-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8. In some embodiments, polyclonality is increased 1000-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1, Figure 36, or Figure 8.

[001853] In some embodiments, PD-L1 expression is determined by the tumor proportion score using one more testing methods as described herein. In some embodiments, the subject or patient with a NSCLC tumor has a < 1% tumor proportion score (TPS). In some embodiments, the NSCLC tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with the NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with a refractory or resistant NSCLC tumor has a < 1% tumor proportion score (TPS). In some embodiments, the subject or patient with a refractory or resistant NSCLC tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the refractory or resistant NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with the refractory or resistant NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment.

[001854] In some embodiments, the NSCLC is an NSCLC that exhibits a tumor proportion score (TPS), or the percentage of viable tumor cells from a patient taken prior to anti-PD-1 or anti-PD-L1 therapy, showing partial or complete membrane staining at any intensity, for the PD-L1 protein that is

less than 1% (TPS < 1%). In some embodiments, the NSCLC is an NSCLC that exhibits a TPS selected from the group consisting of <50%, <45%, <40%, <35%, <30%, <25%, <20%, <15%, <10%, <9%, <8%, <7%, <6%, <5%, <4%, <3%, <2%, <1%, <0.9%, <0.8%, <0.7%, <0.6%, <0.5%, <0.4%, <0.3%, <0.2%, <0.1%, <0.09%, <0.08%, <0.07%, <0.06%, <0.05%, <0.04%, <0.03%, <0.02%, and <0.01%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS selected from the group consisting of about 50%, about 45%, about 40%, about 35%, about 30%, about 25%, about 20%, about 15%, about 10%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.9%, about 0.8%, about 0.7%, about 0.6%, about 0.5%, about 0.4%, about 0.3%, about 0.2%, about 0.1%, about 0.09%, about 0.08%, about 0.07%, about 0.06%, about 0.05%, about 0.04%, about 0.03%, about 0.02%, and about 0.01%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 1%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.9%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.8%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.7%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.6%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.5%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.4%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.3%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.2%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.1%. TPS may be measured by methods known in the art, such as those described in Hirsch, *et al. J. Thorac. Oncol.* **2017,** *12,* 208-222 or those used for the determination of TPS prior to treatment with pembrolizumab or other anti-PD-1 or anti-PD-L1 therapies. Methods for measurement of TPS that have been approved by the U.S. Food and Drug Administration may also be used. In some embodiments, the PD-L1 is exosomal PD-L1. In some embodiments, the PD-L1 is found on circulating tumor cells.

[001855] In some embodiments, the partial membrane staining includes 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99%, or more. In some embodiments, the completed membrane staining includes approximately 100% membrane staining.

[001856] In some embodiments, testing for PD-L1 can involve measuring levels of PD-L1 in patient serum. In these embodiments, measurement of PD-L1 in patient serum removes the uncertainty of tumor heterogeneity and the patient discomfort of serial biopsies.

[001857] In some embodiments, elevated soluble PD-L1 as compared to a baseline or standard level correlates with worsened prognosis in NSCLC. *See*, for example, Okuma, *et al.*, *Clinical Lung Cancer*, **2018,** *19,* 410-417; Vecchiarelli, *et al.*, *Oncotarget,* **2018**, *9,* 17554–17563. In some

embodiments, the PD-L1 is exosomal PD-L1. In some embodiments, the PD-L1 is expressed on circulating tumor cells.

[001858] In some embodiments, the subject or patient has non-small cell lung carcinoma (NSCLC) characterized by at least one of:

i. a predetermined tumor proportion score (TPS) of PD-L1 < 1%,

ii. a TPS score of PD-L1 of 1%-49%, or

iii. a predetermined absence of one or more driver mutations,

wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, an EGFR exon 20 mutation, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation, a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation.

[001859] In other embodiments, the invention provides a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population described herein.

[001860] In other embodiments, the invention provides a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the TIL composition described herein.

[001861] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that prior to administering the therapeutically effective dosage of the therapeutic TIL population and the TIL composition described herein, respectively, a non-myeloablative lymphodepletion regimen has been administered to the subject.

[001862] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m2/day for two days followed by administration of fludarabine at a dose of 25 mg/m2/day for five days.

[001863] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified to further comprise the step of treating the subject with a high-dose IL-2 regimen starting on the day after administration of the TIL cells to the subject.

[001864] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the high-dose IL-2 regimen comprises 600,000 or 720,000 IU/kg administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

[001865] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is a solid tumor.

[001866] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is melanoma, metastatic melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), metastatic NSCLC, lung cancer, bladder cancer, breast cancer, triple negative breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, or renal cell carcinoma.

[001867] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is melanoma, metastatic melanoma, HNSCC, cervical cancers, NSCLC, metastatic NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[001868] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is melanoma.

[001869] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is metastatic melanoma.

[001870] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is HNSCC.

[001871] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is a cervical cancer.

[001872] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is NSCLC.

[001873] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is metastatic NSCLC.

[001874] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is glioblastoma (including GBM).

[001875] In other embodiments, the invention provides a method for treating a subject with cancer described herein modified such that the cancer is gastrointestinal cancer.

[001876] In other embodiments, the invention provides a method for treating a subject with cancer described herein modified such that the cancer is a hypermutated cancer.

[001877] In other embodiments, the invention provides a method for treating a subject with cancer described herein modified such that the cancer is a pediatric hypermutated cancer.

[001878] In other embodiments, the invention provides a therapeutic TIL population described herein for use in a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population.

[001879] In other embodiments, the invention provides a TIL composition described herein for use in a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the TIL composition.

[001880] In other embodiments, the invention provides a therapeutic TIL population described herein or the TIL composition described herein modified such that prior to administering to the subject the therapeutically effective dosage of the therapeutic TIL population described herein or the TIL composition described herein, a non-myeloablative lymphodepletion regimen has been administered to the subject.

[001881] In other embodiments, the invention provides a therapeutic TIL population or the TIL composition described herein modified such that the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[001882] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified to further comprise the step of treating patient with a high-dose IL-2 regimen starting on the day after administration of the TIL cells to the patient.

[001883] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the high-dose IL-2 regimen comprises 600,000 or 720,000 IU/kg administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

[001884] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is a solid tumor.

[001885] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma, metastatic melanoma,

ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), metastatic NSCLC, lung cancer, bladder cancer, breast cancer, triple negative breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, or renal cell carcinoma.

[001886] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma, metastatic melanoma, HNSCC, cervical cancers, NSCLC, metastatic NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[001887] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma.

[001888] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is metastatic melanoma.

[001889] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is HNSCC.

[001890] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is cervical cancer.

[001891] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is NSCLC.

[001892] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is metastatic NSCLC.

[001893] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is glioblastoma.

[001894] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is gastrointestinal cancer.

[001895] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is a hypermutated cancer.

[001896] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is a pediatric hypermutated cancer.

[001897] In other embodiments, the invention provides the use of a therapeutic TIL population described herein in a method of treating cancer in a subject comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population.

[001898] In other embodiments, the invention provides the use of a TIL composition described in any of the preceding paragraphs in a method of treating cancer in a subject comprising administering to the subject a therapeutically effective dosage of the TIL composition.

[001899] In other embodiments, the invention provides the use of a therapeutic TIL population described herein or a TIL composition described herein in a method of treating cancer in a patient comprising administering to the patient a non-myeloablative lymphodepletion regimen and then administering to the subject the therapeutically effective dosage of the therapeutic TIL population described in any of the preceding paragraphs or the therapeutically effective dosage of the TIL composition described herein.

1. Methods of Treating NSCLC

[001900] The compositions and methods described herein can be used in a method for treating non-small-cell lung cancer (NSCLC). In some embodiments, the NSCLC is refractory to treatment with an anti-PD-1 or anti-PD-L1 antibody. In some embodiments the NSCLC is metatstatic NSCLC. In some embodiments the NSCLC is metatstatic stage IV NSCLC. In some embodiments the anit-PD-1 antibody includes, *e.g.*, but is not limited to nivolumab (BMS-936558, Bristol-Myers Squibb; Opdivo®), pembrolizumab (lambrolizumab, MK03475 or MK-3475, Merck; Keytruda®), humanized anti-PD-1 antibody JS001 (ShangHai JunShi), monoclonal anti-PD-1 antibody TSR-042 (Tesaro, Inc.), Pidilizumab (anti-PD-1 mAb CT-011, Medivation), anti-PD-1 monoclonal Antibody BGB-A317 (BeiGene), and/or anti-PD-1 antibody SHR-1210 (ShangHai HengRui), human monoclonal antibody REGN2810 (Regeneron), human monoclonal antibody MDX-1106 (Bristol-Myers Squibb), and/or humanized anti-PD-1 IgG4 antibody PDR001 (Novartis). In some embodiments, the PD-1 antibody is from clone: RMP1-14 (rat A) - BioXcell cat# BP0146. Other suitable antibodies suitable for use in co-administration methods with TILs produced according to Steps A through F as described herein are anti-PD-1 antibodies disclosed in U.S. Patent No. 8,008,449, herein incorporated by reference. In some embodiments, the antibody or antigen-binding portion thereof binds specifically to PD-L1 and inhibits its interaction with PD-1, thereby increasing immune activity. Any antibodies known in the art which bind to PD-L1 and disrupt the interaction between the PD-1 and PD-L1, and stimulates an anti-tumor immu2740274ne response, are include. For example, antibodies that target PD-L1 and are in clinical trials, include BMS-936559 (Bristol-Myers Squibb) and MPDL3280A (Genentech). Other suitable antibodies that target PD-L1 are disclosed in U.S. Patent No. 7,943,743, herein incorporated by reference. It will be understood by one of ordinary skill that any antibody which binds to PD-1 or PD-L1, disrupts the PD-1/PD-L1 interaction, and stimulates an anti-tumor immune response, are included.

[001901] In some embodiments, the NSCLC is refractory to the anti-CTLA-4 and/or anti-PD-1 and a chemotherapeutic agent. In some embodiments, the NSCLC is refractory to the anti-CTLA-4 and/or anti-PD-1 and chemotherapy, wherein the chemotherapeutic agent is carboplatin, paclitaxel, pemetrexed, cisplatin. In some embodiments, the NSCLS is refractory to an anti-CTLA-4 antibody, such as ipilimumab (Yervoy®).

[001902] In some embodiments, the NSCLC is refractory to treatment with combined PD-1 (including for example pembrolizumab) and a chemotherapeutic agent. In some embodiments, the chemotherapeutic agent(s) is a platinum doublet chemotherapeutic agent. In some embodiments, the platinum doublet therapy comprises a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel). In some embodiments, the platinum doublet chemotherapeutic agent is in combination with pemetrexed.

[001903] In some embodiments, the NSCLC is refractory to a combination treatment or combination therapy comprising an anti-PD-1 and a chemotherapeutic agent. In some embodiments, the anti-PD-1 or the anti-PD-L1 antibody is selected from the group consisting of nivolumab, pembrolizumab, JS001, TSR-042, pidilizumab, (BGB-A317, SHR-1210, REGN2810, MDX-1106, PDR001, anti-PD-1 from clone: RMP1-14, an anti-PD-1 antibodies disclosed in U.S. Patent No. 8,008,449, durvalumab, atezolizumab, avelumab, and fragments, derivatives, variants, as well as biosimilars thereof. In some embodiments, the anti-PD-1 is pembrolizumab. In some embodiments, the chemotherapeutic agent is a platinum doublet chemotherapeutic agent. In some embodiments, the chemotherapeutic agent is in combination with pemetrexed. In some embodiments, the NSCLC is refractory to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, and cisplatin. In some embodiments, the NSCLC is refractory to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, cisplatin, nivolumab, and ipilimumab.

[001904] In some embodiments, the NSCLC has undergone no prior therapy. In some embodiments, the NSCLC is naïve to ICI treatment. In some embodiments, the NSCLC is naïve to anti-VEGF (e.g. avastin) treatment. In some embodiments, the NSCLC is naïve to chemotherapy treatment.

[001905] In some embodiments, the NSCLC has been undergoing a maintenance therapy.

[001906] In some embodiments, the NSCLC is PD-1 negative and/or is from a subject that is PD-1.

[001907] In some embodiments, the NSCLC is refractory to a combination therapy comprising the anti-PD-1 or the anti-PD-L1 and a platinum doublet therapy, wherein the platinum doublet therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

[001908] In some embodiments, the NSCLC is refractory to a combination therapy comprising the anti-PD-1 or the anti-PD-L1, pemetrexed, and a platinum doublet therapy, wherein the platinum doublet therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

[001909] In some embodiments, the NSCLC has been treated with an anti-PD-1 antibody. In some embodiments, the NSCLC has been treated with an anti-PD-L1 antibody. In some embodiments, the NSCLC subject is treatment naïve. In some embodiments, the NSCLC has not been treated with an anti-PD-1 antibody. In some embodiments, the NSCLC has not been treated with an anti-PD-L1 antibody. In some embodiments, the NSCLC has been previously treated with a chemotherapeutic agent. In some embodiments, the NSCLC has been previously treated with a chemotherapeutic agent but is not longer being treated with the chemotherapeutic agent. In some embodiments, the NSCLC patient is anti-PD-1/PD-L1 naïve. In some embodiments, the NSCLC subject has low expression of PD-L1. In some embodiments, the NSCLC subject has treatment naïve NSCLC or is post-chemotherapeutic treatment but anti-PD-1/PD-L1 naïve. In some embodiments, the NSCLC subject ist reatment naïve NSCLC or post-chemotherapuetic treament but anti-PD-1/PD-L1 naïve and has low expression of PD-L1. In some embodiments, the NSCLC subject has bulky disease at baseline. In some embodiments, the subject has bulky disease at baseline and has low expression of PD-L1. In some embodiments, the NSCLC subject has no detectable expression of PD-L1. In some embodiments, the NSCLC subject ist reatment naïve NSCLC or post-chemotherapuetic treament but anti-PD-1/PD-L1 naïve and has no detectable expression of PD-L1. In some embodiments, the subject has bulky disease at baseline and has no detectable expression of PD-L1. In some embodiments, the NSCLC subject has treatment naïve NSCLC or post chemotherapy (*e.g.*, post chemotherapeutic agent) but anti-PD-1/PD-L1 naïve who have low expression of PD-L1 and/or have bulky disease at baseline. In some embodiments, bulky disease is indicated where the maximal tumor diameter is greater than 7 cm measured in either the transverse or coronal plane. In some embodiments, bulky disease is indicated when there are swollen lymph nodes with a short-axis diameter of 20 mm or greater. In some embodiments, the chemotherapeutic includes a standard of care therapeutic for NSCLC.

[001910] In some embodiments, PD-L1 expression is determined by the tumor proportion score. In some embodiments, the subject with a refractory NSCLC tumor has a < 1% tumor proportion score (TPS). In some embodiments, the subject with a refractory NSCLC tumor has a ≥ 1% TPS. In some embodiments, subject with the refractory NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to said anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, subject with the refractory NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to said anti-PD-L1 antibody treatment.

[001911] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1 and/or Figure 8, exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 1 and/or Figure 8, such as for example, methods referred to as process 1C methods. In some embodiments, significantly improved polyclonality and/or increased polyclonality is indicative of treatment efficacy and/or increased clinical efficacy for cancer treatment. In some embodiments, polyclonality refers to the T-cell repertoire diversity. In some embodiments, an increase in polyclonality can be indicative of treatment efficacy with regard to administration of the TILs produced by the methods of the present invention. In some embodiments, polyclonality is increased one-fold, two-fold, ten-fold, 100-fold, 500-fold, or 1000-fold as compared to TILs prepared using methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased one-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased two-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased ten-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased 100-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased 500-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1. In some embodiments, polyclonality is increased 1000-fold as compared to an untreated patient and/or as compared to a patient treated with TILs prepared using other methods than those provide herein including for example, methods other than those embodied in Figure 1.

a. **Exemplary PD-L1 Testing Methods**

[001912] In some embodiments, PD-L1 expression is determined by the tumor proportion score using one more testing methods as described herein. In some embodiments, the subject or patient with a NSCLC tumor has a < 1% tumor proportion score (TPS). In some embodiments, the NSCLC tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with the NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with a refractory or resistant NSCLC tumor has a < 1% tumor proportion score (TPS). In some embodiments, the subject or patient with a refractory or resistant NSCLC tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the refractory or resistant NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment. In some embodiments, the subject or patient with the refractory or resistant NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment.

[001913] In some embodiments, the NSCLC is an NSCLC that exhibits a tumor proportion score (TPS), or the percentage of viable tumor cells from a patient taken prior to anti-PD-1 or anti-PD-L1 therapy, showing partial or complete membrane staining at any intensity, for the PD-L1 protein that is less than 1% (TPS < 1%). In some embodiments, the NSCLC is an NSCLC that exhibits a TPS selected from the group consisting of <50%, <45%, <40%, <35%, <30%, <25%, <20%, <15%, <10%, <9%, <8%, <7%, <6%, <5%, <4%, <3%, <2%, <1%, <0.9%, <0.8%, <0.7%, <0.6%, <0.5%, <0.4%, <0.3%, <0.2%, <0.1%, <0.09%, <0.08%, <0.07%, <0.06%, <0.05%, <0.04%, <0.03%, <0.02%, and <0.01%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS selected from the group consisting of about 50%, about 45%, about 40%, about 35%, about 30%, about 25%, about 20%, about 15%, about 10%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.9%, about 0.8%, about 0.7%, about 0.6%, about 0.5%, about 0.4%, about 0.3%, about 0.2%, about 0.1%, about 0.09%, about 0.08%, about 0.07%, about 0.06%, about 0.05%, about 0.04%, about 0.03%, about 0.02%, and about 0.01%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 1%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.9%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.8%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.7%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.6%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS

between 0% and 0.5%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.4%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.3%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.2%. In some embodiments, the NSCLC is an NSCLC that exhibits a TPS between 0% and 0.1%. TPS may be measured by methods known in the art, such as those described in Hirsch, et al. J. Thorac. Oncol. 2017:12, 208-222 or those used for the determination of TPS prior to treatment with pembrolizumab or other anti-PD-1 or anti-PD-L1 therapies. Methods for meansurement of TPS that have been approved by the U.S. Food and Drug Administration may also be used. In some embodiments, the PD-L1 is exosomal PD-L1. In some embodiments, the PD-L1 is found on circulating tumor cells.

[001914] In some embodiments, the partial membrane staining includes 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99%, or more. In some embodiments, the completed membrane staining includes approzimatley 100% membrane staining.

[001915] In some embodiments, testing for PD-L1 can incoclve measuring levels of PD-L1 in patient serum. In these embodiments, measurement of PD-L1 in patient serum removes the uncertainty of tumor heterogeneity and the patient discomfort of serial biopsies.

[001916] In some embodiments, elevated soluble PD-L1 as compared to a baseline or standard level correlates with worsened prognosis in NSCLC. *See*, for example, Okuma, Y. *et al.*, 2018, *Clinical Lung Cancer*, 19(5): 410-417; Vccchiarclli, S., *et al.*, 2018, *Oncotarget,* 9(25):17554–17563. In somc embodiments, the PD-L1 is exosomal PD-L1. In some embodiments, the PD-L1 is expressed on circulating tumor cells.

2. Driver Mutations

[001917] As used herein, the phrases "driver mutation" and/or "actionable mutation" and/or "oncogenic driver mutation" refer to mutations that are typically considered oncogenic drivers (*i.e.*, cancer drivers or cancer inducers). The presence of one or more of these mutations has traditionally been the utilized as the target for a targeted therapy. Often driver mutations are examined and/or analyzed for treatment with targeted therapeutic moieties, including for example tyrosine kinase inhibitors (TKIs). Such driver mutations can, in some embodiments, impact or affect response to a first line therapeutic treatment. TIL therapy methods and compositions described herein are effective for treatment whether such driver mutations are present or absent in the patient or subject. Such driver mutations can be tested and determined by any method known in the art, including whole exome sequencing or methods targeted to the detection of a specific driver mutation.

[001918] In some embodiments, the NSCLC is an NSCLC that exhibits the presence or absence of one or more driver mutations. In some embodiments, the NSCLC is an NSCLC that exhibits the presence of one or more driver mutations. In some embodiments, the NSCLC is an NSCLC that exhibits the absence of one or more driver mutations. In some embodiments, the NSCLC has been analyzed for the absence or presence of one or more driver mutations. In some embodiments, the one or more driver mutations are not present. In some embodiments, the the NSCLC treatment is independent of the presence or absence of one or more driver mutations. In some embodiments, the one or more driver mutations is selected from the group consisting of an EGFR mutation, an EGFR insertion, EGFR exon20, a KRAS mutation, a BRAF-mutation, a BRAF V600E mutation, a BRAF V600K mutation, a BRAF V600 mutation, an ALK mutation, a c-ROS mutation (ROS1-mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation,a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation. In some embodiments, the NSCLC exhibits a TPS of < 1% and has a predetermined absence of one or more driver mutations.

[001919] In some embodiments, the NSCLC is an NSCLC that is not indicated for treatment by an EGFR inhibitor, a BRAF inhibitor, an ALK inhibitor, a c-Ros inhibitor, a RET inhibitor, an ERBB2 inhibitor, BRCA inhibitor, a MAP2K1 inhibitor, PIK3CA inhibitor, CDKN2A inhibitor, a PTEN inhibitor, an UMD inhibitor, an NRAS inhibitor, a KRAS inhibitor, an NF1 inhibitor, MET inhibitor a TP53 inhibitor, a CREBBP inhibitor, a KMT2C inhibitor, a KMT2D mutation, an ARID1A mutation, a RB1 inhibitor, an ATM inhibitor, a SETD2 inhibitor, a FLT3 inhibitor, a PTPN11 inhibitor, a FGFR1 inhibitor, an EP300 inhibitor, a MYC inhibitor, an EZH2 inhibitor, a JAK2 inhibitor, a FBXW7 inhibitor, a CCND3 inhibitor, and a GNA11 inhibitor.

[001920] In some embodiments, the NSCLC exhibits a TPS of < 1% and is a NSCLC that is not indicated for treatment by an EGFR inhibitor, a BRAF inhibitor, an ALK inhibitor, a c-Ros inhibitor, a RET inhibitor, an ERBB2 inhibitor, BRCA inhibitor, a MAP2K1 inhibitor, PIK3CA inhibitor, CDKN2A inhibitor, a PTEN inhibitor, an UMD inhibitor, an NRAS inhibitor, a KRAS inhibitor, an NF1 inhibitor, MET inhibitor a TP53 inhibitor, a CREBBP inhibitor, a KMT2C inhibitor, a KMT2D mutation, an ARID1A mutation, a RB1 inhibitor, an ATM inhibitor, a SETD2 inhibitor, a FLT3 inhibitor, a PTPN11 inhibitor, a FGFR1 inhibitor, an EP300 inhibitor, a MYC inhibitor, an EZH2 inhibitor, a JAK2 inhibitor, a FBXW7 inhibitor, a CCND3 inhibitor, and a GNA11 inhibitor

[001921] In some embodiments, the EGFR mutation results in tumor transformation from NSCLC to small cell lung cancer (SCLC).

[001922] In some embodiments, the NSCLC (or a biopsy thereof) exhibits high-tumor mutational burden (high-TMB; > 10 mut/kb) and/or microsatellite instability high (MSI-high). In some embodiments, the NSCLC (or a biopsy thereof) exhibits high-tumor mutational burden (high-TMB; > 10 mut/kb). In some embodiments, the NSCLC (or a biopsy thereof) exhibits microsatellite instability high (MSI-high). Methods and systems for evaluating tumor mutational burden are known in the art. Exemplary disclosures of such methods and systems can be found in US Patent No. 9,792,403, US Application Publication No. US20180363066A1, International Application publication Nos. WO2013070634 and WO2018106884, as well as Metzker, M. (2010) Nature Biotechnology Reviews 11:31-46, incorporated herein by reference, all of which are incorporated by reference in their entireties.

[001923] In some embodiments, the NSCLC (or a biopsy thereof) exhibits high-tumor mutational burden (high-TMB; > 10 mut/kb) and/or microsatellite instability high (MSI-high). In some embodiments, the NSCLC (or a biopsy thereof) exhibits high-tumor mutational burden (high-TMB; > 10 mut/kb). In some embodiments, the NSCLC (or a biopsy thereof) exhibits microsatellite instability high (MSI-high). Methods and systems for evaluating tumor mutational burden are known in the art. Exemplary disclosures of such methods and systems can be found in US Patent No. 9,792,403, US Application Publication No. US20180363066A1, International Application publication Nos. WO2013070634 and WO2018106884, as well as Metzker, M. (2010) Nature Biotechnology Reviews 11:31-46, incorporated herein by reference, all of which are incorporated by reference in their entireties.

[001924] In some embodiments, the EGFR mutation includes, for example, but is not limited to T790M, Ex19Del, L858R, Exon 20 insertion, delE709-T710insD, I744_K745insKIPVAI, K745_E746insTPVAIK, E709X, E709K, E709A, Exon 18 dclction, G719X, G719A, G719S, L861Q, S768I, L747P, A763_764insFQEA, D770_N771insNPG, A763_764insFQEA, P772_H773insDNP exon 20 insertion, H773_V774insNPH exon 20 insertion, S768I, D770_N771insSVD, V769_D770InsASV, p.K745_E746insIPVAIK, p.K745_E746insTPVAIK, p.I744_K745insKIPVAI, D770_N771insNPG, P772_H773insPNP, A763_Y764insFQEA, and/or EGFR kinase domain duplication (EGFR-KDD). In some embodiments, the EGFR mutation is selected from the group consisting of T790M, Ex19Del, L858R, Exon 20 insertion, delE709-T710insD, I744_K745insKIPVAI, K745_E746insTPVAIK, E709X, E709K, E709A, Exon 18 deletion, G719X, G719A, G719S, L861Q, S768I, L747P, A763_764insFQEA, D770_N771insNPG, A763_764insFQEA, P772_H773insDNP exon 20 insertion, H773_V774insNPH exon 20 insertion, S768I, D770_N771insSVD, V769_D770InsASV, p.K745_E746insIPVAIK,

p.K745_E746insTPVAIK, p.I744_K745insKIPVAI, D770_N771insNPG, P772_H773insPNP, A763_Y764insFQEA, and EGFR kinase domain duplication (EGFR-KDD).

[001925] In some embodiments, the EGFR mutation is a double mutation including for example, but not limited to, L858R/T790M, Ex19Del/T790M, G719X/L861Q, G719X/S768I (or S768I/G719X), S768I/L858R, L858R/E709A, and/or E746_T751delinsA+T790M. In some embodiments, the EGFR mutation is a double mutation selected from group consisting of L858R/T790M, Ex19Del/T790M, G719X/L861Q, G719X/S768I (or S768I/G719X), S768I/L858R, L858R/E709A, and E746_T751delinsA+T790M.

[001926] Additional disclosures of the EGFR mutation are provided in International Application Publication No. WO2010020618, which is incorporated by referenced herein in its entirety.

[001927] In some embodiments, the ALK mutation includes, but not limited to, EML4-ALK Variant 1 (AB274722.1; BAF73611.1), EML4-ALK Variant 2 (AB275889.1; BAF73612.1), EML4-ALK Variant 3a (AB374361.1; BAG55003.1), EML4-ALK Variant 3b (AB374362.1; BAG55004.1), EML4-ALK Variant 4 (AB374363.1; BAG75147.1), EML4-ALK Variant 5a (AB374364.1; BAG75148.1), EML4-ALK Variant 5b (AB374365.1; BAG75149.1), EML4-ALK Variant 6 (AB462411.1; BAH57335.1), EML4-ALK Variant 7 (AB462412.1; BAH57336.1), KIF5B-ALK (AB462413.1; BAH57337.1), NPM-ALK, TPM3-ALK, TFGXL-ALK, TEGL-ALK, TFGS-ALK, A11C-ALK, CLTC-ALK, MSN-ALK, TPM4-ALK, MYH9-ALK, RANBP2-ALK, AL017-ALK, and CARS-ALK (see, for example. Pulford et al., (2004) J. Cell. Physiol. 199:330-358). In addition, a skilled artisan will understand that ALK kinase variants can arise depending upon the particular fusion event between an ALK kinase and its fusion partner (*e.g.*, EML4 can fuse at least exon 2, 6a, 6b, 13, 14, and/or 15, as described, for example, in Horn and Pao, (2009) J. Clin. Oncol. 27:4247-4253) (incorporated by reference in its entirety).

[001928] Additional examples of ALK mutations are described in US Patent Nos. 9,018,230 and 9,458,508, the disclosures of which are incorporated by reference herein.

[001929] In some embodiments, the ROS1 mutation of the present invention is a ROS1 fusion, where a portion of the ROS1 polypeptide that includes the kinase domain of the ROS1 protein (or polynucleotide encoding the same) fused to all or a portion of another polypeptide (or polynucleotide encoding the same) and where the name of that second polypeptide or polynucleotide is named in the fusion. In some embodiments, the ROS1 mutation is determined as ROS1-fusion protein (*e.g.* by IHC) and/or ROS -fusion gene (*e.g.* by FISH), and/or ROS1 mRNA (*e.g.* by qRT-PCR), preferably indicative of a ROS1 -fusion protein selected from the group consisting of SLC34A2-ROS1 (SLC34A2 exons 13del2046 and 4 fused to ROS1 exons 32 and 34), CD74-ROS1 (CD74 exon 6 fused to ROS1 exons 32 and 34), EZR-ROS1 (EZR exon 10 fused to ROS1 exon 34), TPM3-ROS1

(TPM3 exon 8 fused to ROS1 exon 35), LRIG3-ROS1 (LRIG3 exon 16 fused to ROS1 exon 35), SDC4-ROS1 (SDC4 exon 2 and 4 fused to ROS1 exon 32 and SDC4 exon 4 fused to ROS1 exon 34), GOPC-ROS1 , also known as FIG-ROS1 , (GOPC exon 8 fused to ROS1 exon 35 and GOPC exon 4 fused to ROS1 exon 36), and G2032R, i.e. ROS1 ^{G2032R}.

[001930] Additional disclosures of the ROS1 mutations and the ROS fusion have been provided in U.S. Patent Publication Nos. 20100221737, 20150056193, and 20100143918, and PCT Publication No, WO2010/093928, all of which are hereby incorporated by reference in their entirety.In some embodiments, the RET mutation is a RET fusion or point mutation.

[001931] In some embodiments, the RET point mutation includes but is not limited to H6650, K666E, K666M, S686N, G691S, R694Q, M700L, V706M, V706A, E713K, G736R, G748C, A750P, S765P, P766S, E768Q, E768D, L769L, R770Q, D771N, N777S, V7781, Q781R, L790F, Y791F, Y791N, V804L, V804M, V804E, E805K, E806C, Y806E, Y806F, Y806S, Y806G Y806C E818K S8191 G823E Y826M R833C P841L P841P E843D R844W, R844Q, R844L, M848T, 1852M A866W R873W A876V L881V A883F A883S A883T E884K R886W, S891A, R8970, D898V, E901K 5904F S904C2 K907E K907M R908K G911D R912P R912Q M918T, M918V, M918L6, A919V, E921K, S922P S922Y T930M F961L R972G R982C M1009V D1017N V10416, and M1064T.

[001932] In some embodiments, the RET fusion is a fusion between RET and a fusion partner that is selected from the group consisting of BCR, BCR, CLIP 1, KIFSB, CCDC6, PTClex9, NCOA4, TRIM33, ERC1, FGFRIOP, MBD1, RAB61P2, PRKARIA, TRIM24, KTN1, GOLGA5, HOOK3, KIAA1468, TRIM27, AKAP13, FKBP15, SPECCIL, TBL1XR1, CEP55, CUX1, ACBD5, MYH13, PIBF1, KIAA1217, and MPRIP.

[001933] Additional disclosures of the RET mutations has been provided in U.S. Patent No. 10035789, which is hereby incorporated by reference in their entirety.

[001934] In some embodiments, the BRAF mutation is BRAF V600E/K mutation. In other embodiments, the BRAF mutation is a non-V600E/K mutation.

[001935] In some embodiments, the non-V600E/K BRAF mutation is a kinase-activated mutation, a kinase-impaired mutation, or a kinase-unknown mutation, and combinations thereof. In some embodiments, the kinase-activated mutation is selected from the group consisting of R4621, 1463S, G464E, G464R, G464V, G466A, G469A, N58 is, E586K, F595L, L597Q, L597R, L5975, L597V, A598V, T599E, V600R, K601E, 5602D, A728V, and combinations thereof. In some embodiments, the kinase-impaired mutation is selected from the group consisting of G466E, G466R, G466V, Y472C, K483M, D594A, D594E, D594G, D594H, D594N, D594V, G596R, T599A, 5602A, and

combinations thereof. In some embodiments, the kinase-unknown mutation is selected from the group consisting of T4401, 5467L, G469E, G469R, G4695, G469V, L584F, L588F, V600 K6OldelinsE, 56051, Q609L, E611Q, and combinations thereof. In some embodiments, the non-V600E/K BRAF mutation is selected from the group consisting of D594, G469, K601E, L597, T599 duplication, L485W, F247L, G466V, BRAF fusion, BRAF-AGAP3 rearrangement, BRAF exon 15 slice variant, and combinations thereof.

In some embodiments, the Met mutation includes point mutation, deletion mutation, insertion mutation, inversion, aberrant splicing, missense mutation, or gene magnification that causes the increase of at least one bioactivity of c-Met protein, the tyrosine kinase activity such as improved, receptor homolog dimerization Ligand binding of formation, enhancing of body and heterodimer etc. The Met mutation can be located at any part of c-Met genes. In one embodiment, the mutation is in the kinase domain of c-Met protein encoded by the c-MET gene. In some embodiments, the c-Met mutations are point mutation at N375, V13, V923, R175, V136, L229, S323, R988, S1058/T1010 and E168.

[001936] In some embodiments, the ERBB2 mutation is a point mutation in the amino acid sequence of ERBB2. In some embodiments, the point mutation of ERBB2 is one that causes amino acid substitutions, causes mRNA splicing, or is a point mutation in the upstream region. Wherein the mutation comprises a nucleotide mutation causing at least one amino acid substitution selected from the group consisting of Q568E, P601R, I628M, P885S, R143Q, R434Q, and E874K.

[001937] In some embodiments, the ERBB2 mutation is ERBB2 amplification. In some embodiments, the ERBB2 amplification includes point mutation selected from the group consisting of V659E, G309A, G309E, S310F, D769H, D769Y, V777L, P780ins, P780-Y781insGSP, V842I, R896C, K753E, and L755S and can be detected by Polymerase Chain Reaction or any sequencing technique (Bose et al. Cancer Discov. 2013, 3(2), 224-237; Zuo et al. Clin Cancer Res 2016, 22(19), 4859-4869).

[001938] In some embodiments, the BRCA mutation is a mutation in BRCA1 and/or BRCA2, preferably BRCA1, and/or in one or more other genes of which the protein product associates with BRCA1 and/or BRCA2 at DNA damage sites, including ATM, ATR, Chk2, H2AX, 53BP1, NFBD1, Mre11, Rad50, Nibrin, BRCA1-associated RING domain (BARD1), Abraxas, and MSH2. A mutation in one or more of these genes may result in a gene expression pattern that mimics a mutation in BRCA1 and/or BRCA2.

[001939] In certain embodiments the BRCA mutation comprises a non-synonymous mutation. In some embodiments, the BRCA mutation comprises a nonsense mutation. In some embodiments, the BRCA mutation comprises a frameshift mutation. In some embodiments, the BRCA mutation

comprises a splicing mutation. In some embodiments, the BRCA mutation is expressed as a mutant mRNA and ultimately a mutant protein. In some embodiments, the BRCA1/2 protein is functional. In other embodiments, the BRCA1/2 protein has reduced activity. In other embodiments, the BRCA1/2 protein is non-functional.

[001940] As used herein with regard to susbtitions, the "=" sign with regard to mutaitons generally refers to synonymous substitutions, silent codons, and/or silent substitutions. In particular, a synonymous substitution (also called a silent substitution or silent codon) refers to the substitution of one nucleotide base for another in an exon of a gene encoding a protein, wherein the produced amino acid sequence is not modified. This is due to the fact that the genetic code is "degenerate", *i.e.*, that some amino acids are coded for by more than one three-base-pair codon. Because some of the codons for a given amino acid vary by just one base pair from others coding for the same amino acid, a point mutation that replaces the wild-type base by one of the alternatives will result in incorporation of the same amino acid into the elongating polypeptide chain during translation of the gene. In some embodiments, synonymous substitutions and mutations affecting noncoding DNA are often considered silent mutations; however, it is not always the case that the mutation is silent and without any impact. For example, a synonymous mutation can affect transcription, splicing, mRNA transport, and translation, any of which could alter the resulting phenotype, rendering the synonymous mutation non-silent. The substrate specificity of the tRNA to the rare codon can affect the timing of translation, and in turn the co-translational folding of the protein. This is manifested in the codon usage bias that has been observed in many species. A nonsynonymous substitution/mutation results in a change in amino acid that may be arbitrarily classified as conservative (a change to an amino acid with similar physiochemical properties), semi-conservative (*e.g.* negatively to positively charged amino acid), or radical (vastly different amino acid).In some embodiments, the BRCA mutation is a BRCA1 mutation that includes, but is not limited to P871L, K1183R, D693N, S1634G, E1038G, S1040N, S694= (=: silience codon), M1673I, Q356R, S1436=, L771=, K654Sfs*47, S198N, R496H, R841W, R1347G, H619N, S1533I, L30=, A622V, Y655Vfs*18, R496C, E597K, R1443*, E23Vfs*17, L30F, E111Gfs*3, K339Rfs*2, L512F, D693N, P871S, S1140G, Q1240*, P1770S, R7=, L52F, T176M, A224S ,L347=, S561F, E597*, K820E, K893Rfs*107, E962K, M1014I, R1028H, E1258D, E1346K, R1347T, L1439F, H1472R, Q1488*, S1572C, E1602K, R1610C, L1621=, Q1625*, Q1625=, D1754N, R1772Q, R1856*, and any combination thereof.

[001941] In some embodiments, the BRCA mutation is a BRCA2 mutation that includes, but is not limited to V2466A, N289H, N991D, S455= (=: silience codon), N372H, H743=, V1269=, S2414=, V2171=, L1521=, T3033Nfs*11, K1132=, T3033Lfs*29, R2842C, N1784Tfs*7, K3326*, K3326*, D1420Y, I605Yfs*9, I3412V, A2951T, T3085Nfs*26, R2645Nfs*3, S1013*, T1915M, F3090=,

V3244I, A1393V, R2034C, L1356=, E2981Rfs*37, N1784Kfs*3, K3416Nfs*11, K1691Nfs*15, S1982Rfs*22, and any combination thereof.

[001942] In some embodiments, the NRAS mutation of the present invention includes but is not limited to E63K, Q61R, Q61K, G12D, G13D, Q61R, Q61L, Q61K, G12S, G12C, G13R, Q61H, G12V, G12A, Q61L, G13V, Q61H, Q61H, G12R, G13C, Q61P, G13S, G12D, G13A, G13D, A18T, Q61X, G60E, G12S, Q61= (=: silience codon), Q61E, Q61R, A146T, A59T, A59D, Q61=, R68T, A146T, G12A, E62Q, G75=, A91V, and any combination thereof.

[001943] E132KIn some embodiments, the PIK3CA mutation includes substitution mutations, deletion mutations, and insertion mutations. In some embodiments, mutations occur in PIK3CA's helical domain and in its kinase. In other embodiments, in PIK3CA's P85BD domain. In some embodiments, the PIK3CA mutation is in exon 1, 2, 4, 5, 7, 9, 13, 18, and 20. In some embodiments, the PIK3CA mutation is in exons 9 and 20. In yet other embodiments, the PIK3CA mutation is a combination of the any mutations listed above. Any combination of these exons can be tested, optionally in conjunction with testing other exons. Testing for mutations can be done along the whole coding sequence or can be focused in the areas where mutations have been found to cluster. Particular hotspots of mutations occur at nucleotide positions 1624, 1633, 1636, and 3140 of PIK3CA coding sequence.

[001944] In some embodiments, the size of the PIK3CA mutation is small, ranging from 1 to 3 nucleotides. In some embodiments, the PIK3CA mutations include, but are not limited to G1624A, G1633A, C1636A, A3140G, G113A, T1258C, G3129T, C3139T, E542K, E545K, Q546R, H1047L, H1047R and G2702T.

[001945] In some embodiments, the MAP2K1 mutation is a somatic MAP2K1 mutation, optionally a MAP2K1 mutation that upregulates MEK1 levels. In some embodiments, the MAP2K1 mutation is a mutation in one or more genes associated with the RAS/MAPK pathway, comprising: HRAS, KRAS, NRAS, ARAF, BRAF, RAFl, MAP2K2, MAPKl, MAPK3, MAP3K3. In certain embodiments, the MAP2K1 mutation is in one or more genes selected from the group consisting of RASA, PTEN, ENG, ACVRL1, SMAD4, GDF2 or combinations thereof.

[001946] In some embodiments, the MAP2K1 mutation includes, but is not limited to, P124S, Q56P, K57N, E203K, G237*, P124L, G128D, D67N, K57E, E102_I103del, C121S, K57T, K57N, Q56P, P124L, K57N, G128V, Q58_E62del, F53L, I126=, I103_K104del, and any combination thereof.

[001947] In certain embodiments the KRAS mutation comprises a non-synonymous mutation. In some embodiments, the KRAS mutation comprises a nonsense mutation. In some embodiments, the KRAS mutation comprises a frameshift mutation. In some embodiments, the KRAS mutation

comprises a splicing mutation. In some embodiments, the KRAS mutation is expressed as a mutant mRNA and ultimately a mutant protein. In some embodiments, the mutated KRAS protein is functional. In other embodiments, the mutated KRAS protein has reduced activity. In other embodiments, the mutated KRAS protein is non-functional.

[001948] In some embodiments, the KRAS mutation includes but is not limited to G12D, G12V, G13D, G12C, G12A, G12S, G12R, G13C, Q61H, A146T, Q61R, Q61H, Q61L, G13S, A146V, Q61K, G13R, G12F, K117N, G13A, G13V, A59T, V14I, K117N, Q22K, Q61P, A146P, G13D, L19F, L19F, Q61K, G12V, G60=, G12=, G13=, A18D, T58I, Q61E, E63K, G12L, G13V, A59G, G60D, G10R, G10dup, D57N, A59E, , V14G, D33E, G12I, G13dup, and any combination thereof, wherein = is indiciative of silence coding.

[001949] In some embodiments, the NF1 mutation includes substitution mutations, deletion mutations, missense mutations, aberrant splicing mutations, and insertion mutations. In some embodiments, the NF1 mutation is a loss of function (LOF) mutation. In some embodiments, the NF1 mutation is selected from the group consisting of R1947X (C5839T), R304X, exon 37 mutation, exon 4b mutation, exon 7 mutation, exon 10b mutation, and exon 10c mutation (*e.g.*, 1570G→T, E524X).

[001950] In some embodiments, the CDKN2A mutation includes but is not limited to R24P, D108G, D108N, D108Y, G125R, P114L, R80*, R58*, H83Y, W110*, P114L, E88*, W110*, E120*, D108Y, D84Y, D84N, E69*, P81L, Q50*, L78Hfs*41, D108N, S12*, P48L, E61*, Y44*, E88K, R80*, D84G, L16Pfs*9, Y129*, D108H,A148T, A36G, A102V, W15*, H83R, A57V, E33*, D74Y, A76V, E153K, D74N, H83D, V82M, R58*, Y129*, E119*, Y44*, D74A, T18_A19dup, Y44Lfs*76, L32_L37del, V28_E33del, D14_L16del, A68T, or any combination thereof.

[001951] In certain embodiments the PTEN mutation comprises a non-synonymous mutation. In some embodiments, the PTEN mutation comprises a nonsense mutation. In some embodiments, the PTEN mutation comprises a frameshift mutation. In some embodiments, the PTEN mutation comprises a splicing mutation. In some embodiments, the mutated PTEN is expressed as an mRNA and ultimately a protein. In some embodiments, the mutated PTEN protein is functional. In other embodiments, the mutated PTEN protein has reduced activity. In other embodiments, the mutated PTEN protein is non-functional. In some embodiments, the PTEN mutation includes, but is not limited to, R130Q, R130G, T319*, R233*, R130*, K267Rfs*9, N323Mfs*21, N323Kfs*2, R173C, R173H, R335*, Q171*, Q245*, E7*, D268Gfs*30, R130Q, Q214*, R130L, C136R, Q298*, Q17*, H93R, P248Tfs*5, I33del, R233*, E299*, G132D, Y68H, T319Kfs*24, N329Kfs*14, V166Sfs*14, V290*, T319Nfs*6, R142W, P38S, A126T, H61R, F278L, S229*, R130P, G129R, R130Qfs*4, P246L, R130*, G165R, C136Y, R173C, I101T, Y155C, D92E, K164Rfs*3, N184Efs*6, G129E,R130G, G36R, F341V, H123Y, C124S, M35VG127E, G165E and any combination thereof.

[001952] In some embodiments, the TP53 mutation includes, but is not limited to, R175H, G245S, R248Q, R248W, R249S, R273C, R273H, R282W, C135Y, C141Y, P151S, V157F, R158L, Y163C, V173L, V173M, C176F, H179R, H179Y, H179Q, Y205C, Y220C, Y234C, M237I, C238Y, S241F, G245D, G245C, R248L, R249M, V272M, R273L, P278L, R280T, E285K, E286K, R158H, C176Y, I195T, G214R, G245V, G266R, G266E, P278S, R280K, or any combination thereof. In some further embodiments, the TP53 mutation is selected from the group consisting of: G245S; R249S; R273C; R273H; C141Y, V157F, R158L, Y163C, V173L, V173M, Y205C, Y220C, G245C, R249M, V272M, R273L, and E286K. In some embodiments, the TP53 mutation includes one or more of the mutations above.

[001953] In some embodiments, the CREBBP mutation includes, but is not limited to, R1446C, R1446H, S1680del, I1084Sfs*15, P1948L, I1084Nfs*3, ?R386*, S893L, R1341*, P1423Lfs*36, P1488L, Y1503H, R1664C, A1824T, R1173*, R1360*, Y1450C, H2228D, S71L, P928=, D1435N, W1502C, Y1503D, R483*, R601Q, S945L, R1103*, R1288W, R1392*, C1408Y, D1435G, R1446L, H1485Y, Q1491K, Q96*, L361M, L524Wfs*6, Q540*, Q1073*, A1100V, R1169C, C1237Y, R1347W, G1411E, W1472C, I1483F, P1488T, R1498*, Y1503F, Q1856*, R1985C, R2104C, S2328L, V2349=, S2377L, and any combination thereof.

[001954] In some embodiments, the KMT2C mutation includes, but is not limited to, D348N, P350=, R380L, C391*, P309S, C988F, Y987H, S990G, K2797Rfs*26, V346=, R894Q, R284Q, S806=, R1690=, P986=, A1685S, G315S, Q755*, R909K, T316S, S772L, G838S, L291F, P335=, C988F, Q2680=, E765G, K339N, Y816*, R526P, N729D, G845E, I817Nfs*11, G892R, C1103*, S3660L, F4496Lfs*21, G315C, R886C, D348N, S793=, V919L, R2481S, R2884*, R4549C, M305Dfs*28, T316S, P377=, I455M, T820I, S965=, S730Y, P860S, Q873Hfs*40, R904*, R2610Q, R4478*, and any combination thereof.

[001955] In some embodiments, the KMT2D mutation includes, but is not limited to, L1419P, E640D, E541D, E455D, T2131P, K1420R. P2354Lfs*30, G2493=, Q3612=, I942=, T1195Hfs*17, P4170=, P1194H, G1235Vfs*95, P4563=, P647Hfs*283, L449_P457del, P3557=, Q3603=, R1702*, P648Tfs*2, R5501*, R4198*, R4484*, R83Q, R1903*, ,R2685* , R4282*, L5326=, R5432W, R2734*, Q2800*, R2830*, Q3745dup, S4010P, R4904*, G5182Afs*61, R5214H, R1615*, Q2380*, R2687*, R2771*, V3089Wfs*30, Q3799Gfs*212, R4536*, R5030C, R5048C, R5432Q, A221Lfs*40, A476T, A2119Lfs*25,P2557L, R2801*, Q3913*, R4420W, G4641=, R5097*, and any combination thereof.

[001956] In some embodiments, the ARID1A mutation includes, but is not limited to, For example, subject has a mutation of ARID1A selected from the group consisting of a C884* (*: nonsense mutation), E966K, Q1411*, F1720fs (fs: frameshift), G1847fs, C1874fs, D1957E, Q1430, R1721fs,

G1255E, G284fs, R1722*, M274fs, G1847fs, P559fs, R1276*, Q2176fs, H203fs, A591fs, Q1322*, S2264*, Q586*, Q548fs, and N756fs.

[001957] In some embodiments, the RB1 mutation includes, but is not limited to, R320X, R467X, R579X, R455X, R358X, R251X, R787X, R552X, R255X, R556X, Y790X, Q575X, E323X, R661W, R579*, R455*, R556*. R787*, R661W, R445*, R467*, Q217* ,Q471*, W195*, Q395*, I680T, E137*, R255*, Q344*, Q62*, E440K, A488V, P777Lfs*33, E322K, R656W, G617Rfs*36, C221*, E440*,Q93*, Q504*, E125*, S834*, E323*, Q685*, S829*, W516*, G435*, Q257*, E79*, S567L, V654M, V654Sfs*14,G100Efs*11, K715*, and any combination thereof.

[001958] In some embodiments, the ATM mutation is a mutation in the ATM gene sequence including, but is not limited to, 10744A>G;10744A>G; 11482G>A; IVS3-558A>T; 146C>G; 381delA; IVS8-3delGT; 1028delAAAA; 1120C>T; 1930ins16; IVS16+2T>C; 2572T>C; IVS21+1G>A; 3085delA; 3381delTGAC; 3602delTT; 4052delT; 4396C>T; 5188C>T; 5290delC; 5546delT; 5791G>CCT; 6047A>G; IVS44-1G>T; 6672delGC/6677delTACG; 6736dell 1/6749del7; 7159insAGCC; 7671delGTTT; 7705del14; 7865C>T; 7979delTGT; 8177C>T; 8545C>T; 8565T>A; IVS64+1G>T; and 9010del28.

[001959] In some embodiments of the present invention, the SETD2 mutation is an alteration in the gene sequence encoding the SETD2 protein, when the transcription initiation codon position of the mRNA sequence of NCBI accession number NM_014159 is set to 1. In some embodiments, the 7558th G (guanine) is substituted with T (thymine) , 4774 th C (cytosine) is substituted by T, 1210 th A (adenine) is substituted by T, 4883 th is substituted by G, 5290 th C is replaced by T, 7072 th C is replaced by T, 4144 th G Is substituted by T, 1297 is replaced by T, 755 is replaced by G, 7261 is substituted by G, 6700 is replaced by T, 2536 is substituted by T, 7438 is replaced by T Substitution, insertion of A at position 3866, insertion of T at position 6712, insertion of T at position 7572, deletion of 913th A, deletion of 5619th C, deletion of bases 4603-4604, 894-897 Deletion of the 1st base, deletion of the 1936th C, deletion of the 3094-3118 base, insertion of A in the 5289th position, and deletion of the 6323-6333 base One or more mutations selected from the group true luer included.

[001960] In one embodiment of the present invention, the mutation of the SETD2 protein is stopped after 2520 glutamic acid, stop after 1592 arginine, stop after 404 arginine, stop after 1764 glutamine, 1032 of SETD2 amino acid sequence corresponding to NCBI accession number NP_054878 Frameshift after the first serine, Frameshift after the 646 histidine, Frameshift after the 2108th valine, Frameshift after the 1764 glutamine, Frameshift after the 298th isoleucine, Frameshift after the 1289th asparagine, Frameshift since the 289th serine Frameshift after, stop after 2525 lysine, frame shift after 305 threonine, frame shift after 1873 proline, frame shift after 1535 asparagine, stop after 2234 glutamic acid, replace 2536 alanine with threonine, 7438 Glutamine stopped, 1628 Group consisting

of spargine substituted by serine, 2358 th proline by serine, 1382 alanine by serine, 433 th arginine by cytosine, 252nd alanine by glycine, and 2421 threonine by alanine One or more mutations selected from.

[001961] In some embodiments, the FLT3 mutation includes, but is not limited to, (Q569_E648)ins, D835X, (Q569_E648)delins, (D835_I836), D835Y, D835V, D835Y, D835H, T227M, I836del, N676K, D835E, Y597_E598insDYVDFREY,D835E, D835del, F594_D600dup, A680V, D839G, D96=, D835H, V491L, D835E, Q989*, D835V, L561=, I836del, P986Afs*27, D7G, D324N, S451F, D835N, L576P, Y597_E598insDVDFREY, V491L, N841T, D324N, Y572C, R595_L601dup, K663R, N676K,F691L, D835A, I836H, N841K, S993L, L832F, I836M, A66V, and any combination thereof.

[001962] In some embodiments, the PTPN11 mutation includes, but is not limited to, c E76K, A72V, A72T, D61Y, D61V, ,G60V , E69K, E76G, G507V, S506L, G507A, T73I, E76A, E76Q, S506P, D61N, F71L, E76V, F71L, A72D, V432M, T472M, P495L, N58Y, F285S, S506A, S189A, A465T, R502W, G507R, T511K, D61H, D61G, G507E, G60R, G60A, Q514L, E139D, Y197*, N308D, Q514H, Q514H, N58S, E123D, L206=, A465G, P495S, G507R, and any combination thereof.

[001963] In some embodiments, the FGFR1 mutation includes, but is not limited to, N577K, K687E, N577K, D166del, T371M, R476W, T350=, E498K, N577D, D683G, R87C, A154D, N303=, A374V, D550=, S633=, V695L, G728=, R765W, P803S, W19C, P56=, R113C, V149I, S158L, D166dupR220C, N224Kfs*8, D249N, R281W, R281Q, A299S, S424L, S461F, S467F, R506Q, and any combination thereof.

[001964] In some embodiments, the EP300 mutation includes, but is not limited to, D1399N, Y1414C, M1470Cfs*26, Y1111*, H2324Pfs*55, R1627W, N2209_Q2213delinsK, Q2268del, L415P, M1470Nfs*3, E1514K, C1201Y, P1452L, S952*, C1164Y, D1399Y, S507G, Q824*, D1507N, H2324Tfs*29, P925T, P1440L, W1466C, P1502L, A1629V, R1645*, N1700Tfs*9, P1869L, Q65*, A171V, R202*, R580Q, A627V, Q1082*, N1236Kfs*2, N1286S, R1312*, R1356*, C1385F, H1451L, R1462*, Y1467N, Y1467H, R1478H, R1627Q, R86*, R370H, R397*, R754C, P842S, I997V, E1014*,and any combination thereof.

[001965] In some embodiments, the MYC mutation includes, but is limited to, E61T, E68I, R74Q, R75N, W135E, W136E, V394D, L420P, W96E, V325D, L351P, a MYC protein with 41 amino acid deleted at the N-terminus (dN2MYC), N26S, S161L, P74L, V7M, F153S, E54D, P246, L164V, P74S, A59V, T73I, P72T,T73A, H374R, P17S, T73N, S264N, P72S, Q52del, S21T, P74A, S107N, P75S, S77P, P261S, P74Q, S190R, A59T, F153C, P75H, T73I, S77F, N11S, S21N, P78L, P72L, N9K, S190N, S267F, T73P, P78S, G105D, S187C, L71M, Q10H, L191x, Q50x, L191F, R25K, F130L,

Y27S, D195N, D2G, V20A, V6G, V20I, D2H, P75A, G152D, P74T, C40Y, E8K, Q48x, and any combination thereof.

[001966] In some embodiments, the EZH2 mutation is associated with altered histone methylation patterns. In some embodiments, the EZH2 mutation leads to the conversion of amino acid Y641 (equivalent to Y646, catalytic domain), to either F, N, H, S or C resulting in hypertrimethylation of H3K27 and drives lymphomagenesis. In some embodiments, the EZH2 mutation includes EZH2 SET-domain mutations, overexpression of EZH2, overexpression of other PRC2 subunits, loss of function mutations of histone acetyl transferases (HATs), and loss of function of MLL2. Cells that are heterozygous for EZH2 Y646 mutations result in hypertrimethylation of H3K27 relative to cells that are homozygous wild-type (WT) for the EZH2 protein, or to cells that are homozygous for the Y646 mutation.

[001967] In some embodiments, the EZH2 mutation includes, but is not limited to, Y646F, Y646N, D185H, Y646F, Y646S, Y646H, R690H, Y646X, E745K, Y646C, V626M, V679M, R690H, R684H, A682G, E249K, G159R, R288Q, N322S, A692V, R690C, D730* (insertion frameshift), S695L, R684C, M667T, .R288*, S644*, D192N, K550T,Q653E, D664G, R347Q,Y646C,G660R, R213C, A255T, S538L, N693K, I55M, R561H, A692V, K515R,Y733*, R63*, Q570*, Q328*, R25Q, T467P A656V, T573I, C571Y, E725K, R16W, P577L, F145S, V680M, G686D, G135R, K634E, S652F, R298C, G648E, R566H, L149R,, R502Q, Y731D, R313W, N675K, S652C, T374Hfs*3, N152Ifs*15, E401Kfs*22, K406Mfs*17, E246*, S624C, I146T, V626M, L674S, H694R, A581S, and any combination thereof.

[001968] In some embodiments, the JAK2 mutation is a mutation in the JAK2 gene includes, but is not limited to, T1923C mutation in combination with a G1920T mutation, a G1920T / C1922T mutation, or a G1920A mutation. In some embodiments, the JAK2 mutation is a mutant JAK2 protein comprising one or more substitutions include, but are not limited to, V617F, V617I, R683G, N542_E543del, E543_D544del, R683S, R683X, F537_K539delinsL (deletion in frame), K539L, N1108S, R1113H, R1063H, R487C, I540Mfs*3 (deletion-frameshift), R867Q, K539L, G571S, R1113C, R938Q, R228Q, L830*, E1080*, K539L, C618R, R564Q, D1036H, L1088S, H538Nfs*4, D873N, V392M, I682F, L393V, M535I, C618R, T875N, L611V, D319N, L611S, G921S, H538Y, S1035L, and any combination thereof.

[001969] In some embodiments, the FBXW7 mutation is a point mutation selected from the group consisting of W244* (*:stop codon), R222*, R278*, E192A, S282*, E113D, R465H/C, 726+1 G>A splice, R505C, R479Q, R465C, R367*, R499Vfs*25 (fs*: frameshift), R658*, D600Y, D520N, D520Y, and any combination thereof. In further embodiments, the FBXW7 mutation is double- or

triple-mutation includes, but is not limited to, R479Q and S582L, R465H and S582L, D520N, D520Y and R14Q, and R367* and S582L.

[001970] In some embodiments, the CCND3 mutation includes, but is not limited to, S259A, R271Pfs*53 (insertion-caused frameshift), E51*, Q260*, P199S, T283A, T283P, V287D, D286_T288del, R271Gfs*33, Q276*, R241Q, D238G, R33P, I290K, I290T, I290R, P267fs, P284S, P284L, P100S, E253D, S262I, R14W, R114L, D238N, A266E, R167W, and any combination thereof.

[001971] In some embodiments, the GNA11 mutation includes, but is not limited to, Q209L, R183C, T257=, R183C, G208Afs*16, Q209H, R183C, Q209P, Q209R, Q209H, ?T96=, R210W, R256Q, T334=, G48D, S53G, , Q209P, R213Q , and any combination thereof. In some embodiments, the GNA11 mutation has two mutations in exon 4, eg, a mutation in V182 and a mutation in T175, or one or more mutation in exon 5.

3. Combinations with PD-1 and PD-L1 Inhibitors

[001972] Programmed death 1 (PD-1) is a 288-amino acid transmembrane immunocheckpoint receptor protein expressed by T cells, B cells, natural killer (NK) T cells, activated monocytes, and dendritic cells. PD-1, which is also known as CD279, belongs to the CD28 family, and in humans is encoded by the *Pdcd1* gene on chromosome 2. PD-1 consists of one immunoglobulin (Ig) superfamily domain, a transmembrane region, and an intracellular domain containing an immunoreceptor tyrosine-based inhibitory motif (ITIM) and an immunoreceptor tyrosine-based switch motif (ITSM). PD-1 and its ligands (PD-L1 and PD-L2) are known to play a key role in immune tolerance, as described in Keir, *et al.*, *Annu. Rev. Immunol.* **2008,** *26,* 677-704. PD-1 provides inhibitory signals that negatively regulate T cell immune responses. PD-L1 (also known as B7-H1 or CD274) and PD-L2 (also known as B7-DC or CD273) are expressed on tumor cells and stromal cells, which may be encountered by activated T cells expressing PD-1, leading to immunosuppression of the T cells. PD-L1 is a 290 amino acid transmembrane protein encoded by the *Cd274* gene on human chromosome 9. Blocking the interaction between PD-1 and its ligands PD-L1 and PD-L2 by use of a PD-1 inhibitor, a PD-L1 inhibitor, and/or a PD-L2 inhibitor can overcome immune resistance, as demonstrated in recent clinical studies, such as that described in Topalian, *et al.*, *N. Eng. J. Med.* **2012,** *366,* 2443-54. PD-L1 is expressed on many tumor cell lines, while PD-L2 is expressed is expressed mostly on dendritic cells and a few tumor lines. In addition to T cells (which inducibly express PD-1 after activation), PD-1 is also expressed on B cells, natural killer cells, macrophages, activated monocytes, and dendritic cells.

[001973] In some embodiments, TILs and a PD-1 inhibitor are administered as a combination therapy or co-therapy for the treatment of NSCLC.

[001974] In some embodiments, the NSCLC has undergone no prior therapy. In some embodiments, a PD-1 inhibitor is administered as a front-line therapy or initial therapy. In some embodiments, a PD-1 inhibitor is administered as a front-line therapy or initial therapy in combination with the TILs as described herein.

[001975] In some embodiments, the PD-1 inhibitor may be any PD-1 inhibitor or PD-1 blocker known in the art. In particular, it is one of the PD-1 inhibitors or blockers described in more detail in the following paragraphs. The terms "inhibitor," "antagonist," and "blocker" are used interchangeably herein in reference to PD-1 inhibitors. For avoidance of doubt, references herein to a PD-1 inhibitor that is an antibody may refer to a compound or antigen-binding fragments, variants, conjugates, or biosimilars thereof. For avoidance of doubt, references herein to a PD-1 inhibitor may also refer to a small molecule compound or a pharmaceutically acceptable salt, ester, solvate, hydrate, cocrystal, or prodrug thereof.

[001976] In some embodiments, the PD-1 inhibitor is an antibody (*i.e.*, an anti-PD-1 antibody), a fragment thereof, including Fab fragments, or a single-chain variable fragment (scFv) thereof. In some embodiments the PD-1 inhibitor is a polyclonal antibody. In some embodiments, the PD-1 inhibitor is a monoclonal antibody. In some embodiments, the PD-1 inhibitor competes for binding with PD-1, and/or binds to an epitope on PD-1. In some embodiments, the antibody competes for binding with PD-1, and/or binds to an epitope on PD-1.

[001977] In some embodiments, the PD-1 inhibitor is one that binds human PD-1 with a K_D of about 100 pM or lower, binds human PD-1 with a K_D of about 90 pM or lower, binds human PD-1 with a K_D of about 80 pM or lower, binds human PD-1 with a K_D of about 70 pM or lower, binds human PD-1 with a K_D of about 60 pM or lower, binds human PD-1 with a K_D of about 50 pM or lower, binds human PD-1 with a K_D of about 40 pM or lower, binds human PD-1 with a K_D of about 30 pM or lower, binds human PD-1 with a K_D of about 20 pM or lower, binds human PD-1 with a K_D of about 10 pM or lower, or binds human PD-1 with a K_D of about 1 pM or lower.

[001978] In some embodiments, the PD-1 inhibitor is one that binds to human PD-1 with a k_{assoc} of about 7.5×10^5 l/M·s or faster, binds to human PD-1 with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human PD-1 with a k_{assoc} of about 8×10^5 1/M·s or faster, binds to human PD-1 with a k_{assoc} of about 8.5×10^5 1/M·s or faster, binds to human PD-1 with a k_{assoc} of about 9×10^5 1/M·s or faster, binds to human PD-1 with a k_{assoc} of about 9.5×10^5 l/M·s or faster, or binds to human PD-1 with a k_{assoc} of about 1×10^6 1/M·s or faster.

[001979] In some embodiments, the PD-1 inhibitor is one that binds to human PD-1 with a k_{dissoc} of about 2×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.1×10^{-5} 1/s or slower , binds to human PD-1 with a k_{dissoc} of about 2.2×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc}

of about 2.3×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.4×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.5×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.6×10^{-5} 1/s or slower or binds to human PD-1 with a k_{dissoc} of about 2.7×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.8×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.9×10^{-5} 1/s or slower, or binds to human PD-1 with a k_{dissoc} of about 3×10^{-5} 1/s or slower.

[001980] In some embodiments, the PD-1 inhibitor is one that blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 10 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 9 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 8 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 7 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 6 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 5 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 4 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 3 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 2 nM or lower, or blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 1 nM or lower.

[001981] In some embodiments, the PD-1 inhibitor is nivolumab (commercially available as OPDIVO from Bristol-Myers Squibb Co.), or biosimilars, antigen-binding fragments, conjugates, or variants thereof. Nivolumab is a fully human IgG4 antibody blocking the PD-1 receptor. In some embodiments, the anti-PD-1 antibody is an immunoglobulin G4 kappa, anti-(human CD274) antibody. Nivolumab is assigned Chemical Abstracts Service (CAS) registry number 946414-94-4 and is also known as 5C4, BMS-936558, MDX-1106, and ONO-4538. The preparation and properties of nivolumab are described in U.S. Patent No. 8,008,449 and International Patent Publication No. WO 2006/121168, the disclosures of which are incorporated by reference herein. The clinical safety and efficacy of nivolumab in various forms of cancer has been described in Wang, *et al.*, *Cancer Immunol Res.* **2014,** 2, 846-56; Page, *et al.*, *Ann. Rev. Med.*, **2014,** *65,* 185-202; and Weber, *et al.*, *J. Clin. Oncology*, **2013,** *31,* 4311-4318, the disclosures of which are incorporated by reference herein. The amino acid sequences of nivolumab are set forth in Table 18. Nivolumab has intra-heavy chain disulfide linkages at 22-96,140-196, 254-314, 360-418, 22"-96", 140"-196", 254"-314", and 360"-418"; intra-light chain disulfide linkages at 23'-88', 134'-194', 23'"-88'", and 134'"-194'"; inter-heavy-light chain disulfide linkages at 127-214', 127"-214'", inter-heavy-heavy chain disulfide linkages at 219-219" and 222-222"; and N-glycosylation sites (H CH_2 84.4) at 290, 290".

[001982] In some embodiments, a PD-1 inhibitor comprises a heavy chain given by SEQ ID NO:158 and a light chain given by SEQ ID NO:159. In some embodiments, a PD-1 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:158 and SEQ ID NO:159, respectively.

[001983] In some embodiments, the PD-1 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of nivolumab. In some embodiments, the PD-1 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:160, and the PD-1 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:161, and conservative amino acid substitutions thereof. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively.

[001984] In some embodiments, a PD-1 inhibitor comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:162, SEQ ID NO:163, and SEQ ID NO:164, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:165, SEQ ID NO:166, and SEQ ID NO:167, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on PD-1 as any of the aforementioned antibodies.

[001985] In some embodiments, the PD-1 inhibitor is an anti-PD-1 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to nivolumab. In some embodiments, the biosimilar comprises an anti-PD-1 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is nivolumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-PD-1 antibody authorized or submitted for authorization, wherein the anti-PD-1 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is nivolumab. The anti-PD-1 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is nivolumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is nivolumab.

TABLE 18. Amino acid sequences for PD-1 inhibitors related to nivolumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:158 nivolumab heavy chain	QVQLVESGGG VVQPGRSLRL DCKASGITFS NSGMHWVRQA PGKGLEWVAV IWYDGSKRYY ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK	60 120 180 240 300 360 420 440
SEQ ID NO:159 nivolumab light chain	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	60 120 180 214
SEQ ID NO:160 nivolumab variable heavy chain	QVQLVESGGG VVQPGRSLRL DCKASGITFS NSGMHWVRQA PGKGLEWVAV IWYDGSKRYY ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSS	60 113
SEQ ID NO:161 nivolumab variable light chain	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIK	60 107
SEQ ID NO:162	NSGMH	5

Identifier	Sequence (One-Letter Amino Acid Symbols)	
nivolumab heavy chain CDR1		
SEQ ID NO:163 nivolumab heavy chain CDR2	VIWYDGSKRY YADSVKG	17
SEQ ID NO:164 nivolumab heavy chain CDR3	NDDY	4
SEQ ID NO:165 nivolumab light chain CDR1	RASQSVSSYL A	11
SEQ ID NO:166 nivolumab light chain CDR2	DASNRAT	7
SEQ ID NO:167 nivolumab light chain CDR3	QQSSNWPRT	9

[001986] In some embodiments, the PD-1 inhibitor is nivolumab or a biosimilar thereof, and the nivolumab is administered at a dose of about 0.5 mg/kg to about 10 mg/kg. In some embodiments, the PD-1 inhibitor is nivolumab or a biosimilar thereof, and the nivolumab is administered at a dose of about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 4.5 mg/kg, about 5 mg/kg, about 5.5 mg/kg, about 6 mg/kg, about 6.5 mg/kg, about 7 mg/kg, about 7.5 mg/kg, about 8 mg/kg, about 8.5 mg/kg, about 9 mg/kg, about 9.5 mg/kg, or about 10 mg/kg. In some embodiments, the nivolumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the nivolumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the nivolumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the nivolumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001987] In some embodiments, the PD-1 inhibitor is nivolumab or a biosimilar thereof, and the nivolumab is administered at a dose of about 200 mg to about 500 mg. In some embodiments, the PD-1 inhibitor is nivolumab or a biosimilar thereof, and the nivolumab is administered at a dose of about 200 mg, about 220 mg, about 240 mg, about 260 mg, about 280 mg, about 300 mg, about 320 mg, about 340 mg, about 360 mg, about 380 mg, about 400 mg, about 420 mg, about 440 mg, about 460 mg, about 480 mg, or about 500 mg. In some embodiments, the nivolumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the nivolumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the nivolumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample

from the subject or patient). In some embodiments, the nivolumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001988] In some embodiments, the PD-1 inhibitor is nivolumab or a biosimilar thereof, and the nivolumab is administered every 2 weeks, every 3 weeks, every 4 weeks, every 5 weeks, or every 6 weeks. In some embodiments, the nivolumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the nivolumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the nivolumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the nivolumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001989] In some embodiments, the nivolumab is administered to treat metastatic non-small cell lung cancer. In some embodiments, the nivolumab is administered to treat metastatic non-small cell lung cancer at about 3 mg/kg every 2 weeks along with ipilimumab at about 1 mg/kg every 6 weeks. In some embodiments, the nivolumab is administered to treat metastatic non-small cell lung cancer at about 360 mg every 3 weeks with ipilimumab 1 mg/kg every 6 weeks and 2 cycles of platinum-doublet chemotherapy. In some embodiments, the nivolumab is administered to treat metastatic non-small cell lung cancer at about 240 mg every 2 weeks or 480 mg every 4 weeks. In some embodiments, the nivolumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the nivolumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the nivolumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the nivolumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001990] In some embodiments, the PD-1 inhibitor comprises pembrolizumab (commercially available as KEYTRUDA from Merck & Co., Inc., Kenilworth, NJ, USA), or antigen-binding fragments, conjugates, or variants thereof. Pembrolizumab is assigned CAS registry number 1374853-91-4 and is also known as lambrolizumab, MK-3475, and SCH-900475. Pembrolizumab has an immunoglobulin G4, anti-(human protein PDCD1 (programmed cell death 1)) (human-Mus musculus monoclonal heavy chain), disulfide with human-Mus musculus monoclonal light chain, dimer structure. The structure of pembrolizumab may also be described as immunoglobulin G4, anti-(human programmed cell death 1); humanized mouse monoclonal [228-L-proline(H10-S>P)]γ4 heavy chain (134-218')-disulfide with humanized mouse monoclonal κ light chain dimer (226-226":229-229")-bisdisulfide. The properties, uses, and preparation of pembrolizumab are described in International Patent Publication No. WO 2008/156712 A1, U.S. Patent No. 8,354,509 and U.S. Patent Application Publication Nos. US 2010/0266617 A1, US 2013/0108651 A1, and US 2013/0109843 A2, the

disclosures of which are incorporated herein by reference. The clinical safety and efficacy of pembrolizumab in various forms of cancer is described in Fuerst, *Oncology Times,* **2014,** *36,* 35-36; Robert, *et al.*, *Lancet,* **2014,** *384,* 1109-17; and Thomas, *et al.*, *Exp. Opin. Biol. Ther.*, **2014,** *14,* 1061-1064. The amino acid sequences of pembrolizumab are set forth in Table 19. Pembrolizumab includes the following disulfide bridges: 22-96, 22"-96", 23'-92', 23'"-92'", 134-218', 134"-218'", 138'-198', 138'"-198'", 147-203, 147"-203", 226-226", 229-229", 261-321, 261"-321", 367-425, and 367"-425", and the following glycosylation sites (N): Asn-297 and Asn-297". Pembrolizumab is an IgG4/kappa isotype with a stabilizing S228P mutation in the Fc region; insertion of this mutation in the IgG4 hinge region prevents the formation of half molecules typically observed for IgG4 antibodies. Pembrolizumab is heterogeneously glycosylated at Asn297 within the Fc domain of each heavy chain, yielding a molecular weight of approximately 149 kDa for the intact antibody. The dominant glycoform of pembrolizumab is the fucosylated agalacto diantennary glycan form (G0F).

[001991] In some embodiments, a PD-1 inhibitor comprises a heavy chain given by SEQ ID NO:168 and a light chain given by SEQ ID NO:169. In some embodiments, a PD-1 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively. In some embodiments, a PD-1 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:168 and SEQ ID NO:169, respectively.

[001992] In some embodiments, the PD-1 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of pembrolizumab. In some embodiments, the PD-1 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:170, and the PD-1 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:171, or conservative amino acid substitutions thereof. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 97% identical

to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively. In some embodiments, a PD-1 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively.

[001993] In some embodiments, a PD-1 inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:172, SEQ ID NO:173, and SEQ ID NO:174, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:175, SEQ ID NO:176, and SEQ ID NO:177, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on PD-1 as any of the aforementioned antibodies.

[001994] In some embodiments, the PD-1 inhibitor is an anti-PD-1 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to pembrolizumab. In some embodiments, the biosimilar comprises an anti-PD-1 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is pembrolizumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-PD-1 antibody authorized or submitted for authorization, wherein the anti-PD-1 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is pembrolizumab. The anti-PD-1 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is pembrolizumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is pembrolizumab.

TABLE 19. Amino acid sequences for PD-1 inhibitors related to pembrolizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:168 pembrolizumab heavy chain	QVQLVQSGVE VKKPGASVKV SCKASGYTFT NYYMYWVRQA PGQGLEWMGG INPSNGGTNF NEKFKNRVTL TTDSSTTTAY MELKSLQFDD TAVYYCARRD YRFDMGFDYW GQGTTVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK	60 120 180 240 300 360 420 447
SEQ ID NO:169 pembrolizumab light chain	EIVLTQSPAT LSLSPGERAT LSCRASKGVS TSGYSYLHWY QQKPGQAPRL LIYLASYLES GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRDLPL TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC	60 120 180 218
SEQ ID NO:170 pembrolizumab variable heavy chain	QVQLVQSGVE VKKPGASVKV SCKASGYTFT NYYMYWVRQA PGQGLEWMGG INPSNGGTNF NEKFKNRVTL TTDSSTTTAY MELKSLQFDD TAVYYCARRD YRFDMGFDYW GQGTTVTVSS	60 120
SEQ ID NO:171 pembrolizumab variable light chain	EIVLTQSPAT LSLSPGERAT LSCRASKGVS TSGYSYLHWY QQKPGQAPRL LIYLASYLES GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRDLPL TFGGGTKVEI K	60 111
SEQ ID NO:172 pembrolizumab heavy chain CDR1	NYYMY	5
SEQ ID NO:173 pembrolizumab heavy chain CDR2	GINPSNGGTN FNEKFK	16
SEQ ID NO:174 pembrolizumab heavy chain CDR3	RDYRFDMGFD Y	11
SEQ ID NO:175 pembrolizumab light chain CDR1	RASKGVSTSG YSYLH	15
SEQ ID NO:176 pembrolizumab light chain CDR2	LASYLES	7
SEQ ID NO:177 pembrolizumab light chain CDR3	QHSRDLPLT	9

[001995] In some embodiments, the PD-1 inhibitor is pembrolizumab or a biosimilar thereof, and the pembrolizumab is administered at a dose of about 0.5 mg/kg to about 10 mg/kg. In some embodiments, the PD-1 inhibitor is pembrolizumab or a biosimilar thereof, and the pembrolizumab is administered at a dose of about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 4.5 mg/kg, about 5 mg/kg, about 5.5 mg/kg, about 6 mg/kg, about 6.5 mg/kg, about 7 mg/kg, about 7.5 mg/kg, about 8 mg/kg, about 8.5 mg/kg, about 9 mg/kg, about 9.5 mg/kg, or about 10 mg/kg. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the

pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001996] In some embodiments, the PD-1 inhibitor is pembrolizumab or a biosimilar thereof, wherein the pembrolizumab is administered at a dose of about 200 mg to about 500 mg. In some embodiments, the PD-1 inhibitor is pembrolizumab or a biosimilar thereof, and the nivolumab is administered at a dose of about 200 mg, about 220 mg, about 240 mg, about 260 mg, about 280 mg, about 300 mg, about 320 mg, about 340 mg, about 360 mg, about 380 mg, about 400 mg, about 420 mg, about 440 mg, about 460 mg, about 480 mg, or about 500 mg. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001997] In some embodiments, the PD-1 inhibitor is pembrolizumab or a biosimilar thereof, wherein the pembrolizumab is administered every 2 weeks, every 3 weeks, every 4 weeks, every 5 weeks, or every 6 weeks. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001998] In some embodiments, the pembrolizumab is administered to treat NSCLC. In some embodiments, the pembrolizumab is administered to treat NSCLC at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat NSCLC at about 400 mg every 6 weeks. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[001999] In some embodiments, the pembrolizumab is administered to treat small cell lung cancer (SCLC). In some embodiments, the pembrolizumab is administered to treat SCLC at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat SCLC at about

400 mg every 6 weeks. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[002000] In some embodiments, if the patient or subject is an adult, *i.e.*, treatment of adult indications, and additional dosing regimen of 400 mg every 6 weeks can be employed. In some embodiments, the pembrolizumab administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the pembrolizumab administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the pembrolizumab can also be administered 1, 2, 3, 4 or 5 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, the pembrolizumab can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient).

[002001] In some embodiments, the PD-1 inhibitor is a commercially-available anti-PD-1 monoclonal antibody, such as anti-m-PD-1 clones J43 (Cat # BE0033-2) and RMP1-14 (Cat # BE0146) (Bio X Cell, Inc., West Lebanon, NH, USA). A number of commercially-available anti-PD-1 antibodies are known to one of ordinary skill in the art.

[002002] In some embodiments, the PD-1 inhibitor is an antibody disclosed in U.S. Patent No. 8,354,509 or U.S. Patent Application Publication Nos. 2010/0266617 A1, 2013/0108651 A1, 2013/0109843 A2, the disclosures of which are incorporated by reference herein. In some embodiments, the PD-1 inhibitor is an anti-PD-1 antibody described in U.S. Patent Nos. 8,287,856, 8,580,247, and 8,168,757 and U.S. Patent Application Publication Nos. 2009/0028857 A1, 2010/0285013 A1, 2013/0022600 A1, and 2011/0008369 A1, the teachings of which are hereby incorporated by reference. In some embodiments, the PD-1 inhibitor is an anti-PD-1 antibody disclosed in U.S. Patent No. 8,735,553 B1, the disclosure of which is incorporated herein by reference. In some embodiments, the PD-1 inhibitor is pidilizumab, also known as CT-011, which is described in U.S. Patent No. 8,686,119, the disclosure of which is incorporated by reference herein.

[002003] In some embodiments, the PD-1 inhibitor may be a small molecule or a peptide, or a peptide derivative, such as those described in U.S. Patent Nos. 8,907,053; 9,096,642; and 9,044,442 and U.S. Patent Application Publication No. US 2015/0087581; 1,2,4-oxadiazole compounds and derivatives such as those described in U.S. Patent Application Publication No. 2015/0073024; cyclic peptidomimetic compounds and derivatives such as those described in U.S. Patent Application Publication No. US 2015/0073042; cyclic compounds and derivatives such as those described in U.S.

Patent Application Publication No. US 2015/0125491; 1,3,4-oxadiazole and 1,3,4-thiadiazole compounds and derivatives such as those described in International Patent Application Publication No. WO 2015/033301; peptide-based compounds and derivatives such as those described in International Patent Application Publication Nos. WO 2015/036927 and WO 2015/04490, or a macrocyclic peptide-based compounds and derivatives such as those described in U.S. Patent Application Publication No. US 2014/0294898; the disclosures of each of which are hereby incorporated by reference in their entireties.

[002004] In some embodiments, TILs and a PD-L1 inhibitor or a PD-L2 inhibitor are administered as a combination therapy or co-therapy for the treatment of NSCLC.

[002005] In some embodiments, the NSCLC has undergone no prior therapy. In some embodiments, a PD-L1 inhibitor or a PD-L2 inhibitor is administered as a front-line therapy or initial therapy. In some embodiments, a PD-L1 inhibitor or a PD-L2 inhibitor is administered as a front-line therapy or initial therapy in combination with the TILs as described herein.

[002006] In some embodiments, the PD-L1 or PD-L2 inhibitor may be any PD-L1 or PD-L2 inhibitor, antagonist, or blocker known in the art. In particular, it is one of the PD-L1 or PD-L2 inhibitors, antagonist, or blockers described in more detail in the following paragraphs. The terms "inhibitor," "antagonist," and "blocker" are used interchangeably herein in reference to PD-L1 and PD-L2 inhibitors. For avoidance of doubt, references herein to a PD-L1 or PD-L2 inhibitor that is an antibody may refer to a compound or antigen-binding fragments, variants, conjugates, or biosimilars thereof. For avoidance of doubt, references herein to a PD-L1 or PD-L2 inhibitor may refer to a compound or a pharmaceutically acceptable salt, ester, solvate, hydrate, cocrystal, or prodrug thereof.

[002007] In some embodiments, the compositions, processes and methods described herein include a PD-L1 or PD-L2 inhibitor. In some embodiments, the PD-L1 or PD-L2 inhibitor is a small molecule. In some embodiments, the PD-L1 or PD-L2 inhibitor is an antibody (*i.e.*, an anti-PD-1 antibody), a fragment thereof, including Fab fragments, or a single-chain variable fragment (scFv) thereof. In some embodiments the PD-L1 or PD-L2 inhibitor is a polyclonal antibody. In some embodiments, the PD-L1 or PD-L2 inhibitor is a monoclonal antibody. In some embodiments, the PD-L1 or PD-L2 inhibitor competes for binding with PD-L1 or PD-L2, and/or binds to an epitope on PD-L1 or PD-L2. In some embodiments, the antibody competes for binding with PD-L1 or PD-L2, and/or binds to an epitope on PD-L1 or PD-L2.

[002008] In some embodiments, the PD-L1 inhibitors provided herein are selective for PD-L1, in that the compounds bind or interact with PD-L1 at substantially lower concentrations than they bind or interact with other receptors, including the PD-L2 receptor. In certain embodiments, the compounds bind to the PD-L1 receptor at a binding constant that is at least about a 2-fold higher

concentration, about a 3-fold higher concentration, about a 5-fold higher concentration, about a 10-fold higher concentration, about a 20-fold higher concentration, about a 30-fold higher concentration, about a 50-fold higher concentration, about a 100-fold higher concentration, about a 200-fold higher concentration, about a 300-fold higher concentration, or about a 500-fold higher concentration than to the PD-L2 receptor.

[002009] In some embodiments, the PD-L2 inhibitors provided herein are selective for PD-L2, in that the compounds bind or interact with PD-L2 at substantially lower concentrations than they bind or interact with other receptors, including the PD-L1 receptor. In certain embodiments, the compounds bind to the PD-L2 receptor at a binding constant that is at least about a 2-fold higher concentration, about a 3-fold higher concentration, about a 5-fold higher concentration, about a 10-fold higher concentration, about a 20-fold higher concentration, about a 30-fold higher concentration, about a 50-fold higher concentration, about a 100-fold higher concentration, about a 200-fold higher concentration, about a 300-fold higher concentration, or about a 500-fold higher concentration than to the PD-L1 receptor.

[002010] Without being bound by any theory, it is believed that tumor cells express PD-L1, and that T cells express PD-1. However, PD-L1 expression by tumor cells is not required for efficacy of PD-1 or PD-L1 inhibitors or blockers. In some embodiments, the tumor cells express PD-L1. In some embodiments, the tumor cells do not express PD-L1. In some embodiments, the methods can include a combination of a PD-1 and a PD-L1 antibody, such as those described herein, in combination with a TIL. The administration of a combination of a PD-1 and a PD-L1 antibody and a TIL may be simultaneous or sequential.

[002011] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that binds human PD-L1 and/or PD-L2 with a K_D of about 100 pM or lower, binds human PD-L1 and/or PD-L2 with a K_D of about 90 pM or lower, binds human PD-L1 and/or PD-L2 with a K_D of about 80 pM or lower, binds human PD-L1 and/or PD-L2 with a K_D of about 70 pM or lower, binds human PD-L1 and/or PD-L2 with a K_D of about 60 pM or lower, a K_D of about 50 pM or lower, binds human PD-L1 and/or PD-L2 with a K_D of about 40 pM or lower, or binds human PD-L1 and/or PD-L2 with a KD of about 30 pM or lower,

[002012] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that binds to human PD-L1 and/or PD-L2 with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a k_{assoc} of about 8×10^5 1/M·s or faster, binds to human PD-L1 and/ or PD-L2 with a k_{assoc} of about 8.5×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a k_{assoc} of about 9×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a k_{assoc} of about 9.5×10^5 1/M·s and/or faster, or binds to human PD-L1 and/or PD-L2 with a k_{assoc} of about 1×10^6 1/M·s or faster.

[002013] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that binds to human PD-L1 or PD-L2 with a k_{dissoc} of about 2×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.1×10^{-5} 1/s or slower , binds to human PD-1 with a k_{dissoc} of about 2.2×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.3×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.4×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.5×10^{-5} 1/s or slower, binds to human PD-1 with a k_{dissoc} of about 2.6×10^{-5} 1/s or slower, binds to human PD-L1 or PD-L2 with a k_{dissoc} of about 2.7×10^{-5} 1/s or slower, or binds to human PD-L1 or PD-L2 with a k_{dissoc} of about 3×10^{-5} 1/s or slower.

[002014] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 10 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 9 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 8 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 7 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 6 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 5 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 4 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 3 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC_{50} of about 2 nM or lower; or blocks human PD-1, or blocks binding of human PD-L1 or human PD-L2 to human PD-l with an IC_{50} of about 1 nM or lower.

[002015] In some embodiments, the PD-L1 inhibitor is durvalumab, also known as MEDI4736 (which is commercially available from Medimmune, LLC, Gaithersburg, Maryland, a subsidiary of AstraZeneca plc.), or antigen-binding fragments, conjugates, or variants thereof. In some embodiments, the PD-L1 inhibitor is an antibody disclosed in U.S. Patent No. 8,779,108 or U.S. Patent Application Publication No. 2013/0034559, the disclosures of which are incorporated by reference herein. The clinical efficacy of durvalumab has been described in Page, *et al.*, *Ann. Rev. Med.*, **2014,** *65,* 185-202; Brahmer, *et al.*, *J. Clin. Oncol.* **2014,** *32,* 5s (supplement, abstract 8021); and McDermott, *et al.*, *Cancer Treatment Rev.*, **2014,** *40,* 1056-64. The preparation and properties of durvalumab are described in U.S. Patent No. 8,779,108, the disclosure of which is incorporated by reference herein. The amino acid sequences of durvalumab are set forth in Table 20. The durvalumab monoclonal antibody includes disulfide linkages at 22-96, 22"-96", 23'-89', 23'"-89'", 135'-195', 135'"-195'", 148-204, 148"-204", 215'-224, 215'"-224", 230-230", 233-233", 265-325, 265"-325", 371-429, and 371"-429'; and N-glycosylation sites at Asn-301 and Asn-301".

[002016] In some embodiments, a PD-L1 inhibitor comprises a heavy chain given by SEQ ID NO:178 and a light chain given by SEQ ID NO:179. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:178 and SEQ ID NO:179, respectively.

[002017] In some embodiments, the PD-L1 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of durvalumab. In some embodiments, the PD-L1 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:180, and the PD-L1 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:181, or conservative amino acid substitutions thereof. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively.

[002018] In some embodiments, a PD-L1 inhibitor comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:182, SEQ ID NO:183, and SEQ ID NO:184, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:185, SEQ ID NO:186, and SEQ ID NO:187, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on PD-L1 as any of the aforementioned antibodies.

[002019] In some embodiments, the PD-L1 inhibitor is an anti-PD-L1 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to durvalumab. In some embodiments, the biosimilar comprises an anti-PD-L1 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is durvalumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-PD-L1 antibody authorized or submitted for authorization, wherein the anti-PD-L1 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is durvalumab. The anti-PD-L1 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is durvalumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is durvalumab.

TABLE 20. Amino acid sequences for PD-L1 inhibitors related to durvalumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:178 durvalumab heavy chain	EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMSWVRQA PGKGLEWVAN IKQDGSEKYY VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAREG GWFGELAFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPEFEG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPASIEKTI SKAKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K	60 120 180 240 300 360 420 451
SEQ ID NO:179 durvalumab light chain	EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMSWVRQA PGKGLEWVAN EIVLTQSPGT LSLSPGERAT LSCRASQRVS SSYLAWYQQK PGQAPRLLIY DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSLPWTFG QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC	60 120 180 240 265
SEQ ID NO:180 durvalumab variable heavy chain	EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMSWVRQA PGKGLEWVAN IKQDGSEKYY VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAREG GWFGELAFDY WGQGTLVTVS S	60 120 121
SEQ ID NO:181 durvalumab	EIVLTQSPGT LSLSPGERAT LSCRASQRVS SSYLAWYQQK PGQAPRLLIY DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSLPWTFG QGTKVEIK	60 108

Identifier	Sequence (One-Letter Amino Acid Symbols)	
variable light chain		
SEQ ID NO:182 durvalumab heavy chain CDR1	RYWMS	5
SEQ ID NO:183 durvalumab heavy chain CDR2	NIKQDGSEKY YVDSVKG	17
SEQ ID NO:184 durvalumab heavy chain CDR3	EGGWFGELAF DY	12
SEQ ID NO:185 durvalumab light chain CDR1	RASQRVSSSY LA	12
SEQ ID NO:186 durvalumab light chain CDR2	DASSRAT	7
SEQ ID NO:187 durvalumab light chain CDR3	QQYGSLPWT	9

[002020] In some embodiments, the PD-L1 inhibitor is avelumab, also known as MSB0010718C (commercially available from Merck KGaA/EMD Serono), or antigen-binding fragments, conjugates, or variants thereof. The preparation and properties of avelumab are described in U.S. Patent Application Publication No. US 2014/0341917 A1, the disclosure of which is specifically incorporated by reference herein. The amino acid sequences of avelumab are set forth in Table 21. Avelumab has intra-heavy chain disulfide linkages (C23-C104) at 22-96, 147-203, 264-324, 370-428, 22"-96", 147"-203", 264"-324", and 370"-428"; intra-light chain disulfide linkages (C23-C104) at 22'-90', 138'-197', 22'"-90'", and 138'"-197'"; intra-heavy-light chain disulfide linkages (h 5-CL 126) at 223-215' and 223"-215'"; intra-heavy-heavy chain disulfide linkages (h 11, h 14) at 229-229" and 232-232"; N-glycosylation sites (H CH_2 N84.4) at 300, 300"; fucosylated complex bi-antennary CHO-type glycans; and H CHS K2 C-terminal lysine clipping at 450 and 450'.

[002021] In some embodiments, a PD-L1 inhibitor comprises a heavy chain given by SEQ ID NO:188 and a light chain given by SEQ ID NO:189. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each

at least 97% identical to the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:188 and SEQ ID NO:189, respectively.

[002022] In some embodiments, the PD-L1 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of avelumab. In some embodiments, the PD-L1 inhibitor heavy chain variable region (VH) comprises the sequence shown in SEQ ID NO:190, and the PD-L1 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:191, or conservative amino acid substitutions thereof. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively.

[002023] In some embodiments, a PD-L1 inhibitor comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:192, SEQ ID NO:193, and SEQ ID NO:194, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:195, SEQ ID NO:196, and SEQ ID NO:197, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on PD-L1 as any of the aforementioned antibodies.

[002024] In some embodiments, the PD-L1 inhibitor is an anti-PD-L1 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to avelumab. In some embodiments, the biosimilar comprises an anti-PD-L1 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is avelumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the

biosimilar is an anti-PD-L1 antibody authorized or submitted for authorization, wherein the anti-PD-L1 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is avelumab. The anti-PD-L1 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is avelumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is avelumab.

TABLE 21. Amino acid sequences for PD-L1 inhibitors related to avelumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:188 avelumab heavy chain	EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYIMMWVRQA PGKGLEWVSS IYPSGGITFY ADTVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARIK LGTVTTVDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK	60 120 180 240 300 360 420 450
SEQ ID NO:189 avelumab light chain	QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI YDVSNRPSGV SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTRV FGTGTKVTVL GQPKANPTVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADGSPVK AGVETTKPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS	60 120 180 216
SEQ ID NO:190 avelumab variable heavy chain	EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYIMMWVRQA PGKGLEWVSS IYPSGGITFY ADTVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARIK LGTVTTVDYW GQGTLVTVSS	60 120
SEQ ID NO:191 avelumab variable light chain	QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI YDVSNRPSGV SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTRV FGTGTKVTVL	60 110
SEQ ID NO:192 avelumab heavy chain CDR1	SYIMM	5
SEQ ID NO:193 avelumab heavy chain CDR2	SIYPSGGITF YADTVKG	17
SEQ ID NO:194 avelumab heavy chain CDR3	IKLGTVTTVD Y	11
SEQ ID NO:195 avelumab light chain CDR1	TGTSSDVGGY NYVS	14
SEQ ID NO:196 avelumab	DVSNRPS	7

Identifier	Sequence (One-Letter Amino Acid Symbols)
light chain CDR2	
SEQ ID NO:197 avelumab light chain CDR3	SSYTSSSTRV 10

[002025] In some embodiments, the PD-L1 inhibitor is atezolizumab, also known as MPDL3280A or RG7446 (commercially available as TECENTRIQ from Genentech, Inc., a subsidiary of Roche Holding AG, Basel, Switzerland), or antigen-binding fragments, conjugates, or variants thereof. In some embodiments, the PD-L1 inhibitor is an antibody disclosed in U.S. Patent No. 8,217,149, the disclosure of which is specifically incorporated by reference herein. In some embodiments, the PD-L1 inhibitor is an antibody disclosed in U.S. Patent Application Publication Nos. 2010/0203056 A1, 2013/0045200 A1, 2013/0045201 A1, 2013/0045202 A1, or 2014/0065135 A1, the disclosures of which are specifically incorporated by reference herein. The preparation and properties of atezolizumab are described in U.S. Patent No. 8,217,149, the disclosure of which is incorporated by reference herein. The amino acid sequences of atezolizumab are set forth in Table 22. Atezolizumab has intra-heavy chain disulfide linkages (C23-C104) at 22-96, 145-201, 262-322, 368-426, 22"-96", 145"-201", 262"-322", and 368"-426"; intra-light chain disulfide linkages (C23-C104) at 23'-88', 134'-194', 23'"-88'", and 134'"-194'"; intra-heavy-light chain disulfide linkages (h 5-CL 126) at 221-214' and 221"-214'"; intra-heavy-heavy chain disulfide linkages (h 11, h 14) at 227-227" and 230-230"; and N-glycosylation sites (H CH_2 N84.4>A) at 298 and 298'.

[002026] In some embodiments, a PD-L1 inhibitor comprises a heavy chain given by SEQ ID NO:198 and a light chain given by SEQ ID NO:199. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively. In some embodiments, a PD-L1 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:198 and SEQ ID NO:199, respectively.

[002027] In some embodiments, the PD-L1 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of atezolizumab. In some embodiments, the PD-L1 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:200, and the PD-L1 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:201, or conservative amino acid substitutions thereof. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively. In some embodiments, a PD-L1 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively.

[002028] In some embodiments, a PD-L1 inhibitor comprises heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:202, SEQ ID NO:203, and SEQ ID NO:204, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:205, SEQ ID NO:206, and SEQ ID NO:207, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on PD-L1 as any of the aforementioned antibodies.

[002029] In some embodiments, the anti-PD-L1 antibody is an anti-PD-L1 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to atezolizumab. In some embodiments, the biosimilar comprises an anti-PD-L1 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is atezolizumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-PD-L1 antibody authorized or submitted for authorization, wherein the anti-PD-L1 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is atezolizumab. The anti-PD-L1 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In

some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is atezolizumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is atezolizumab.

TABLE 22. Amino acid sequences for PD-L1 inhibitors related to atezolizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:198 atezolizumab heavy chain	EVQLVESGGG LVQPGGSLRL SCAASGFTFS DSWIHWVRQA PGKGLEWVAW ISPYGGSTYY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARRH WPGGFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK	60 120 180 240 300 360 420 448
SEQ ID NO:199 atezolizumab light chain	DIQMTQSPSS LSASVGDRVT ITCRASQDVS TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLYHPATFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	60 120 180 214
SEQ ID NO:200 atezolizumab variable heavy chain	EVQLVESGGG LVQPGGSLRL SCAASGFTFS DSWIHWVRQA PGKGLEWVAW ISPYGGSTYY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARRH WPGGFDYWGQ GTLVTVSA	60 118
SEQ ID NO:201 atezolizumab variable light chain	DIQMTQSPSS LSASVGDRVT ITCRASQDVS TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLYHPATFGQ GTKVEIKR	60 108
SEQ ID NO:202 atezolizumab heavy chain CDR1	GFTFSDSWIH	10
SEQ ID NO:203 atezolizumab heavy chain CDR2	AWISPYGGST YYADSVKG	18
SEQ ID NO:204 atezolizumab heavy chain CDR3	RHWPGGFDY	9
SEQ ID NO:205 atezolizumab light chain CDR1	RASQDVSTAV A	11
SEQ ID NO:206 atezolizumab light chain CDR2	SASFLYS	7
SEQ ID NO:207 atezolizumab light chain CDR3	QQYLYHPAT	9

[002030] In some embodiments, PD-L1 inhibitors include those antibodies described in U.S. Patent Application Publication No. US 2014/0341917 A1, the disclosure of which is incorporated by reference herein. In some embodiments, antibodies that compete with any of these antibodies for binding to PD-L1 are also included. In some embodiments, the anti-PD-L1 antibody is MDX-1105, also known as BMS-935559, which is disclosed in U.S. Patent No. US 7,943,743, the disclosures of which are incorporated by reference herein. In some embodiments, the anti-PD-L1 antibody is selected from the anti-PD-L1 antibodies disclosed in U.S. Patent No. US 7,943,743, which are incorporated by reference herein.

[002031] In some embodiments, the PD-L1 inhibitor is a commercially-available monoclonal antibody, such as INVIVOMAB anti-m-PD-L1 clone 10F.9G2 (Catalog # BE0101, Bio X Cell, Inc., West Lebanon, NH, USA). In some embodiments, the anti-PD-L1 antibody is a commercially-available monoclonal antibody, such as AFFYMETRIX EBIOSCIENCE (MIH1). A number of commercially-available anti-PD-L1 antibodies are known to one of ordinary skill in the art.

[002032] In some embodiments, the PD-L2 inhibitor is a commercially-available monoclonal antibody, such as BIOLEGEND 24F.10C12 Mouse IgG2a, κ isotype (catalog # 329602 Biolegend, Inc., San Diego, CA), SIGMA anti-PD-L2 antibody (catalog # SAB3500395, Sigma-Aldrich Co., St. Louis, MO), or other commercially-available anti-PD-L2 antibodies known to one of ordinary skill in the art.

4. Combinations with CTLA-4 Inhibitors

[002033] In some embodiments, TILs and a CTLA-4 inhibitor are administered as a combination therapy or co-therapy for the treatment of NSCLC.

[002034] In some embodiments, the NSCLC has undergone no prior therapy. In some embodiments, the CTLA-4 inhibitor is administered as a front-line therapy or initial therapy. In some embodiments, the CTLA-4 inhibitor is administered as a front-line therapy or initial therapy in combination with the TILs as described herein.

[002035] Cytotoxic T lymphocyte antigen 4 (CTLA-4) is a member of the immunoglobulin superfamily and is expressed on the surface of helper T cells. CTLA-4 is a negative regulator of CD28-dependent T cell activation and acts as a checkpoint for adaptive immune responses. Similar to the T cell costimulatory protein CD28, the CTLA-4 binding antigen presents CD80 and CD86 on the cells. CTLA-4 delivers a suppressor signal to T cells, while CD28 delivers a stimulus signal. Human antibodies against human CTLA-4 have been described as immunostimulatory modulators in many disease conditions, such as treating or preventing viral and bacterial infections and for treating cancer (WO 01/14424 and WO 00/37504). Various preclinical studies have shown that CTLA-4 blockade by

CTLA-4 inhibitors such as monoclonal antibodies enhances host immune responses against immunogenic tumors and can even rule out established tumors. A number of fully human anti-human CTLA-4 monoclonal antibodies (mAbs) have been studied in clinical trials for the treatment of various types of solid tumors, including, but limited to, ipilimumab (MDX-010) and tremelimumab (CP-675,206).

[002036] In some embodiments, a CTLA-4 inhibitor may be any CTLA-4 inhibitor or CTLA-4 blocker known in the art. In particular, it is one of the CTLA-4 inhibitors or blockers described in more detail in the following paragraphs. The terms "inhibitor," "antagonist," and "blocker" are used interchangeably herein in reference to CTLA-4 inhibitors. For avoidance of doubt, references herein to a CTLA-4 inhibitor that is an antibody may refer to a compound or antigen-binding fragments, variants, conjugates, or biosimilars thereof. For avoidance of doubt, references herein to a CTLA-4 inhibitor may also refer to a small molecule compound or a pharmaceutically acceptable salt, ester, solvate, hydrate, cocrystal, or prodrug thereof.

[002037] Suitable CTLA-4 inhibitors for use in the methods of the invention, include, without limitation, anti-CTLA-4 antibodies, human anti-CTLA-4 antibodies, mouse anti-CTLA-4 antibodies, mammalian anti-CTLA-4 antibodies, humanized anti-CTLA-4 antibodies, monoclonal anti-CTLA-4 antibodies, polyclonal anti-CTLA-4 antibodies, chimeric anti-CTLA-4 antibodies, MDX-010 (ipilimumab), tremelimumab, anti-CD28 antibodies, anti-CTLA-4 adnectins, anti-CTLA-4 domain antibodies, single chain anti-CTLA-4 fragments, heavy chain anti-CTLA-4 fragments, light chain anti-CTLA-4 fragments, inhibitors of CTLA-4 that agonize the co-stimulatory pathway, the antibodies disclosed in PCT Publication No. WO 2001/014424, the antibodies disclosed in PCT Publication No. WO 2004/035607, the antibodies disclosed in U.S. Publication No. 2005/0201994, and the antibodies disclosed in granted European Patent No. EP 1212422 B1, the disclosures of each of which are incorporated herein by reference. Additional CTLA-4 antibodies are described in U.S. Pat. Nos. 5,811,097, 5,855,887, 6,051,227, and 6,984,720; in PCT Publication Nos. WO 01/14424 and WO 00/37504; and in U.S. Publication Nos. 2002/0039581 and 2002/086014, the disclosures of each of which are incorporated herein by reference. Other anti-CTLA-4 antibodies that can be used in a method of the present invention include, for example, those disclosed in: WO 98/42752; U.S. Pat. Nos. 6,682,736 and 6,207,156; Hurwitz et al., Proc. Natl. Acad. Sci. USA, 95(17):10067-10071 (1998); Camacho et al., J. Clin. Oncology, 22(145): Abstract No. 2505 (2004) (antibody CP-675206); Mokyr et al., Cancer Res., 58:5301-5304 (1998), and U.S. Pat. Nos. 5,977,318, 6,682,736, 7,109,003, and 7,132,281, the disclosures of each of which are incorporated herein by reference the non-myeloablative lymphodepletion regimen.

[002038] Additional CTLA-4 inhibitors include, but are not limited to, the following: any inhibitor that is capable of disrupting the ability of CD28 antigen to bind to its cognate ligand, to inhibit the

ability of CTLA-4 to bind to its cognate ligand, to augment T cell responses via the co-stimulatory pathway, to disrupt the ability of B7 to bind to CD28 and/or CTLA-4, to disrupt the ability of B7 to activate the co-stimulatory pathway, to disrupt the ability of CD80 to bind to CD28 and/or CTLA-4, to disrupt the ability of CD80 to activate the co-stimulatory pathway, to disrupt the ability of CD86 to bind to CD28 and/or CTLA-4, to disrupt the ability of CD86 to activate the co-stimulatory pathway, and to disrupt the co-stimulatory pathway, in general from being activated. This necessarily includes small molecule inhibitors of CD28, CD80, CD86, CTLA-4, among other members of the co-stimulatory pathway; antibodies directed to CD28, CD80, CD86, CTLA-4, among other members of the co-stimulatory pathway; antisense molecules directed against CD28, CD80, CD86, CTLA-4, among other members of the co-stimulatory pathway; adnectins directed against CD28, CD80, CD86, CTLA-4, among other members of the co-stimulatory pathway, RNAi inhibitors (both single and double stranded) of CD28, CD80, CD86, CTLA-4, among other members of the co-stimulatory pathway, among other CTLA-4 inhibitors.

[002039] In some embodiments a CTLA-4 inhibitor binds to CTLA-4 with a Kd of about 10^{-6} M or less, 10^{-7}M or less, 10^{-8} M or less, 10^{-9} M or less, 10^{-10} M or less, 10^{-11} M or less, 10^{-12} M or less, *e.g.*, between 10^{-13} M and 10^{-16} M, or within any range having any two of the afore-mentioned values as endpoints. In some embodiments a CTLA-4 inhibitor binds to CTLA-4 with a Kd of no more than 10-fold that of ipilimumab, when compared using the same assay. In some embodiments a CTLA-4 inhibitor binds to CTLA-4 with a Kd of about the same as, or less (*e.g.*, up to 10-fold lower, or up to 100-fold lower) than that of ipilimumab, when compared using the same assay. In some embodiments, the IC50 values for inhibition by a CTLA-4 inhibitor of CTLA-4 binding to CD80 or CD86 is no more than 10-fold greater than that of ipilimumab-mediated inhibition of CTLA-4 binding to CD80 or CD86, respectively, when compared using the same assay. In some embodiments, the IC50 values for inhibition by a CTLA-4 inhibitor of CTLA-4 binding to CD80 or CD86 is about the same or less (*e.g.*, up to 10-fold lower, or up to 100-fold lower) than that of ipilimumab-mediated inhibition of CTLA-4 binding to CD80 or CD86, respectively, when compared using the same assay.

[002040] In some embodiments a CTLA-4 inhibitor is used in an amount sufficient to inhibit expression and/or decrease biological activity of CTLA-4 by at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% relative to a suitable control, *e.g.*, between 50% and 75%, 75% and 90%, or 90% and 100%. In some embodiments a CTLA-4 pathway inhibitor is used in an amount sufficient to decrease the biological activity of CTLA-4 by reducing binding of CTLA-4 to CD80, CD86, or both by at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% relative to a suitable control, *e.g.*, between 50% and 75%, 75% and 90%, or 90% and 100% relative to a suitable control. A suitable control in the context of assessing or quantifying the effect of an agent of interest is typically a comparable biological system (*e.g.*, cells or a subject) that has not been exposed to or

treated with the agent of interest, *e.g.*, CTLA-4 pathway inhibitor (or has been exposed to or treated with a negligible amount). In some embodiments a biological system may serve as its own control (*e.g.*, the biological system may be assessed before exposure to or treatment with the agent and compared with the state after exposure or treatment has started or finished. In some embodiments a historical control may be used.

[002041] In some embodiments, the CTLA-4 inhibitor is ipilimumab (commercially available as Yervoy from Bristol-Myers Squibb Co.), or biosimilars, antigen-binding fragments, conjugates, or variants thereof. As is known in the art, ipilimumab refers to an anti-CTLA-4 antibody, a fully human IgG 1κ antibody derived from a transgenic mouse with human genes encoding heavy and light chains to generate a functional human repertoire. is there. Ipilimumab can also be referred to by its CAS Registry Number 477202-00-9, and in PCT Publication Number WO 01/14424, which is incorporated herein by reference in its entirety for all purposes. It is disclosed as antibody 10DI. Specifically, ipilimumab contains a light chain variable region and a heavy chain variable region (having a light chain variable region comprising SEQ ID NO: 516 and having a heavy chain variable region comprising SEQ ID NO: 515). Represents a human monoclonal antibody or its antigen binding site that specifically binds to CTLA-4. A pharmaceutical composition of ipilimumab includes all pharmaceutically acceptable compositions containing ipilimumab and one or more diluents, vehicles and / or excipients. An example of a pharmaceutical composition containing ipilimumab is described in PCT Publication No. WO 2007/67959. Impilimumab can be administered intravenously (IV).

[002042] In some embodiments, a CTLA-4 inhibitor comprises a heavy chain given by SEQ ID NO:208 and a light chain given by SEQ ID NO:209. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:208 and SEQ ID NO:209, respectively.

[002043] In some embodiments, the CTLA-4 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of ipilimumab. In some embodiments, the CTLA-4 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:210, and the CTLA-4 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:211, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively.

[002044] IIn some embodiments, a CTLA-4 inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:212, SEQ ID NO:213, and SEQ ID NO:214, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:215, SEQ ID NO:216, and SEQ ID NO:217, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on CTLA-4 as any of the aforementioned antibodies.

[002045] In some embodiments, the CTLA-4 inhibitor is a CTLA-4 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to ipilimumab. In some embodiments, the biosimilar comprises an anti-CTLA-4 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ipilimumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. The amino acid sequences of ipilimumab are set forth in Table 23. In some embodiments, the biosimilar is an anti-CTLA-4 antibody authorized or submitted for authorization, wherein the anti-CTLA-4 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ipilimumab. The anti-CTLA-4 antibody may be authorized by a drug regulatory authority such as the

U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ipilimumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ipilimumab.

TABLE 23. Amino acid sequences for ipilimumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:208 ipilimumab heavy chain	1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVTF ISYDGNNKYY 61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG WLGPFDYWGQ GTLVTVSSAS 121 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL 181 YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTH
SEQ ID NO:209 ipilimumab light chain	1 EIVLTQSPGT LSLSPGERAT LSCRASQSVG SSYLAWYQQK PGQAPRLLIY GAFSRATGIP 61 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG QGTKVEIKRT VAAPSVFIFP 121 PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 181 TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC
SEQ ID NO:210 ipilimumab variable heavy chain	1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVTF ISYDGNNKYY 61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG WLGPFDYWGQ GTLVTVSS
SEQ ID NO:211 ipilimumab variable light chain	1 EIVLTQSPGT LSLSPGERAT LSCRASQSVG SSYLAWYQQK PGQAPRLLIY GAFSRATGIP 61 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG QGTKVEIK
SEQ ID NO:212 ipilimumab heavy chain CDR1	GFTFSSYT 8
SEQ ID NO:213 ipilimumab heavy chain CDR2	TFISYDGNNK 10
SEQ ID NO:214 ipilimumab heavy chain CDR3	ARTGWLGPFD Y 11
SEQ ID NO:215 ipilimumab light chain CDR1	QSVGSSY 7
SEQ ID NO:216 ipilimumab light chain CDR2	GAF 3
SEQ ID NO:217 ipilimumab light chain CDR3	QQYGSSPWT 9

[002046] In some embodiments, the CTLA-4 inhibitor is ipilimumab or a biosimilar thereof, and the ipilimumab is administered at a dose of about 0.5 mg/kg to about 10 mg/kg. In some embodiments,

the CTLA-4 inhibitor is ipilimumab or a biosimilar thereof, and the ipilimumab is administered at a dose of about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 4.5 mg/kg, about 5 mg/kg, about 5.5 mg/kg, about 6 mg/kg, about 6.5 mg/kg, about 7 mg/kg, about 7.5 mg/kg, about 8 mg/kg, about 8.5 mg/kg, about 9 mg/kg, about 9.5 mg/kg, or about 10 mg/kg. In some embodiments, the ipilimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the ipilimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient).

[002047] In some embodiments, the CTLA-4 inhibitor is ipilimumab or a biosimilar thereof, and the ipilimumab is administered at a dose of about 200 mg to about 500 mg. In some embodiments, the CTLA-4 inhibitor is ipilimumab or a biosimilar thereof, and the ipilimumab is administered at a dose of about 200 mg, about 220 mg, about 240 mg, about 260 mg, about 280 mg, about 300 mg, about 320 mg, about 340 mg, about 360 mg, about 380 mg, about 400 mg, about 420 mg, about 440 mg, about 460 mg, about 480 mg, or about 500 mg. In some embodiments, the ipilimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the ipilimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient).

[002048] In some embodiments, the CTLA-4 inhibitor is ipilimumab or a biosimilar thereof, and the ipilimumab is administered every 2 weeks, every 3 weeks, every 4 weeks, every 5 weeks, or every 6 weeks. In some embodiments, the ipilimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the ipilimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the tremelimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient).

[002049] In some embodiments, the ipilimumab is administered to treat metastatic non-small cell lung cancer. In some embodiments, the ipilimumab is administered to treat metastatic non-small cell lung cancer at about 1 mg/kg every 6 weeks with nivolumab 3 mg/kg every 2 weeks. In some embodiments, the ipilimumab is administered to treat metastatic non-small cell lung cancer at about 1 mg/kg every 6 weeks with nivolumab 360 mg every 3 weeks and 2 cycles of platinum-doublet chemotherapy. In some embodiments, the ipilimumab administration is begun 1, 2, 3, 4, or 5 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient). In some embodiments, the ipilimumab administration is begun 1, 2, or 3 weeks pre-resection (i.e., prior to obtaining the tumor sample from the subject or patient).

[002050] Tremelimumab (also known as CP-675,206) is a fully human IgG2 monoclonal antibody and has the CAS number 745013-59-6. Tremelimumab is disclosed as antibody 11.2.1 in U.S. Patent No: 6,682,736 (incorporated herein by reference). The amino acid sequences of the heavy chain and light chain of tremelimumab are set forth in Table 24, respectively. Tremelimumab has been investigated in clinical trials for the treatment of various tumors, including melanoma and breast cancer; in which Tremelimumab was administered intravenously either as single dose or multiple doses every 4 or 12 weeks at the dose range of 0.01 and 15 mg/kg. In the regimens provided by the present invention, tremelimumab is administered locally, particularly intradermally or subcutaneously. The effective amount of tremelimumab administered intradermally or subcutaneously is typically in the range of 5 - 200 mg/dose per person. In some embodiments, the effective amount of tremelimumab is in the range of 10 -150 mg/dose per person per dose. In some particular embodiments, the effective amount of tremelimumab is about 10, 25, 37.5, 40, 50, 75, 100, 125, 150, 175, or 200 mg/dose per person.

[002051] In some embodiments, a CTLA-4 inhibitor comprises a heavy chain given by SEQ ID NO:218 and a light chain given by SEQ ID NO:219. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are

each at least 95% identical to the sequences shown in SEQ ID NO:218 and SEQ ID NO:219, respectively.

[002052] In some embodiments, the CTLA-4 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of tremelimumab. In some embodiments, the CTLA-4 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:220, and the CTLA-4 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:221, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively.

[002053] In some embodiments, a CTLA-4 inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:222, SEQ ID NO:223, and SEQ ID NO:224, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:225, SEQ ID NO:226, and SEQ ID NO:227, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on CTLA-4 as any of the aforementioned antibodies.

[002054] In some embodiments, the CTLA-4 inhibitor is an anti-CTLA-4 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to tremelimumab. In some embodiments, the biosimilar comprises an anti-CTLA-4 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tremelimumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. The amino acid sequences of tremelimumab are set forth in Table 24. In some embodiments, the biosimilar is an anti-CTLA-4 antibody authorized or submitted for authorization, wherein the anti-CTLA-4 antibody is provided in a formulation which differs from the formulations of a reference

medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tremelimumab. The anti-CTLA-4 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tremelimumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is tremelimumab.

TABLE 24. Amino acid sequences for tremelimumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:218 tremelimumab heavy chain	1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV IWYDGSNKYY 61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDP RGATLYYYYY GMDVWGQGTT 121 VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA 181 VLQSSGLYSL SSVVTVPSSN FGTQTYTCNV DHKPSNTKVD KTVERKCCVE CPPCPAPPVA 241 GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVQFN WYVDGVEVHN AKTKPREEQF 301 NSTFRVVSVL TVVHQDWLNG KEYKCKVSNK GLPAPIEKTI SKTKGQPREP QVYTLPPSRE 361 EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP MLDSDGSFFL YSKLTVDKSR 421 WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K
SEQ ID NO:219 tremelimumab light chain	1 DIQMTQSPSS LSASVGDRVT ITCRASQSIN SYLDWYQQKP GKAPKLLIYA ASSLQSGVPS 61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSTPFTFGP GTKVEIKRTV AAPSVFIFPP 121 SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 181 LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC
SEQ ID NO:220 tremelimumab variable heavy chain	1 GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY YADSVKGRFT 61 ISRDNSKNTL YLQMNSLRAE DTAVYYCARD PRGATLYYYY YGMDVWGQGT TVTVSSASTK 121 GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVH
SEQ ID NO:221 tremelimumab variable light chain	1 PSSLSASVGD RVTITCRASQ SINSYLDWYQ QKPGKAPKLL IYAASSLQSG VPSRFSGSGS 61 GTDFTLTISS LQPEDFATYY CQQYYSTPFT FGPGTKVEIK RTVAAPSVFI FPPSDEQLKS 121 GTASVVCLLN NFYPREAKV
SEQ ID NO:222 tremelimumab heavy chain CDR1	GFTFSSYGMH 10
SEQ ID NO:223 tremelimumab heavy chain CDR2	VIWYDGSNKY YADSV 15
SEQ ID NO:224 tremelimumab heavy chain CDR3	DPRGATLYYY YYGMDV 16
SEQ ID NO:225 tremelimumab light chain CDR1	RASQSINSYL D 11
SEQ ID NO:226 tremelimumab light chain CDR2	AASSLQS 7
SEQ ID NO:227	QQYYSTPFT 9

Identifier	Sequence (One-Letter Amino Acid Symbols)
tremelimumab light chain CDR3	

[002055] In some embodiments, the CTLA-4 inhibitor is tremelimumab or a biosimilar thereof, and the tremelimumab is administered at a dose of about 0.5 mg/kg to about 10 mg/kg. In some embodiments, the CTLA-4 inhibitor is tremelimumab or a biosimilar thereof, and the tremelimumab is administered at a dose of about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 4.5 mg/kg, about 5 mg/kg, about 5.5 mg/kg, about 6 mg/kg, about 6.5 mg/kg, about 7 mg/kg, about 7.5 mg/kg, about 8 mg/kg, about 8.5 mg/kg, about 9 mg/kg, about 9.5 mg/kg, or about 10 mg/kg.

[002056] In some embodiments, the CTLA-4 inhibitor is tremelimumab or a biosimilar thereof, and the tremelimumab is administered at a dose of about 200 mg to about 500 mg. In some embodiments, the CTLA-4 inhibitor is tremelimumab or a biosimilar thereof, and the tremelimumab is administered at a dose of about 200 mg, about 220 mg, about 240 mg, about 260 mg, about 280 mg, about 300 mg, about 320 mg, about 340 mg, about 360 mg, about 380 mg, about 400 mg, about 420 mg, about 440 mg, about 460 mg, about 480 mg, or about 500 mg.

[002057] In some embodiments, the CTLA-4 inhibitor is tremelimumab or a biosimilar thereof, and the tremelimumab is administered every 2 weeks, every 3 weeks, every 4 weeks, every 5 weeks, or every 6 weeks.

[002058] In some embodiments, the CTLA-4 inhibitor is zalifrelimab from Agenus, or biosimilars, antigen-binding fragments, conjugates, or variants thereof. Zalifrelimab is a fully human monoclonal antibody. Zalifrelimab is assigned Chemical Abstracts Service (CAS) registry number 2148321-69-9 and is also known as also known as AGEN1884. The preparation and properties of zalifrelimab are described in U.S. Patent No. 10,144,779 and US Patent Application Publication No. US2020/0024350 A1, the disclosures of which are incorporated by reference herein.

[002059] In some embodiments, a CTLA-4 inhibitor comprises a heavy chain given by SEQ ID NO:228 and a light chain given by SEQ ID NO:229. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:228 and SEQ ID NO:229, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:228 and SEQ ID NO:229, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:228 and SEQ ID

NO:229, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:228 and SEQ ID NO:229, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:228 and SEQ ID NO:229, respectively. In some embodiments, a CTLA-4 inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:228 and SEQ ID NO:229, respectively.

[002060] In some embodiments, the CTLA-4 inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of zalifrelimab. In some embodiments, the CTLA-4 inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:230, and the CTLA-4 inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:231, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively. In some embodiments, a CTLA-4 inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively.

[002061] In some embodiments, a CTLA-4 inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:231, SEQ ID NO:233, and SEQ ID NO:234, respectively, or conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:235, SEQ ID NO:236, and SEQ ID NO:237, respectively, or conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on CTLA-4 as any of the aforementioned antibodies.

[002062] In some embodiments, the CTLA-4 inhibitor is a CTLA-4 biosimilar monoclonal antibody approved by drug regulatory authorities with reference to zalifrelimab. In some embodiments, the biosimilar comprises an anti-CTLA-4 antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is

zalifrelimab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. The amino acid sequences of zalifrelimab are set forth in Table 25. In some embodiments, the biosimilar is an anti-CTLA-4 antibody authorized or submitted for authorization, wherein the anti-CTLA-4 antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is zalifrelimab. The anti-CTLA-4 antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is zalifrelimab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is zalifrelimab.

TABLE 25. Amino acid sequences for zalifrelimab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:228 zalifrelimab heavy chain	1 EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS ISSSSSYIYY 61 ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG LMGPFDIWGQ GTMVTVSSAS 121 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL 181 YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS 241 VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 301 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSREEMT 361 KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ 421 GNVFSCSVMH EALHNHYTQK SLSLSPGK
SEQ ID NO:229 zalifrelimab light chain	1 EIVLTQSPGT LSLSPGERAT LSCRASQSVS RYLGWYQQKP GQAPRLLIYG ASTRATGIPD 61 RFSGSGSGTD FTLTITRLEP EDFAVYYCQQ YGSSPWTFGQ GTKVEIKRTV AAPSVFIFPP 121 SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 181 LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC
SEQ ID NO:230 zalifrelimab variable heavy chain	1 EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS ISSSSSYIYY 61 ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG LMGPFDIWGQ GTMVTVSS
SEQ ID NO:231 zalifrelimab variable light chain	1 EIVLTQSPGT LSLSPGERAT LSCRASQSVS RYLGWYQQKP GQAPRLLIYG ASTRATGIPD 61 RFSGSGSGTD FTLTITRLEP EDFAVYYCQQ YGSSPWTFGQ GTKVEIK

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:232 zalifrelimab heavy chain CDR1	GFTFSSYS	8
SEQ ID NO:233 zalifrelimab heavy chain CDR2	ISSSSSYI	8
SEQ ID NO:234 zalifrelimab heavy chain CDR3	ARVGLMGPFD I	11
SEQ ID NO:235 zalifrelimab light chain CDR1	QSVSRY	6
SEQ ID NO:236 zalifrelimab light chain CDR2	GAS	3
SEQ ID NO:237 zalifrelimab light chain CDR3	QQYGSSPWT	9

[002063] Examples of additional anti-CTLA-4 antibodies includes, but are not limited to: AGEN1181, BMS-986218, BCD-145, ONC-392, CS1002, REGN4659, and ADG116, which are known to one of ordinary skill in the art.

[002064] In some embodiments, the anti-CTLA-4 antibody is an anti-CTLA-4 antibody disclosed in any of the following patent publications (incorporated herein by reference): US2019/0048096A1; US2020/0223907; US2019/0201334; US2019/0201334; US2005/0201994; EP 1212422 B1; WO2018204760; WO2018204760; WO2001014424; WO2004035607; WO2003086459; WO2012120125; WO2000037504; WO2009100140; WO200609649; WO2005092380; WO2007123737; WO2006029219; WO20100979597; WO200612168; and WO1997020574. Additional CTLA-4 antibodies are described in U.S. Pat. Nos. 5,811,097, 5,855,887, 6,051,227, and 6,984,720; in PCT Publication Nos. WO 01/14424 and WO 00/37504; and in U.S. Publication Nos. 2002/0039581 and 2002/086014; and/or U.S. Patent Nos. 5,977,318, 6,682,736, 7,109,003, and 7,132,281, incorporated herein by reference). In some embodiments, the anti-CTLA-4 antibody is an, for example, those disclosed in: WO 98/42752; U.S. Pat. Nos. 6,682,736 and 6,207,156; Hurwitz et al., *Proc. Natl. Acad. Sci.* USA, 95(17): 10067-10071 (1998); Camacho et al., *J. Clin. Oncol.,*

22(145): Abstract No. 2505 (2004) (antibody CP-675206); Mokyr et al., *Cancer Res.*, 58:5301-5304 (1998) (incorporated herein by reference).

[002065] In some embodiments, the CTLA-4 inhibitor is a CTLA-4 ligand as disclosed in WO1996040915 (incorporated herein by reference).

[002066] In some embodiments, the CTLA-4 inhibitor is a nucleic acid inhibitor of CTLA-4 expression. For example, anti-CTLA-4 RNAi molecules may take the form of the molecules described by Mello and Fire in PCT Publication Nos. WO 1999/032619 and WO 2001/029058; U.S. Publication Nos. 2003/0051263, 2003/0055020, 2003/0056235, 2004/265839, 2005/0100913, 2006/0024798, 2008/0050342, 2008/0081373, 2008/0248576, and 2008/055443; and/or U.S. Pat. Nos. 6,506,559, 7,282,564, 7,538,095, and 7,560,438 (incorporated herein by reference). In some instances, the anti-CTLA-4 RNAi molecules take the form of double stranded RNAi molecules described by Tuschl in European Patent No. EP 1309726 (incorporated herein by reference). In some instances, the anti-CTLA-4 RNAi molecules take the form of double stranded RNAi molecules described by Tuschl in U.S. Pat. Nos. 7,056,704 and 7,078,196 (incorporated herein by reference). In some embodiments, the CTLA-4 inhibitor is an aptamer described in PCT Publication No. WO2004081021 (incorporated herein by reference).

[002067] In other embodiments, the anti-CTLA-4 RNAi molecules of the present invention are RNA molecules described by Crooke in U.S. Patent Nos. 5,898,031, 6,107,094, 7,432,249, and 7,432,250, and European Application No. EP 0928290 (incorporated herein by reference).

5. Combinations with VEGF-A Inhibitors

[002068] In some embodiments, TILs and a VEGF-A inhibitor are administered as a combination therapy or co-therapy for the treatment of NSCLC.

[002069] In some embodiments, the NSCLC has undergone no prior therapy. In some embodiments, the VEGF-A inhibitor is administered as a front-line therapy or initial therapy. In some embodiments, the VEGF-A inhibitor is administered as a front-line therapy or initial therapy in combination with the TILs as described herein.

[002070] VEGF-A (polynucleotide and polypeptide sequences shown in SEQ ID NOs: 1 and 2, respectively) is a secreted, disulfide-linked homodimeric glycoprotein belonging to the VEGF/PDGF (platelet-derived growth factor) group of the cystine-knot superfamily of hormones and extracellular signaling molecules (see Vitt et al., Mol. Endocrinol., 15:681-694, 2001), which are all characterized by the presence of eight conserved cysteine residues forming the typical cystine-knot structure (named after cystine, a dimer of two cysteines linked by a disulfide bond). Five human VEGF-A isoforms of 121, 145, 165, 189 or 206 amino acids in length (VEGF-A121-206), encoded by distinct mRNA

splice variants, have been described, all of which are capable of stimulating mitogenesis in endothelial cells. These isoforms differ in biological activity, receptor specificity, and affinity for cell surface- and extracellular matrix-associated heparan-sulfate proteoglycans, which behave as low affinity receptors for VEGF-A: VEGF-A121 does not bind to either heparin or heparan-sulfate; VEGF-A145 and VEGF-A165 (GenBank Acc. No. M32977) are both capable of binding to heparin; and VEGF-A189 and VEGF-A206 show the strongest affinity for heparin and heparan-sulfates. VEGF-A121, VEGF-A145, and VEGF-A165 are secreted in a soluble form, although most of VEGF-A165 is confined to cell surface and extracellular matrix proteoglycans, whereas VEGF-A189 and VEGF-A206 remain associated with extracellular matrix. Both VEGF-A189 and VEGF-A206 can be released by treatment with heparin or heparinase, indicating that these isoforms are bound to extracellular matrix via proteoglycans. Cell-bound VEGF-A180 can also be cleaved by proteases such as plasmin, resulting in release of an active soluble VEGF-A110.

[002071] VEGF-A-driven angiogenesis has a major role in the pathogenesis of diverse human diseases, including cancer, eye disorders, and rheumatoid arthritis. See Carmeliet et al., Nature 407:249-257, 2000. Recognition of the importance of VEGF-A for the development of several important classes of cancer recently culminated in the approval of AVASTIN™, a humanized monoclonal antibody to VEGF-A, for the treatment of metastatic colorectal cancer. See Ferrara et al., Nat. Rev. Drug Discov. 2004, 3:391-400, 2004. Similarly, the importance of VEGF-A in the pathogenesis of neovascular ocular disorders is reflected in the recent approval of LUCENTIS™, a humanized monoclonal antibody fragment, for the treatment of neovascular (wet) age-related macular degeneration (AMD).

[002072] VEGF-A inhibitors for use within the present invention include molecules that bind to VEGF-A or a VEGF-A receptor and thereby reduce the activity of VEGF-A on cells that express the receptor such as, *e.g.*, VEGFR-1, VEGFR-2, neuropilin-1, and/or neuropilin-2. In particular, VEGF-A inhibitors include anti-VEGF-A antibodies. Other suitable VEGF-A inhibitors include soluble VEGF-A receptors comprising a VEGFR extracellular domain, as well as small molecule antagonists capable of inhibiting the interaction of VEGF-A with its receptor or otherwise capable in inhibiting VEGF-A-induced intracellular signaling through a VEGF-A receptor. In addition, binding proteins based on non-antibody scaffolds may be employed. (See, *e.g.*, Koide et al., J. Mol. Biol. 284:1141-1151, 1998; Hosse et al. Protein Sci. 15:14-27, 2006, and references therein.) Preferred VEGF-A inhibitors for use within the invention include antibodies that specifically bind to VEGF-A, including bispecific antibodies that also comprise a binding site for PDGFRβ. Antibodies that are specific for VEGF-A bind at least the soluble secreted forms of VEGF-A, and preferably also bind cell surface-associated forms.

[002073] In some embodiments, the VEGF-A inhibitor may be any VEGF-A inhibitor or VEGF-A blocker known in the art. In particular, it is one of the VEGF-A inhibitors or blockers described in more detail in the following paragraphs. The terms "inhibitor," "antagonist," and "blocker" are used interchangeably herein in reference to VEGF-A inhibitors. For avoidance of doubt, references herein to a VEGF-A inhibitor that is an antibody may refer to a compound or antigen-binding fragments, variants, conjugates, or biosimilars thereof. For avoidance of doubt, references herein to a VEGF-A inhibitor may also refer to a small molecule compound or a pharmaceutically acceptable salt, ester, solvate, hydrate, cocrystal, or prodrug thereof.

[002074] In some embodiments, the VEGF-A inhibitor may be any VEGF-A inhibitor or VEGF-A blocker known in the art. In particular, it is one of the VEGF-A inhibitors or blockers described in more detail in the following paragraphs. The terms "inhibitor," "antagonist," and "blocker" are used interchangeably herein in reference to VEGF-A inhibitors. For avoidance of doubt, references herein to a VEGF-A inhibitor that is an antibody may refer to a compound or antigen-binding fragments, variants, conjugates, or biosimilars thereof. For avoidance of doubt, references herein to a VEGF-A inhibitor may also refer to a small molecule compound or a pharmaceutically acceptable salt, ester, solvate, hydrate, cocrystal, or prodrug thereof.

[002075] In some embodiments, the VEGF-A inhibitor is an antibody (*i.e.*, an anti-VEGF-A antibody), a fragment thereof, including Fab fragments, or a single-chain variable fragment (scFv) thereof. In some embodiments the VEGF-A inhibitor is a polyclonal antibody. In some embodiments, the VEGF-A inhibitor is a monoclonal antibody. In some embodiments, the VEGF-A inhibitor competes for binding with VEGF-A, and/or binds to an epitope on VEGF-A. In some embodiments, the antibody competes for binding with VEGF-A, and/or binds to an epitope on VEGF-A.

[002076] In some embodiments, the VEGF-A inhibitor is one that binds human VEGF-A with a K_D of about 100 pM or lower, binds human VEGF-A with a K_D of about 90 pM or lower, binds human VEGF-A with a K_D of about 80 pM or lower, binds human VEGF-A with a K_D of about 70 pM or lower, binds human VEGF-A with a K_D of about 60 pM or lower, binds human VEGF-A with a K_D of about 50 pM or lower, binds human VEGF-A with a K_D of about 40 pM or lower, binds human VEGF-A with a K_D of about 30 pM or lower, binds human VEGF-A with a K_D of about 20 pM or lower, binds human VEGF-A with a K_D of about 10 pM or lower, or binds human VEGF-A with a K_D of about 1 pM or lower.

[002077] In some embodiments, the VEGF-A inhibitor is one that binds to human VEGF-A with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human VEGF-A with a k_{assoc} of about 7.5×10^5 1/M·s or faster, binds to human VEGF-A with a k_{assoc} of about 8×10^5 1/M·s or faster, binds to human VEGF-A with a k_{assoc} of about 8.5×10^5 1/M·s or faster, binds to human VEGF-A with a k_{assoc} of

about 9×10^5 1/M·s or faster, binds to human VEGF-A with a k_{assoc} of about 9.5×10^5 1/M·s or faster, or binds to human VEGF-A with a k_{assoc} of about 1×10^6 1/M·s or faster.

[002078] In some embodiments, the VEGF-A inhibitor is one that binds to human VEGF-A with a k_{dissoc} of about 2×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.1×10^{-5} 1/s or slower , binds to human VEGF-A with a k_{dissoc} of about 2.2×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.3×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.4×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.5×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.6×10^{-5} 1/s or slower or binds to human VEGF-A with a k_{dissoc} of about 2.7×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.8×10^{-5} 1/s or slower, binds to human VEGF-A with a k_{dissoc} of about 2.9×10^{-5} 1/s or slower, or binds to human VEGF-A with a k_{dissoc} of about 3×10^{-5} 1/s or slower.

[002079] In some embodiments, the VEGF-A inhibitor is one that blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 10 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 9 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 8 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 7 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 6 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 5 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 4 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 3 nM or lower, blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 2 nM or lower, or blocks or inhibits binding of human VEGFR-1 receptor or human VEGFR-2 receptor to human VEGF-A with an IC_{50} of about 1 nM or lower.

[002080] In some embodiments, the VEGF-A inhibitor is bevacizumab, or biosimilars, antigen-binding fragments, conjugates, or variants thereof. Bevacizumab (CAS registry number 216974-75-3, AVASTIN®, Genentech) is an anti-VEGF monoclonal antibody against vascular endothelial growth factor used in cancer treatment (US 7227004; US 6884879; US 7060269; US 7169901; US 7297334), which inhibits tumor growth by blocking neovascularization. Bevacizumab is the first clinically available angiogenesis inhibitor in the United States. It was approved by the FDA in 2004 in combination with standard chemotherapy for the treatment of metastatic colon cancer and most forms of metastatic non-small cell lung cancer. Several post-clinical studies are underway to determine its safety and effectiveness in patients with the following diseases: auxiliary / non-metastatic colon

cancer, metastatic breast cancer, metastatic renal cell carcinoma, metastatic polymorphic glioblastoma Neoplasms, metastatic ovarian cancer, metastatic hormone refractory prostate cancer and metastasis Metastatic pancreatic cancer or unresectable locally advanced pancreatic cancer.

[002081] Bevacizumab includes a mutant human IgG1 framework region and an antigen-binding complementarity determining region from a murine anti-hVEGF monoclonal antibody A.4.6.1 that blocks the binding of human VEGF to its receptor. About 93% of the bevacizumab amino acid sequences (including most framework regions) are derived from human IgG1 and about 7% of the sequences are derived from the murine antibody A4.6.1. Bevacizumab has a molecular mass of about 149,000 daltons and is glycosylated. Bevacizumab and other humanized anti-VEGF antibodies are further described in US 6884879. Additional anti-VEGF antibodies include G6 or B20 series antibodies (eg G6-31, B20-4.1) as described in any of Figures 27-29 of International Patent Publication No. WO 2005/012359. In one embodiment, the B20 series antibodies bind to functional epitopes on human VEGF containing residues F17, M18, D19, Y21, Y25, Q89, I91, K101, E103, and C104. Additional VEGF antibodies are in are described in International Patent Publication No. WO2010148223.

[002082] In some embodiments, a VEGF-A inhibitor comprises a heavy chain given by SEQ ID NO:207 and a light chain given by SEQ ID NO:208. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:207 and SEQ ID NO:208, respectively.

[002083] In some embodiments, the VEGF-A inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of bevacizumab. In some embodiments, the VEGF-A inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:209, and the VEGF-A inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:210, and conservative amino acid substitutions thereof. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L

regions that are each at least 99% identical to the sequences shown in SEQ ID NO:209 and SEQ ID NO:210, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:209 and SEQ ID NO:210, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:209 and SEQ ID NO:210, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:209 and SEQ ID NO:210, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:209 and SEQ ID NO:210, respectively.

[002084] In some embodiments, a VEGF-A inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:211, SEQ ID NO:212, and SEQ ID NO:213, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:214, SEQ ID NO:215, and SEQ ID NO:216, respectively, and conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on VEGF-A as any of the aforementioned antibodies.

[002085] In some embodiments, the VEGF-A inhibitor is a VEGF-A biosimilar monoclonal antibody approved by drug regulatory authorities with reference to bevacizumab. In some embodiments, the biosimilar comprises an anti-VEGF-A antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is bevacizumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-VEGF-A antibody authorized or submitted for authorization, wherein the anti-VEGF-A antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is bevacizumab. The anti-VEGF-A antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is bevacizumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are

the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is bevacizumab.

TABLE 26. Amino acid sequences for bevacizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:207 bevacizumab heavy chain	1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW INTYTGEPTY 61 AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP HYYGSSHWYF DVWGQGTLVT 121 VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL 181 QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL 241 LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 301 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 361 REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF FLYSKLTVDK 421 SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK
SEQ ID NO:208 bevacizumab light chain	1 DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF TSSLHSGVPS 61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP 121 SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 181 LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC
SEQ ID NO:209 bevacizumab variable heavy chain	1 EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW INTYTGEPTY 61 AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP HYYGSSHWYF DVWGQGTLVT 121 VSS
SEQ ID NO:210 bevacizumab variable light chain	1 DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF TSSLHSGVPS 61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ GTKVEIKR
SEQ ID NO:211 bevacizumab heavy chain CDR1	GYTFTNYGMN 10
SEQ ID NO:212 bevacizumab heavy chain CDR2	WINTYTGEPT YAADFK 16
SEQ ID NO:213 bevacizumab heavy chain CDR3	YPHYYGSSHW YFDV 14
SEQ ID NO:214 bevacizumab light chain CDR1	SASQDISNYL N 11
SEQ ID NO:215 bevacizumab light chain CDR2	FTSSLHS 7
SEQ ID NO:216 bevacizumab light chain CDR3	QQYSTVPWT 9

[002086] In some embodiments, the VEGF-A inhibitor is ranibizumab, or biosimilars, antigen-binding fragments, conjugates, or variants thereof. Ranibizumab (CAS registry number 347396-82-1, Lucentis®) is a monoclonal antibody fragment (Fab) created from the same parent mouse antibody as bevacizumab. It is an anti-angiogenic that has been approved to treat age-related macular degeneration (AMD, also ARMD), a common form of age-related vision loss. Its rates of side effects is similar to that of bevacizumab. However, ranibizumab typically costs $2,000 a dose, while the equivalent dose of bevacizumab typically costs $50.

[002087] In some embodiments, a VEGF-A inhibitor comprises a heavy chain given by SEQ ID NO:217 and a light chain given by SEQ ID NO:218. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains having the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:217 and SEQ ID NO:218, respectively.

[002088] In some embodiments, the VEGF-A inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of ranibizumab. In some embodiments, the VEGF-A inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:219, and the VEGF-A inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:220, and conservative amino acid substitutions thereof. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:219 and SEQ ID NO:220, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:219 and SEQ ID NO:220, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:219 and SEQ ID NO:220, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:219 and SEQ ID NO:220, respectively. In some

embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:219 and SEQ ID NO:220, respectively.

[002089] In some embodiments, a VEGF-A inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:221, SEQ ID NO:222, and SEQ ID NO:223, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:224, SEQ ID NO:225, and SEQ ID NO:226, respectively, and conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on VEGF-A as any of the aforementioned antibodies.

[002090] In some embodiments, the VEGF-A inhibitor is a VEGF-A biosimilar monoclonal antibody approved by drug regulatory authorities with reference to ranibizumab. In some embodiments, the biosimilar comprises an anti-VEGF-A antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.*, 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ranibizumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-VEGF-A antibody authorized or submitted for authorization, wherein the anti-VEGF-A antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ranibizumab. The anti-VEGF-A antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ranibizumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is ranibizumab.

TABLE 27. Amino acid sequences for ranibizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:217 ranibizumab heavy chain	1 EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW INTYTGEPTY 61 AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP YYYGTSHWYF DVWGQGTLVT 121 VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL 181 QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKK VEPKSCDKTH L
SEQ ID NO:218 ranibizumab light chain	1 DIQLTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF TSSLHSGVPS 61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP 121 SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 181 LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC
SEQ ID NO:219 ranibizumab variable heavy chain	1 EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW INTYTGEPTY 61 AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP YYYGTSHWYF DVWGQGTLVT 121 VSS
SEQ ID NO:220 ranibizumab variable light chain	1 DIQLTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF TSSLHSGVPS 61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ GTKVEIKR
SEQ ID NO:221 ranibizumab heavy chain CDR1	GYDFTHYGMN 10
SEQ ID NO:222 ranibizumab heavy chain CDR2	WINTYTGEPT YAADFKR 17
SEQ ID NO:223 ranibizumab heavy chain CDR3	YPYYYGTSHW YFDV 14
SEQ ID NO:224 ranibizumab light chain CDR1	SASQDISNYL N 11
SEQ ID NO:225 ranibizumab light chain CDR2	FTSSLHS 7
SEQ ID NO:226 ranibizumab light chain CDR3	QQYSTVPWT 9

[002091] In some embodiments, the VEGF-A inhibitor is icrucumab, or biosimilars, antigen-binding fragments, conjugates, or variants thereof. Icrucumab (CAS registry number 1024603-92-6, also known as IMC-18F1) is a human monoclonal antibody designed for the treatment of solid tumors. A fully human IgG1 monoclonal antibody directed against human vascular endothelial growth factor receptor 1 (VEGFR-1/FLT-1) with potential antiangiogenesis and antineoplastic activities. Icrucumab specifically binds to and inhibits the activity of VEGFR-1, which may prevent the activation of downstream signaling pathways and so inhibit tumor angiogenesis; the subsequent reduction in tumor nutrient supply may inhibit tumor cell proliferation. Tumor cell overexpression of VEGFR-1 may be associated with tumor angiogenesis and tumor cell proliferation and invasion; VEGFR-1 may modulate VEGFR-2 signaling.

[002092] In some embodiments, a VEGF-A inhibitor comprises a heavy chain given by SEQ ID NO:227 and a light chain given by SEQ ID NO:228. In some embodiments, a VEGF-A inhibitor

comprises heavy and light chains having the sequences shown in SEQ ID NO:227 and SEQ ID NO: 564, respectively, or antigen binding fragments, Fab fragments, single-chain variable fragments (scFv), variants, or conjugates thereof. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 99% identical to the sequences shown in SEQ ID NO:227 and SEQ ID NO:228, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 98% identical to the sequences shown in SEQ ID NO:227 and SEQ ID NO:228, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 97% identical to the sequences shown in SEQ ID NO:227 and SEQ ID NO:228, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 96% identical to the sequences shown in SEQ ID NO:227 and SEQ ID NO:228, respectively. In some embodiments, a VEGF-A inhibitor comprises heavy and light chains that are each at least 95% identical to the sequences shown in SEQ ID NO:227 and SEQ ID NO:228, respectively.

[002093] In some embodiments, the VEGF-A inhibitor comprises the heavy and light chain CDRs or variable regions (VRs) of icrucumab. In some embodiments, the VEGF-A inhibitor heavy chain variable region (V_H) comprises the sequence shown in SEQ ID NO:229, and the VEGF-A inhibitor light chain variable region (V_L) comprises the sequence shown in SEQ ID NO:230, and conservative amino acid substitutions thereof. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 99% identical to the sequences shown in SEQ ID NO:229 and SEQ ID NO:230, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 98% identical to the sequences shown in SEQ ID NO:229 and SEQ ID NO:230, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 97% identical to the sequences shown in SEQ ID NO:229 and SEQ ID NO:230, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 96% identical to the sequences shown in SEQ ID NO:229 and SEQ ID NO:230, respectively. In some embodiments, a VEGF-A inhibitor comprises V_H and V_L regions that are each at least 95% identical to the sequences shown in SEQ ID NO:229 and SEQ ID NO:230, respectively.

[002094] In some embodiments, a VEGF-A inhibitor comprises the heavy chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:231, SEQ ID NO:232, and SEQ ID NO:233, respectively, and conservative amino acid substitutions thereof, and light chain CDR1, CDR2 and CDR3 domains having the sequences set forth in SEQ ID NO:234, SEQ ID NO:235, and SEQ ID NO:236, respectively, and conservative amino acid substitutions thereof. In some embodiments, the antibody competes for binding with, and/or binds to the same epitope on VEGF-A as any of the aforementioned antibodies.

[002095] In some embodiments, the VEGF-A inhibitor is a VEGF-A biosimilar monoclonal antibody approved by drug regulatory authorities with reference to icrucumab. In some embodiments, the biosimilar comprises an anti-VEGF-A antibody comprising an amino acid sequence which has at least 97% sequence identity, *e.g.,* 97%, 98%, 99% or 100% sequence identity, to the amino acid sequence of a reference medicinal product or reference biological product and which comprises one or more post-translational modifications as compared to the reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is icrucumab. In some embodiments, the one or more post-translational modifications are selected from one or more of: glycosylation, oxidation, deamidation, and truncation. In some embodiments, the biosimilar is an anti-VEGF-A antibody authorized or submitted for authorization, wherein the anti-VEGF-A antibody is provided in a formulation which differs from the formulations of a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is icrucumab. The anti-VEGF-A antibody may be authorized by a drug regulatory authority such as the U.S. FDA and/or the European Union's EMA. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is icrucumab. In some embodiments, the biosimilar is provided as a composition which further comprises one or more excipients, wherein the one or more excipients are the same or different to the excipients comprised in a reference medicinal product or reference biological product, wherein the reference medicinal product or reference biological product is icrucumab.

TABLE 28. Amino acid sequences for icrucumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:227 icrucumab heavy chain	1 QAQVVESGGG VVQSGRSLRL SCAASGFAFS SYGMHWVRQA PGKGLEWVAV IWYDGSNKYY 61 ADSVRGRFTI SRDNSENTLY LQMNSLRAED TAVYYCARDH YGSGVHHYFY YGLDVWGQGT 121 TVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP 181 AVLQSSGLYS LSSVVTVPSS SLGTQTYICN VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK
SEQ ID NO:228 icrucumab light chain	1 EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY GASSRATGIP 61 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLTFG GGTKVEIKRT VAAPSVFIFP 121 PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 181 TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC
SEQ ID NO:229 icrucumab variable heavy chain	QAQWESGGGVVQSGRSLRLSCAASGFAFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSEN TLYLQMNSLRAEDTAVYYCARDHYGSGVHHYFYYGLDVWGQGTTVTVSS
SEQ ID NO:230 icrucumab variable light chain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTI SRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIK
SEQ ID NO:231	VVQSGRS

Identifier	Sequence (One-Letter Amino Acid Symbols)
icrucumab heavy chain CDR1	
SEQ ID NO:232 icrucumab heavy chain CDR2	SGFAFSSYG
SEQ ID NO:233 icrucumab heavy chain CDR3	WVAVIWYDGSNKYYADS
SEQ ID NO:234 icrucumab light chain CDR1	LSPGERA
SEQ ID NO:235 icrucumab light chain CDR2	QSV
SEQ ID NO:236 icrucumab light chain CDR3	APRLLIYGAS

[002096] In some embodiments, the VEGF-A inhibitor is a decoy VEGF receptor (also known as VEGF trap), such as Aflibercept (Eylea, Zaltrap), which is disclosed in US Patent Application Publication No. US2019/0298801 and International Patent Application Publication No. WO2014006113A1 (disclosure incorporated herein by reference) or Conbercept, which is disclosed in US Patent Application Publication Nos. US2019/0002546 and US2019/0343918 (disclosure incorporated herein by reference). Additional disclosure and examples of decoy VEGF receptor is provided in US Patent Nos. 6,383,486, 6,375,929, 6,348,333, 6,100,071, and 9,777,261, the disclosure of which are incorporated herein by reference in their entireties.

[002097] In some embodiments, the VEGF-A inhibitor is a small molecule tyrosine kinases inhibitor. Small molecule tyrosine kinases are known to those of ordinary skill in the art. Examples of small molecule tyrosine kinases inhibitor include, but are not limited to, Pegaptanib, Pazopanib, lapatinib, Sunitinib, sorafenib, regorafenib, Ponatinib, lenvatinib, axitinib (AG-013736), Cediranib (AZD2171), vatalanib, and/or Lucitanib.

[002098] In some embodiments, the VEGF-A inhibitor is an anti-VEGFR ribozyme, an anti-VEGFR antisense, and an siRNA that inhibits a VEGFR that are disclosed in US Patent No. 7,148,342 and International Patent Application No. WO2010058426 (disclosure incorporated herein by reference in their entireties).

6. Lymphodepletion Preconditioning of Patients

[002099] In some embodiments, the invention includes a method of treating a cancer with a population of TILs, wherein a patient is pre-treated with non-myeloablative chemotherapy prior to an

infusion of TILs according to the present disclosure. In some embodiments, the invention includes a population of TILs for use in the treatment of cancer in a patient which has been pre-treated with non-myeloablative chemotherapy. In some embodiments, the population of TILs is for administration by infusion. In some embodiments, the non-myeloablative chemotherapy is cyclophosphamide 60 mg/kg/d for 2 days (days 27 and 26 prior to TIL infusion) and fludarabine 25 mg/m^2/d for 5 days (days 27 to 23 prior to TIL infusion). In some embodiments, after non-myeloablative chemotherapy and TIL infusion (at day 0) according to the present disclosure, the patient receives an intravenous infusion of IL-2 (aldesleukin, commercially available as PROLEUKIN) intravenously at 720,000 IU/kg every 8 hours to physiologic tolerance. In certain embodiments, the population of TILs is for use in treating cancer in combination with IL-2, wherein the IL-2 is administered after the population of TILs.

[002100] Experimental findings indicate that lymphodepletion prior to adoptive transfer of tumor-specific T lymphocytes plays a key role in enhancing treatment efficacy by eliminating regulatory T cells and competing elements of the immune system ('cytokine sinks'). Accordingly, some embodiments of the invention utilize a lymphodepletion step (sometimes also referred to as "immunosuppressive conditioning") on the patient prior to the introduction of the TILs of the invention.

[002101] In general, lymphodepletion is achieved using administration of fludarabine or cyclophosphamide (the active form being referred to as mafosfamide) and combinations thereof. Such methods are described in Gassner, *et al., Cancer Immunol. Immunother.* **2011**, *60,* 75–85, Muranski, *et al.*, *Nat. Clin. Pract. Oncol.,* **2006,** *3,* 668–681, Dudley, *et al.*, *J. Clin. Oncol.* **2008**, *26,* 5233-5239, and Dudley, *et al.*, *J. Clin. Oncol.* **2005**, *23,* 2346–2357, all of which are incorporated by reference herein in their entireties.

[002102] In some embodiments, the fludarabine is administered at a concentration of 0.5 μg/mL to 10 μg/mL fludarabine. In some embodiments, the fludarabine is administered at a concentration of 1 μg/mL fludarabine. In some embodiments, the fludarabine treatment is administered for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days or more. In some embodiments, the fludarabine is administered at a dosage of 10 mg/kg/day, 15 mg/kg/day, 20 mg/kg/day, 25 mg/kg/day, 30 mg/kg/day, 35 mg/kg/day, 40 mg/kg/day, or 45 mg/kg/day. In some embodiments, the fludarabine treatment is administered for 2-7 days at 35 mg/kg/day. In some embodiments, the fludarabine treatment is administered for 4-5 days at 35 mg/kg/day. In some embodiments, the fludarabine treatment is administered for 4-5 days at 25 mg/kg/day.

[002103] In some embodiments, the mafosfamide, the active form of cyclophosphamide, is obtained at a concentration of 0.5 μg/mL to 10 μg/mL by administration of cyclophosphamide. In some

embodiments, mafosfamide, the active form of cyclophosphamide, is obtained at a concentration of 1 μg/mL by administration of cyclophosphamide. In some embodiments, the cyclophosphamide treatment is administered for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days or more. In some embodiments, the cyclophosphamide is administered at a dosage of 100 mg/m^2/day, 150 mg/m^2/day, 175 mg/m^2/day, 200 mg/m^2/day, 225 mg/m^2/day, 250 mg/m^2/day, 275 mg/m^2/day, or 300 mg/m^2/day. In some embodiments, the cyclophosphamide is administered intravenously *(i.e.*, i.v.). In some embodiments, the cyclophosphamide treatment is administered for 2-7 days at 35 mg/kg/day. In some embodiments, the cyclophosphamide treatment is administered for 4-5 days at 250 mg/m^2/day i.v. In some embodiments, the cyclophosphamide treatment is administered for 4 days at 250 mg/m^2/day i.v.

[002104] In some embodiments, lymphodepletion is performed by administering the fludarabine and the cyclophosphamide together to a patient. In some embodiments, fludarabine is administered at 25 mg/m^2/day i.v. and cyclophosphamide is administered at 250 mg/m^2/day i.v. over 4 days.

[002105] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[002106] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days and administration of fludarabine at a dose of 25 mg/m^2/day for five days, wherein cyclophosphamide and fludarabine are both administered on the first two days, and wherein the lymphodepletion is performed in five days in total.

[002107] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of about 50 mg/m^2/day for two days and administration of fludarabine at a dose of about 25 mg/m^2/day for five days, wherein cyclophosphamide and fludarabine are both administered on the first two days, and wherein the lymphodepletion is performed in five days in total.

[002108] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of about 50 mg/m^2/day for two days and administration of fludarabine at a dose of about 20 mg/m^2/day for five days, wherein cyclophosphamide and fludarabine are both administered on the first two days, and wherein the lymphodepletion is performed in five days in total.

[002109] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of about 40 mg/m^2/day for two days and administration of fludarabine at a dose of about 20 mg/m^2/day for five days, wherein cyclophosphamide and fludarabine are both administered on the first two days, and wherein the lymphodepletion is performed in five days in total.

[002110] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of about 40 mg/m^2/day for two days and administration of fludarabine at a dose of about 15 mg/m^2/day for five days, wherein cyclophosphamide and fludarabine are both administered on the first two days, and wherein the lymphodepletion is performed in five days in total.

[002111] In some embodiments, the lymphodepletion is performed by administration of cyclophosphamide at a dose of 60 mg/m^2/day and fludarabine at a dose of 25 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

[002112] In some embodiments, the cyclophosphamide is administered with mesna. In some embodiments, mesna is administered at 15 mg/kg. In some embodiments where mesna is infused, and if infused continuously, mesna can be infused over approximately 2 hours with cyclophosphamide (on Days -5 and/or -4), then at a rate of 3 mg/kg/hour for the remaining 22 hours over the 24 hours starting concomitantly with each cyclophosphamide dose.

[002113] In some embodiments, the lymphodepletion comprises the step of treating the patient with an IL-2 regimen starting on the day after administration of the third population of TILs to the patient.

[002114] In some embodiments, the lymphodepletion comprises the step of treating the patient with an IL-2 regimen starting on the same day as administration of the third population of TILs to the patient.

[002115] In some embodiments, the lymphodeplete comprises 5 days of preconditioning treatment. In some embodiments, the days are indicated as days -5 through -1, or Day 0 through Day 4. In some embodiments, the regimen comprises cyclophosphamide on days -5 and -4 (*i.e.*, days 0 and 1). In some embodiments, the regimen comprises intravenous cyclophosphamide on days -5 and -4 (*i.e.*, days 0 and 1). In some embodiments, the regimen comprises 60 mg/kg intravenous cyclophosphamide on days -5 and -4 (*i.e.*, days 0 and 1). In some embodiments, the cyclophosphamide is administered with mesna. In some embodiments, the regimen further comprises fludarabine. In some embodiments, the regimen further comprises intravenous fludarabine. In some embodiments, the regimen further comprises 25 mg/m^2 intravenous fludarabine. In some embodiments, the regimen further comprises 25 mg/m^2 intravenous fludarabine on days -5 and -1 (*i.e.*, days 0 through 4). In some embodiments, the regimen further comprises 25 mg/m^2 intravenous fludarabine on days -5 and -1 (*i.e.*, days 0 through 4).

[002116] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day and fludarabine at a dose of 25

mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[002117] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[002118] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

[002119] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day and fludarabine at a dose of 25 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

[002120] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day and fludarabine at a dose of 25 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for one day.

[002121] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

[002122] In some embodiments, the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day and fludarabine at a dose of 25 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

[002123] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 29.

TABLE 29. Exemplary lymphodepletion and treatment regimen.

Day	**-5**	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 60 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 25 mg/m^2/day	X	X	X	X	X					
TIL infusion						X				

[002124] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 30.

TABLE 30. Exemplary lymphodepletion and treatment regimen.

Day	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 60 mg/kg	X	X							
Mesna (as needed)	X	X							
Fludarabine 25 mg/m^2/day	X	X	X	X					
TIL infusion					X				

[002125] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 31.

TABLE 31. Exemplary lymphodepletion and treatment regimen.

Day	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 60 mg/kg	X	X						
Mesna (as needed)	X	X						
Fludarabine 25 mg/m^2/day	X	X	X					
TIL infusion				X				

[002126] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 32.

TABLE 32. Exemplary lymphodepletion and treatment regimen.

Day	**-5**	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 60 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 25 mg/m^2/day			X	X	X					
TIL infusion						X				

[002127] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 33.

TABLE 33. Exemplary lymphodepletion and treatment regimen.

Day	**-5**	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 300 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 30 mg/m^2/day	X	X	X	X	X					

Day	-5	-4	-3	-2	-1	0	1	2	3	4
TIL infusion						X				

[002128] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 34.

TABLE 34. Exemplary lymphodepletion and treatment regimen.

Day	-4	-3	-2	-1	0	1	2	3	4
Cyclophosphamide 300 mg/kg	X	X							
Mesna (as needed)	X	X							
Fludarabine 30 mg/m^2/day	X	X	X	X					
TIL infusion					X				

[002129] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 35.

TABLE 35. Exemplary lymphodepletion and treatment regimen.

Day	-3	-2	-1	0	1	2	3	4
Cyclophosphamide 300 mg/kg	X	X						
Mesna (as needed)	X	X						
Fludarabine 30 mg/m^2/day	X	X	X					
TIL infusion				X				

[002130] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 36.

TABLE 36. Exemplary lymphodepletion and treatment regimen.

Day	-5	-4	-3	-2	-1	0	1	2	3	4
Cyclophosphamide 300 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 30 mg/m^2/day			X	X	X					
TIL infusion						X				

[002131] In some embodiments, the TIL infusion used with the foregoing embodiments of myeloablative lymphodepletion regimens may be any TIL composition described herein, as well as the addition of IL-2 regimens and administration of co-therapies (such as PD-1 and PD-L1 inhibitors) as described herein.

7. IL-2 Regimens

[002132] In some embodiments, the IL-2 regimen comprises a high-dose IL-2 regimen, wherein the high-dose IL-2 regimen comprises aldesleukin, or a biosimilar or variant thereof, administered intravenously starting on the day after administering a therapeutically effective portion of the therapeutic population of TILs, wherein the aldesleukin or a biosimilar or variant thereof is administered at a dose of 0.037 mg/kg or 0.044 mg/kg IU/kg (patient body mass) using 15-minute bolus intravenous infusions every eight hours until tolerance, for a maximum of 14 doses. Following 9 days of rest, this schedule may be repeated for another 14 doses, for a maximum of 28 doses in total. In some embodiments, IL-2 is administered in 1, 2, 3, 4, 5, or 6 doses. In some embodiments, IL-2 is administered at a maximum dosage of up to 6 doses.

[002133] In some embodiments, the IL-2 regimen comprises a decrescendo IL-2 regimen. Decrescendo IL-2 regimens have been described in O'Day, *et al.*, *J. Clin. Oncol.* **1999,** *17,* 2752-61 and Eton, *et al.*, *Cancer* **2000,** *88,* 1703-9, the disclosures of which are incorporated herein by reference. In some embodiments, a decrescendo IL-2 regimen comprises 18×10^6 IU/m^2 aldesleukin, or a biosimilar or variant thereof, administered intravenously over 6 hours, followed by 18×10^6 IU/m^2 administered intravenously over 12 hours, followed by 18×10^6 IU/m^2 administered intravenously over 24 hours, followed by 4.5×10^6 IU/m^2 administered intravenously over 72 hours. This treatment cycle may be repeated every 28 days for a maximum of four cycles. In some embodiments, a decrescendo IL-2 regimen comprises 18,000,000 IU/m^2 on day 1, 9,000,000 IU/m^2 on day 2, and 4,500,000 IU/m^2 on days 3 and 4.

[002134] In some embodiments, the IL-2 regimen comprises a low-dose IL-2 regimen. Any low-dose IL-2 regimen known in the art may be used, including the low-dose IL-2 regimens described in Dominguez-Villar and Hafler, *Nat. Immunology* **2000,** *19,* 665-673; Hartemann, *et al.*, *Lancet Diabetes Endocrinol.* **2013**, *1*, 295-305; and Rosenzwaig, *et al.*, *Ann. Rheum. Dis.* **2019,** *78,* 209–217, the disclosures of which are incorporated herein by reference. In some embodiments, a low-dose IL-2 regimen comprises 18×10^6 IU per m^2 of aldesleukin, or a biosimilar or variant thereof, per 24 hours, administered as a continuous infusion for 5 days, followed by 2-6 days without IL-2 therapy, optionally followed by an an additional 5 days of intravenous aldesleukin or a biosimilar or variant thereof, as a continuous infusion of 18×10^6 IU per m^2 per 24 hours, optionally followed by 3 weeks without IL-2 therapy, after which additional cycles may be administered.

[002135] In some embodiments, IL-2 is administered at a maximum dosage of up to 6 doses. In some embodiments, the high-dose IL-2 regimen is adapted for pediatric use. In some embodiments, a dose of 600,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6

doses is used. In some embodiments, a dose of 500,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used. In some embodiments, a dose of 400,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used. In some embodiments, a dose of 500,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used. In some embodiments, a dose of 300,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used. In some embodiments, a dose of 200,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used. In some embodiments, a dose of 100,000 international units (IU)/kg of aldesleukin every 8–12 hours for up to a maximum of 6 doses is used.

[002136] In some embodiments, the IL-2 regimen comprises administration of pegylated IL-2 every 1, 2, 4, 6, 7, 14 or 21 days at a dose of 0.10 mg/day to 50 mg/day. In some embodiments, the IL-2 regimen comprises administration of bempegaldesleukin, or a fragment, variant, or biosimilar thereof, every 1, 2, 4, 6, 7, 14 or 21 days at a dose of 0.10 mg/day to 50 mg/day.

[002137] In some embodiments, the IL-2 regimen comprises administration of THOR-707, or a fragment, variant, or biosimilar thereof, every 1, 2, 4, 6, 7, 14 or 21 days at a dose of 0.10 mg/day to 50 mg/day.

[002138] In some embodiments, the IL-2 regimen comprises administration of nemvaleukin alfa, or a fragment, variant, or biosimilar thereof, following administration of TIL. In certain embodiments, the patient the nemvaleukin is administered every 1, 2, 4, 6, 7, 14 or 21 days at a dose of 0.10 mg/day to 50 mg/day.

[002139] In some embodiments, the IL-2 regimen comprises administration of an IL-2 fragment engrafted onto an antibody backbone. In some embodiments, the IL-2 regimen comprises administration of an antibody-cytokine engrafted protein that binds the IL-2 low affinity receptor. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain variable region (V_H), comprising complementarity determining regions HCDR1, HCDR2, HCDR3; a light chain variable region (V_L), comprising LCDR1, LCDR2, LCDR3; and an IL-2 molecule or a fragment thereof engrafted into a CDR of the V_H or the V_L, wherein the antibody cytokine engrafted protein preferentially expands T effector cells over regulatory T cells. In some embodiments, the antibody cytokine engrafted protein comprises a heavy chain variable region (V_H), comprising complementarity determining regions HCDR1, HCDR2, HCDR3; a light chain variable region (V_L), comprising LCDR1, LCDR2, LCDR3; and an IL-2 molecule or a fragment thereof engrafted into a CDR of the V_H or the V_L, wherein the IL-2 molecule is a mutein, and wherein the antibody cytokine engrafted protein preferentially expands T effector cells over regulatory T cells. In some embodiments, the IL-2 regimen comprises administration of an antibody comprising a heavy chain selected from the group

consisting of SEQ ID NO:29 and SEQ ID NO:38 and a light chain selected from the group consisting of SEQ ID NO:37 and SEQ ID NO:39, or a fragment, variant, or biosimilar thereof, every 1, 2, 4, 6, 7, 14 or 21 days at a dose of 0.10 mg/day to 50 mg/day.

[002140] In some embodiments, the antibody cytokine engrafted protein described herein has a longer serum half-life that a wild-type IL-2 molecule such as, but not limited to, aldesleukin (Proleukin®) or a comparable molecule.

[002141] In some embodiments, the TIL infusion used with the foregoing embodiments of myeloablative lymphodepletion regimens may be any TIL composition described herein and may also include infusions of MILs and PBLs in place of the TIL infusion, as well as the addition of IL-2 regimens and administration of co-therapies (such as PD-1 and/or PD-L1 inhibitors and/or CTLA-4 inhibitors) as described herein.

8. Additional Methods of Treatment

[002142] In some embodiments, the invention provides a method of treating non-small cell lung carcinoma (NSCLC) by administering a population of tumor infiltrating lymphocytes (TILs) to a subject or patient in need thereof, wherein the subject or patient has at least one of:

i. a predetermined tumor proportion score (TPS) of of PD-L1 < 1%,

ii. a TPS score of of PD-L1 of 1%-49%, or

iii. a predetermined absence of one or more driver mutations, wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, an EGFR exon 20 mutation, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation,a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation, and wherein the method comprises:

(a) obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments;
(b) adding the first population of TILs into a closed system;
(c) performing a first expansion by culturing the first population of TILs in a cell culture

medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (b) to step (c) occurs without opening the system;

(d) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) harvesting therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

(f) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system;

(g) cryopreserving the infusion bag comprising the harvested TIL population from step (f) using a cryopreservation process; and

(h) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (g) to the subject or patient.

[002143] In some embodiments, the invention provides a method of treating non-small cell lung carcinoma (NSCLC) by administering a population of tumor infiltrating lymphocytes (TILs) to a patient in need thereof, wherein the method comprises:

(a) testing the patient's tumor for PD-L1 expression and tumor proportion score (TPS) of PD-L1,

(b) testing the patient for the absence of one or more driver mutations, wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, an EGFR exon 20 mutation, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation,a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation,

an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation,

(c) determining that the patient has a TPS score for PD-L1 of about 1% to about 49% and determining that the patient also has no driver mutations,

(d) obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments;

(e) adding the first population of TILs into a closed system;

(f) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

(i) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system;

(j) cryopreserving the infusion bag comprising the harvested TIL population from step (f) using a cryopreservation process; and

(k) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (g) to the subject or patient.

[002144] In some embodiments, the invention provides a method of treating non-small cell lung carcinoma (NSCLC) by administering a population of tumor infiltrating lymphocytes (TILs) to a patient in need thereof, wherein the method comprises:

(a) testing the patient's tumor for PD-L1 expression and tumor proportion score (TPS) of PD-L1,

(b) testing the patient for the absence of one or more driver mutations, wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, an EGFR exon 20 mutation, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation,a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation,

(c) determining that the patient has a TPS score for PD-L1 of less than about 1% and determining that the patient also has no driver mutations,

(d) obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments;

(e) adding the first population of TILs into a closed system;

(f) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

(i) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system;

(j) cryopreserving the infusion bag comprising the harvested TIL population from step (f) using a cryopreservation process; and

(k) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (g) to the subject or patient.

[002145] In some embodiments, the invention provides a method of treating non-small cell lung carcinoma (NSCLC) by administering a population of tumor infiltrating lymphocytes (TILs) to a patient in need thereof, wherein the method comprises:

(a) testing the patient's tumor for PD-L1 expression and tumor proportion score (TPS) of PD-L1,

(b) testing the patient for the absence of one or more driver mutations, wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, or a RET fusion,

(c) determining that the patient has a TPS score for PD-L1 of about 1% to about 49% and determining that the patient also has no driver mutations,

(d) obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments;

(e) adding the first population of TILs into a closed system;

(f) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

(i) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system;

(j) cryopreserving the infusion bag comprising the harvested TIL population from step (f) using a cryopreservation process; and

(k) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (g) to the subject or patient.

[002146] In some embodiments, the invention provides a method of treating non-small cell lung carcinoma (NSCLC) by administering a population of tumor infiltrating lymphocytes (TILs) to a patient in need thereof, wherein the method comprises:

(a) testing the patient's tumor for PD-L1 expression and tumor proportion score (TPS) of PD-L1,

(b) testing the patient for the absence of one or more driver mutations, wherein the driver mutation is selected from the group consisting of an EGFR mutation, an EGFR insertion, a KRAS mutation, a BRAF mutation, an ALK mutation, a c-ROS mutation (ROS1 mutation), a ROS1 fusion, a RET mutation, or a RET fusion,

(c) determining that the patient has a TPS score for PD-L1 of less than about 1% and determining that the patient also has no driver mutations,

(d) obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments;

(e) adding the first population of TILs into a closed system;

(f) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (f) to step (g) occurs without opening the system;

(h) harvesting therapeutic population of TILs obtained from step (d), wherein the transition from step (d) to step (e) occurs without opening the system; and

(i) transferring the harvested TIL population from step (e) to an infusion bag, wherein the transfer from step (e) to (f) occurs without opening the system;

(j) cryopreserving the infusion bag comprising the harvested TIL population from step (f) using a cryopreservation process; and

(k) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (g) to the subject or patient.

[002147] In some embodiments, the second population of TILs is at least 50-fold greater in number than the first population of TILs,

[002148] In some embodiments, the invention provides a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population described in any of the preceding paragraphs above.

[002149] In some embodiments, the invention provides a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the TIL composition described in any of the preceding paragraphs above.

[002150] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that prior to administering the therapeutically effective dosage of the therapeutic TIL population and the TIL composition described in any of the preceding paragraphs above, respectively, a non-myeloablative lymphodepletion regimen has been administered to the subject.

[002151] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[002152] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified to further comprise the step of treating the subject with a high-dose IL-2 regimen starting on the day after administration of the TIL cells to the subject.

[002153] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the high-dose IL-2 regimen comprises 600,000 or 720,000 IU/kg administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

[002154] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is a solid tumor.

[002155] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, or renal cell carcinoma.

[002156] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is melanoma, HNSCC, cervical cancers, NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[002157] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is melanoma.

[002158] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is HNSCC.

[002159] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is a cervical cancer.

[002160] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is NSCLC.

[002161] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is glioblastoma (including GBM).

[002162] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is gastrointestinal cancer.

[002163] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is a hypermutated cancer.

[002164] In some embodiments, the invention provides the method for treating a subject with cancer described in any of the preceding paragraphs above modified such that the cancer is a pediatric hypermutated cancer.

[002165] In some embodiments, the invention provides the therapeutic TIL population described in any of the preceding paragraphs above for use in a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population.

[002166] In some embodiments, the invention provides the TIL composition described in any of the preceding paragraphs above for use in a method for treating a subject with cancer comprising administering to the subject a therapeutically effective dosage of the TIL composition.

[002167] In some embodiments, the invention provides the therapeutic TIL population described in any of the preceding paragraphs above or the TIL composition described in any of the preceding paragraphs above modified such that prior to administering to the subject the therapeutically effective dosage of the therapeutic TIL population described in any of the preceding paragraphs above or the TIL composition described in any of the preceding paragraphs above, a non-myeloablative lymphodepletion regimen has been administered to the subject.

[002168] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[002169] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified to further comprise the step of treating patient with a high-dose IL-2 regimen starting on the day after administration of the TIL cells to the patient.

[002170] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the high-dose IL-2 regimen comprises 600,000 or 720,000 IU/kg administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

[002171] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is a solid tumor.

[002172] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (NSCLC), lung cancer, bladder cancer, breast cancer, cancer caused by human papilloma virus, head and neck cancer (including head

and neck squamous cell carcinoma (HNSCC)), glioblastoma (including GBM), gastrointestinal cancer, renal cancer, or renal cell carcinoma.

[002173] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is melanoma, HNSCC, cervical cancers, NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[002174] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is melanoma.

[002175] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is HNSCC.

[002176] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is a cervical cancer.

[002177] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is NSCLC.

[002178] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is glioblastoma (including GBM).

[002179] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is gastrointestinal cancer.

[002180] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is a hypermutated cancer.

[002181] In some embodiments, the invention provides the therapeutic TIL population or the TIL composition described in any of the preceding paragraphs above modified such that the cancer is a pediatric hypermutated cancer.

[002182] In some embodiments, the invention provides the use of the therapeutic TIL population described in any of any of the preceding paragraphs above in a method of treating cancer in a subject

comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population.

[002183] In some embodiments, the invention provides the use of the TIL composition described in any of the preceding paragraphs above in a method of treating cancer in a subject comprising administering to the subject a therapeutically effective dosage of the TIL composition.

[002184] In some embodiments, the invention provides the use of the therapeutic TIL population described in any of the preceding paragraphs above or the TIL composition described in any of the preceding paragraphs above in a method of treating cancer in a subject comprising administering to the subject a non-myeloablative lymphodepletion regimen and then administering to the subject the therapeutically effective dosage of the therapeutic TIL population described in any of the preceding paragraphs above or the therapeutically effective dosage of the TIL composition described in any of the preceding paragraphs above.

EXAMPLES

[002185] The embodiments encompassed herein are now described with reference to the following examples. These examples are provided for the purpose of illustration only and the disclosure encompassed herein should in no way be construed as being limited to these examples, but rather should be construed to encompass any and all variations which become evident as a result of the teachings provided herein.

EXAMPLE 1: PREPARATION OF MEDIA FOR PRE-REP AND REP PROCESSES

[002186] This Example describes the procedure for the preparation of tissue culture media for use in protocols involving the culture of tumor infiltrating lymphocytes (TIL) derived from various tumor types including non-small cell lung carcinoma (NSCLC). This media can be used for preparation of any of the TILs described in the present application and Examples.

Preparation of CM1

[002187] Removed the following reagents from cold storage and warmed them in a 37°C water bath: (RPMI1640, Human AB serum, 200mM L-glutamine). Prepared CM1 medium according to Table 37 below by adding each of the ingredients into the top section of a 0.2um filter unit appropriate to the volume to be filtered. Store at 4°C.

TABLE 37: Preparation of CM1

Ingredient	Final concentration	Final Volume 500 ml	Final Volume IL

RPMI1640	NA	450 ml	900 ml
Human AB serum, heat-inactivated 10%	50 ml	100 ml	
200mM L-glutamine	2 mM	5 ml	10 ml
55mM BME	55 µM	0.5 ml	1 ml
50mg/mL gentamicin sulfate	50 µg/mL	0.5 ml	1 ml

[002188] On the day of use, prewarmed required amount of CM1 in 37°C water bath and add 6000 IU/ml IL-2.

[002189] Additional supplementation - as needed according to Table 38.

TABLE 38: Additional supplementation of CM1, as needed.

Supplement	Stock concentration	Dilution	Final concentration
GlutaMAX™	200mM	1:100	2mM
Penicillin/streptomycin	10,000 U/mL penicillin 10,000µg/mL streptomycin	1:100	100 U/mL penicillin 100 µg/mL streptomycin
Amphotericin B	250µg/mL	1:100	2.5µg/mL

Preparation of CM2

[002190] Removed prepared CM1 from refrigerator or prepare fresh CM1 as per Section 7.3 above. Removed AIM-V® from refrigerator and prepared the amount of CM2 needed by mixing prepared CM1 with an equal volume of AIM-V® in a sterile media bottle. Added 3000 IU/mL IL-2 to CM2 medium on the day of usage. Made sufficient amount of CM2 with 3000 IU/mL IL-2 on the day of usage. Labeled the CM2 media bottle with its name, the initials of the preparer, the date it was filtered/prepared, the two-week expiration date and store at 4°C until needed for tissue culture.

Preparation of CM3

[002191] Prepared CM3 on the day it was required for use. CM3 was the same as AIM-V® medium, supplemented with 3000 IU/mL IL-2 on the day of use. Prepared an amount of CM3 sufficient to experimental needs by adding IL-2 stock solution directly to the bottle or bag of AIM-V. Mixed well by gentle shaking. Label bottle with "3000 IU/mL IL-2" immediately after adding to the AIM-V. If there was excess CM3, stored it in bottles at 4°C labeled with the media name, the initials of the preparer, the date the media was prepared, and its expiration date (7 days after preparation). Discarded media supplemented with IL-2 after 7 days storage at 4°C.

Preparation of CM4

[002192] CM4 was the same as CM3, with the additional supplement of 2mM GlutaMAX™ (final concentration). For every 1L of CM3, added 10ml of 200mM GlutaMAX™. Prepared an amount of CM4 sufficient to experimental needs by adding IL-2 stock solution and GlutaMAX™ stock solution directly to the bottle or bag of AIM-V. Mixed well by gentle shaking. Labeled bottle with "3000 IL/nil IL-2 and GlutaMAX" immediately after adding to the AIM-V. If there was excess CM4, stored it in bottles at 4°C labeled with the media name, "GlutaMAX", and its expiration date (7 days after preparation). Discarded media supplemented with IL-2 after 7-days storage at 4°C.

EXAMPLE 2: USE OF IL-2, IL-15, AND IL-21 CYTOKINE COCKTAIL

[002193] This example describes the use of IL-2, IL-15, and IL-21 cytokines, which serve as additional T cell growth factors, in combination with the TIL process of Examples A to G.

[002194] Using the processes described herein, TILs can be grown from non-small cell lung carcinoma (NSCLC) tumors in presence of IL-2 in one arm of the experiment and, in place of IL-2, a combination of IL-2, IL-15, and IL-21 in another arm at the initiation of culture. At the completion of the pre-REP, cultures were assessed for expansion, phenotype, function (CD107a+ and IFN-γ) and TCR Vβ repertoire. IL-15 and IL-21 are described elsewhere herein and in Gruijl, et al., IL-21 promotes the expansion of CD27+CD28+ tumor infiltrating lymphocytes with high cytotoxic potential and low collateral expansion of regulatory T cells, *Santegoets, S. J.,* J Transl Med., **2013,** *11*:37 (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3626797/).

[002195] The results can show that enhanced TIL expansion (>20%), in both $CD4^+$ and $CD8^+$ cells in the IL-2, IL-15, and IL-21 treated conditions can observed relative to the IL-2 only conditions. There was a skewing towards a predominantly $CD8^+$ population with a skewed TCR Vβ repertoire in the TILs obtained from the IL-2, IL-15, and IL-21 treated cultures relative to the IL-2 only cultures. IFN-γ and CD107a were elevated in the IL-2, IL-15, and IL-21 treated TILs, in comparison to TILs treated only IL-2.

EXAMPLE 3: QUALIFYING INDIVIDUAL LOTS OF GAMMA-IRRADIATED PERIPHERAL MONONUCLEAR CELLS

[002196] This Example describes an abbreviated procedure for qualifying individual lots of gamma-irradiated peripheral mononuclear cells (PBMCs, also known as mononuclear cells or MNCs) for use as allogeneic feeder cells in the exemplary methods described herein.

[002197] Each irradiated MNC feeder lot was prepared from an individual donor. Each lot or donor was screened individually for its ability to expand TIL in the REP in the presence of purified anti-CD3 (clone OKT3) antibody and interleukin-2 (IL-2). In addition, each lot of feeder cells was tested without the addition of TIL to verify that the received dose of gamma radiation was sufficient to render them replication incompetent.

[002198] Gamma-irradiated, growth-arrested MNC feeder cells are required for REP of TILs. Membrane receptors on the feeder MNCs bind to anti-CD3 (clone OKT3) antibody and crosslink to TILs in the REP flask, stimulating the TIL to expand. Feeder lots were prepared from the leukapheresis of whole blood taken from individual donors. The leukapheresis product was subjected to centrifugation over Ficoll-Hypaque, washed, irradiated, and cryopreserved under GMP conditions.

[002199] It is important that patients who received TIL therapy not be infused with viable feeder cells as this can result in graft-versus-host disease (GVHD). Feeder cells are therefore growth-arrested by dosing the cells with gamma-irradiation, resulting in double strand DNA breaks and the loss of cell viability of the MNC cells upon re-culture.

[002200] Feeder lots were evaluated on two criteria: (1) their ability to expand TILs in co-culture >100-fold and (2) their replication incompetency.

[002201] Feeder lots were tested in mini-REP format utilizing two primary pre-REP TIL lines grown in upright T25 tissue culture flasks. Feeder lots were tested against two distinct TIL lines, as each TIL line is unique in its ability to proliferate in response to activation in a REP. As a control, a lot of irradiated MNC feeder cells which has historically been shown to meet the criteria above was run alongside the test lots.

[002202] To ensure that all lots tested in a single experiment receive equivalent testing, sufficient stocks of the same pre-REP TIL lines were available to test all conditions and all feeder lots.

[002203] For each lot of feeder cells tested, there was a total of six T25 flasks: Pre-REP TIL line #1 (2 flasks); Pre-REP TIL line #2 (2 flasks); and feeder control (2 flasks). Flasks containing TIL

lines #1 and #2 evaluated the ability of the feeder lot to expand TIL. The feeder control flasks evaluated the replication incompetence of the feeder lot.

A. Experimental Protocol

[002204] Day -2/3, Thaw of TIL lines. Prepare CM2 medium and warm CM2 in 37°C water bath. Prepare 40 mL of CM2 supplemented with 3000 IU/mL IL-2. Keep warm until use. Place 20 mL of pre-warmed CM2 without IL-2 into each of two 50 mL conical tubes labeled with names of the TIL lines used. Removed the two designated pre-REP TIL lines from LN2 storage and transferred the vials to the tissue culture room. Thawed vials by placing them inside a sealed zipper storage bag in a 37°C water bath until a small amount of ice remains.

[002205] Using a sterile transfer pipet, the contents of each vial were immediately transferred into the 20 mL of CM2 in the prepared, labeled 50 mL conical tube. QS to 40 mL using CM2 without IL-2 to wash cells and centrifuged at 400 × CF for 5 minutes. Aspirated the supernatant and resuspend in 5 mL warm CM2 supplemented with 3000 IU/mL IL-2.

[002206] A small aliquot (20 µL) was removed in duplicate for cell counting using an automated cell counter. The counts were recorded. While counting, the 50 mL conical tube with TIL cells was placed into a humidified 37°C, 5% CO_2 incubator, with the cap loosened to allow for gas exchange. The cell concentration was determined, and the TILs were diluted to 1×10^6 cells/mL in CM2 supplemented with IL-2 at 3000 IU/mL.

[002207] Cultured in 2 mL/well of a 24-well tissue culture plate in as many wells as needed in a humidified 37°C incubator until Day 0 of the mini-REP. The different TIL lines were cultured in separate 24-well tissue culture plates to avoid confusion and potential cross-contamination.

[002208] Day 0, initiate Mini-REP. Prepared enough CM2 medium for the number of feeder lots to be tested. (*e.g.*, for testing 4 feeder lots at one time, prepared 800 mL of CM2 medium). Aliquoted a portion of the CM2 prepared above and supplemented it with 3000 IU/mL IL-2 for the culturing of the cells. (*e.g.*, for testing 4 feeder lots at one time, prepare 500 mL of CM2 medium with 3000 IU/mL IL-2).

[002209] Working with each TIL line separately to prevent cross-contamination, the 24-well plate with TIL culture was removed from the incubator and transferred to the BSC.

[002210] Using a sterile transfer pipet or 100-1000 µL pipettor and tip, about 1 mL of medium was removed from each well of TILs to be used and placed in an unused well of the 24-well tissue culture plate.

[002211] Using a fresh sterile transfer pipet or 100-1000 µL pipettor and tip, the remaining medium was mixed with TILs in wells to resuspend the cells and then transferred the cell suspension to a 50 mL conical tube labeled with the TIL lot name and recorded the volume.

[002212] Washed the wells with the reserved media and transferred that volume to the same 50 mL conical tube. Spun the cells at 400 × CF to collect the cell pellet. Aspirated off the media supernatant and resuspend the cell pellet in 2-5 mL of CM2 medium containing 3000 IU/mL IL-2, volume to be used based on the number of wells harvested and the size of the pellet – volume should be sufficient to ensure a concentration of $>1.3 \times 10^6$ cells/mL.

[002213] Using a serological pipet, the cell suspension was mixed thoroughly and the volume was recorded. Removed 200 µL for a cell count using an automated cell counter. While counting, placed the 50 mL conical tube with TIL cells into a humidified, 5% CO_2, 37ºC incubator, with the cap loosened to allow gas exchange. Recorded the counts.

[002214] Removed the 50 mL conical tube containing the TIL cells from the incubator and resuspend them cells at a concentration of 1.3×10^6 cells/mL in warm CM2 supplemented with 3000 IU/mL IL-2. Returned the 50 mL conical tube to the incubator with a loosened cap.

[002215] The steps above were repeated for the second TIL line.

[002216] Just prior to plating the TIL into the T25 flasks for the experiment, TIL were diluted 1:10 for a final concentration of 1.3×10^5 cells/mL as per below.

[002217] Prepare MACS GMP CD3 pure (OKT3) working solution. Took out stock solution of OKT3 (1 mg/mL) from 4°C refrigerator and placed in BSC. A final concentration of 30 ng/mL OKT3 was used in the media of the mini-REP.

[002218] 600 ng of OKT3 were needed for 20 mL in each T25 flask of the experiment; this was the equivalent of 60 µL of a 10 µg/mL solution for each 20 mL, or 360 µL for all 6 flasks tested for each feeder lot.

[002219] For each feeder lot tested, made 400 µL of a 1:100 dilution of 1 mg/mL OKT3 for a working concentration of 10 µg/mL (*e.g.*, for testing 4 feeder lots at one time, make 1600 µL of a 1:100 dilution of 1 mg/mL OKT3: 16 µL of 1 mg/mL OKT3 + 1.584 mL of CM2 medium with 3000 IU/mL IL-2.)

[002220] Prepare T25 flasks. Labeled each flask and filled flask with the CM2 medium prior to preparing the feeder cells. Placed flasks into 37°C humidified 5% CO_2 incubator to keep media warm while waiting to add the remaining components. Once feeder cells were prepared, the components will be added to the CM2 in each flask.

[0003] Further information is provided in Table 39.

TABLE 39. Solution information.

Component	**Volume in co-culture flasks**	**Volume in control (feeder only) flasks**
CM2 + 3000 IU/mL IL-2	18 mL	19 mL
MNC: 1.3×10^7/mL in CM2 + 3000 IU IL-2 (final concentration 1.3×10^7/flask)	1 mL	1 mL
OKT3: 10 µL/mL in CM2 = 3000 IU IL-2	60 µL	60 µL
TIL: 1.3×10^5/mL in CM2 with 3000 IU of IL-2 (final concentration 1.3×10^5/flask)	1 mL	0

[002221] Prepare Feeder Cells. A minimum of 78×10^6 feeder cells were needed per lot tested for this protocol. Each 1 mL vial frozen by SDBB had 100×10^6 viable cells upon freezing. Assuming a 50% recovery upon thaw from liquid N_2 storage, it was recommended to thaw at least two 1 mL vials of feeder cells per lot giving an estimated 100×10^6 viable cells for each REP. Alternately, if supplied in 1.8 mL vials, only one vial provided enough feeder cells.

[002222] Before thawing feeder cells, approximately 50 mL of CM2 without IL-2 was pre-warmed for each feeder lot to be tested. The designated feeder lot vials were removed from LN2 storage, placed in zipper storage bag, and placed on ice. Vials were thawed inside closed zipper storage bag by immersing in a 37°C water bath. Vials were removed from zipper bag, sprayed or wiped with 70% EtOH, and transferred to a BSC.

[002223] Using a transfer pipet, the contents of feeder vials were immediately transferred into 30 mL of warm CM2 in a 50 mL conical tube. The vial was washed with a small volume of CM2 to remove any residual cells in the vial and centrifuged at 400 × CF for 5 minutes. Aspirated the supernatant and resuspended in 4 mL warm CM2 plus 3000 IU/mL IL-2. Removed 200 µL for cell counting using the automated cell counter. Recorded the counts.

[002224] Resuspended cells at 1.3×10^7 cells/mL in warm CM2 plus 3000 IU/mL IL-2. Diluted TIL cells from 1.3×10^6 cells/mL to 1.3×10^5 cells/mL.

[002225] Setup Co-Culture. Diluted TIL cells from 1.3×10^6 cells/mL to 1.3×10^5 cells/mL. Added 4.5 mL of CM2 medium to a 15 mL conical tube. Removed TIL cells from incubator and resuspended well using a 10 mL serological pipet. Removed 0.5 mL of cells from the 1.3×10^6 cells/mL TIL suspension and added to the 4.5 mL of medium in the 15 mL conical tube. Returned TIL stock vial to incubator. Mixed well. Repeated for the second TIL line.

[002226] Transferred flasks with pre-warmed media for a single feeder lot from the incubator to the BSC. Mixed feeder cells by pipetting up and down several times with a 1 mL pipet tip and transferred 1 mL (1.3×10^7 cells) to each flask for that feeder lot. Added 60 µL of OKT3 working stock (10 µg/mL) to each flask. Returned the two control flasks to the incubator.

[002227] Transferred 1 mL (1.3×10^5) of each TIL lot to the correspondingly labeled T25 flask. Returned flasks to the incubator and incubate upright. Did not disturb until Day 5. This procedure was repeated for all feeder lots tested.

[002228] Day 5, Media change. Prepared CM2 with 3000 IU/mL IL-2. 10 mL is needed for each flask. With a 10 mL pipette, transferred 10 mL warm CM2 with 3000 IU/mL IL-2 to each flask. Returned flasks to the incubator and incubated upright until day 7. Repeated for all feeder lots tested.

[002229] Day 7, Harvest. Removed flasks from the incubator and transfer to the BSC, care as taken not to disturb the cell layer on the bottom of the flask. Without disturbing the cells growing on the bottom of the flasks, 10 mL of medium was removed from each test flask and 15 mL of medium from each of the control flasks.

[002230] Using a 10 mL serological pipet, the cells were resuspended in the remaining medium and mix well to break up any clumps of cells. After thoroughly mixing cell suspension by pipetting, removed 200 µL for cell counting. Counted the TIL using the appropriate standard operating procedure in conjunction with the automatic cell counter equipment. Recorded counts in day 7. This procedure was repeated for all feeder lots tested.

[002231] Feeder control flasks were evaluated for replication incompetence and flasks containing TIL were evaluated for fold expansion from day 0.

[002232] Day 7, Continuation of Feeder Control Flasks to Day 14. After completing the day 7 counts of the feeder control flasks, 15 mL of fresh CM2 medium containing 3000 IU/mL IL-2 was added to each of the control flasks. The control flasks were returned to the incubator and incubated in an upright position until day 14.

[002233] Day 14, Extended Non-proliferation of Feeder Control Flasks. Removed flasks from the incubator and transfer to the BSC, care was taken not to disturb the cell layer on the bottom of the

flask. Without disturbing the cells growing on the bottom of the flasks, approximately 17 mL of medium was removed from each control flasks. Using a 5 mL serological pipet, the cells were resuspended in the remaining medium and mixed well to break up any clumps of cells. The volumes were recorded for each flask.

[002234] After thoroughly mixing the cell suspension by pipetting, 200 µL was removed for cell counting. The TIL were counted using the appropriate standard operating procedure in conjunction with the automatic cell counter equipment and the counts were recorded. This procedure was repeated for all feeder lots tested.

B. Results and Acceptance Criteria Protocol

[002235] Results. The dose of gamma irradiation was sufficient to render the feeder cells replication incompetent. All lots were expected to meet the evaluation criteria and also demonstrated a reduction in the total viable number of feeder cells remaining on day 7 of the REP culture compared to day 0. All feeder lots were expected to meet the evaluation criteria of 100-fold expansion of TIL growth by day 7 of the REP culture. Day 14 counts of Feeder Control flasks were expected to continue the non-proliferative trend seen on day 7.

[002236] Acceptance Criteria. The following acceptance criteria were met for each replicate TIL line tested for each lot of feeder cells. Acceptance criteria were two-fold, as shown in Table 40 below.

TABLE 40. Embodiments of acceptance criteria.

Test	**Acceptance criteria**
Irradiation of MNC and Replication Incompetence	No growth observed at 7 and 14 days
TIL expansion	At least a 100-fold expansion of each TIL (minimum of 1.3×10^7 viable cells)

[002237] The dose of radiation was evaluated for its sufficiency to render the MNC feeder cells replication incompetent when cultured in the presence of 30 ng/mL OKT3 antibody and 3000 IU/mL IL-2. Replication incompetence was evaluated by total viable cell count (TVC) as determined by automated cell counting on day 7 and day 14 of the REP.

[002238] The acceptance criteria was "No Growth," meaning the total viable cell number has not increased on day 7 and day 14 from the initial viable cell number put into culture on Day 0 of the REP.

[002239] The ability of the feeder cells to support TIL expansion was evaluated. TIL growth was measured in terms of fold expansion of viable cells from the onset of culture on day 0 of the REP to day 7 of the REP. On day 7, TIL cultures achieved a minimum of 100-fold expansion, (i.e., greater than 100 times the number of total viable TIL cells put into culture on REP day 0), as evaluated by automated cell counting.

[002240] Contingency Testing of MNC Feeder Lots that do not meet acceptance criteria. In the event that an MNC feeder lot did not meet the either of the acceptance criteria outlined above, the following steps will be taken to retest the lot to rule out simple experimenter error as its cause.

[002241] If there are two or more remaining satellite testing vials of the lot, then the lot was retested. If there were one or no remaining satellite testing vials of the lot, then the lot was failed according to the acceptance criteria listed above.

[002242] In order to be qualified, the lot in question and the control lot had to achieve the acceptance criteria above. Upon meeting these criteria, the lot is released for use.

EXAMPLE 4: PREPARATION OF IL-2 STOCK SOLUTION (CELLGENIX)

[002243] This Example describes the process of dissolving purified, lyophilized recombinant human interleukin-2 into stock samples suitable for use in further tissue culture protocols, including all of those described in the present application and Examples, including those that involve using rhIL-2.

Procedure

[002244] Prepared 0.2% Acetic Acid solution (HAc). Transferred 29mL sterile water to a 50mL conical tube. Added lmL 1N acetic acid to the 50mL conical tube. Mixed well by inverting tube 2-3 times. Sterilized the HAc solution by filtration using a Steriflip filter

[002245] Prepare 1% HSA in PBS. Added 4mL of 25% HSA stock solution to 96mL PBS in a 150mL sterile filter unit. Filtered solution. Stored at 4°C. For each vial of rhIL-2 prepared, fill out forms.

[002246] Prepared rhIL-2 stock solution (6×10^6 IU/mL final concentration). Each lot of rhIL-2 was different and required information found in the manufacturer's Certificate of Analysis (COA), such as: 1) Mass of rhIL-2 per vial (mg), 2) Specific activity of rhIL-2 (IU/mg) and 3) Recommended 0.2% HAc reconstitution volume (mL).

[002247] Calculated the volume of 1% HSA required for rhIL-2 lot by using the equation below:

$$\left(\frac{Vial\ Mass\ (mg)\ x\ Biological\ Activity\ (\frac{IU}{mg})}{6x10^6\ \frac{IU}{mL}}\right) - HAc\ vol\ (mL) = 1\%\ HSA\ vol\ (mL)$$

[002248] For example, according to CellGenix's rhIL-2 lot 10200121 COA, the specific activity for the lmg vial is $25x10^6$ IU/mg. It recommends reconstituting the rhIL-2 in 2mL 0.2% HAc.

$$\left(\frac{1mg\ x\ 25x10^6\ \frac{IU}{mg}}{6x10^6\ \frac{IU}{mL}}\right) - 2mL = 2.167mL\ HSA$$

[002249] Wiped rubber stopper of IL-2 vial with alcohol wipe. Using a 16G needle attached to a 3mL syringe, injected recommended volume of 0.2% HAc into vial. Took care to not dislodge the stopper as the needle is withdrawn. Inverted vial 3 times and swirled until all powder is dissolved. Carefully removed the stopper and set aside on an alcohol wipe. Added the calculated volume of 1% HSA to the vial.

[002250] Storage of rhIL-2 solution. For short-term storage (<72hrs), stored vial at 4°C. For long-term storage (>72hrs), aliquoted vial into smaller volumes and stored in cryovials at -20°C until ready to use. Avoided freeze/thaw cycles. Expired 6 months after date of preparation. Rh-IL-2 labels included vendor and catalog number, lot number, expiration date, operator initials, concentration and volume of aliquot.

EXAMPLE 5: CRYOPRESERVATION PROCESS

[002251] This example describes a cryopreservation process method for TILs prepared with the procedure described herein using the CryoMed Controlled Rate Freezer, Model 7454 (Thermo Scientific).

[002252] The equipment used was as follows: aluminum cassette holder rack (compatible with CS750 freezer bags), cryostorage cassettes for 750 mL bags, low pressure (22 psi) liquid nitrogen tank, refrigerator, thermocouple sensor (ribbon type for bags), and CryoStore CS750 freezing bags (OriGen Scientific).

[002253] The freezing process provides for a 0.5 °C rate from nucleation to -20 °C and 1 °C per minute cooling rate to -80 °C end temperature. The program parameters are as follows: Step 1 - wait at 4 °C; Step 2: 1.0 °C/min (sample temperature) to -4 °C; Step 3: 20.0 °C/min (chamber temperature) to -45 °C; Step 4: 10.0 °C/min (chamber temperature) to -10.0 °C; Step 5: 0.5 °C/min (chamber temperature) to -20 °C; and Step 6: 1.0 °C/min (sample temperature) to -80 °C.

EXAMPLE 6: TUMOR EXPANSION PROCESSES WITH DEFINED MEDIUM

[002254] The processes disclosed above may be performed substituting the CM1 and CM2 media with a defined medium according (*e.g.*, CTS™ OpTmizer™ T-Cell Expansion SFM, ThermoFisher, including for example DM1 and DM2).

EXAMPLE 7: NSCLC TREATMENT WITH ANTI-PD-1 ANTIBODIES

Patient population:

[002255] Treatment naïve NSCLC or post chemotherapy but anti-PD-1/PD-L1 naïve

Treatment schedules:

[002256] Tumor fragment, treat with up to 4 doses of anti-PD-1/PD-L1, treat the primary refractory patients with TIL product which is cryo-preserved and ready for use upon immediate progression. Primary refractory patients may have progressed after 2 doses.

[002257] Relapse patients can also be treated upon progression (the timing may vary from months to years later).

[002258] Full strength IL-2 up to 6 doses.

[002259] Patient populations to further consider with the same manufacturing permutations noted earlier:

- Treatment naïve NSCLC or post chemotherapy but anti-PD-1/PD-L1 naïve
- Treatment naïve NSCLC or post chemotherapy but anti-PD-1/PD-L1 naïve who have low expression of PD-L1
- Treatment naïve NSCLC or post chemotherapy but anti-PD-1/PD-L1 naïve who have low expression of PD-L1 and/or have bulky disease at baseline (for example, bulky disease is

indicated where the maximal tumor diameter is greater than 7 cm measured in either the transverse or coronal plane or swollen lymph nodes with a short-axis diameter of 20 mm or greater on CT were defined as bulky; see for example, Samejima, J., *Japanese Journal of Clinical Oncology*, 45(11): 1050–10541 2015, incorporated herein by referece)

EXAMPLE 8: EXEMPLARY GEN 2 PRODUCTION OF A CRYOPRESERVED TIL CELL THERAPY

[002260] This example describes the the cGMP manufacture of Iovance Biotherapeutics, Inc. TIL Cell Therapy Process in G-REX Flasks according to current Good Tissue Practices and current Good Manufacturing Practices. This example describes an exemplary cGMP manufacture of TIL Cell Therapy Process in G-REX Flasks according to current Good Tissue Practices and current Good Manufacturing Practices.

TABLE 41. Process Expansion Exemplary Plan.

Estimated Day (post-seed)	Activity	Target Criteria	Anticipated Vessels	Estimated Total Volume (mL)
0	Tumor Dissection	≤ 50 desirable tumor fragments per G-REX-100MCS	G-REX-100MCS 1 flask	≤1000
11	REP Seed	5 – 200 × 10^6viable cells per G-REX-500MCS	G-REX-500MCS 1 flasks	≤5000
16	REP Split	1 × 10^9viable cells per G-REX-500MCS	G-REX-500MCS ≤5 flasks	≤25000
22	Harvest	Total available cells	3-4 CS-750 bags	≤530

TABLE 42. Flask Volumes.

Flask Type	Working Volume/Flask
G-REX-100MCS	1000
G-REX-500MCS	5000

[002261] Day 0 CM1 Media Preparation. In the BSC added reagents to RPMI 1640 Media bottle. Added the following reagents t Added per bottle: Heat Inactivated Human AB Serum (100.0 mL); GlutaMax™ (10.0 mL); Gentamicin sulfate, 50 mg/mL (1.0 mL); 2-mercaptoethanol (1.0 mL)

[002262] Removed unnecessary materials from BSC. Passed out media reagents from BSC, left Gentamicin Sulfate and HBSS in BSC for Formulated Wash Media preparation.

[002263] Thawed IL-2 aliquot. Thawed one 1.1 mL IL-2 aliquot ($6x10^6$ IU/mL) (BR71424) until all ice had melted. Recorded IL-2: Lot # and Expiry

[002264] Transferred IL-2 stock solution to media. In the BSC, transferred 1.0 mL of IL-2 stock solution to the CM1 Day 0 Media Bottle prepared. Added CM1 Day 0 Media 1 bottle and IL-2 (6x106 IU/mL) 1.0 mL.

[002265] Passed G-REX100MCS into BSC. Aseptically passed G-REX100MCS (W3013130) into the BSC.

[002266] Pumped all Complete CM1 Day 0 Media into G-REX100MCS flask. Tissue Fragments Conical or GRex100MCS .

[002267] Day 0 Tumor Wash Media Preparation. In the BSC, added 5.0 mL Gentamicin (W3009832 or W3012735) to 1 x 500 mL HBSS Media (W3013128) bottle. Added per bottle: HBSS (500.0 mL); Gentamicin sulfate, 50 mg/mL (5.0 mL). Filtered HBSS containing gentamicin prepared through a 1L 0.22-micron filter unit (W1218810).

[002268] Day 0 Tumor Processing. Obtained tumor specimen and transferred into suite at 2-8 °C immediately for processing. Aliquoted tumor wash media. Tumor wash 1 is performed using 8" forceps (W3009771). The tumor is removed from the specimen bottle and transferred to the "Wash 1" dish prepared. This is followed by tumor wash 2 and tumor wash 3. Measured and assessed tumor. Assessed whether > 30% of entire tumor area observed to be necrotic and/or fatty tissue. Clean up dissection if applicable. If tumor was large and >30% of tissue exterior was observed to be necrotic/fatty, performed "clean up dissection" by removing necrotic/fatty tissue while preserving tumor inner structure using a combination of scalpel and/or forceps. Dissect tumor. Using a combination of scalpel and/or forceps, cut the tumor specimen into even, appropriately sized fragments (up to 6 intermediate fragments). Transferred intermediate tumor fragments. Dissected tumor fragments into pieces approximately 3x3x3mm in size. Stored Intermediate Fragments to prevent drying. Repeated intermediate fragment dissection. Determined number of pieces collected. If desirable tissue remains, selected additional favorable tumor pieces from the "favorable intermediate fragments" 6-well plate to fill the drops for a maximum of 50 pieces.

[002269] Prepared conical tube. Transferred tumor pieces to 50 mL conical tube. Prepared BSC for G-REX100MCS. Removed G-REX100MCS from incubator. Aseptically passed G-REX100MCS flask into the BSC. Added tumor fragments to G-REX100MCS flask. Evenly distributed pieces.

[002270] Incubated G-REX100MCS at the following parameters: Incubated G-REX flask: Temperature LED Display: 37.0±2.0 °C; CO_2 Percentage: 5.0±1.5 %CO_2. Calculations: Time of incubation; lower limit = time of incubation + 252 hours; upper limit = time of incubation + 276 hours.

[002271] After process was complete, discarded any remaining warmed media and thawed aliquots of IL-2.

[002272] Day 11 – Media Preparation. Monitored incubator. Incubator parameters: Temperature LED Display: 37.0±2.0 °C; CO2 Percentage: 5.0±1.5 %CO2.

[002273] Warmed 3× 1000 mL RPMI 1640 Media (W3013112) bottles and 3× 1000 mL AIM-V (W3009501) bottles in an incubator for ≥ 30 minutes. Removed RPMI 1640 Media from incubator. Prepared RPMI 1640 Media. Filter Media. Thawed 3 x 1.1 mL aliquots of IL-2 (6x106 IU/mL) (BR71424). Removed AIM-V Media from the incubator. Add IL-2 to AIM-V. Aseptically transferred a 10 L Labtainer Bag and a repeater pump transfer set into the BSC.

[002274] Prepared 10 L Labtainer media bag. Prepared Baxa pump. Prepared 10L Labtainer media bag. Pumped media into 10 L Labtainer. Removed pumpmatic from Labtainer bag.

[002275] Mixed media. Gently massaged the bag to mix. Sample media per sample plan. Removed 20.0 mL of media and place in a 50 mL conical tube. Prepared cell count dilution tubes. In the BSC, added 4.5 mL of AIM-V Media that had been labelled with "For Cell Count Dilutions" and lot number to four 15 mL conical tubes. Transferred reagents from the BSC to 2-8°C. Prepared 1 L Transfer Pack. Outside of the BSC weld (per Process Note 5.11) a 1L Transfer Pack to the transfer set attached to the "Complete CM2 Day 11 Media" bag prepared. Prepared feeder cell transfer pack. Incubated Complete CM2 Day 11 Media.

[002276] Day 11 - TIL Harvest. Preprocessing table. Incubator parameters: Temperature LED display: 37.0±2.0 °C; CO_2 Percentage: 5.0±1.5 % CO_2. Removed G-REX100MCS from incubator. Prepared 300 mL Transfer Pack. Welded transfer packs to G-REX100MCS.

[002277] Prepare flask for TIL Harvest and initiation of TIL Harvest. TIL Harvested. Using the GatheRex, transferred the cell suspension through the blood filter into the 300 mL transfer pack. Inspect membrane for adherent cells.

[002278] Rinsed flask membrane. Closed clamps on G-REX100MCS. Ensured all clamps are closed. Heat sealed the TIL and the "Supernatant" transfer pack. Calculated volume of TIL suspension. Prepared Supernatant Transfer Pack for Sampling.

[002279] Pulled Bac-T Sample. In the BSC, draw up approximately 20.0 mL of supernatant from the 1L "Supernatant" transfer pack and dispense into a sterile 50 mL conical tube.

[002280] Inoculated BacT per Sample Plan. Removed a 1.0 mL sample from the 50 mL conical labeled BacT prepared using an appropriately sized syringe and inoculated the anaerobic bottle.

[002281] Incubated TIL. Placed TIL transfer pack in incubator until needed. Performed cell counts and calculations. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Viability ÷ 2. Viable Cell Concentration ÷ 2. Determined Upper and Lower Limit for counts. Lower Limit: Average of Viable Cell Concentration x 0.9. Upper Limit: Average of Viable Cell Concentration x 1.1. Confirmed both counts within acceptable limits. Determined an average Viable Cell Concentration from all four counts performed.

[002282] Adjusted Volume of TIL Suspension: Calculate the adjusted volume of TIL suspension after removal of cell count samples. Total TIL Cell Volume (A). Volume of Cell Count Sample Removed (4.0 mL) (B) Adjusted Total TIL Cell Volume C=A-B.

[002283] Calculated Total Viable TIL Cells. Average Viable Cell Concentration*: Total Volume; Total Viable Cells: C = A x B.

[002284] Calculation for flow cytometry: if the Total Viable TIL Cell count from was ≥ $4.0x10^7$, calculated the volume to obtain 1.0×10^7cells for the flow cytometry sample.

[002285] Total viable cells required for flow cytometry: 1.0×10^7cells. Volume of cells required for flow cytometry: Viable cell concentration divided by 1.0×10^7cells A.

[002286] Calculated the volume of TIL suspension equal to 2.0×10^8viable cells. As needed, calculated the excess volume of TIL cells to remove and removed excess TIL and placed TIL in incubator as needed. Calculated total excess TIL removed, as needed.

[002287] Calculated amount of CS-10 media to add to excess TIL cells with the target cell concentration for freezing is 1.0×10^8 cells/mL. Centrifuged excess TILs, as needed. Observed conical tube and added CS-10.

[002288] Filled Vials. Aliquoted 1.0 mL cell suspension, into appropriately sized cryovials. Aliquoted residual volume into appropriately sized cryovial. If volume is ≤0.5 mL, add CS10 to vial until volume is 0.5 mL.

[002289] Calculated the volume of cells required to obtain $1x10^7$cells for cryopreservation. Removed sample for cryopreservation. Placed TIL in incubator.

[002290] Cryopreservation of sample. Observed conical tube and added CS-10 slowly and record volume of 0.5 mL of CS10 added.

[002291] Day 11 - Feeder Cells. Obtained feeder cells. Obtained 3 bags of feeder cells with at least two different lot numbers from LN2 freezer. Kept cells on dry ice until ready to thaw. Prepared water bath or cryotherm. Thawed feeder cells at 37.0 ± 2.0°C in the water bath or cytotherm for ~3-5 minutes or until ice has just disappeared. Removed media from incubator. Pooled thawed feeder cells. Added feeder cells to transfer pack. Dispensed the feeder cells from the syringe into the transfer pack. Mixed pooled feeder cells and labeled transfer pack.

[002292] Calculated total volume of feeder cell suspension in transfer pack. Removed cell count samples. Using a separate 3 mL syringe for each sample, pulled 4x1.0 mL cell count samples from Feeder Cell Suspension Transfer Pack using the needless injection port. Aliquoted each sample into the cryovials labeled. Performed cell counts and determine multiplication factors, elected protocols and entered multiplication factors. Determined the average of viable cell concentration and viability of the cell counts performed. Determined upper and lower limit for counts and confirm within limits.

[002293] Adjusted volume of feeder cell suspension. Calculated the adjusted volume of feeder cell suspension after removal of cell count samples. Calculated total viable feeder cells. Obtained additional feeder cells as needed. Thawed additional feeder cells as needed. Placed the 4th feeder cell bag into a zip top bag and thaw in a 37.0 ± 2.0°C water bath or cytotherm for ~3-5 minutes and pooled additional feeder cells. Measured volume. Measured the volume of the feeder cells in the syringe and recorded below (B). Calculated the new total volume of feeder cells. Added feeder cells to transfer pack.

[002294] Prepared dilutions as needed, adding 4.5 mL of AIM-V Media to four 15 mL conical tubes. Prepared cell counts. Using a separate 3 mL syringe for each sample, removed 4 x 1.0 mL cell count samples from Feeder Cell Suspension transfer pack, using the needless injection port. Performed cell counts and calculations. Determined an average viable cell concentration from all four counts performed. Adjusted volume of feeder cell suspension and calculated the adjusted volume of feeder cell suspension after removal of cell count samples. Total Feeder Cell Volume minues 4.0 mL removed. Calculated the volume of Feeder Cell Suspension that was required to obtain $5x10^9$viable feeder cells. Calculated excess feeder cell volume. Calculated the volume of excess feeder cells to remove. Removed excess feeder cells.

[002295] Using a 1.0 mL syringe and 16G needle, drew up 0.15 mL of OKT3 and added OKT3. Heat sealed the feeder cell suspension transfer pack.

[002296] Day 11 G-REX Fill and Seed Set up G-REX500MCS. Removed "Complete CM2 Day 11 Media", from incubator and pumped media into G-REX500MCS. Pumped 4.5L of media into the G-REX500MCS, filling to the line marked on the flask. Heat sealed and incubated flask as needed. Welded the Feeder Cell suspension transfer pack to the G-REX500MCS. Added Feeder Cells to G-REX500MCS. Heat sealed. Welded the TIL Suspension transfer pack to the flask. Added TIL to G-REX500MCS. Heat sealed. Incubated G-REX500MCS at 37.0±2.0 °C, CO2 Percentage: 5.0±1.5 %CO2.

[002297] Calculated incubation window. Performed calculations to determine the proper time to remove G-REX500MCS from incubator on Day 16. Lower limit: Time of incubation + 108 hours. Upper limit: Time of incubation + 132 hours.

[002298] Day 11 Excess TIL Cryopreservation. Applicable: Froze Excess TIL Vials. Verified the CRF has been set up prior to freeze. Perform Cryopreservation. Transferred vials from Controlled Rate Freezer to the appropriate storage. Upon completion of freeze, transfer vials from CRF to the appropriate storage container. Transferred vials to appropriate storage. Recorded storage location in LN2.

[002299] Day 16 Media Preparation. Pre-warmed AIM-V Media. Calculated time Media was warmed for media bags 1, 2, and 3. Ensured all bags have been warmed for a duration between 12 and 24 hours. Setup 10L Labtainer for Supernatant. Attached the larger diameter end of a fluid pump transfer set to one of the female ports of a 10L Labtainer bag using the Luer connectors. Setup 10L Labtainer for Supernatant and label. Setup 10L Labtainer for Supernatant. Ensure all clamps were closed prior to removing from the BSC. NOTE: Supernatant bag was used during TIL Harvest, which may be performed concurrently with media preparation.

[002300] Thawed IL-2. Thawed 5×1.1 mL aliquots of IL-2 (6×10^6 IU/mL) (BR71424) per bag of CTS AIM V media until all ice had melted. Aliquoted 100.0 mL GlutaMax™. Added IL-2 to GlutaMax™. Prepared CTS AIM V media bag for formulation. Prepared CTS AIM V media bag for formulation. Stage Baxa Pump. Prepared to formulate media. Pumped GlutaMax™ +IL-2 into bag. Monitored parameters: Temperature LED Display: 37.0±2.0 °C, CO_2 Percentage: 5.0±1.5% CO_2. Warmed Complete CM4 Day 16 Media. Prepared Dilutions.

[002301] Day 16 REP Spilt. Monitored Incubator parameters: Temperature LED display: 37.0±2.0 °C, CO_2 Percentage: 5.0±1.5 %CO_2. Removed G-REX500MCS from the incubator. Prepared and labeled 1 L Transfer Pack as TIL Suspension and weighed 1L.

[002302] Volume Reduction of G-REX500MCS. Transferred ~4.5L of culture supernatant from the G-REX500MCS to the 10L Labtainer.

[002303] Prepared flask for TIL harvest. After removal of the supernatant, closed all clamps to the red line.

[002304] Initiation of TIL Harvest. Vigorously tap flask and swirl media to release cells and ensure all cells have detached.

[002305] TIL Harvest. Released all clamps leading to the TIL suspension transfer pack. Using the GatheRex transferred the cell suspension into the TIL Suspension transfer pack. NOTE: Be sure to maintain the tilted edge until all cells and media are collected. Inspected membrane for adherent cells. Rinsed flask membrane. Closed clamps on G-REX500MCS. Heat sealed the Transfer Pack containing the TIL. Heat sealed the 10L Labtainer containing the supernatant. Recorded weight of Transfer Pack with cell suspension and calculate the volume suspension. Prepared transfer pack for sample removal. Removed testing samples from cell supernatant.

[002306] Sterility & BacT testing sampling. Removed a 1.0 mL sample from the 15 mL conical labeled BacT prepared. Removed Cell Count Samples. In the BSC, using separate 3 mL syringes for each sample, removed 4x1.0 mL cell count samples from "TIL Suspension" transfer pack.

[002307] Removed mycoplasma samples. Using a 3 mL syringe, removed 1.0 mL from TIL Suspension transfer pack and place into 15 mL conical labeled "Mycoplasma diluent" prepared.

[002308] Prepared transfer pack for seeding. Placed TIL in incubator. Removed cell suspension from the BSC and place in incubator until needed. Performed cell counts and calculations. Diluted cell count samples initially by adding 0.5 mL of cell suspension into 4.5 mL of AIM-V media prepared which gave a 1:10 dilution. Determined the average of viable cell concentration and viability of the cell counts performed. Determined upper and lower limit for counts. Note: dilution may be adjusted according based off the expected concentration of cells. Determined an average viable cell concentration from all four counts performed. Adjusted volume of TIL suspension. Calculated the adjusted volume of TIL suspension after removal of cell count samples. Total TIL cell volume minus 5.0 mL removed for testing.

[002309] Calculated total viable TIL cells. Calculated the total number of flasks to seed. NOTE: The maximum number of G-REX500MCS flasks to seed was five. If the calculated number of flasks to seed exceeded five, only five were seeded using the entire volume of cell suspension available.

[002310] Calculate number of flasks for subculture. Calculated the number of media bags required in addition to the bag prepared. Prepared one 10L bag of "CM4 Day 16 Media" for every two G-REX-500M flask needed as calculated. Proceeded to seed the first GREX-500M flask(s) while additional media is prepared and warmed. Prepared and warmed the calculated number of additional

media bags determined. Filled G-REX500MCS. Prepared to pump media and pumped 4.5L of media into G-REX500MCS. Heat Sealed. Repeated Fill. Incubated flask. Calculated the target volume of TIL suspension to add to the new G-REX500MCS flasks. If the calculated number of flasks exceeds five only five will be seeded, USING THE ENTIRE VOLUME OF CELL SUSPENSION. Prepared Flasks for Seeding. Removed G-REX500MCS from the incubator. Prepared G-REX500MCS for pumping. Closed all clamps on except large filter line. Removed TIL from incubator. Prepared cell suspension for seeding. Sterile welded (per Process Note 5.11) "TIL Suspension" transfer pack to pump inlet line. Placed TIL suspension bag on a scale.

[002311] Seeded flask with TIL Suspension. Pump the volume of TIL suspension calculated into flask. Heat sealed. Filled remaining flasks.

[002312] Monitored Incubator. Incubator parameters: Temperature LED Display: 37.0±2.0 °C, CO_2 Percentage: 5.0±1.5 % CO_2. Incubated Flasks.

[002313] Determined the time range to remove G-REX500MCS from incubator on Day 22.

[002314] Day 22 Wash Buffer Preparation. Prepared 10 L Labtainer Bag. In BSC, attach a 4" plasma transfer set to a 10L Labtainer Bag via luer connection. Prepared 10 L Labtainer Bag. Closed all clamps before transferring out of the BSC. NOTE: Prepared one 10L Labtainer Bag for every two G-REX500MCS flasks to be harvested. Pumped Plasmalyte into 3000 mL bag and removed air from 3000 mL Origen bag by reversing the pump and manipulating the position of the bag. Added human albumin 25% to 3000 mL Bag. Obtain a final volumeof 120.0 mL of human albumin 25%.

[002315] Prepared IL-2 diluent. Using a 10 mL syringe, removed 5.0 mL of LOVO Wash Buffer using the needleless injection port on the LOVO Wash Buffer bag. Dispensed LOVO wash buffer into a 50 mL conical tube.

[002316] CRF blank bag LOVO wash buffer aliquotted. Using a 100 mL syringe, drew up 70.0 mL of LOVO Wash Buffer from the needleless injection port.

[002317] Thawed one 1.1 mL of IL-2 (6x106 IU/mL), until all ice has melted. Added 50 µL IL-2 stock (6×10^6 IU/mL) to the 50 mL conical tube labeled "IL-2 Diluent."

[002318] Cryopreservation preparation. Placed 5 cryo-cassettes at 2-8°C to precondition them for final product cryopreservation.

[002319] Prepared cell count dilutions. In the BSC, added 4.5 mL of AIM-V Media that has been labelled with lot number and "For Cell Count Dilutions" to 4 separate 15 mL conical tubes. Prepared cell counts. Labeled 4 cryovials with vial number (1-4). Kept vials under BSC to be used.

[002320] Day 22 TIL Harvest. Monitored Incubator. Incubator Parameters Temperature LED display: 37 ± 2.0°C, CO2 Percentage: 5%±1.5%. Removed G-REX500MCS Flasks from Incubator. Prepared TIL collection bag and labeled. Sealed off extra connections. Volume Reduction: Transferred ~4.5L of supernatant from the G-REX500MCS to the Supernatant bag.

[002321] Prepared flask for TIL harvest. Initiated collection of TIL. Vigorously tap flask and swirl media to release cells. Ensure all cells have detached. Initiated collection of TIL. Released all clamps leading to the TIL suspension collection bag. TIL Harvest. Using the GatheRex, transferred the TIL suspension into the 3000 mL collection bag. Inspect membrane for adherent cells. Rinsed flask membrane. Closed clamps on G- Rex500MCS and ensured all clamps are closed. Transferred cell suspension into LOVO source bag. Closed all clamps. Heat Sealed. Removed 4x1.0 mL Cell Counts Samples

[002322] Performed Cell Counts. Performed cell counts and calculations utilizing NC-200 and Process Note 5.14. Diluted cell count samples initially by adding 0.5 mL of cell suspension into 4.5 mL of AIM-V media prepared. This gave a 1:10 dilution. Determined the average viability, viable cell concentration, and total nucleated cell concentration of the cell counts performed. Determined Upper and Lower Limit for counts. Determined the average viability, viable cell concentration, and total nucleated cell concentration of the cell counts performed. Weighed LOVO source bag. Calculated total viable TIL Cells. Calculated total nucleated cells.

[002323] Prepared Mycoplasma Diluent. Removed 10.0 mL from one supernatant bag via luer sample port and placed in a 15 mL conical.

[002324] Performed "TIL G-REX Harvest" protocol and determined the final product target volume. Loaded disposable kit. Removed filtrate bag. Entered Filtrate capacity. Placed Filtrate container on benchtop. Attached PlasmaLyte. Verified that the PlasmaLyte was attached and observed that the PlasmaLyte is moving. Attached Source container to tubing and verified Source container was attached. Confirmed PlasmaLyte was moving.

[002325] Final Formulation and Fill. Target volume/bag calculation. Calculated volume of CS-10 and LOVO wash buffer to formulate blank bag. Prepared CRF Blank.

[002326] Calculated the volume of IL-2 to add to the Final Product. Final IL-2 Concentration desired (IU/mL) – 300IU/mL. IL-2 working stock: 6×10^4 IU/mL. Assembled connect apparatus. Sterile welded a 4S-4M60 to a CC2 cell connection. Sterile welded the CS750 cryobags to the harness prepared. Welded CS-10 bags to spikes of the 4S-4M60. Prepared TIL with IL-2. Using an appropriately sized syringe, removed amount of IL-2 determined from the "IL-2 $6x10^4$" aliquot. Labeled forumlated TIL Bag. Added the formulated TIL bag to the apparatus. Added CS10. Switched

Syringes. Drew ~10 mL of air into a 100 mL syringe and replaced the 60 mL syringe on the apparatus. Added CS10. Prepared CS-750 bags. Dispensed cells.

[002327] Removed air from final product bags and take retain. Once the last final product bag was filled, closed all clamps. Drew 10 mL of air into a new 100 mL syringe and replace the syringe on the apparatus. Dispensed retain into a 50 mL conical tube and label tube as "Retain" and lot number. Repeat air removal step for each bag.

[002328] Prepared final product for cryopreservation, including visual inspection. Held the cryobags on cold pack or at 2-8°C until cryopreservation.

[002329] Removed cell count sample. Using an appropriately sized pipette, remove 2.0 mL of retain and place in a 15 mL conical tube to be used for cell counts. Performed cell counts and calculations. NOTE: Diluted only one sample to appropriate dilution to verify dilution is sufficient. Diluted additional samples to appropriate dilution factor and proceed with counts. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Determined Upper and Lower Limit for counts. NOTE: Dilution may be adjusted according based off the expected concentration of cells. Determined the Average of Viable Cell Concentration and Viability. Determined Upper and Lower Limit for counts. Calculated IFN-γ. Heat Sealed Final Product bags.

[002330] Labeled and collected samples per exemplary sample plan below.

TABLE 43. Sample plan.

Sample	Number of Containers	Sample Volume to Add to Each	Container Type
*Mycoplasma	1	1.0 mL	15 mL Conical
Endotoxin	2	1.0 mL	2 mL Cryovial
Gram Stain	1	1.0 mL	2 mL Cryovial
IFN-γ	1	1.0 mL	2 mL Cryovial
Flow Cytometry	1	1.0 mL	2 mL Cryovial
**Bac-T Sterility	2	1.0 mL	Bac-T Bottle
QC Retain	4	1.0 mL	2 mL Cryovial
Satellite Vials	10	0.5 mL	2 mL Cryovial

[002331] Sterility and BacT testing. Testing Sampling. In the BSC, remove a 1.0 mL sample from the retained cell suspension collected using an appropriately sized syringe and inoculate the anaerobic bottle. Repeat the above for the aerobic bottle.

[002332] Final Product Cryopreservation. Prepared controlled rate freezer (CRF). Verified the CRF had been set up. Set up CRF probes. Placed final product and samples in CRF. Determined the time needed to reach 4 °C ± 1.5 °C and proceed with the CRF run. CRF completed and stored. Stopped the CRF after the completion of the run. Remove cassettes and vials from CRF. Transferred cassettes and vials to vapor phase LN2 for storage. Recorded storage location.

[002333] Post-Processing and analysis of final drug product included the following tests: (Day 22) Determination of CD3+ cells on Day 22 REP by flow cytometry; (Day 22) Gram staining method (GMP); (Day 22) Bacterial endotoxin test by Gel Clot LAL Assay (GMP); (Day 16) BacT Sterility Assay (GMP); (Day 16) Mycoplasma DNA detection by TD-PCR (GMP); Acceptable appearance attributes; (Day 22) BacT sterility assay (GMP)(Day 22); (Day 22) IFN-gamma assay. Other potency assay as described herein are also employed to analyze TIL products.

EXAMPLE 9: AN EXEMPLARY EMBODIMENT OF THE GEN 3 EXPANSION PLATFORM

DAY 0

[002334] Prepared tumor wash media. Media warmed prior to start. Added 5 mL of gentamicin (50mg/mL) to the 500 mL bottle of HBSS. Added 5mL of Tumor Wash Media to a 15mL conical to be used for OKT3 dilution. Prepared feeder cell bags. Sterilely transfered feeder cells to feeder cell bags and stored at 37 °C until use or freeze. Counted feeder cells if at 37 °C. Thawed and then counted feeder cells if frozen.

[002335] Optimal range for the feeder cell concentration is between 5×10^4 and 5×10^6 cells/mL. Prepared four conical tubes with 4.5 mL of AIM-V. Added 0.5 mL of cell fraction for each cell count. If total viable feeder cell number was $\geq 1 \times 10^9$ cells, proceeded to adjust the feeder cell concentration. Calculated the volume of feeder cells to remove from the first feeder cell bag in order to add 1×10^9 cells to a second feeder cell bag.

[002336] Using the p1000 micropipette, transferred 900 µL of Tumor Wash Media to the OKT3 aliquot (100µL). Using a syringe and sterile technique, drew up 0.6 mL of OKT3 and added into the second feeder cell bag. Adjusted media volume to a total volume of 2L. Transferred the second feeder cells bag to the incubator.

[002337] OKT3 formulation details: OKT3 may be aliquoted and frozen in original stock concentration from the vial (1 mg/mL) in 100 µL aliquots. ~10X aliquots per 1 mL vial. Stored at -80C. Day 0: 15 µg/flask, *i.e.* 30 ng/mL in 500 mL – 60 µL max ~ 1 aliquot.

[002338] Added 5 mL of Tumor Wash Medium into all wells of the 6-well plate labelled Excess Tumor Pieces. Kept the Tumor Wash Medium available for further use in keeping the tumor hydrated during dissection. Added 50 mL of Tumor Wash Medium to each 100 mm petri dish.

[002339] Dissected the tumor into 27 mm^3 fragments (3×3×3mm), using the ruler under the Dissection dish lid as a reference. Dissected intermediate fragment until 60 fragments were reached. Counted total number of final fragments and prepared G-REX-100MCS flasks according to the number of final fragments generated (generally 60 fragments per flask).

[002340] Retained favorable tissue fragments in the conical tubes labeled as Fragments Tube 1 through Fragments Tube 4. Calculated the number of G-REX-100MCS flasks to seed with feeder cell suspension according to the number of fragments tubes originated.

[002341] Removed feeder cells bag from the incubator and seed the G-REX-100MCS. Label as D0 (Day 0).

[002342] Tumor fragment addition to culture in G-REX-100 MCS. Under sterile conditions, unscrewed the cap of the G-REX-100MCS labelled Tumor Fragments Culture (D0) 1 and the 50 mL conical tube labelled Fragments Tube. Swirled the opened Fragments Tube 1 and, at the same time, slightly lifted the cap of the G-REX100MCS. Added the medium with the fragments to the G-REX100MCS while being swirled. Recorded the number of fragments transferred into the G-REX100MCS.

[002343] Once the fragments were located at the bottom of the GREX flask, drew 7 mL of media and created seven 1 mL aliquots – 5 mL for extended characterization and 2 mL for sterility samples. Stored the 5 aliquots (final fragment culture supernatant) for extended characterization at -20°C until needed.

[002344] Inoculated one anaerobic BacT/Alert bottle and one aerobic BacT/Alert bottle each with 1 mL of final fragment culture supernatant. Repeat for each flask sampled.

AT DAY 7-8

[002345] Prepared feeder cell bags. Thawed feeder bags for 3-5 minutes in 37°C water bath when frozen. Counted feeder cells if frozen. Optimal range for the feeder cell concentration is between 5×10^4 and 5×10^6 cells/mL. Prepared four conical tubes with 4.5 mL of AIM-V. Added 0.5

mL of cell fraction for each cell count into a new cryovial tube. Mixed the samples well and proceeded with the cell count.

[002346] If total viable feeder cell number was ≥ 2 x10^9 cells, proceeded to the next step to adjust the feeder cell concentration. Calculated the volume of feeder cells to remove from the first feeder cell bag in order to add 2 × 10^9 cells to the second feeder cell bag.

[002347] Using the p1000 micropipette, transfer 900 µL of HBSS to a 100µL OKT3 aliquot. Mix by pipetting up and down 3 times. Prepared two aliquots.

[002348] OKT3 formulation details: OKT3 may be aliquoted and frozen in original stock concentration from the vial (1 mg/mL) in 100 µL aliquots. ~10× aliquots per 1 mL vial. Stored at -80C. Day7/8: 30 µg/flask, *i.e.* 60 ng/mL in 500 mL – 120 µl max ~ 2 aliquots.

[002349] Using a syringe and sterile technique, drew up 0.6 mL of OKT3 and added into the feeder cell bag, ensuring all added. Adjusted media volume to a total volume of 2 L. Repeated with second OKT3 aliquot and added to the feeder cell bag. Transferred the second feeder cells bag to the incubator.

[002350] Preparation of G-REX100MCS flask with feeder cell suspension. Recorded the number of G-REX-100MCS flasks to process according to the number of G-REX flasks generated on Day 0. Removed G-REX flask from incubator and removed second feeder cells bag from incubator.

[002351] Removal of supernatant prior to feeder cell suspension addition. Connected one 10 mL syringe to the G-REX100 flask and drew up 5 mL of media. Created five 1 mL aliquots – 5 mL for extended characterization and storeed the 5 aliquots (final fragment culture supernatant) for extended characterization at -20°C until requested by sponsor. Labeled and repeated for each G-REX100 flask.

[002352] 5-20 × 1 mL samples for characterization, dependeding on number of flasks:

- 5 mL = 1flask
- 10 mL = 2 flasks
- 15 mL = 3 flasks
- 20 mL = 4 flasks

[002353] Continued seeding feeder cells into the G-REX100 MCS and repeated for each G-REX100 MCS flask. Using sterile transfer methods, gravity transferred 500 mL of the second feeder cells bag by weight (assume 1 g = 1 mL) into each G-REX-100MCS flask and recoreded amount. Labeled as Day 7 culture and repeated for each G-REX100 flask. Transferred G-REX-100MCS flasks to the incubator.

DAY 10-11

[002354] Removed the first G-REX-100MCS flask and using sterile conditions removed 7 mL of pre-process culture supernatant using a 10 mL syringe. Created seven 1 mL aliquots – 5 mL for extended characterization and 2 mL for sterility samples.

[002355] Mixed the flask carefully and using a new 10 mL syringe remove 10 mL supernatant and transfer to a 15 mL tube labelled as D10/11 mycoplasma supernatant.

[002356] Mixed the flask carefully and using a new syringe removed the volume below according to how many flasks were to be processed:

- 1 flask = 40 mL
- 2 flask = 20 mL/flask
- 3 flask = 13.3 mL/flask
- 4 flask = 10 mL/flask

[002357] A total of 40 mL should be pulled from all flasks and pooled in a 50 mL conical tube labeled 'Day 10/11 QC Sample' and stored in the incubator until needed. Performed a cell count and allocated the cells.

[002358] Stored the 5 aliquots (pre-process culture supernatant) for extended characterization at ≤-20°C until needed. Inoculated one anaerobic BacT/Alert bottle and one aerobic BacT/Alert bottle each with 1 mL of pre-process culture supernatant.

[002359] Continued with cell suspension transferred to the G-REX-500MCS and repeated for each G-REX-100MCS. Using sterile conditions, transferred the contents of each G-REX-100MCS into a G-REX-500MCS, monitoring about 100 mL of fluid transfer at a time. Stopped transfer when the volume of the G-REX-100MCS was reduced to 500 mL.

[002360] During transfer step, used 10 mL syringe and drew 10 mL of cell suspension into the syringe from the G-REX-100MCS. Followed the instructions according to the number of flasks in culture. If only 1 flask: Removed 20 mL total using two syringes. If 2 flasks: removed 10 mL per flask. If 3 flasks: removed 7 mL per flask. If 4 flasks: removed 5 mL per flask. Transferred the cell suspension to one common 50 mL conical tube. Keep in the incubator until the cell count step and QC sample. Total number of cells needed for QC was ~ 20e6 cells: 4 x 0.5 mL cell counts (cell counts were undiluted first).

[002361] The quantities of cells needed for assays are as follows:

1. 10×10^6 cells minimum for potency assays, such as those described herein, or for an IFN-γ or granzyme B assay

2. 1×10^6 cells for mycoplasma

3. 5×10^6 cells for flow cytometry for CD3+/CD45+

[002362] Transferred the G-REX-500MCS flasks to the incubator.

[002363] Prepared QC Samples. At least 15×10^8 cells were needed for the assays in this embodiment. Assays included: Cell count and viability; Mycoplasma (1×10^6 cells/ average viable concentration;) flow (5×10^6 cells/ average viable concentration;) and IFN-g assay (5×10^6 cells – 1×10^6 cells; 8-10×10^6 cells are required for the IFN-γ assay.

[002364] Calculated the volume of cells fraction for cryopreservation at 10×10^6 cells/mL and calculated the number of vials to prepare

DAY 16-17

[002365] Wash Buffer preparation (1% HSA Plasmalyte A). Transferred HSA and Plasmalyte to 5 L bag to make LOVO wash buffer. Using sterile conditions, transferred a total volume of 125 mL of 25% HSA to the 5L bag. Removed and transferred 10 mL or 40 mL of wash buffer in the 'IL-2 6×10^4 IU/mL' tube (10 mL if IL-2 was prepared in advance or 40 mL if IL-2 was prepared fresh).

[002366] Calculated volume of reconstituted IL-2 to add to Plasmalyte + 1% HSA: volume of reconstituted IL-2 = (Final concentration of IL-2 x Final volume)/ specific activity of the IL-2 (based on standard assay). The Final Concentration of IL-2 was 6×10^4 IU/mL. The final volume was 40 mL.

[002367] Removed calculated initial volume of IL-2 needed of reconstituted IL-2 and transfer to the 'IL-2 $6x10^4$ IU/mL' tube. Added 100µL of IL-2 $6x10^6$ IU/mL from the aliquot prepared in advance to the tube labelled 'IL-2 $6x10^4$ IU/mL' containing 10 mL of LOVO wash buffer.

[002368] Removed about 4500 mL of supernatant from the G-REX-500MCS flasks. Swirled the remaining supernatant and transferred cells to the Cell Collection Pool bag. Repeated with all G-REX-500MCS flasks.

[002369] Removed 60 mL of supernatant and add to supernatant tubes for quality control assays, including mycoplasma detection. Stored at +2-8°C.

[002370] Cell collection. Counted cells. Prepare four 15 mL conicals with 4.5 mL of AIM-V. These may be prepared in advance. Optimal range = is between 5×10^4 and 5×10^6 cells/mL. (1:10 dilution was recommended). For 1:10 dilution, to 4500 µL of AIM V prepared previously, add 500 µL of CF. Recorded dilution factor.

[002371] Calculated the TC (Total Cells) pre-LOVO (live + dead) =

Average Total Cell

Concentration (TC conc pre LOVO)

(live + dead)

X

Volume of Source bag

[002372] Calculated the TVC (Total Viable Cells) pre-LOVO (live) =

Average Total Viable Cell

Concentration (TVC pre LOVO)

(live)

X

Volume of LOVO Source Bag

[002373] When the total cell (TC) number was > 5×10^9, remove 5×10^8 cells to be cryopreserved as MDA retention samples. $5 \times 10^8 \div$ avg TC concentration (step 14.44) = volume to remove.

[002374] When the total cell (TC) number was $\leq 5 \times 10^9$, remove 4×10^6 cells to be cryopreserved as MDA retention samples. $4 \times 10^6 \div$ avg TC concentration = volume to remove.

[002375] When the total cell number was determined, the number of cells to remove should allow retention of 150×10^9 viable cells. Confirm TVC pre-LOVO 5×10^8 or 4×10^6 or not applicable. Calculated the volume of cells to remove.

[002376] Calculated the remaining Total Cells Remaining in Bag. Calculated the TC (Total Cells) pre-LOVO. [Avg. Total cell concentration X Remaining Volume = TC pre-LOVO Remaining]

[002377] According to the total number of cells remaining, the corresponding process in Table 44 is selected.

TABLE 44. Total number of cells.

Total cells:	*Retentate (mL)*
$0 <$ Total cells $\leq 31 \times 10^9$	115
$31 \times 10^9 <$ Total cells $\leq 71 \times 10^9$	165
$71 \times 10^9 <$ Total Cells $\leq 110 \times 10^9$	215

$110 \times 10^9 <$ Total Cells$\leq 115 \times 10^9$	265

[002378] Chose the volume of IL-2 to add corresponding to the used process. Volume calculated as: Retentate Volume × 2 × 300 IU/mL = IU of IL-2 required. IU of IL-2 required / 6×10^4 IU/mL = Volume of IL-2 to add Post LOVO bag. Recorded all volumes added. Obtained samples in cryovial for further analyses.

[002379] Mixed the cell product well. Sealed all bags for further processing, included cryopreservation when applicable.

[002380] Performed endotoxin, IFN-γ, sterility, and other assays as needed on cryovial samples obtained.

EXAMPLE 10: GEN 2 AND GEN 3 EXEMPLARY PROCESSES

[002381] This example demonstrates the Gen 2 and Gen 3 processes. Process Gen 2 and Gen 3 TILs are generally composed of autologous TIL derived from an individual patient through surgical resection of a tumor and then expanded ex vivo. The priming first expansion step of the Gen 3 process was a cell culture in the presence of interleukin-2 (IL-2) and the monoclonal antibody OKT3, which targets the T-cell co-receptor CD3 on a scaffold of irradiated peripheral blood mononuclear cells (PBMCs).

[002382] The manufacture of Gen 2 TIL products consists of two phases: 1) pre-Rapid Expansion (Pre-REP) and 2) Rapid Expansion Protocol (REP). During the Pre-REP resected tumors were cut up into ≤ 50 fragments 2-3 mm in each dimension which were cultured with serum-containing culture medium (RPMI 1640 media containing 10% HuSAB supplemented) and 6,000 IU/mL of Interleukin-2 (IL-2) for a period of 11 days. On day 11 TIL were harvested and introduced into the large-scale secondary REP expansion. The REP consists of activation of $\leq 200 \times 10^6$ of the viable cells from pre-REP in a co-culture of $5x10^9$ irradiated allogeneic PBMCs feeder cells loaded with 150 µg of monoclonal anti-CD3 antibody (OKT3) in a 5 L volume of CM2 supplemented with 3000 IU/mL of rhIL-2 for 5 days. On day 16 the culture is volume reduced 90% and the cell fraction is split into multiple G-REX-500 flasks at $\geq 1 \times 10^9$ viable lymphocytes/flask and QS to 5L with CM4. TIL are incubated an additional 6 days. The REP is harvested on day 22, washed, formulated, and cryo-preserved prior to shipping at -150°C to the clinical site for infusion.

[002383] The manufacture of Gen 3 TIL products consists of three phases: 1) Priming First Expansion Protocol, 2) Rapid Second Expansion Protocol (also referred to as rapid expansion phase

or REP), and 3) Subculture Split. To effect the Priming First Expansion TIL propagation, resected tumor was cut up into ≤ 120 fragments 2-3 mm in each dimension. On day 0 of the Priming First Expansion, a feeder layer of approximately 2.5×10^8 allogeneic irradiated PBMCs feeder cells loaded with OKT-3 was established on a surface area of approximately $100cm^2$ in each of 3 100 MCS vessels. The tumor fragments were distributed among and cultured in the 3 100 MCS vessels each with 500 mL serum-containing CM1 culture medium and 6,000 IU/mL of Interleukin-2 (IL-2) and 15 ug OKT-3 for a period of 7 days. On day 7, REP was initiated by incorporating an additional feeder cell layer of approximately $5x10^8$ allogeneic irradiated PBMCs feeder cells loaded with OKT-3 into the tumor fragmented culture phase in each of the three 100 MCS vessels and culturing with 500 mL CM2 culture medium and 6,000 IU/mL IL-2 and 30 µg OKT-3. The REP initiation was enhanced by activating the entire Priming First Expansion culture in the same vessel using closed system fluid transfer of OKT3 loaded feeder cells into the 100MCS vessel. For Gen 3, the TIL scale up or split involved process steps where the whole cell culture was scaled to a larger vessel through closed system fluid transfer and was transferred (from 100 M flask to a 500 M flask) and additional 4 L of CM4 media was added. The REP cells were harvested on day 16, washed, formulated, and cryo-preserved prior to shipping at -150 °C to the clinical site for infusion.

[002384] Overall, the Gen 3 process is a shorter, more scalable, and easily modifiable expansion platform that will accommodate to fit robust manufacturing and process comparability.

TABLE 45. Comparison of Exemplary Gen 2 and Exemplary Gen 3 manufacturing process.

Step	Process (Gen 2)	Process (Gen 3)
Pre REP-day 0	Up to 50 fragments, 1 G-REX-100MCS, 11 days In 1 L of CM1 media + IL-2 (6000 IU/mL)	Whole tumor up to 120 fragments divided evenly among up to 3 flasks. 1 flask: 1-60 fragments 2 flasks: 61-89 fragments 3 flasks 90-120 fragments 7 days in 500 mL of CM1 media + IL-2 (6000 IU/mL) 2.5×10^8 feeder cells/flask 15 ug OKT-3/flask
REP Initiation	Direct to REP, Day 11, <200×10^6 TIL (1)G-REX-500MCS in 5L CM2 media	Direct to REP, Day 7, all cells, same G-REX-100MCS Add 500 CM2 media IL-2 (6000 IU/mL)

	IL-2 (3000 IU/mL) 5×10^9 feeder cells 150ug OKT-3	5×10^8 feeder cells/flask 30ug OKT-3/flask
TIL propagation or Scale up	Volume reduce and split cell fraction in up to 5 G-REX-500MCS 4.5L CM4 media + IL-2 (3000 IU/mL) $\geq 1\times10^9$ TVC / flask Split day 16	Each G-REX-100MCS(1L) transfers to 1 G-REX-500MCS Add 4L CM4 media +IL-2 (3000 IU/mL) Scale up on day 9 to 11
Harvest	Harvest day 22, LOVO-automated cell washer	Harvest day 16 LOVO- automated cell washer
Final formulation	Cryopreserved Product 300 IU/mL IL2- CS10 in LN_2, multiple aliquots	Cryopreserved product 300 IU/mL IL-2-CS10 in LN_2, multiple aliquots
Process time	**22 days**	**16 days**

[002385] On day 0, for both processes, the tumor was washed 3 times and the fragments were randomized and divided into two pools; one pool per process. For the Gen 2 Process, the fragments were transferred to one -GREX 100MCS flask with 1 L of CM1 media containing 6,000IU/mL rhIL-2. For the Gen 3 Process, fragments were transferred to one G-REX-100MCS flask with 500 mL of CM1 containing 6,000IU/mL rhIL-2, 15 ug OKT-3 and 2.5×10^8 feeder cells. Seeding of TIL for Rep initiation day occurred on different days according to each process. For the Gen 2 Process, in which the G-REX-100MCS flask was 90% volume reduced, collected cell suspension was transferred to a new G-REX-500MCS to start REP initiation on day 11 in CM2 media containing IL-2 (3000 IU/mL), plus 5×10^9 feeder cells and OKT-3 (30 ng/mL). Cells were expanded and split on day 16 into multiple G-REX-500 MCS flasks with CM4 media with IL-2 (3000 IU/mL) per protocol. The culture was then harvested and cryopreserved on day 22 per protocol. For the Gen 3 process, the REP initiation occurred on day 7, in which the same G-REX-100MCS used for REP initiation. Briefly, 500 mL of

CM2 media containing IL-2 (6000 IU/mL) and 5×10^8 feeder cells with 30ug OKT-3 was added to each flask. On day 9-11 the culture was scaled up. The entire volume of the G-REX100M (1 L) was transferred to a G-REX-500MCS and 4L of CM4 containing IL-2 (3000 IU/mL) was added. Flasks were incubated 5 days. Cultures were harvested and cryopreserved on Day 16.

[002386] Three different tumors were included in the comparison, two lung tumors (L4054 and L4055) and one melanoma tumor (M1085T).

[002387] CM1 (culture media 1), CM2 (culture media 2), and CM4 (culture media 4) media were prepared in advance and held at 4°C for L4054 and L4055. CM1 and CM2 media were prepared without filtration to compare cell growth with and without filtration of media.

[002388] Media was warmed at 37°C up to 24 hours in advance for L4055 tumor on REP initiation and scale-up.

[002389] Results. Gen 3 results fell within 30% of Gen 2 for total viable cells achieved. Gen 3 final product exhibited higher production of IFN-γ after restimulation. Gen 3 final product exhibited increased clonal diversity as measured by total unique CDR3 sequences present. Gen 3 final product exhibited longer mean telomere length.

[002390] Pre-REP and REP expansion on Gen 2 and Gen 3 processes followed the procedures described above. For each tumor, the two pools contained equal number of fragments. Due to the small size of tumors, the maximum number of fragments per flask was not achieved. Total pre-REP cells (TVC) were harvested and counted at day 11 for the Gen 2 process and at day 7 for the Gen 3 process. To compare the two pre-REP arms, the cell count was divided over the number of fragments provided in the culture in order to calculate an average of viable cells per fragment. As indicated in Table 46 below, the Gen 2 process consistently grew more cells per fragment compared to the Gen 3 Process. An extrapolated calculation of the number of TVC expected for Gen 3 process at day 11, which was calculated dividing the pre-REP TVC by 7 and then multiply by 11.

TABLE 46. Pre-REP cell counts

Tumor ID	**L4054**		**L4055***		**M1085T**	
Process	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**
pre-REP TVC	1.42E+08	4.32E+07	2.68E+07	1.38E+07	1.23E+07	3.50E+06
Number of fragments	21	21	24	24	16	16
Average TVC per fragment at pre-REP	6.65E+06	2.06E+06	1.12E+06	5.75E+05	7.66E+05	2.18E+05
Gen 3 extrapolated value at pre REP day 11	N/A	6.79E+07	N/A	2.17E+07	N/A	5.49E+06

* L4055, unfiltered media.

[002391] For the Gen 2 and Gen 3 processes, TVC was counted per process condition and percent viable cells was generated for each day of the process. On harvest, day 22 (Gen 2) and day 16 (Gen 3) cells were collected and the TVC count was established. The TVC was then divided by the number of fragments provided on day 0, to calculate an average of viable cells per fragment. Fold expansion was calculated by dividing harvest TVC by over the REP initiation TVC. As exhibited in Table 47, comparing Gen 2 and the Gen 3, fold expansions were similar for L4054; in the case of L4055, the fold expansion was higher for the Gen 2 process. Specifically, in this case, the media was warmed up 24 in advance of REP initiation day. A higher fold expansion was also observed in Gen 3 for M1085T. An extrapolated calculation of the number of TVC expected for Gen 3 process at day 22, which was calculated dividing the REP TVC by 16 and then multiply by 22.

TABLE 47. Total viable cell count and fold expansion on TIL final product.

Tumor ID	**L4054**		**L4055**		**M1085T**	
Process	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**
# Fragments	**21**	**21**	**24**	**24**	**16**	**16**
TVC /fragment (at Harvest)	3.18E+09	8.77E+08	2.30E+09	3.65E+08	7.09E+08	4.80E+08
REP initiation	1.42E+08	4.32E+07	2.68E+07	1.38E+07	1.23E+07	3.50E+06
Scale up	3.36E+09	9.35E+08	3.49E+09	8.44E+08	1.99E+09	3.25E+08
Harvest	6.67E+10	1.84E+10	5.52E+10	8.76E+09	1.13E+10	7.68E+09
Fold Expansion Harvest/ REP initiation	**468.4**	**425.9**	**2056.8**	**634.6**	**925.0**	**2197.2**
Gen 3 extrapolated value at REP harvest day 22	**N/A**	**2.53E+10**	**N/A**	**1.20E+10**	**N/A**	**1.06E+10**

* L4055, unfiltered media.

[002392] Table 48: %Viability of TIL final product: Upon harvest, the final TIL REP products were compared against release criteria for % viability. All of the conditions for the Gen 2 and Gen 3 processes surpassed the 70% viability criterion and were comparable across processes and tumors.

[002393] Upon harvest, the final TIL REP products were compared against release criteria for % viability. All of the conditions for the Gen 2 and Gen 3 processes surpassed the 70% viability criterion and were comparable across processes and tumors.

TABLE 48. % Viability of REP (TIL Final Product)

Tumor ID	**L4054**		**L4055**		**M1085T**	
Process	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**	**Gen 2**	**Gen 3**
REP initiation	98.23%	97.97%	97.43%	92.03%	81.85%	68.27%
Scale up	94.00%	93.57%	90.50%	95.93%	78.55%	71.15%
Harvest	87.95%	89.85%	87.50%	86.70%	86.10%	87.45%

[002394] Due to the number of fragments per flask below the maximum required number, an estimated cell count at harvest day was calculated for each tumor. The estimation was based on the expectation that clinical tumors were large enough to seed 2 or 3 flasks on day 0.

TABLE 49. Extrapolated estimate cell count calculation to full scale 2 and 3 flask on Gen 3 Process.

Tumor ID	**L4054**		**L4055**		**M1085T**	
Gen 3 Process	**2 flasks**	**3 Flasks**	**2 flasks**	**3 Flasks**	**2 flasks**	**3 Flasks**
Estimate Harvest	3.68E+10	5.52E+10	1.75E+10	2.63E+10	1.54E+10	2.30E+10

[002395] Immunophenotyping - phenotypic marker comparisons on TIL final product. Three tumors L4054, L4055, and M1085T underwent TIL expansion in both the Gen 2 and Gen 3 processes. Upon harvest, the REP TIL final products were subjected to flow cytometry analysis to test purity, differentiation, and memory markers. For all the conditions the percentage of TCR a/b+ cells was over 90%.

[002396] TIL harvested from the Gen 3 process showed a higher expression of CD8 and CD28 compared to TIL harvested from the Gen 2 process. The Gen 2 process showed a higher percentage of CD4+.

[002397] TIL harvested from the Gen 3 process showed a higher expression on central memory compartments compared to TIL from the Gen 2 process.

[002398] Activation and exhaustion markers were analyzed in TIL from two, tumors L4054 and L4055 to compare the final TIL product by from the Gen 2 and Gen 3 TIL expansion processes. Activation and exhaustion markers were comparable between the Gen 2 and Gen 3 processes.

[002399] Interferon gamma secretion upon restimulation. On harvest day, day 22 for Gen 2 and day 16 for Gen 3, TIL underwent an overnight restimulation with coated anti-CD3 plates for L4054 and L4055. The restimulation on M1085T was performed using anti-CD3, CD28, and CD137 beads. Supernatant was collected after 24 hours of the restimulation in all conditions and the supernatant was frozen. IFNγ analysis by ELISA was assessed on the supernatant from both processes at the same time using the same ELISA plate. Higher production of IFNγ from the Gen 3 process was observed in the three tumors analyzed.

[002400] Measurement of IL-2 levels in culture media. To compare the IL-2 consumption between Gen 2 and Gen 3 process, cell supernatant was collected on REP initiation, scale up, and harvest day, on tumor L4054 and L4055. The quantity of IL-2 in cell culture supernatant was measured by Quantitate ELISA Kit from R&D. The general trend indicates that the IL-2 concentration

remains higher in the Gen 3 process when compared to the Gen 2 process. This is likely due to the higher concentration of IL-2 on REP initiation (6000 IU/mL) for Gen 3 coupled with the carryover of the media throughout the process.

[002401] Metabolic substrate and metabolite analysis. The levels of metabolic substrates such as D-glucose and L-glutamine were measured as surrogates of overall media consumption. Their reciprocal metabolites, such lactic acid and ammonia, were measured. Glucose is a simple sugar in media that is utilized by mitochondria to produce energy in the form of ATP. When glucose is oxidized, lactic acid is produced (lactate is an ester of lactic acid). Lactate is strongly produced during the cells exponential growth phase. High levels of lactate have a negative impact on cell culture processes.

[002402] Spent media for L4054 and L4055 was collected at REP initiation, scale up, and harvest days for both process Gen 2 and Gen 3. The spent media collection was for Gen 2 on Day 11, day 16 and day 22; for Gen 3 was on day 7, day 11 and day 16. Supernatant was analyzed on a CEDEX Bio-analyzer for concentrations of glucose, lactic acid, glutamine, GlutaMax™, and ammonia.

[002403] L-glutamine is an unstable essential amino acid required in cell culture media formulations. Glutamine contains an amine, and this amide structural group can transport and deliver nitrogen to cells. When L-glutamine oxidizes, a toxic ammonia by-product is produced by the cell. To counteract the degradation of L-glutamine the media for the Gen 2 and Gen 3 processes was supplemented with GlutaMax™, which is more stable in aqueous solutions and does not spontaneously degrade. In the two tumor lines, the Gen 3 arm showed a decrease in L-glutamine and GlutaMax™ during the process and an increase in ammonia throughout the REP. In the Gen 2 arm a constant concentration of L-glutamine and GlutaMax™, and a slight increase in the ammonia production was observed. The Gen 2 and Gen 3 processes were comparable at harvest day for ammonia and showed a slight difference in L-glutamine degradation.

[002404] Telomere repeats by Flow-FISH. Flow-FISH technology was used to measure the average length of the telomere repeat on L4054 and L4055 under Gen 2 and Gen 3 process. The determination of a relative telomere length (RTL) was calculated using Telomere PNA kit/FITC for flow cytometry analysis from DAKO. Gen 3 showed comparable telomere length to Gen 2.

[002405] CD3 Analysis. To determine the clonal diversity of the cell products generated in each process, TIL final product harvested for L4054 and L4055, were sampled and assayed for clonal diversity analysis through sequencing of the CDR3 portion of the T-cell receptors.

[002406] Table 50 shows a comparison between Gen 2 and Gen 3 of percentage shared unique CDR3 sequences on L4054 on TIL harvested cell product. 199 sequences are shared between Gen 3 and Gen 2 final product, corresponding to 97.07% of top 80% of unique CDR3 sequences from Gen 2 shared with Gen 3 final product.

TABLE 50. Comparison of shared uCDR3 sequences between Gen 2 and Gen 3 processes on L4054.

# uCDR3 (% Overlap)	All uCDR3's		Top 80% uCDR3's	
	Gen 2	Gen 3	Gen 2	Gen 3
Gen 2-L4054	8915	4355 (48.85%)	205	199 (97.07%)
Gen 3-L4054	-	18130	-	223

[002407] Table 51 shows a comparison between Gen 2 and Gen 3 of percentage shared unique CDR3 sequences on L4055 on TIL harvested cell product. 1833 sequences are shared between Gen 3 and Gen 2 final product, corresponding to 99.45% of top 80% of unique CDR3 sequences from Gen 2 shared with Gen 3 final product.

TABLE 51. Comparison of shared uCDR3 sequences between Gen 2 and Gen 3 processes on L4055.

# uCDR3 (% Overlap)	All uCDR3's		Top 80% uCDR3's	
	Gen 2	Gen 3	Gen 2	Gen 3
Gen 2-L4055	12996	6599 (50.77%)	1843	1833 (99.45%)
Gen 3-L4055	-	27246	-	2616

[002408] CM1 and CM2 media was prepared in advanced without filtration and held at 4 degree C until use for tumor L4055 to use on Gen 2 and Gen 3 process.

[002409] Media was warmed up at 37 degree C for 24 hours in advance for tumor L4055 on REP initiation day for Gen 2 and Gen 3 process.

[002410] LDH was not measured in the supernatants collected on the processes.

[002411] M1085T TIL cell count was executed with K2 cellometer cell counter.

[002412] On tumor M1085T, samples were not available such as supernatant for metabolic analysis, TIL product for activation and exhaustion markers analysis, telomere length and CD3 - TCR vb Analysis.

[002413] Conclusions. This example compares 3 independent donor tumors tissue in terms of functional quality attributes, plus extended phenotypic characterization and media consumption among Gen 2 and Gen 3 processes.

[002414] Gen 2 and Gen 3 pre-REP and REP expansion comparison were evaluated in terms of total viable cells generated and viability of the total nucleated cell population. TVC cell doses at harvest day was not comparable between Gen 2 (22 days) and Gen 3 (16 days). Gen 3 cell doses were lower than Gen 2 at around 40% of total viable cells collected at harvest.

[002415] An extrapolated cell number was calculated for Gen 3 process assuming the pre-REP harvest occurred at day 11 instead day 7 and REP Harvest at Day 22 instead day 16. In both cases, Gen 3 shows a closer number on TVC compared to the Gen 2 process, indicating that the early activation enhanced TIL growth.

[002416] In the case of extrapolated value for extra flasks (2 or 3) on Gen 3 process assuming a bigger size of tumor processed, and reaching the maximum number of fragments required per process as described. It was observed that a similar dose can be reachable on TVC at Day 16 Harvest for Gen 3 process compared to Gen 2 process at Day 22. This observation is important and indicates an early activation of the culture reduced TIL processing time.

[002417] Gen 2 and Gen 3 pre-REP and REP expansion comparison were evaluated in terms of total viable cells generated and viability of the total nucleated cell population. TVC cell doses at harvest day was not comparable between Gen 2 (22 days) and Gen 3 (16 days). Gen 3 cell doses were lower than Gen 2 at around 40% of total viable cells collected at harvest.

[002418] In terms of phenotypic characterization, a higher CD8+ and CD28+ expression was observed on three tumors on Gen 3 process compared to Gen 2 process.

[002419] Gen 3 process showed slightly higher central memory compartments compared to Gen 2 process.

[002420] Gen 2 and Gen 3 process showed comparable activation and exhaustion markers, despite the shorter duration of the Gen 3 process.

[002421] IFN gamma (IFNγ) production was 3 times higher on Gen 3 final product compared to Gen 2 in the three tumors analyzed. This data indicates the Gen 3 process generated a highly functional and more potent TIL product as compared to the Gen 2 process, possibly due to the higher expression of CD8 and CD28 expression on Gen 3. Phenotypic characterization suggested positive trends in Gen 3 toward CD8+, CD28+ expression on three tumors compared to Gen 2 process.

[002422] Telomere length on TIL final product between Gen 2 and Gen 3 were comparable.

[002423] Glucose and Lactate levels were comparable between Gen 2 and Gen 3 final product, suggesting the levels of nutrients on the media of Gen 3 process were not affected due to the non-execution of volume reduction removal in each day of the process and less volume media overall in the process, compared to Gen 2.

[002424] Overall Gen 3 process showed a reduction almost two times of the processing time compared to Gen 2 process, which would yield a substantial reduction on the cost of goods (COGs) for TIL product expanded by the Gen 3 process.

[002425] IL-2 consumption indicates a general trend of IL-2 consumption on Gen 2 process, and in Gen 3 process IL-2 was higher due to the non-removal of the old media.

[002426] The Gen 3 process showed a higher clonal diversity measured by CDR3 TCRab sequence analysis.

[002427] The addition of feeders and OKT-3 on day 0 of the pre-REP allowed an early activation of TIL and allowed for TIL growth using the Gen 3 process.

[002428] Table 52 describes various embodiments and outcomes for the Gen 3 process as compared to the current Gen 2 process.

TABLE 52. Exemplary Gen 3 process features.

Step	Process Gen 2 embodiment	Process Gen 3 embodiment
Pre REP-day 0	≤50 fragments 1X G-REX-100MCS 1 L media IL-2 (6000 IU/mL) 11 days	≤240 fragments ≤60 fragments/flask ≤4 flasks ≤2L media (500 mL/flask) IL-2 (6000 IU/mL) $2.5x10^8$ feeder cells/flask 15ug OKT3/flask
REP Initiation	Fresh TIL direct to REP Day 11 $\leq 200e^6$ viable cells 5×10^9 feeder cells G-REX-500MCS 5L CM2 media + IL-2 (3000 IU/mL)	Fresh TIL direct to REP Day 7 Activate entire culture 5×10^8 feeder cells 30 µg OKT3/flask

	150 μg OKT3	G-REX-100MCS 500 mL media+ IL-2 (6000 IU/mL)
TIL Sub-culture or Scale up	≤5 G-REX-500MCS ≤1x10 viable cells/ flask 5 L/flask Day 16	≤4 G-REX-500MCS Scale up entire culture 4 L/flask Day 10-11
Harvest	Harvest Day 22, LOVO-automated cell washer 2 wash cycles	Harvest Day 16 LOVO-automated cell washer 5 wash cycles
Final formulation	Cryopreserved Product 300 IU/mL IL2- CS10 in LN_2, multiple aliquots	Cryopreserved product 300 IU/mL IL-2-CS10 in LN_2, multiple aliquots
Process time	22 days	16 days

EXAMPLE 11: AN EXEMPLARY GEN 3 PROCESS (ALSO REFERRED TO AS GEN 3.1)

[002429] This example describes further studies regarding the "Comparability between the Gen 2 and Gen 3 processes for TIL expansion". The Gen 3 process was modified to include an activation step early in the process with the goal of increasing the final total viable cell (TVC) output, while maintaining the phenotypic and functional profiles. As described below, a Gen 3 embodiment was modified as a further embodiment and is referred to herein in this example as Gen 3.1.

[002430] In some embodiments, the Gen 3.1 TIL manufacturing process has four operator interventions:

1. Tumor Fragment Isolation and Activation: On Day 0 of the process the tumor was dissected and the final fragments generated awe~3x3mm each (up to 240 fragments total) and cultured in 1-4 G-REX100MCS flasks. Each flask contained up to 60 fragments, 500 mL of

CM1 or DM1 media, and supplemented with 6,000 IU rhIL-2, 15 μg OKT3, and $2.5x10^8$ irradiated allogeneic mononuclear cells. The culture was incubated at 37°C for 6-8 days.

2. TIL Culture Reactivation: On Day 7-8 the culture was supplemented through slow addition of CM2 or DM1 media supplemented with 6,000 IU rhIL-2, 30 μg OKT3, and $5x10^8$ irradiated allogeneic mononuclear cells in both cases. Care was taken to not disturb the existing cells at the bottom of the flask. The culture was incubated at 37°C for 3-4 days.

3. Culture Scale Up: Occurs on day 10-11. During the culture scale-up, the entire contents of the G-REX100MCS was transferred to a G-REX500MCS flask containing 4L of CM4 or DM2 supplemented with 3,000 IU/mL of IL-2 in both cases. Flasks were incubated at 37°C for 5-6 days until harvest.

4. Harvest/Wash/Formulate: On day 16-17 the flasks are volume reduced and pooled. Cells were concentrated and washed with PlasmaLyte A pH 7.4 containing 1% HSA. The washed cell suspension was formulated at a 1:1 ratio with CryoStor10 and supplemented with rhIL-2 to a final concentration of 300 IU/mL.

[002431] The DP was cryopreserved with a controlled rate freeze and stored in vapor phase liquid nitrogen. *Complete Standard TIL media 1, 2, or 4 (CM1, CM2, CM4) could be substituted for CTS™OpTmizer™ T-Cell serum free expansion Medium, referred to as Defined Medium (DM1 or DM2), as noted above.

[002432] Process description. On day 0, the tumor was washed 3 times, then fragmented in 3x3x3 final fragments. Once the whole tumor was fragmented, then the final fragments were randomized equally and divided into three pools. One randomized fragment pool was introduced to each arm, adding the same number of fragments per the three experimental matrices.

[002433] Tumor L4063 expansion was performed with Standard Media and tumor L4064 expansion was performed with Defined Media (CTS OpTmizer) for the entire TIL expansion process. Components of the media are described herein.

[002434] CM1 Complete Media 1: RPMI+ Glutamine supplemented with 2mM GlutaMax™, 10% Human AB Serum, Gentamicin (50ug/mL), 2-Mercaptoethanol (55uM). Final media formulation supplemented with 6000IU/mL IL-2.

[002435] CM2 Complete Media 2: 50% CM1 medium + 50% AIM-V medium. Final media formulation supplemented with 6000IU/mL IL-2.

[002436] CM4 Complete Media 4: AIM-V supplemented with GlutaMax™ (2mM). Final media formulation supplemented with 3000IU/mL IL-2.

[002437] CTS OpTmizer CTS™OpTmizer™ T-Cell Expansion Basal Medium supplemented with CTS™ OpTmizer™ T-Cell Expansion Supplement (26 mL/L).

[002438] DM1: CTS™OpTmizer™ T-Cell Expansion Basal Medium supplemented with CTS™ OpTmizer™ T-Cell Expansion Supplement (26 mL/L), and CTS™ Immune Cell SR (3%), with GlutaMax™ (2mM). Final formulation supplemented with 6,000 IU/mL of IL-2.

[002439] DM2: CTS™OpTmizer™ T-Cell Expansion Basal Medium supplemented with CTS™ OpTmizer™ T-Cell Expansion Supplement (26 mL/L), and CTS™ Immune Cell SR (3%), with GlutaMax™ (2mM). Final formulation supplemented with 3,000 IU/mL of IL-2.

[002440] All types of media used, *i.e.*, Complete (CM) and Defined (DM) media, were prepared in advance, held at 4°C degree until the day before use, and warmed at 37°C in an incubator for up to 24 hours in advance prior to process day.

[002441] TIL culture reactivation occurred on Day 7 for both tumors. Scale-up occurred on day 10 for L4063 and day 11 for L4064. Both cultures were harvested and cryopreserved on Day 16.

[002442] Results Achieved. Cells counted and % viability for Gen 3.0 and Gen 3.1 processes were determined. Expansion in all the conditions followed details described in this example.

[002443] For each tumor, the fragments were divided into three pools of equal numbers. Due to the small size of the tumors, the maximum number of fragments per flask was not achieved. For the three different processes, the total viable cells and cell viability were assessed for each condition. Cell counts were determined as TVC on day 7 for reactivation, TVC on day 10 (L4064) or day 11 (L4063) for scale-up, and TVC at harvest on day 16/17.

[002444] Cell counts for Day 7 and Day 10/11 were taken FIO. Fold expansion was calculated by dividing the harvest day 16/17 TVC by the day 7 reactivation day TVC. To compare the three arms, the TVC on harvest day was divided by the number of fragments added in the culture on Day 0 in order to calculate an average of viable cells per fragment.

[002445] Cell counts and viability assays were performed for L4063 and L4064. The Gen 3.1-Test process yielded more cells per fragment than the Gen 3.0 Process on both tumors.

[002446] Total viable cell count and fold expansion; % Viability during the process. On reactivation, scale up and harvest the percent viability was performed on all conditions. On day 16/17 harvest, the final TVC were compared against release criteria for % viability. All of the conditions assessed surpassed the 70% viability criterion and were comparable across processes and tumors.

[002447] Immunophenotyping - Phenotypic characterization on TIL final product. The final products were subjected to flow cytometry analysis to test purity, differentiation, and memory markers. Percent populations were consistent for TCRα/β, CD4+ and CD8+ cells for all conditions.

[002448] Extended phenotypic analysis of REP TIL was performed. TIL product showed a higher percentage of CD4+ cells for Gen 3.1 conditions compared to Gen 3.0 on both tumors, and higher percentage of CD28+ cells from CD8+ population for Gen 3.0 compared to Gen 3.1 conditions on both conditions.

[002449] TIL harvested from the Gen 3.0 and Gen 3.1 processes showed comparable phenotypic markers as CD27 and CD56 expression on CD4+and CD8+ cells, and a comparable CD28 expression on CD4+ gated cells population. Memory markers comparison on TIL final product:

[002450] Frozen samples of TIL harvested on day 16 were stained for analysis. TIL memory status was comparable between Gen 3.0 and Gen 3.1 processes. Activation and exhaustion markers comparison on TIL final product:

[002451] Activation and exhaustion markers were comparable between the Gen 3.0 and Gen 3.1 processes gated on CD4+ and CD8+ cells.

[002452] Interferon gamma secretion upon restimulation. Harvested TIL underwent an overnight restimulation with coated anti-CD3 plates for L4063 and L4064. Higher production of IFNγ from the Gen 3.1 process was observed in the two tumors analyzed compared to Gen 3.0 process.

[002453] Measurement of IL-2 levels in culture media. To compare the levels of IL-2 consumption between all of the conditions and processes, cell supernatants were collected at initiation of reactivation on Day 7, at scale-up Day 10 (L4064) / 11 (L4063), and at harvest Day 16 / 17, and frozen. The supernatants were subsequently thawed and then analyzed. The quantity of IL-2 in cell culture supernatant was measured by the manufacturer protocol.

[002454] Overall Gen 3 and Gen 3.1 processes were comparable in terms of IL-2 consumption during the complete process assessed across same media conditions. IL-2 concentration (pg/mL) analysis on spent media collected for L4063 and L4064.

[002455] Metabolite analysis. Spent media supernatants was collected from L4063 and L4064 at reactivation initiation on day 7, scale-up on day 10 (L4064) or day 11 (L4063), and at harvest on days 16/17 for L4063 and L4064, for every condition. Supernatants were analyzed on a CEDEX Bio-analyzer for concentrations of glucose, lactate, glutamine, GlutaMax™, and ammonia.

[002456] Defined media has a higher glucose concentration of 4.5 g/L compared to complete media (2g/L). Overall, the concentration and consumption of glucose were comparable for Gen 3.0 and Gen 3.1 processes within each media type.

[002457] An increase in lactate was observed and increase in lactate was comparable between the Gen 3.0 and Gen 3.1 conditions and between the two media used for reactivation expansion (complete media and defined media).

[002458] In some instances, the standard basal media contained 2 mM L-glutamine and was supplemented with 2mM GlutaMax™ to compensate for the natural degradation of L-glutamine in culture conditions to L-glutamate and ammonia.

[002459] In some instances, defined (serum free) media used did not contain L-glutamine on the basal media, and was supplemented only with GlutaMax™ to a final concentration of 2mM. GlutaMax™ is a dipeptide of L-alanine and L-glutamine, is more stable than L-glutamine in aqueous solutions and does not spontaneously degrade into glutamate and ammonia. Instead, the dipeptide is gradually dissociated into the individual amino acids, thereby maintaining a lower but sufficient concentration of L-glutamine to sustain robust cell growth.

[002460] In some instances, the concentration of glutamine and GlutaMax™ slightly decreased on the scale-up day, but at harvest day showed an increase to similar or closer levels compared to reactivation day. For L4064, glutamine and GlutaMax™ concentration showed a slight degradation in a similar rate between different conditions, during the whole process.

[002461] Ammonia concentrations were higher samples grown in standard media containing 2 mM glutamine + 2 mM GlutaMax™) than those grown in defined media containing 2 mM GlutaMax™). Further, as expected, there was a gradual increase or accumulation of ammonia over the course of the culture. There were no differences in ammonia concentrations across the three different test conditions.

[002462] Telomere repeats by Flow – FISH. Flow-FISH technology was used to measure the average length of the telomere repeat on L4063 and L4064 under Gen 3 and Gen 3.1 processes. The determination of a relative telomere length (RTL) was calculated using Telomere PNA kit/FITC for flow cytometry analysis from DAKO. Telomere assay was performed. Telomere length in samples were compared to a control cell line (1301 leukemia). The control cell line is a tetraploid cell line having long stable telomeres that allows calculation of a relative telomere length. Gen 3 and Gen 3.1 processes assessed in both tumors showed comparable telomere length.

TCR Vβ repertoire Analysis

[002463] To determine the clonal diversity of the cell products generated in each process, TIL final products were assayed for clonal diversity analysis through sequencing of the CDR3 portion of the T-cell receptors.

[002464] Three parameters were compared between the three conditions:

- Diversity index of Unique CDR3 (uCDR3)
- % shared uCDR3
- For the top 80% of uCDR3:
    - Compare the % shared uCDR3 copies
    - Compare the frequency of unique clonotypes

[002465] Control and Gen 3.1 Test, percentage shared unique CDR3 sequences on TIL harvested cell product for: 975 sequences are shared between Gen 3 and Gen 3.1 Test final product, equivalent to 88% of top 80% of unique CDR3 sequences from Gen 3 shared with Gen 3.1.

[002466] Control and Gen 3.1 Test, percentage shared unique CDR3 sequences on TIL harvested cell product for: 2163 sequences are shared between Gen 3 and Gen 3.1 Test final product, equivalent to 87% of top 80% of unique CDR3 sequences from Gen 3 shared with Gen 3.1.

[002467] The number of unique CD3 sequences identified from $1x10^6$ cells collected on Harvest day 16, for the different processes. Gen 3.1 Test condition showed a slightly higher clonal diversity compared to Gen 3.0 based on the number of unique peptide CDRs within the sample.

[002468] The Shannon entropy diversity index is a reliable and common metric for comparison, because Gen 3.1 conditions on both tumors showed slightly higher diversity than Gen 3 process, suggesting that TCR Vβ repertoire for Gen 3.1 Test condition was more polyclonal than the Gen 3.0 process.

[002469] Additionally, the TCR Vβ repertoire for Gen 3.1 Test condition showed more than 87% overlap with the corresponding repertoire for Gen 3.0 process on both tumor L4063 and L4064.

[002470] The value of IL-2 concentration on spent media for Gen 3.1 Test L4064 on reactivation day was below to the expected value (similar to Gen 3.1 control and Gen 3.0 condition).

[002471] The low value could be due to a pipetting error, but because of the minimal sample taken it was not possible to repeat the assay.

[002472] Conclusions. Gen 3.1 test condition including feeders and OKT-3 on Day 0 showed a higher TVC of cell doses at Harvest day 16 compared to Gen 3.0 and Gen 3.1 control. TVC on the final product for Gen 3.1 test condition was around 2.5 times higher than Gen 3.0.

[002473] Gen 3.1 test condition with the addition of OKT-3 and feeders on day 0, for both tumor samples tested, reached a maximum capacity of the flask at harvest. Under these conditions, if a maximum of 4 flasks on day 0 is initiated, the final cell dose could be between 80 - 100×10^9 TILs.

[002474] All the quality attributes such as phenotypic characterization including purity, exhaustion, activation and memory markers on final TIL product were maintained between Gen 3.1 Test and Gen 3.0 process.

[002475] IFN-γ production on final TIL product was 3 times higher on Gen 3.1 with feeder and OKT-3 addition on day 0, compared to Gen 3.0 in the two tumors analyzed, suggesting Gen 3.1 process generated a potent TIL product.

[002476] No differences observed in glucose or lactate levels across test conditions. No differences observed on glutamine and ammonia between Gen 3.0 and Gen 3.1 processes across media conditions. The low levels of glutamine on the media are not limiting cell growth and suggest the addition of GlutaMax™ only in media is sufficient to give the nutrients needed to make cells proliferate.

[002477] The scale up on day 11 and day 10 respectively and did not show major differences in terms of cell number reached on the harvest day of the process and metabolite consumption was comparable in both cases during the whole process. This observation suggests of Gen 3.0 optimized process can have flexibility on processing days, thereby facilitating flexibility in the manufacturing schedule.

[002478] Gen 3.1 process with feeder and OKT-3 addition on day 0 showed a higher clonal diversity measured by CDR3 TCRab sequence analysis compared to Gen 3.0.

[002479] Figure 32 describes an embodiment of the Gen 3 process (Gen 3 Optimized process). Standard media and CTS Optimizer serum free media can be used for Gen 3 Optimized process TIL expansion. In case of CTS Optimizer serum free media is recommended to increase the GlutaMax™ on the media to final concentration 4mM.

EXAMPLE 12: AN EXEMPLARY EMBODIMENT OF SELECTING AND EXPANDING PBLS FROM PBMCS IN CLL PATIENTS.

[002480] PBMCs are collected from patients and either frozen for later use, or used fresh. Enough volume of peripheral blood is collected to yield at least about 400,000,000 (400×10^6) PBMCs for starting material in the method of the present invention. On Day 0 of the method, IL-2 at $6x10^6$ IU/mL is either prepared fresh or thawed, and stored at 4°C or on ice until ready to use. 200 mL of CM2 medium is prepared by combining 100 mL of CM1 medium (containing GlutaMAX®), then diluting it with 100 mL (1:1) with AIM-V to make CM2. The CM2 is protected from light, and sealed tightly when not in use.

[002481] All of the following steps are performed under sterile cell culture conditions. An aliquot of CM2 is warmed in a 50mL conical tube in a 37°C water bath for use in thawing and/or washing a frozen PBMC sample. If a frozen PBMC sample is used, the sample is removed from freezer storage and kept on dry ice until ready to thaw. When ready to thaw the PBMC cryovial, 5 mL of CM2 medium is placed in a sterile 50 mL conical tube. The PBMC sample cryovial is placed in a 37°C water bath until only a few ice crystals remain. Warmed CM2 medium is added, dropwise, to the sample vial in a 1:1 volume ratio of sample:medium (about 1 mL). The entire contents is removed from the cryovial and transferred to the remaining CM2 medium in the 50 mL conical tube. An additional 1-2 mL of CM2 medium is used to rinse the cryovial and the entire contents of the cryovial is removed and transferred to the 50 mL conical tube. The volume in the conical tube is then adjusted with additional CM2 medium to 15 mL, and swirled gently to rinse the cells. The conical tube is then centrifuged at 400g for 5 minutes at room temperature in order to collect the cell pellet.

[002482] The supernatant is removed from the pellet, the conical tube is capped, and then the cell pellet is disrupted by, for example, scraping the tube along a rough surface. About 1mL of CM2 medium is added to the cell pellet, and the pellet and medium are aspirated up and down 5-10 times with a pipette to break up the cell pellet. An additional 3-5 mL of CM2 medium is added to the tube and mixed via pipette to suspend the cells. At this point, the volume of the cell suspension is recorded. Remove 100 uL of the cell suspension from the tube for cell counting with an automatic cell counter, for example, a Nexcelom Cellometer K2. Determine the number of live cells in the sample and record.

[002483] Reserve a minimum of 5×10^6 cells for phenotyping and other characterization experiments. Spin the reserved cells at 400g for 5 minutes at room temperature to collect the cell pellet. Resuspend the cell pellet in freezing medium (sterile, heat-inactivated FBS containing 20% DMSO). Freeze one or two aliquots of the reserved cells in freezing medium, and slow-freeze the aliquots in a cell freezer (Mr. Frosty) in a -80°C freezer. Transfer to liquid nitrogen storage after a minimum of 24 hours at -80°C.

[002484] For the following steps, use pre-cooled solutions, work quickly, and keep the cells cold. The next step is to purify the T-cell fraction of the PBMC sample. This is completed using a Pan T-cell Isolation Kit (Miltenyi, catalog # 130-096-535). Prepare the cells for purification by washing the cells with a sterile-filtered wash buffer containing PBS, 0.5% BSA, and 2mM EDTA at pH 7.2. The PBMC sample is centrifuged at 400g for 5 minutes to collect the cell pellet. The supernatant is aspirated off and the cell pellet is resuspended in 40 uL of wash buffer for every 10^7 cells. Add 10 uL of Pan T Cell Biotin-Antibody Cocktail for every 10^7 cells. Mix well and incubate for 5 minutes in refrigerator or on ice. Add 30 uL of wash buffer for every 10^7 cells. Add 20 uL of Pan T-cell MicroBead Cocktail for every 10^7 cells. Mix well and incubate for 10 minutes in refrigerator or on ice. Prepare an LS column and magnetically separate cells from the microbeads. The LS column is placed in the QuadroMACS magnetic field. The LS column is washed with 3 mL of cold wash buffer, and the wash is collected and discarded. The cell suspension is applied to the column and the flow-through (unlabeled cells) is collected. This flow-through is the enriched T-cell fraction (PBLs). Wash the column with 3 mL of wash buffer and collect the flow-through in the same tube as the initial flow-through. Cap the tube and place on ice. This is the T-cell fraction, or PBLs. Remove the LS column from the magnetic field, wash the column with 5 mL of wash buffer, and collect the non-T-cell fraction (magnetically labeled cells) into another tube. Centrifuge both fractions at 400g for 5 minutes to collect the cell pellets. Supernatants are aspirated from both samples, disrupt the pellet, and resuspend the cells in 1 mL of CM2 medium supplemented with 3000 IU/mL IL-2 to each pellet, and pipette up and down 5-10 times to break up the pellets. Add 1-2 mL of CM2 to each sample, and mix each sample well, and store in tissue culture incubator for next steps. Remove about a 50 uL aliquot from each sample, count cells, and record count and viability.

[002485] The T-cells (PBLs) are then cultured with Dunabeads™ Human T-Expander CD3/CD28. A stock vial of Dynabeads is vortexed for 30 seconds at medium spead. A required aliquot of beads is removed from the stock vial into a sterile 1.5 mL microtube. The beads are washed with bead wash solution by adding 1 mL of bead wash to the 1.5 mL microtube containing the beads. Mix gently. Place the tube onto the DynaMag™-2 magnet and let sit for 30 minutes while beads draw toward the magnet. Aspirate the wash solution off the beads and remove tube from the magnet. 1mL of CM2 medium supplemented with 3000 IU/mL IL-2 is added to the beads. The entire contents of the microtube is transferred to a 15 or 50 mL conical tube. Bring the beads to a final concentration of about 500,000/mL using CM2 medium with IL-2.

[002486] The T-cells (PBLs) and beads are cultured together as follows. On day 0: In a G-Rex-REX 24 well plate, in a total of 7mL per well, add 500,000 T-cells, 500,000 CD3/CD28 Dynabeads, and CM2 supplemented with IL-2. The G-Rex-REX plate is placed into a humidified 37°C, 5% CO_2 incubator until the next step in the process (on Day 4). Remaining cells are frozen in CS10

cryopreservation medium using a Mr. Frosty cell freezer. The non-T-cell fraction of cells are frozen in CS10 cryopreservation medium using a Mr. Frosty cell freezer. On day 4, medium is exchanged. Half of the medium (about 3.5mL) is removed from each well of the G-rex plate. A sufficient volume (about 3.5mL) of CM4 medium supplemented with 3000 IU/mL IL-2 warmed to 37°C is added to replace the medium removed from each sample well. The G-rex plate is returned to the incubator.

[002487] On day 7, cells are prepared for expansion by REP. The G-rex plate is removed from the incubator and half of medium is removed from each well and discarded. The cells are resuspended in the remaining medium and transferred to a 15 mL conical tube. The wells are washed with 1 mL each of CM4 supplemented with 3000 IU/mL IL-2 warmed to 37°C and the wash medium is transferred to the same 15 mL tube with the cells. A representative sample of cells is removed and counted using an automated cell counter. If there are less than $1x10^6$ live cells, the Dynabead expansion process at Day 0 is repeated. The remainder of the cells are frozen for back-up expansion or for phenotyping and other characterization studies. If there are $1x10^6$ live cells or more, the REP expansion is set up in replicate according to the protocol from Day 0. Alternatively, with enough cells, the expansion may be set up in a G-rex 10M culture flask using $10\text{-}15x10^6$ PBLs per flask and a 1:1 ratio of Dynabeads:PBLs in a final volume of 100mL/well of CM4 medium supplemented with 3000 IU/mL IL-2. The plate and/or flask is returned to the incubator. Excess PBLs may be aliquotted and slow-frozen in a Mr. Frosty cell freezer in a -80°C freezer, and the transferred to liquid nitrogen storage after a minimum of 24 hours at -80°C. These PBLs may be used as back-up samples for expansion or for phenotyping or other characterization studies.

[002488] On Day 11, the medium is exchanged. Half of the medium is removed from either each well of the G-rex plate or the flask and replaced with the same amount of fresh CM4 medium supplemented with 3000 IU/mL IL-2 at 37°C.

[002489] On Day 14, the PBLs are harvested. If the G-rex plate is used, about half of the medium is removed from each well of the plate and discarded. The PBLs and beads are suspended in the remaining medium and transferred to a sterile 15 mL conical tube (Tube 1). The wells are washed with 1-2 mL of fresh AIM-V medium warmed to 37°C, and the wash is transferred to Tube 1. Tube 1 is capped and placed in the DynaMag™-15 Magnet for 1 minute to allow the beads to be drawn to the magnet. The cell suspension is transferred into a new 15 mL tube (Tube 2), and the beads are washed with 2mL of fresh AIM-V at 37°C. Tube 1 is placed back in the magnet for an additional 1 minute, and the wash medium is then transferred to Tube 2. The wells may be combined if desired, after the final washing step. Remove a representative sample of cells and count, record count and viability. Tubes may be placed in the incubator while counting. Additional AIM-V medium may be added to the Tube 2 if cells appear very dense. If a flask is used, the volume in the flask should be reduced to about 10 mL. The contents of the flask is mixed and transferred to a 15 mL conical tube (Tube A).

The flask is washed with 2mL of the AIM-V medium as described above and the wash medium is also transferred to Tube A. Tube A is capped and placed in the DynaMag™-15 Magnet for 1 minute to allow the beads to be drawn to the magnet. The cell suspension is transferred into a new 15 mL tube (Tube B), and the beads are washed with 2mL of fresh AIM-V at 37°C. Tube A is placed back in the magnet for an additional 1 minute, and the wash medium is then transferred to Tube B. The wells may be combined if desired, after the final washing step. Remove a representative sample of cells and count, record count and viability. Tubes may be placed in the incubator while counting. Additional AIM-V medium may be added to the Tube B if cells appear very dense. Cells may be used fresh or frozen in CS10 preservation medium at desired concentrations.

EXAMPLE 13: A PHASE 2, MULTICENTER STUDY OF AUTOLOGOUS TUMOR INFILTRATING LYMPHOCYTES IN PATIENTS WITH SOLID TUMORS

[002490] **STUDY DESIGN**

[002491] Overview

[002492] This example describes a prospective, open-label, multi-cohort, non-randomized, multicenter Phase 2 study evaluating ACT using TIL in combination with pembrolizumab or TIL as a single therapy, using TILs prepared as described in the present application as well as in this example.

[002493] Objectives:

[002494] *Primary:*

[002495] To evaluate the efficacy of autologous TIL in combination with pembrolizumab in MM, HNSCC, or NSCLC patients or TIL as a single therapy in relapsed or refractory (r/r) NSCLC patients, who had previously progressed on or after treatment with CPIs, as determined by objective response rate (ORR), using the Response Evaluation Criteria in Solid Tumors (RECIST 1.1), as assessed by Investigator.

[002496] To characterize the safety profile of TIL in combination with pembrolizumab in MM, HNSCC, and NSCLC patients or TIL as a single therapy in r/r NSCLC patients as measured by the incidence of Grade $\geq$ 3 treatment-emergent adverse events (TEAEs).

[002497] *Secondary:*

[002498] To further evaluate the efficacy of autologous TIL in combination with pembrolizumab in MM, HNSCC, and NSCLC patients or TIL as a single therapy in r/r NSCLC patients using complete

response (CR) rate, duration of response (DOR), disease control rate (DCR), progression-free survival (PFS) using RECIST 1.1, as assessed by Investigator, and overall survival (OS).

[002499] Cohorts:

[002500] Cohort 1A: TIL therapy in combination with pembrolizumab in patients with Stage IIIC or Stage IV unresectable or MM with ≤ 3 prior lines of systemic therapy excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002501] Cohort 2A: TIL therapy in combination with pembrolizumab in patients with advanced, recurrent or metastatic HNSCC (*e.g.*, Stages T1N1-N2B, T2-4N0-N2b) with ≤ 3 prior lines of systemic therapy, excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002502] Cohort 3A: TIL therapy in combination with pembrolizumab in patients with locally advanced or metastatic (Stage III– IV) NSCLC with ≤3 prior lines of systemic therapy, excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002503] Cohort 3B: TIL therapy as a single agent in patients Stage III or Stage IV NSCLC who have previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1) as part of ≤ 3 prior lines of systemic therapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002504] Patients in Cohorts 3A and 3B (NSCLC) with oncogene-driven tumors with available effective targeted therapy must have received at least one line of targeted therapy.

[002505] All patients received autologous cryopreserved TIL therapy (with or without pembrolizumab, depending on cohort assignment), preceded by a nonmyeloablative lymphodepletion (NMA-LD) preconditioning regimen consisting of cyclophosphamide and fludarabine. Following TIL infusion, up to 6 IV interleukin-2 (IL-2) doses maximum were administered.

[002506] The following general study periods took place in all 4 cohorts, unless specified otherwise.

[002507] Screening and Tumor Resection: Up to 4 weeks (28 days) from study entry; manufacturing of the TIL Product: approximately ≤22 days from tumor resection; and treatment period, as discussed below.

[002508] Treatment Period (Cohorts 1A, 2A, and 3A): up to 2 years, including NMA-LD (7 days), TIL infusion (1 day) followed by IL-2 administrations (1 to 4 days).Patients receive a single infusion

of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans but before the initiation of the NMA-LD regimen. The next dose of pembrolizumab will be no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter for ≤ 2 years (24 months) or until disease progression or unacceptable toxicity, whichever occurs first. The end-of-treatment (EOT) visit occurred within 30 days after the last dose of pembrolizumab. The visit could be combined with end-of-assessment (EOA) visit if applicable (*e.g.*, pembrolizumab discontinuation occurred at disease progression or at the start of new anticancer therapy).

[002509] Treatment Period (Cohort 3B): up to 12 days, including NMA-LD (7 days), TIL, infusion (1 day) followed by IL-2 administrations (1 to 4 days). The EOT visit occurred once a patient received the last dose of IL-2. The EOT visit was performed within 30 days after treatment discontinuation and it may be combined with any scheduled visit occurring within this interval during the assessment period.

[002510] Assessment Period: began after TIL infusion on Day 0 and ends upon disease progression, with the start of a new anticancer therapy, partial withdrawal of consent to study assessments, or 5 years (Month 60), whichever occurred first. An end-of assessment (EOA) visit occurred once a patient reached disease progression or started a new anticancer therapy.

[002511] The TIL autologous therapy with the TILs prepared as described herein was comprised of the following steps:

[002512] 1. Tumor resection to provide the autologous tissue that serves as the source of the TIL cellular product;

[002513] 2. TIL product produced at a central Good Manufacturing Practice (GMP) facility;

[002514] 3. A 7-day NMA-LD preconditioning regimen;

[002515] 4. Cohorts 1A, 2A, and 3A: Patients receive a single infusion of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans but before the initiation of NMA-LD regimen. The next dose of pembrolizumab will be no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter.

[002516] 5. Infusion of the autologous TIL product (Day 0); and

[002517] 6. IV IL-2 administrations for up to 6 doses maximum.

[002518] In Cohorts 1A, 2A, and 3A, the next dose of pembrolizumab was no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter for ≤ 2 years (24 months), or until disease progression or unacceptable toxicity, whichever occurred first.

[002519] Flowcharts for Cohorts 1A, 2A, and 3A can be found in Figure 7. The Flowchart for Cohort 3B can be found in Figure 8. Patients were assigned to the appropriate cohort by tumor indication.

[002520] TIL Therapy + Pembrolizumab (Cohorts 1A, 2A, and 3A)

[002521] Patients were screened and scheduled for surgery for tumor resection. Patients then had one or more tumor lesions resected, which were sent to a central manufacturing facility for TIL production.

[002522] Next, the NMA-LD regimen was imitated and consisted of 2 days of IV cyclophosphamide (60 mg/kg) with mesna (per site standard of care or USPI/SmPC) on Days -7 and Day -6 followed by 5 days of IV fludarabine (25 mg/m2: Day -5 through Day -1).

[002523] Patients in Cohorts 1A, 2A, and 3A received a single infusion of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans and before the initiation of NMA-LD regimen. IL-2 administrations at a dose of 600,000 IU/kg IV begun as soon as 3 hours after, but no later than 24 hours after, completion of the TIL infusion on Day 0. Additional IL-2 administrations will be given approximately every 8 to 12 hours for up to 6 doses maximum. The second dose of pembrolizumab was no earlier than following the completion of IL-2. Patients should have recovered from all IL-2-related toxicities (Grade $\leq$2), prior to the second pembrolizumab administration. Pembrolizumab will continue Q3W $\pm$ 3 days thereafter for $\leq$2 years (24 months) or until disease progression or unacceptable toxicity, whichever occurred first.

[002524] TIL Therapy as a Single Agent (Cohort 3B)

[002525] Patients were screened and scheduled for surgery for tumor resection. Patients then had one or more tumor lesions resected, which were sent to a central manufacturing facility for TIL production.

[002526] Next, the NMA-LD regimen consisted of 2 days of IV cyclophosphamide (60 mg/kg) with mesna (per site standard of care or USPI/SmPC) on Day -7 and Day -6 followed by 5 days of IV fludarabine (25 mg/m2: Day -5 through Day -1).

[002527] Infusion of the tumor-derived autologous TIL product occurred no sooner than 24 hours after last dose of fludarabine. IL-2 administrations at a dose of 600,000 IU/kg IV may have begun as soon as 3 hours after, but no later than 24 hours after, completion of the TIL infusion.

[002528] Additional IL-2 administrations were given approximately every 8 to 12 hours for up to 6 doses maximum.

[002529] Production and Expansion of Tumor Infiltrating Lymphocytes

[002530] The TIL autologous cellular product was composed of viable cytotoxic T lymphocytes derived from a patient's tumor/lesion, which are manufactured ex vivo at a central GMP facility. An exemplary flow diagram depicting the TIL production process is provided in Figure 9, for example.

[002531] The TIL manufacturing process begun at the clinical site after surgical excision of a primary or secondary metastatic tumor lesion(s) of ≥1.5 cm in diameter in each individual patient. Multiple tumor lesions from various anatomical locations can be excised to compile a total aggregate of tumor tissue; however, the aggregate should not exceed 4.0 cm in diameter, or 10 g in weight, due to the limited quantity of the biopreservation media present in the transport bottle.

[002532] Once the tumor lesion(s) was placed in the biopreservation transport bottle, it is shipped at 2°C to 8°C using an express courier to a central GMP manufacturing facility. Upon arrival, the tumor specimen(s) were dissected into fragments, which were then cultured in a pre-rapid expansion protocol (Pre-REP) with human recombinant IL-2 for ~11 days.

[002533] These pre-REP cells were then further expanded using a rapid expansion protocol (REP) for 11 days in the presence of IL-2, OKT3 (a murine monoclonal antibody to human CD3, also known as [muromonab-CD3]) and irradiated allogenic peripheral blood mononuclear cells (PBMC) as feeder cells.

[002534] The expanded cells were then harvested, washed, formulated, cryopreserved, and shipped to the clinical site via an express courier. The dosage form of the TIL cellular product was a cryopreserved autologous "live-cell suspension" that was ready for infusion into the patient from whom the TIL were derived. Patients were to receive the full dose of product that was manufactured and released, which contained between 1×10^9 and 150×10^9 viable cells per the product specification. Clinical experience indicated that objective tumor responses were achieved across this dose range, which has also been shown to be safe (Radvanyi L.G., *et al.*, Clin Cancer Res. **2012**;18(24):6758-70). The full dose of product was provided in up to four infusion bags.

[002535] Preparation of Patients to Receive the TIL Cellular Product

[002536] The NMA-LD preconditioning regimen used in this study (i.e., 2 days of cyclophosphamide plus mesna, followed by 5 days of fludarabine) was based on the method developed and tested by the National Cancer Institute (Rosenberg S.A., et al., Clin Cancer Res. **2011**;17(13):4550-7; Radvanyi L.G., et al., Clin Cancer Res. **2012**;18(24):6758-70; Dudley M.E., et al., J Clin Oncol. **2008**;26(32):5233-9; Pilon-Thomas S, et al., J Immunother. **2012**;35(8):615-20; Dudley M.E., et al., J Clin Oncol. **2005**;23(10):2346-57; and Dudley M.E., et al., Science. **2002**;298(5594):850-4). Following the 7-day preconditioning regimen, the patient was infused with the TIL cellular product.

[002537] The TIL infusion was followed by the administration of IV IL-2 (600,000 IU/kg) every 8 to 12 hours, with the first dose administered between 3 and 24 hours after the completion of the TIL infusion and continuing for up to 6 doses maximum. Per institutional standards, the doses of IL-2 can be calculated on the basis of actual weight.

[002538] SELECTION OF PATIENT POPULATIONS

[002539] *Cohort 1A:*

[002540] Patients had a confirmed diagnosis of unresectable MM (Stage IIIC or Stage IV, histologically confirmed as per American Joint Committee on Cancer [AJCC] staging system). Ocular melanoma patients were excluded. Patients must not have received prior immuno-oncology targeted agents. If BRAF-mutation positive, patient could have received prior BRAF/MEKtargeted therapy.

[002541] *Cohort 2A:*

[002542] Patients had advanced, recurrent and/or metastatic HNSCC and can be treatment naive; histologic diagnosis of the primary tumor is required via the pathology report. Patients must not have received prior immunotherapy regimens.

[002543] *Cohort 3A:*

[002544] Patients had a confirmed diagnosis of Stage III or Stage IV NSCLC (squamous, adenocarcinoma, large cell carcinoma). Patients with oncogene-driven tumors with available effective targeted therapy had received at least one line of targeted therapy.

[002545] *Cohort 3B:*

[002546] Patients had a confirmed diagnosis of Stage III or Stage IV NSCLC (squamous, adenocarcinoma, large cell carcinoma) and had previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1). Patients with oncogene-driven tumors with available effective targeted therapy had received at least one line of targeted therapy.

[002547] All patients had received up to 3 prior systemic anticancer therapies (see, inclusion criteria below), excluding immunotherapy for Cohorts 1A, 2A, and 3A. If previously treated, patients had radiographically confirmed progression on or after most recent therapy.

[002548] *Inclusion Criteria*

[002549] Patients must have met ALL of the following inclusion criteria for participation in the study:

[002550] 1. All patients had a histologically or pathologically confirmed diagnosis of malignancy of their respective histologies:

- Unresectable or metastatic melanoma (Cohort 1A)
- Advanced, recurrent or metastatic squamous cell carcinoma of the head and neck (Cohort 2A)
- Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, large cell carcinoma) (Cohorts 3A and 3B).

[002551] 2. Cohorts 1A, 2A, and 3A only: Patients were immunotherapy naïve. If previously treated, patients had progressed on or after most recent therapy. Cohorts 1A, 2A, and 3A may have received up to 3 prior systemic anticancer therapies, specifically:

- In Cohort 1A: Patients with unresectable or metastatic melanoma (Stage IIIC or Stage IV); if BRAF mutation-positive, patients could have received a BRAF inhibitor.
- In Cohort 2A: Patients with unresectable or metastatic HNSCC. Those who had received initial chemo-radiotherapy were allowed.
- In Cohort 3A: Patients with Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, or large cell carcinoma) and who were immunotherapy naïve and progressed after ≤3 lines of prior systemic therapy in the locally advanced or metastatic setting. Patients who received systemic therapy in the adjuvant or neoadjuvant setting, or as part of definitive chemoradiotherapy, were eligible and were considered to have had one line of therapy if the disease has progressed within 12 months of completion of prior systemic therapy. Patients with known oncogene drivers (*e.g.*, EGFR, ALK, ROS) who had mutations that were sensitive to targeted therapies must had progressed after at least 1 line of targeted therapy.

[002552] 3. Cohort 3B only: Patients with Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, or large cell carcinoma) who had previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1) as part of ≤ 3 prior lines of systemic therapy.

- Patients had radiographically confirmed progression on or after most recent therapy.
- Patients who received systemic therapy in the adjuvant or neoadjuvant setting, or as part of definitive chemoradiotherapy, were eligible and were considered to have had 1 line of therapy if the disease had progressed within 12 months of completion of prior systemic therapy.

- Patients with known oncogene drivers (*e.g.*, EGFR, ALK, ROS) who had mutations that are sensitive to targeted therapies must have progressed after at least 1 line of targeted therapy.

[002553] 4. Patients had at least 1 resectable lesion (or aggregate lesions) of a minimum 1.5 cm in diameter post-resection for TIL investigational product production. It was encouraged that tumor tissue be obtained from multiple and diverse metastatic lesions, as long as the surgical resection did not pose additional risks to the patient.

- If the lesion considered for resection for TIL generation is within a previously irradiated field, the lesion must have demonstrated radiographic progression prior to resection.
- Patients must have an adequate histopathology specimen for protocol-required testing.

[002554] 5. Patients had remaining measurable disease as defined by the standard and well known RECIST 1.1 guidelines (*see*, for example, Eisenhauer, European Journal of Cancer 45:228–247 (2009), also available on the World Wide Web at project.eortc.org/recist/wp-content/uploads/sites/4/2015/03/RECISTGuidelines.pdf) following tumor resection for TIL manufacturing:

- Lesions in previously irradiated areas were not be selected as target lesions unless there had been demonstrated progression of disease in those lesions;
- Lesions that were partially resected for TIL generation that were still measurable per RECIST may be selected as nontarget lesions but could not serve as a target lesion for response assessment.

[002555] 6. Patients were ≥ 18 years at the time of consent.

[002556] 7. Patients had an Eastern Cooperative Oncology Group (ECOG) performance status of 0 or 1, and an estimated life expectancy of ≥3 months.

[002557] 8. Patients of childbearing potential or those with partners of childbearing potential had to be willing to practice an approved method of highly effective birth control during treatment and continue for 12 months after receiving all protocol-related therapy (Note: Females of reproductive potential were to use effective contraception during treatment and for 12 months after their last dose of IL-2, or 4 months after their last dose of pembrolizumab whichever occurred later). Males could not donate sperm during the study or for 12 months after treatment discontinuation, whichever occurred later.

[002558] 9. Patients had the following hematologic parameters:

- Absolute neutrophil count (ANC) ≥1000/mm3;
- Hemoglobin ≥9.0 g/dL;
- Platelet count ≥100,000/mm3.

[002559] 10. Patients had adequate organ function:

- Serum alanine aminotransferase (ALT)/serum glutamic-pyruvic transaminase (SGPT) and aspartate aminotransferase (AST)/SGOT ≤3 times the upper limit of normal (ULN), patients with liver metastasis ≤5 times ULN.
- An estimated creatinine clearance ≥40 mL/min using the Cockcroft Gault formula at Screening.
- Total bilirubin ≤2 mg/dL.
- Patients with Gilbert's Syndrome must have a total bilirubin ≤3 mg/dL.

[002560] 11. Patients were seronegative for the human immunodeficiency virus (HIV1 and HIV2). Patients with positive serology for hepatitis B virus surface antigen (HBsAg), hepatitis B core antibody (anti HBc), or hepatitis C virus (anti-HCV) indicating acute or chronic infection were enrolled depending on the viral load based on polymerase chain reaction (PCR) and the local prevalence of certain viral exposures.

[002561] 12. Patients had a washout period from prior anticancer therapy(ies) of a minimum duration, as detailed below prior to the first study treatment (*i.e.*, start of NMA-LD or pembrolizumab):

- Targeted therapy: prior targeted therapy with an epidermal growth factor receptor (EGFR), MEK, BRAF, ALK, ROS1 or other-targeted agents (*e.g.*, erlotinib, afatinib, dacomitinib, osimertinib, crizotinib, ceritinib, lorlatinib) was allowed provided the washout is a minimum of 14 days prior to the start of treatment.
- Chemotherapy: adjuvant, neoadjuvant or definitive chemotherapy/ chemoradiation was allowed provided the washout is a minimum of 21 days prior to the start of treatment.
- Immunotherapy for Cohort 3B only, prior checkpoint-targeted therapy with an anti-PD-1, other mAbs, or vaccines were allowed with a washout period of ≥ 21 days before the start of NMA-LD.

- Palliative radiation therapy: prior external beam radiation was allowed provided all radiation-related toxicities were resolved to Grade 1 or baseline, excluding alopecia, skin pigmentation change, or other clinically insignificant events, *e.g.*, small area radiation dermatitis or rectal or urinary urgency
- The tumor lesion(s) being assessed as target for response via RECIST 1.1 were outside of the radiation portal; however, if within the portal, they must have demonstrated progression (see Inclusion Criterion above).
- Surgery/pre-planned procedure: previous surgical procedure(s) was permitted provided that wound healing had occurred, all complications had resolved, and at least 14 days have elapsed (for major operative procedures) prior to the tumor resection.

[002562] 13. Patients had recovered from all prior anticancer treatment-related adverse events (TRAEs) to Grade ≤1 (per Common Terminology Criteria for Adverse Events [CTCAE]), except for alopecia or vitiligo, prior to cohort assignment.

[002563] 14. Patients with stable Grade ≥2 toxicity from prior anticancer therapy were considered on a case by case basis after consultation with the Medical Monitor.

[002564] 15. Cohorts 1A, 2A, and 3A patients with irreversible toxicity not reasonably expected to be exacerbated by treatment with pembrolizumab were included only after consultation with the Medical Monitor. For patients in Cohort 3B only, patients with documented Grade ≥2 or higher diarrhea or colitis as a result of a previous treatment with immune checkpoint inhibitor CPI(s) must have been asymptomatic for at least 6 months or had a normal by visual assessment colonoscopy post-treatment prior to tumor resection.

[002565] 16. Patients must have provided written authorization for use and disclosure of protected health information.

[002566] *Exclusion Criteria*

[002567] Patients who meet ANY of the following criteria were excluded from the study:

[002568] 1. Patients with melanoma of uveal/ocular origin

[002569] 2. Patients who had received an organ allograft or prior cell transfer therapy that included a nonmyeloablative or myeloablative chemotherapy regimen within the past 20 years. (Note: This criterion was applicable for patients undergoing retreatment with TIL, with the exception that they had a prior NMA-LD regimen with their

[002570] prior TIL treatment.)

[002571] 3. Patients with symptomatic and/or untreated brain metastases.

- • Patients with definitively-treated brain metastases will be considered for enrollment

[002572] after discussion with Medical Monitor; if, prior to the start of treatment the patient is

[002573] clinically stable for ≥2 weeks, there are no new brain lesions via magnetic resonance

[002574] imaging (MRI) post-treatment, and the patient does not require ongoing

[002575] corticosteroid treatment.

[002576] 4. Patients who are on a systemic steroid therapy within 21 days of enrollment.

[002577] 5. Patients who are pregnant or breastfeeding.

[002578] 6. Patients who had an active medical illness(es), which in the opinion of the Investigator, posed increased risks for study participation; such as systemic infections (*e.g.*, syphilis or any other infection requiring antibiotics), coagulation disorders, or other active major medical illnesses of the cardiovascular, respiratory, or immune systems.

[002579] 7. Patients may not have active or prior documented autoimmune or inflammatory disorders (including pneumonitis, inflammatory bowel disease [*e.g.*, colitis or Crohn's disease], diverticulitis [with the exception of diverticulosis], systemic lupus erythematosus, sarcoidosis syndrome, or Wegener syndrome [granulomatosis with polyangiitis, Graves' disease, rheumatoid arthritis, hypophysitis, uveitis, etc.]). The following were exceptions to this criterion:

- Patients with vitiligo or alopecia.
- Patients with hypothyroidism (*e.g.*, following Hashimoto syndrome) stable on
- hormone replacement.
- Any chronic skin condition that did not require systemic therapy.
- Patients with celiac disease controlled by diet alone.

[002580] 8. Patients who had received a live or attenuated vaccination within 28 days prior to the start of treatment.

[002581] 9. Patients who had any form of primary immunodeficiency (such as severe combined immunodeficiency disease [SCID] and acquired immune deficiency syndrome [AIDS]).

[002582] 10. Patients with a history of hypersensitivity to any component of the study drugs. TILs were not administered to patients with a known hypersensitivity to any component of TIL product formulation including, but not limited to any of the following:

- • NMA-LD (cyclophosphamide, mesna, and fludarabine)
- • Prolcukin®, aldcslcukin, IL-2
- • Antibiotics of the aminoglycoside group (*i.e.*, streptomycin, gentamicin [excluding those who are skin-test negative for gentamicin hypersensitivity])
- • Any component of the TIL product formulation including dimethyl sulfoxide
- [DMSO], HSA, IL-2, and dextran-40
- • Pembrolizumab

[002583] 11. Patients who had a left ventricular ejection fraction (LVEF) <45% or who are New York Heart Association Class II or higher. A cardiac stress test demonstrating any irreversible wall movement abnormality in any patients ≥60 years of age or in patients who have a history of ischemic heart disease, chest pain, or clinically significant atrial and/or ventricular arrhythmias.

- Patients with an abnormal cardiac stress test could be enrolled if they had adequate ejection fraction and cardiology clearance with approval of the Sponsor's Medical Monitor.

[002584] 12. Patients who had obstructive or restrictive pulmonary disease and have a documented FEV1 (forced expiratory volume in 1 second) of ≤60% of predicted normal.

- • If a patient was not able to perform reliable spirometry due to abnormal upper airway anatomy (*i.e.*, tracheostomy), a 6-minute walk test was used to assess pulmonary function. Patients who were unable to walk a distance of at least 80% predicted for age and sex or demonstrates evidence of hypoxia at any point during the test (SpO2<90%) are excluded.

[002585] 13. Patients who had another primary malignancy within the previous 3 years (except for those which did not require treatment or had been curatively treated greater than 1 year ago, and in the judgment of the Investigator, did not pose a significant risk of recurrence including, but not limited to, non-melanoma skin cancer, DCIS, LCIS, prostate cancer Gleason score ≤6 or bladder cancer).

[002586] 14. Participation in another clinical study with an investigational product within 21 days of the initiation of treatment.

[002587] Study Endpoints and Planned Analyses

[002588] The primary and secondary endpoints were analyzed separately by cohort.

[002589] *Primary Endpoints:*

[002590] The ORR was defined as the proportion of patients who achieved either a confirmed PR or CR as best response as assessed by Investigators per RECIST 1.1 among the efficacy analysis set.

[002591] Objective response was evaluated per each disease assessment and the ORR was expressed as a binomial proportion with the corresponding 2-sided 90% CI. The primary analysis for each cohort occurred when all treated patients per cohort have an opportunity to be followed for 12 months, unless progressed/expired or discontinued early from the assessment period.

[002592] The safety primary endpoint was measured by any Grade 3 or higher TEAE incidence rate within each cohort expressed as binomial proportions with the corresponding 2-sided 90% CI.

[002593] *Secondary Endpoints:*

[002594] *Efficacy:*

[002595] The secondary efficacy endpoints were defined as follows:

[002596] CR rate as based on responders who achieved confirmed CR as assessed by Investigators. DCR was derived as the sum of the number of patients who achieved confirmed PR/CR or sustained SD (at least 6 weeks) divided by the number of patients in the efficacy analysis set × 100%. The CR rate and DCR was summarized using a point estimate and its 2-sided 90% CI.

[002597] DOR was defined among patients who achieved objective response. It was measured from the first-time response (PR/CR) criteria are met until the first date that recurrent or progressive disease was objectively documented, or receipt of subsequent anticancer therapy or the patient dies (whichever is first recorded). Patients not experiencing PD or have not died prior to the time of data cut or the final database lock will have their event times censored on the last date that an adequate assessment of tumor status is made.

[002598] PFS was defined as the time (in months) from the time of lymphodepletion to PD, or death due to any cause, whichever event is earlier. Patients not experiencing PD or not having expired at the time of the data cut or the final database lock had their event times censored on the last date that an adequate assessment of tumor status is made.

[002599] OS was defined as the time (in months) from the time of lymphodepletion to death due to any cause. Patients not having expired by the time of data cut or the final database lock had their event times censored on the last date of their known survival status.

[002600] DOR, PFS, and OS was subjected to right censoring. The Kaplan-Meier method will be used to summarize the time-to-event efficacy endpoints. The baseline data for the tumor assessment was the last scan before the lymphodepletion for all cohorts.

[002601] The above efficacy parameters will be estimated for applicable cohort for subsets defined by baseline disease characteristics; BRAF status (Cohort 1A only), HPV status (Cohort 2A only), squamous or non-squamous lung disease (Cohorts 3A and 3B only), and anti-PD-L1 status.

EXAMPLE 14: A PHASE 2, MULTICENTER STUDY OF AUTOLOGOUS TUMOR INFILTRATING LYMPHOCYTES IN PATIENTS WITH SOLID TUMORS

STUDY DESIGN

[002602] Overview

[002603] This example describes a prospective, open-label, multi-cohort, non-randomized, multicenter Phase 2 study evaluating ACT using TIL in combination with pembrolizumab or TIL as a single therapy, using TILs prepared as described in the present application as well as in this example.

[002604] Objectives:

[002605] *Primary:*

[002606] To evaluate the efficacy of autologous TIL in combination with pembrolizumab in MM, HNSCC, or NSCLC patients or TIL as a single therapy in relapsed or refractory (r/r) NSCLC patients, who had previously progressed on or after treatment with CPIs, as determined by objective response rate (ORR), using the Response Evaluation Criteria in Solid Tumors (RECIST 1.1), as assessed by Investigator.

[002607] To characterize the safety profile of TIL in combination with pembrolizumab in MM, HNSCC, and NSCLC patients or TIL as a single therapy in r/r NSCLC patients as measured by the incidence of Grade $\geq$ 3 treatment-emergent adverse events (TEAEs).

[002608] *Secondary:*

[002609] To further evaluate the efficacy of autologous TIL in combination with pembrolizumab in MM, HNSCC, and NSCLC patients or TIL as a single therapy in r/r NSCLC patients using complete

response (CR) rate, duration of response (DOR), disease control rate (DCR), progression-free survival (PFS) using RECIST 1.1, as assessed by Investigator, and overall survival (OS).

[002610] Cohorts:

[002611] Cohort 1A: TIL therapy in combination with pembrolizumab in patients with Stage IIIC or Stage IV unresectable or MM with ≤ 3 prior lines of systemic therapy excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002612] Cohort 2A: TIL therapy in combination with pembrolizumab in patients with advanced, recurrent or metastatic HNSCC (*e.g.*, Stages T1N1-N2B, T2-4N0-N2b) with ≤ 3 prior lines of systemic therapy, excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002613] Cohort 3A: TIL therapy in combination with pembrolizumab in patients with locally advanced or metastatic (Stage III– IV) NSCLC with ≤3 prior lines of systemic therapy, excluding immunotherapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002614] Cohort 3B: TIL therapy as a single agent in patients Stage III or Stage IV NSCLC who have previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1) as part of ≤ 3 prior lines of systemic therapy. If previously treated, patients must have had radiographically documented progression on or after most recent therapy.

[002615] Patients in Cohorts 3A and 3B (NSCLC) with oncogene-driven tumors with available effective targeted therapy must have received at least one line of targeted therapy.

[002616] All patients received autologous cryopreserved TIL therapy (with or without pembrolizumab, depending on cohort assignment), preceded by a nonmyeloablative lymphodepletion (NMA-LD) preconditioning regimen consisting of cyclophosphamide and fludarabine. Following TIL infusion, up to 6 IV interleukin-2 (IL-2) doses maximum were administered.

[002617] The following general study periods took place in all 4 cohorts, unless specified otherwise.

[002618] Screening and Tumor Resection: Up to 4 weeks (28 days) from study entry; manufacturing of the TIL Product: approximately ≤22 days from tumor resection; and treatment period, as discussed below.

[002619] Treatment Period (Cohorts 1A, 2A, and 3A): up to 2 years, including NMA-LD (7 days), TIL infusion (1 day) followed by IL-2 administrations (1 to 4 days).Patients receive a single infusion

of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans but before the initiation of the NMA-LD regimen. The next dose of pembrolizumab will be no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter for ≤ 2 years (24 months) or until disease progression or unacceptable toxicity, whichever occurs first. The end-of-treatment (EOT) visit occurred within 30 days after the last dose of pembrolizumab. The visit could be combined with end-of-assessment (EOA) visit if applicable (*e.g.*, pembrolizumab discontinuation occurred at disease progression or at the start of new anticancer therapy).

[002620] Treatment Period (Cohort 3B): up to 12 days, including NMA-LD (7 days), TIL, infusion (1 day) followed by IL-2 administrations (1 to 4 days). The EOT visit occurred once a patient received the last dose of IL-2. The EOT visit was performed within 30 days after treatment discontinuation and it may be combined with any scheduled visit occurring within this interval during the assessment period.

[002621] Assessment Period: began after TIL infusion on Day 0 and ends upon disease progression, with the start of a new anticancer therapy, partial withdrawal of consent to study assessments, or 5 years (Month 60), whichever occurred first. An end-of assessment (EOA) visit occurred once a patient reached disease progression or started a new anticancer therapy.

[002622] The TIL autologous therapy with the TILs prepared as described herein was comprised of the following steps:

[002623] 1. Tumor resection to provide the autologous tissue that serves as the source of the TIL cellular product;

[002624] 2. TIL product produced at a central Good Manufacturing Practice (GMP) facility;

[002625] 3. A 7-day NMA-LD preconditioning regimen;

[002626] 4. Cohorts 1A, 2A, and 3A: Patients receive a single infusion of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans but before the initiation of NMA-LD regimen. The next dose of pembrolizumab will be no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter.

[002627] 5. Infusion of the autologous TIL product (Day 0); and

[002628] 6. IV IL-2 administrations for up to 6 doses maximum.

[002629] In Cohorts 1A, 2A, and 3A, the next dose of pembrolizumab was no earlier than following the completion of IL-2 and continue Q3W ± 3 days thereafter for ≤ 2 years (24 months), or until disease progression or unacceptable toxicity, whichever occurred first.

[002630] Flowcharts for Cohorts 1A, 2A, and 3A can be found in Figure 7. The Flowchart for Cohort 3B can be found in Figure 8. Patients were assigned to the appropriate cohort by tumor indication.

[002631] TIL Therapy + Pembrolizumab (Cohorts 1A, 2A, and 3A)

[002632] Patients were screened and scheduled for surgery for tumor resection. Patients then had one or more tumor lesions resected, which were sent to a central manufacturing facility for TIL production.

[002633] Next, the NMA-LD regimen was imitated and consisted of 2 days of IV cyclophosphamide (60 mg/kg) with mesna (per site standard of care or USPI/SmPC) on Days -7 and Day -6 followed by 5 days of IV fludarabine (25 mg/m2: Day -5 through Day -1).

[002634] Patients in Cohorts 1A, 2A, and 3A received a single infusion of pembrolizumab after the completion of their tumor resection for TIL production and baseline scans and before the initiation of NMA-LD regimen. IL-2 administrations at a dose of 600,000 IU/kg IV begun as soon as 3 hours after, but no later than 24 hours after, completion of the TIL infusion on Day 0. Additional IL-2 administrations will be given approximately every 8 to 12 hours for up to 6 doses maximum. The second dose of pembrolizumab was no earlier than following the completion of IL-2. Patients should have recovered from all IL-2-related toxicities (Grade $\leq$2), prior to the second pembrolizumab administration. Pembrolizumab will continue Q3W $\pm$ 3 days thereafter for $\leq$2 years (24 months) or until disease progression or unacceptable toxicity, whichever occurred first.

[002635] TIL Therapy as a Single Agent (Cohort 3B)

[002636] Patients were screened and scheduled for surgery for tumor resection. Patients then had one or more tumor lesions resected, which were sent to a central manufacturing facility for TIL production.

[002637] Next, the NMA-LD regimen consisted of 2 days of IV cyclophosphamide (60 mg/kg) with mesna (per site standard of care or USPI/SmPC) on Day -7 and Day -6 followed by 5 days of IV fludarabine (25 mg/m2: Day -5 through Day -1).

[002638] Infusion of the tumor-derived autologous TIL product occurred no sooner than 24 hours after last dose of fludarabine. IL-2 administrations at a dose of 600,000 IU/kg IV may have begun as soon as 3 hours after, but no later than 24 hours after, completion of the TIL infusion.

[002639] Additional IL-2 administrations were given approximately every 8 to 12 hours for up to 6 doses maximum.

[002640] Production and Expansion of Tumor Infiltrating Lymphocytes

[002641] The TIL autologous cellular product was composed of viable cytotoxic T lymphocytes derived from a patient's tumor/lesion, which are manufactured ex vivo at a central GMP facility. An exemplary flow diagram depicting the TIL production process is provided in Figure 9, for example.

[002642] The TIL manufacturing process begun at the clinical site after surgical excision of a primary or secondary metastatic tumor lesion(s) of ≥1.5 cm in diameter in each individual patient. Multiple tumor lesions from various anatomical locations can be excised to compile a total aggregate of tumor tissue; however, the aggregate should not exceed 4.0 cm in diameter, or 10 g in weight, due to the limited quantity of the biopreservation media present in the transport bottle.

[002643] Once the tumor lesion(s) was placed in the biopreservation transport bottle, it is shipped at 2°C to 8°C using an express courier to a central GMP manufacturing facility. Upon arrival, the tumor specimen(s) were dissected into fragments, which were then cultured in a pre-rapid expansion protocol (Pre-REP) with human recombinant IL-2 for ~11 days.

[002644] These pre-REP cells were then further expanded using a rapid expansion protocol (REP) for 11 days in the presence of IL-2, OKT3 (a murine monoclonal antibody to human CD3, also known as [muromonab-CD3]) and irradiated allogenic peripheral blood mononuclear cells (PBMC) as feeder cells.

[002645] The expanded cells were then harvested, washed, formulated, cryopreserved, and shipped to the clinical site via an express courier. The dosage form of the TIL cellular product was a cryopreserved autologous "live-cell suspension" that was ready for infusion into the patient from whom the TIL were derived. Patients were to receive the full dose of product that was manufactured and released, which contained between 1×10^9 and 150×10^9 viable cells per the product specification. Clinical experience indicated that objective tumor responses were achieved across this dose range, which has also been shown to be safe (Radvanyi L.G., *et al.*, Clin Cancer Res. **2012**;18(24):6758-70). The full dose of product was provided in up to four infusion bags.

[002646] Preparation of Patients to Receive the TIL Cellular Product

[002647] The NMA-LD preconditioning regimen used in this study (i.e., 2 days of cyclophosphamide plus mesna, followed by 5 days of fludarabine) was based on the method developed and tested by the National Cancer Institute (Rosenberg S.A., et al., Clin Cancer Res. **2011**;17(13):4550-7; Radvanyi L.G., et al., Clin Cancer Res. **2012**;18(24):6758-70; Dudley M.E., et al., J Clin Oncol. **2008**;26(32):5233-9; Pilon-Thomas S, et al., J Immunother. **2012**;35(8):615-20; Dudley M.E., et al., J Clin Oncol. **2005**;23(10):2346-57; and Dudley M.E., et al., Science. **2002**;298(5594):850-4). Following the 7-day preconditioning regimen, the patient was infused with the TIL cellular product.

[002648] The TIL infusion was followed by the administration of IV IL-2 (600,000 IU/kg) every 8 to 12 hours, with the first dose administered between 3 and 24 hours after the completion of the TIL infusion and continuing for up to 6 doses maximum. Per institutional standards, the doses of IL-2 can be calculated on the basis of actual weight.

[002649] SELECTION OF PATIENT POPULATIONS

[002650] *Cohort 1A:*

[002651] Patients had a confirmed diagnosis of unresectable MM (Stage IIIC or Stage IV, histologically confirmed as per American Joint Committee on Cancer [AJCC] staging system). Ocular melanoma patients were excluded. Patients must not have received prior immuno-oncology targeted agents. If BRAF-mutation positive, patient could have received prior BRAF/MEKtargeted therapy.

[002652] *Cohort 2A:*

[002653] Patients had advanced, recurrent and/or metastatic HNSCC and can be treatment naive; histologic diagnosis of the primary tumor is required via the pathology report. Patients must not have received prior immunotherapy regimens.

[002654] *Cohort 3A:*

[002655] Patients had a confirmed diagnosis of Stage III or Stage IV NSCLC (squamous, adenocarcinoma, large cell carcinoma). Patients with oncogene-driven tumors with available effective targeted therapy had received at least one line of targeted therapy.

[002656] *Cohort 3B:*

[002657] Patients had a confirmed diagnosis of Stage III or Stage IV NSCLC (squamous, adenocarcinoma, large cell carcinoma) and had previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1). Patients with oncogene-driven tumors with available effective targeted therapy had received at least one line of targeted therapy.

[002658] All patients had received up to 3 prior systemic anticancer therapies (see, inclusion criteria below), excluding immunotherapy for Cohorts 1A, 2A, and 3A. If previously treated, patients had radiographically confirmed progression on or after most recent therapy.

[002659] *Inclusion Criteria*

[002660] Patients must have met ALL of the following inclusion criteria for participation in the study:

[002661] 1. All patients had a histologically or pathologically confirmed diagnosis of malignancy of their respective histologies:

- Unresectable or metastatic melanoma (Cohort 1A)
- Advanced, recurrent or metastatic squamous cell carcinoma of the head and neck (Cohort 2A)
- Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, large cell carcinoma) (Cohorts 3A and 3B).

[002662] 2. Cohorts 1A, 2A, and 3A only: Patients were immunotherapy naïve. If previously treated, patients had progressed on or after most recent therapy. Cohorts 1A, 2A, and 3A may have received up to 3 prior systemic anticancer therapies, specifically:

- In Cohort 1A: Patients with unresectable or metastatic melanoma (Stage IIIC or Stage IV); if BRAF mutation-positive, patients could have received a BRAF inhibitor.
- In Cohort 2A: Patients with unresectable or metastatic HNSCC. Those who had received initial chemo-radiotherapy were allowed.
- In Cohort 3A: Patients with Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, or large cell carcinoma) and who were immunotherapy naïve and progressed after $\leq$3 lines of prior systemic therapy in the locally advanced or metastatic setting. Patients who received systemic therapy in the adjuvant or neoadjuvant setting, or as part of definitive chemoradiotherapy, were eligible and were considered to have had one line of therapy if the disease has progressed within 12 months of completion of prior systemic therapy. Patients with known oncogene drivers (*e.g.*, EGFR, ALK, ROS) who had mutations that were sensitive to targeted therapies must had progressed after at least 1 line of targeted therapy.

[002663] 3. Cohort 3B only: Patients with Stage III or Stage IV NSCLC (squamous, nonsquamous, adenocarcinoma, or large cell carcinoma) who had previously received systemic therapy with CPIs (*e.g.*, anti-PD-1/anti-PD-L1) as part of $\leq$ 3 prior lines of systemic therapy.

- Patients had radiographically confirmed progression on or after most recent therapy.
- Patients who received systemic therapy in the adjuvant or neoadjuvant setting, or as part of definitive chemoradiotherapy, were eligible and were considered to have had 1 line of therapy if the disease had progressed within 12 months of completion of prior systemic therapy.

- Patients with known oncogene drivers (*e.g.*, EGFR, ALK, ROS) who had mutations that are sensitive to targeted therapies must have progressed after at least 1 line of targeted therapy.

[002664] 4. Patients had at least 1 resectable lesion (or aggregate lesions) of a minimum 1.5 cm in diameter post-resection for TIL investigational product production. It was encouraged that tumor tissue be obtained from multiple and diverse metastatic lesions, as long as the surgical resection did not pose additional risks to the patient.

- If the lesion considered for resection for TIL generation is within a previously irradiated field, the lesion must have demonstrated radiographic progression prior to resection.
- Patients must have an adequate histopathology specimen for protocol-required testing.

[002665] 5. Patients had remaining measurable disease as defined by the standard and well known RECIST 1.1 guidelines (*see*, for example, Eisenhauer, European Journal of Cancer 45:228–247 (2009), also available on the World Wide Web at project.eortc.org/recist/wp-content/uploads/sites/4/2015/03/RECISTGuidelines.pdf) following tumor resection for TIL manufacturing:

- Lesions in previously irradiated areas were not be selected as target lesions unless there had been demonstrated progression of disease in those lesions;
- Lesions that were partially resected for TIL generation that were still measurable per RECIST may be selected as nontarget lesions but could not serve as a target lesion for response assessment.

[002666] 6. Patients were ≥ 18 years at the time of consent.

[002667] 7. Patients had an Eastern Cooperative Oncology Group (ECOG) performance status of 0 or 1, and an estimated life expectancy of ≥3 months.

[002668] 8. Patients of childbearing potential or those with partners of childbearing potential had to be willing to practice an approved method of highly effective birth control during treatment and continue for 12 months after receiving all protocol-related therapy (Note: Females of reproductive potential were to use effective contraception during treatment and for 12 months after their last dose of IL-2, or 4 months after their last dose of pembrolizumab whichever occurred later). Males could not donate sperm during the study or for 12 months after treatment discontinuation, whichever occurred later.

[002669] 9. Patients had the following hematologic parameters:

- Absolute neutrophil count (ANC) ≥1000/mm3;
- Hemoglobin ≥9.0 g/dL;
- Platelet count ≥100,000/mm3.

[002670] 10. Patients had adequate organ function:

- Serum alanine aminotransferase (ALT)/serum glutamic-pyruvic transaminase (SGPT) and aspartate aminotransferase (AST)/SGOT ≤3 times the upper limit of normal (ULN), patients with liver metastasis ≤5 times ULN.
- An estimated creatinine clearance ≥40 mL/min using the Cockcroft Gault formula at Screening.
- Total bilirubin ≤2 mg/dL.
- Patients with Gilbert's Syndrome must have a total bilirubin ≤3 mg/dL.

[002671] 11. Patients were seronegative for the human immunodeficiency virus (HIV1 and HIV2). Patients with positive serology for hepatitis B virus surface antigen (HBsAg), hepatitis B core antibody (anti HBc), or hepatitis C virus (anti-HCV) indicating acute or chronic infection were enrolled depending on the viral load based on polymerase chain reaction (PCR) and the local prevalence of certain viral exposures.

[002672] 12. Patients had a washout period from prior anticancer therapy(ies) of a minimum duration, as detailed below prior to the first study treatment (*i.e.*, start of NMA-LD or pembrolizumab):

- Targeted therapy: prior targeted therapy with an epidermal growth factor receptor (EGFR), MEK, BRAF, ALK, ROS1 or other-targeted agents (*e.g.*, erlotinib, afatinib, dacomitinib, osimertinib, crizotinib, ceritinib, lorlatinib) was allowed provided the washout is a minimum of 14 days prior to the start of treatment.
- Chemotherapy: adjuvant, neoadjuvant or definitive chemotherapy/ chemoradiation was allowed provided the washout is a minimum of 21 days prior to the start of treatment.
- Immunotherapy for Cohort 3B only, prior checkpoint-targeted therapy with an anti-PD-1, other mAbs, or vaccines were allowed with a washout period of ≥ 21 days before the start of NMA-LD.

- Palliative radiation therapy: prior external beam radiation was allowed provided all radiation-related toxicities were resolved to Grade 1 or baseline, excluding alopecia, skin pigmentation change, or other clinically insignificant events, *e.g.*, small area radiation dermatitis or rectal or urinary urgency
- The tumor lesion(s) being assessed as target for response via RECIST 1.1 were outside of the radiation portal; however, if within the portal, they must have demonstrated progression (see Inclusion Criterion above).
- Surgery/pre-planned procedure: previous surgical procedure(s) was permitted provided that wound healing had occurred, all complications had resolved, and at least 14 days have elapsed (for major operative procedures) prior to the tumor resection.

[002673] 13. Patients had recovered from all prior anticancer treatment-related adverse events (TRAEs) to Grade ≤1 (per Common Terminology Criteria for Adverse Events [CTCAE]), except for alopecia or vitiligo, prior to cohort assignment.

[002674] 14. Patients with stable Grade ≥2 toxicity from prior anticancer therapy were considered on a case by case basis after consultation with the Medical Monitor.

[002675] 15. Cohorts 1A, 2A, and 3A patients with irreversible toxicity not reasonably expected to be exacerbated by treatment with pembrolizumab were included only after consultation with the Medical Monitor. For patients in Cohort 3B only, patients with documented Grade ≥2 or higher diarrhea or colitis as a result of a previous treatment with immune checkpoint inhibitor CPI(s) must have been asymptomatic for at least 6 months or had a normal by visual assessment colonoscopy post-treatment prior to tumor resection.

[002676] 16. Patients must have provided written authorization for use and disclosure of protected health information.

[002677] *Exclusion Criteria*

[002678] Patients who meet ANY of the following criteria were excluded from the study:

[002679] 1. Patients with melanoma of uveal/ocular origin

[002680] 2. Patients who had received an organ allograft or prior cell transfer therapy that included a nonmyeloablative or myeloablative chemotherapy regimen within the past 20 years. (Note: This criterion was applicable for patients undergoing retreatment with TIL, with the exception that they had a prior NMA-LD regimen with their

[002681] prior TIL treatment.)

[002682] 3. Patients with symptomatic and/or untreated brain metastases.

- • Patients with definitively-treated brain metastases will be considered for enrollment

[002683] after discussion with Medical Monitor; if, prior to the start of treatment the patient is

[002684] clinically stable for ≥2 weeks, there are no new brain lesions via magnetic resonance

[002685] imaging (MRI) post-treatment, and the patient does not require ongoing

[002686] corticosteroid treatment.

[002687] 4. Patients who are on a systemic steroid therapy within 21 days of enrollment.

[002688] 5. Patients who are pregnant or breastfeeding.

[002689] 6. Patients who had an active medical illness(es), which in the opinion of the Investigator, posed increased risks for study participation; such as systemic infections (*e.g.*, syphilis or any other infection requiring antibiotics), coagulation disorders, or other active major medical illnesses of the cardiovascular, respiratory, or immune systems.

[002690] 7. Patients may not have active or prior documented autoimmune or inflammatory disorders (including pneumonitis, inflammatory bowel disease [*e.g.*, colitis or Crohn's disease], diverticulitis [with the exception of diverticulosis], systemic lupus erythematosus, sarcoidosis syndrome, or Wegener syndrome [granulomatosis with polyangiitis, Graves' disease, rheumatoid arthritis, hypophysitis, uveitis, etc.]). The following were exceptions to this criterion:

- Patients with vitiligo or alopecia.
- Patients with hypothyroidism (*e.g.*, following Hashimoto syndrome) stable on
- hormone replacement.
- Any chronic skin condition that did not require systemic therapy.
- Patients with celiac disease controlled by diet alone.

[002691] 8. Patients who had received a live or attenuated vaccination within 28 days prior to the start of treatment.

[002692] 9. Patients who had any form of primary immunodeficiency (such as severe combined immunodeficiency disease [SCID] and acquired immune deficiency syndrome [AIDS]).

[002693] 10. Patients with a history of hypersensitivity to any component of the study drugs. TILs were not administered to patients with a known hypersensitivity to any component of TIL product formulation including, but not limited to any of the following:

- o • NMA-LD (cyclophosphamide, mesna, and fludarabine)
- o • Prolcukin®, aldcslcukin, IL-2
- o • Antibiotics of the aminoglycoside group (*i.e.*, streptomycin, gentamicin [excluding those who are skin-test negative for gentamicin hypersensitivity])
- o • Any component of the TIL product formulation including dimethyl sulfoxide
- o [DMSO], HSA, IL-2, and dextran-40
- o • Pembrolizumab

[002694] 11. Patients who had a left ventricular ejection fraction (LVEF) <45% or who are New York Heart Association Class II or higher. A cardiac stress test demonstrating any irreversible wall movement abnormality in any patients ≥60 years of age or in patients who have a history of ischemic heart disease, chest pain, or clinically significant atrial and/or ventricular arrhythmias.

- o Patients with an abnormal cardiac stress test could be enrolled if they had adequate ejection fraction and cardiology clearance with approval of the Sponsor's Medical Monitor.

[002695] 12. Patients who had obstructive or restrictive pulmonary disease and have a documented FEV1 (forced expiratory volume in 1 second) of ≤60% of predicted normal.

- o • If a patient was not able to perform reliable spirometry due to abnormal upper airway anatomy (*i.e.*, tracheostomy), a 6-minute walk test was used to assess pulmonary function. Patients who were unable to walk a distance of at least 80% predicted for age and sex or demonstrates evidence of hypoxia at any point during the test (SpO2<90%) are excluded.

[002696] 13. Patients who had another primary malignancy within the previous 3 years (except for those which did not require treatment or had been curatively treated greater than 1 year ago, and in the judgment of the Investigator, did not pose a significant risk of recurrence including, but not limited to, non-melanoma skin cancer, DCIS, LCIS, prostate cancer Gleason score ≤6 or bladder cancer).

[002697] 14. Participation in another clinical study with an investigational product within 21 days of the initiation of treatment.

[002698] Study Endpoints and Planned Analyses

[002699] The primary and secondary endpoints were analyzed separately by cohort.

[002700] *Primary Endpoints:*

[002701] The ORR was defined as the proportion of patients who achieved either a confirmed PR or CR as best response as assessed by Investigators per RECIST 1.1 among the efficacy analysis set.

[002702] Objective response was evaluated per each disease assessment and the ORR was expressed as a binomial proportion with the corresponding 2-sided 90% CI. The primary analysis for each cohort occurred when all treated patients per cohort have an opportunity to be followed for 12 months, unless progressed/expired or discontinued early from the assessment period.

[002703] The safety primary endpoint was measured by any Grade 3 or higher TEAE incidence rate within each cohort expressed as binomial proportions with the corresponding 2-sided 90% CI.

[002704] *Secondary Endpoints:*

[002705] *Efficacy:*

[002706] The secondary efficacy endpoints were defined as follows:

[002707] CR rate as based on responders who achieved confirmed CR as assessed by Investigators. DCR was derived as the sum of the number of patients who achieved confirmed PR/CR or sustained SD (at least 6 weeks) divided by the number of patients in the efficacy analysis set × 100%. The CR rate and DCR was summarized using a point estimate and its 2-sided 90% CI.

[002708] DOR was defined among patients who achieved objective response. It was measured from the first-time response (PR/CR) criteria are met until the first date that recurrent or progressive disease was objectively documented, or receipt of subsequent anticancer therapy or the patient dies (whichever is first recorded). Patients not experiencing PD or have not died prior to the time of data cut or the final database lock will have their event times censored on the last date that an adequate assessment of tumor status is made.

[002709] PFS was defined as the time (in months) from the time of lymphodepletion to PD, or death due to any cause, whichever event is earlier. Patients not experiencing PD or not having expired at the time of the data cut or the final database lock had their event times censored on the last date that an adequate assessment of tumor status is made.

[002710] OS was defined as the time (in months) from the time of lymphodepletion to death due to any cause. Patients not having expired by the time of data cut or the final database lock had their event times censored on the last date of their known survival status.

[002711] DOR, PFS, and OS was subjected to right censoring. The Kaplan-Meier method will be used to summarize the time-to-event efficacy endpoints. The baseline data for the tumor assessment was the last scan before the lymphodepletion for all cohorts.

[002712] The above efficacy parameters will be estimated for applicable cohort for subsets defined by baseline disease characteristics; BRAF status (Cohort 1A only), HPV status (Cohort 2A only), squamous or non-squamous lung disease (Cohorts 3A and 3B only), and anti-PD-L1 status.

EXAMPLE 15: A PHASE 2, MULTICENTER STUDY OF AUTOLOGOUS TUMOR INFILTRATING LYMPHOCYTES IN PATIENTS WITH SOLID TUMORS

[002713] The study in this example is a phase 2, multicenter, global, open label study of autologous tumor infiltrating lymphocytes (TIL) in patients with select solid tumors (metastatic melanoma, head and neck squamous cell cancer, and non-small cell lung cancer (NSCLC)). The example uses the TIL product manufactured according to the Examples herein, including Examples 10-17, as well as dresibed in throughout the present application, which is cryopreserved and has a 22-day manufacturing process. A single infusion of TIL produce was given after patients had completed the preparatory regimen of non-myeloablative lymphodepletion with cyclophosphamide (60mg/kg x2 days) and fludarabine ($25mg^2/m \times 5$ days). There are 4 patient cohorts as described below:

- Cohort 1A (combination cohort): Stage IIIC or IV unresectable or metastatic melanoma patients who are immunotherapy naïve with ≤3 prior lines of systemic therapy. These patients will be receiving TIL product in combination with pembrolizumab.
- Cohort 2A (combination cohort): Advanced, recurrent or metastatic head and neck squamous cell carcinoma patients who are immunotherapy naïve with ≤3 prior lines of systemic therapy. These patients will be receiving TIL product in combination with pembrolizumab.
- Cohort 3A (combination cohort): Locally advanced or metastatic (Stage III-IV) NSCLC patients who are immunotherapy naïve with ≤3 prior lines of systemic therapy. These patients will be receiving TIL product in combination with pembrolizumab.
- Cohort 3B (single agent cohort): Stage III- IV NSCLC patients who have previously received systemic therapy with checkpoint inhibitors (anti-PD-1/anti-PD-L1) as part of ≤3 prior lines of systemic therapy. These patients will be receiving TIL product as single agent.

[002714] Two patients with NSCLC have been enrolled in Cohort 3B (TIL alone post immune checkpoint inhibitor) who had completed their first response assessment visit at day 42) are described below.

[002715] Patient A is a 63-year old female diagnosed with Stage IVA lung adenocarcinoma. She had received 3 prior lines of systemic therapy which included pembrolizumab, carboplatin/ bevacizumab and vinorelbine. Her best response to prior pembrolizumab therapy was progressive disease; to carboplatin/bevacizumab was a partial response, and her vinorelbine response was non-evaluable (she discontinued prior to response assessment). She underwent left lower lobe lung resection for TIL generation and was infused with 3.75×10^9 cells of TIL product. The patient had her first response assessment (Day 42) visit, at which computerized tomography (CT) scans showed a 4% reduction in the tumor load compared to baseline scans, which is a stable disease response per RECIST 1.1.

[002716] Patient B is a 70-year old female diagnosed with Stage IVB basaloid squamous cell carcinoma. She had received 3 prior lines of therapy which included carboplatin/abraxane, nivolumab and cisplatin/gemcitabine. Her best response to prior carbo/abraxane was not evaluable (therapy discontinued due to toxicity); to nivolumab was progressive disease and for cisplatin/gemcitabine was a partial response. She underwent splenic lesion resection for TIL generation and was infused with 39×10^9 cells of TIL product. The patient had her first response assessment (Day 42) visit, at which CT scans showed a 44% reduction in the tumor load compared to baseline scans, which is a partial response per RECIST 1.1.

EXAMPLE 16: A PHASE 2, MULTICENTER STUDY OF AUTOLOGOUS TUMOR INFILTRATING LYMPHOCYTES IN PATIENTS WITH LOCALLY ADVANCED OR METASTATIC NON-SMALL-CELL LUNG CANCER

[002717] This example relates to treatment of patients with locally advanced, unresectable or metastatic non-small-cell lung cancer (NSCLC) without any actionable driver mutations who have disease progression on or following a single line of approved systemic therapy consisting of combined checkpoint inhibitor (CPI) + chemotherapy ± bevacizumab (including bevacizumab (AVASTIN), a VEGFA inhibitor) and the cohorts for treatment are summarized below:

- Cohort 1: Patients whose tumors did not express programmed cell death-ligand 1 (PD-L1) (tumor proportion score [TPS] < 1%) prior to their CPI treatment.
- Cohort 2: Patients whose tumors expressed PD-L1 (TPS ≥ 1%) prior to their CPI treatment. Cohort 3: Patients whose tumors did not express PD-L1 (TPS < 1%) prior to their CPI treatment and who are unable to safely undergo a surgical harvest for TIL generation due to at least one of the followin:
    - Unacceptable surgical risk, or

- Surgically approachable lesion was required for Response Evaluation Criteria in Solid Tumors (RECIST) v1.1 assessment.

- Cohort 4: Retreatment cohort: Patients who had been previously treated with TIL-based immunotherapy in Cohort 1, 2 or 3 of this study.

[002718] Treatment will be given using autologous TIL-based immunotherapy derived from an individual patient's tumor for patient-directed therapy

Study Details

Autologous TIL Therapy Regimen

[002719] The TIL-based immunotherapy treatment regimen involved a course of the NMA-LD preparative regimen using cyclophosphamide and fludarabine for a total of 5 days prior to TIL-based immunotherapy infusion, and a limited course of IL-2 administration (up to six doses) following the TIL-based immunotherapy infusion. The NMA-LD preparative regimen and IL-2 were included in the regimen to support the engraftment, expansion, and activation of the transferred TIL

[002720] Several preparative regimens had been used in conjunction with TIL therapies. NMA-LD preparative regimens included cyclophosphamide/fludarabine, total body irradiation (TBI), or the combination of both. The present exemplary study utilized the cy-flu regimen. The NMA-LD preparative regimen used in the current study was based on the method developed and tested by the National Cancer Institute (NCI), which involves 2 days of cyclophosphamide concomitant with 5 days of fludarabine in an effort to shorten the duration of the hospital stay of patients. Each patient would undergo an NMA-LD preparative regimen prior to infusion of TIL-based immunotherapy.

Brief description of the Treatment

[002721] The therapy was a ready-to-infuse, autologous TIL-based immunotherapy. The TIL-based immunotherapy was composed of autologous TIL, which were obtained from an individual patient's tumor and expanded *ex vivo* through cell culture in the presence of the cytokine IL-2 and a murine monoclonal antibody (mAb) to human CD3 (OKT3).

[002722] The final drug product was a cryopreserved live-cell suspension that was formulated for IV infusion. The *ex vivo* expanded autologous TIL were formulated in CryoStor® CS10 cryopreservation medium/PlasmaLyte (final dimethyl sulfoxide [DMSO] concentration: 5%), with 0.5% human serum albumin (HSA) and 300 IU/mL (12 ng/mL) of IL-2. The formulated product was frozen at a controlled rate to < -150°C in vapor phase liquid nitrogen, shipped in a cryoshipper to the appropriate clinical site, and thawed before use for infusion into the patient.

Production and Expansion of TIL

[002723] The manufacturing process began at the clinical site with the surgical resection or core biopsy of a tumor lesion containing viable tumor material. An aggregate of multiple separate lesion biopsies could also be resected from the patient and was encouraged if patient safety allows. The tumor specimen was placed in transport media and shipped by express courier at 2–8°C to the Good Manufacturing Practices (GMP) manufacturing facility. Upon arrival at the GMP manufacturing facility, the tumor specimen was dissected into fragments, which are then activated (initial expansion step) to generate the minimum number of viable cells required for the rapid expansion protocol (REP) stage. The tumors could also be enzymatically dissociated, and TIL could be selected for expression of biomarkers prior to proceeding to the REP. The REP stage (second expansion step) further expands the cells in the presence of IL-2, OKT3, and irradiated allogeneic peripheral blood mononuclear cells (PBMC). The REP-expanded cells are then harvested, washed, and formulated in a blood transport/infusion bag for shipment by courier to the clinical site. A diagram of the manufacturing process for TIL-based immunotherapy is provided in Figures 34 and 35.

[002724] Each cryopreservation bag of the TIL-based immunotherapy final product was labeled with a patient-specific label. TIL-based immunotherapy was shipped from the manufacturing facility to clinical sites for administration to patients.

[002725] This example related to a prospective, open-label, multi-cohort, non-randomized, multicenter phase 2 study evaluating TIL-based immunotherapy in patients with locally advanced unresectable or metastatic NSCLC.

The following cohorts were studied:

[002726] Cohort 1: TIL-based immunotherapy as single-agent therapy in patients with Stage IV NSCLC whose tumors did not express PD-L1 (tumor proportion score [TPS] < 1%) prior to their CPI treatment without a known actionable driver mutation, who had disease progression on or following a single line of approved systemic therapy consisting of combined CPI + chemotherapy ± bevacizumab, who had at least one resectable lesion (or aggregate lesions) of a minimum 1.5 cm in diameter for TIL production and, following the resection, had at least one remaining measurable lesion, as defined by RECIST 1.1..

[002727] Cohort 2: TIL-based immunotherapy as single-agent therapy in patients with Stage IV NSCLC whose tumors expressed PD-L1 (TPS ≥1%) prior to their CPI treatment, without any known actionable driver mutations, who had disease progression on or following a single line of approved systemic therapy consisting of combined CPI + chemotherapy ± bevacizumab, and who had at least one resectable lesion (or aggregate lesions) of a minimum 1.5 cm in diameter for TIL production and, following the resection, had at least one remaining measurable lesion, as defined by RECIST 1.1.

[002728] Cohort 3: TIL-based immunotherapy as single-agent therapy in patients with Stage IV NSCLC whose tumors did not express PD-L1 (TPS < 1%) prior to their CPI treatment, without any known actionable driver mutations, who had disease progression on or following a single line of approved systemic therapy consisting of combined CPI + chemotherapy ± bevacizumab, and who were unable to safely undergo a surgical harvest for TIL generation due to at least one of the following: 1) unacceptable surgical risk, or 2) surgically approachable lesion is required for RECIST assessment.

[002729] Cohort 4: TIL-based immunotherapy single agent therapy as retreatment in patients who previously received TIL-based immunotherapy as part of their participation in Cohorts 1, 2 or 3.

[002730] For Cohorts 1, 2, 3, and 4, all patients received autologous cryopreserved TIL-based immunotherapy, preceded by a nonmyeloablative lymphodepletion (NMA-LD) preconditioning regimen consisting of cyclophosphamide and fludarabine. Following TIL-based immunotherapy infusion, up to 6 doses of IV IL-2 (such as aldesleukin or a biosimilar or variant thereof) were administered. Alternatively, descrescendo IL-2 or low-dose IL-2 may be used as set forth herein.

[002731] The autologous TIL therapy with TIL-based immunotherapy included the following general steps:

- Tumor harvest to provide the autologous tissue that served as the source of the autologous TIL cellular product,
- Production of autologous TIL-based immunotherapy investigational product (IP) at a central Good Manufacturing Practice (GMP) facility,
- A 5-day nonmyeloablative lymphodepletion (NMA-LD) preconditioning regimen,
- Infusion of the TIL-based immunotherapy product (Day 0) , and
- Administration of ≤ 6 doses IV IL-2.

Primary Objectives:

[002732] Evaluated the efficacy of TIL-based immunotherapy in patients with locally advanced unresectable or metastatic NSCLC without an actionable driver mutation who have disease progression on or following a single line of approved systemic therapy consisting of combined checkpoint inhibitor(s) (CPI[s]) + chemotherapy ± bevacizumab, as determined by objective response rate (ORR), using the Response Evaluation Criteria in Solid Tumors (RECIST 1.1), as assessed by the Independent Review Committee (IRC) (Cohorts 1 and 2) or by the Investigator Cohort 3 and Cohort 4).

Secondary Objectives:

[002733] Evaluated the efficacy of TIL-based immunotherapy as determined by ORR, using RECIST 1.1, and as assessed by the Investigator (Cohorts 1 and 2).

[002734] Further evaluated the efficacy of TIL-based immunotherapy using complete response (CR) rate; duration of response (DOR); disease control rate (DCR); progression-free survival (PFS) using RECIST 1.1, as assessed by the IRC (Cohorts 1 and 2) and Investigator (all cohorts); and overall survival (OS).

[002735] Characterized the safety profile of TIL-based immunotherapy in NSCLC patients, as measured by the incidence of Grade ≥ 3 treatment-emergent adverse events (TEAEs).

[002736] For Cohort 3 only: Evaluated the efficiency of generating TIL-based immunotherapy from core biopsies.

Exploratory Objectives:

[002737] Evaluated the persistence of TIL-based immunotherapy and to identify immune correlates that may affect response, outcome, and toxicity variables.

[002738] Assessed respective, indication-specific, health-related quality of life (HRQoL) parameters.

Endpoints - Primary Endpoint:

[002739] ORR was assessed per RECIST 1.1 by the IRC (Cohorts 1 and 2) or by the Investigator (Cohorts 3 and 4).

Endpoints - Secondary Endpoints:

[002740] Incidence of severity, seriousness, relationship to study treatment, and characteristics of treatment-emergent adverse events (TEAEs), including serious AEs (SAEs), therapy-related AEs, and AEs leading to early discontinuation from treatment or withdrawal from the Assessment Period or death.

[002741] CR (complete response) rate, DOR (duration of response), DCR (disease control rate), and PFS (progression-free survival) as assessed by IRC per RECIST 1.1 (Cohorts 1 and 2).

[002742] ORR (objective response rate), CR rate, DOR, DCR, and PFS as assessed by the Investigator per RECIST 1.1 (all cohorts).

[002743] OS (overall survival).

[002744] Percentage successful TIL products generated from core biopsies (Cohort 3).

Endpoints - Exploratory Endpoints:

[002745] *In vivo* persistence of the T cells comprising the TIL product was assessed by monitoring the presence of TIL product-specific T-cell receptor-beta complementarity determining region 3 (CDR3) sequences in the patient's blood over time. The CDR3 sequences present in the product and peripheral blood samples were identified using deep sequencing.

[002746] Exploratory endpoints aimed at identifying predictive and pharmacodynamic clinical biomarkers of the activity of TIL-based immunotherapy:

- Phenotypic and functional characteristics of TIL-based immunotherapy;
- Immune profile of the tumor tissues;
- Gene expression profiles of the TIL product, tumor tissues, and/or PBMCs;
- Mutational landscape of the tumors;
- Circulating immune factors; and
- Immune composition of PBMC.

[002747] HRQoL (health-related quality of life) as assessed per the European Organization for Research and Treatment of Cancer (EORTC) quality of life questionnaire (QLQ) C30 and QLQ LC13.

Study Design Details:

[002748] A prospective, open-label, multi-cohort, non-randomized, multicenter phase 2 study evaluated adoptive cell therapy (ACT) with TIL-based immunotherapy.

[002749] All patients received TIL-based immunotherapy, consisting of these steps:

- Tumor harvest provided the autologous tissue that serves as the source of the autologous TIL cellular product,
- Production of autologous TIL-based immunotherapy investigational product (IP) at a central Good Manufacturing Practice (GMP) facility,
- A 5-day nonmyeloablative lymphodepletion (NMA-LD) preconditioning regimen,
- Infusion of the TIL-based immunotherapy product (Day 0) , and
- Administration of $\leq$ 6 doses IV IL-2.

[002750] The following general sequential periods will occur in all 4 cohorts, unless otherwise specified:

1. *Screening Period*: From informed consent form (ICF) signature to enrollment

2. *Pre-treatment Period*: From enrollment to initiation of preparative NMA-LD regimen.

3. *Treatment Period*: From initiation of preparative NMA-LD to End of Treatment (EOT) Visit. This consisted of 8 to 9 days of therapy, including NMA-LD (Days - 5 to -1), TIL-based immunotherapy infusion (Day 0), followed by IL-2 administrations (Days 0 or 1 to 3 or 4). The EOT occurred approximately 30 days after Day 0.

4. *Posttreatment Follow-up period*, which is composed of:

a. *Posttreatment Efficacy Follow-up Period (TEFU)*: From EOT Visit to study completion (at 5 years [Month 60] after treatment) or the End of Efficacy Assessment (EOEA) Visit, which would be prompted by disease progression or start of a new anticancer therapy, whichever occurs first.

b. *Long-Term Follow-up Period (LTFU)*: From EOEA, as described above, to study completion (at 5 years [Month 60] after treatment).

[002751] Study participants (enrolled patients) will transition early to LTFU (*e.g.*, at partial withdrawal of consent, or if is determined that they would not receive TIL-based immunotherapy for any reason). Early study withdrawal was prompted by either consent withdrawal, death, lost to follow-up, or study termination by Sponsor. A flowchart for the study design is presented in Figure 36.

Detailed Doses and Treatment Schedule:

TIL-Based Immunotherapy

[002752] Patients will undergo a 5-day preconditioning NMA-LD regimen that was initiated prior to the planned TIL-based immunotherapy infusion on Day 0 (*i.e.*, Days -5 through -1). The NMA LD regimen consisted of 2 days of intravenous (IV) cyclophosphamide (60 mg/kg) with mesna (per site standard of care or USPI/SmPC) on Days -5 and -4, and 5 days of fludarabine IV (25 mg/m2, Days -5 through -1).

[002753] IL-2 IV administrations at a dose of 600,000 IU/kg began as soon as 3 hours after, but no later than 24 hours after, completion of the TIL-based immunotherapy infusion on Day 0. Additional IL-2 doses were given approximately every 8 to 12 hours for up to 6 total doses.

Table 53: Treatment administration regimen

Treatment Administration										
	-5	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
Cyclophosphamide 60 mg/kg	X	X								
Mesna	X	X								
Fludarabine 25 mg/m^2/day	X	X	X	X	X					
TIL-based immunotherapy infusion						X				

Treatment Administration										
	-5	-4	-3	-2	-1	0	1	2	3	4
IL-2 600,000 IU/kg						(X)[a]	X	X	X	(X)[a]

[a] () = If applicable.

Mesna Preparation

[002754] Mesna was administered to reduce the risk of hemorrhagic cystitis related to cyclophosphamide administration. Mesna was administered as a continuous or intermittent infusion as per local standards.

[002755] The total dose of mesna was not adjusted if the amount of cyclophosphamide is reduced. Dilute the volume of mesna injection or infusion per institutional standard.

Infusion of Cyclophosphamide and Mesna

[002756] Cyclophosphamide (60 mg/kg) in a total volume of 250 mL or 500 mL (*e.g.*, 5% dextrose in water [D5W] or 0.9 % sodium chloride [NaCl]).

[002757] Mesna (15 mg/kg), if infused continuously, was infused over approximately 2 hours with cyclophosphamide (on Days -5 and -4), then at a rate of 3 mg/kg/hour for the remaining 22 hours in a suitable diluent over 24 hours starting concomitantly with each cyclophosphamide dose.

[002758] The total dose administered was at least 1.3 times that of the dose of cyclophosphamide. Higher or continued doses of mesna could be administered for prevention of hemorrhagic cystitis.

Infusion of Fludarabine

[002759] Fludarabine (25 mg/m2) was to be given IV over approximately 30 minutes once daily for 5 consecutive days during Day -5 to Day -1.

Duration of Participation:

[002760] Overall, the study participation time will be up to 5 years from treatment to completion.

Selected Inclusion Criteria:

[002761] Had histologically or pathologically confirmed diagnosis of NSCLC (squamous, nonsquamous, adenocarcinoma, large cell, or mixed histologies), and must have documented PD-L1 expression status, as determined by the tumor proportion score (TPS) prior to the CPI treatment that they received (ie, the historic TPS that informed the initial treatment choice) (TPS < 1% for Cohorts 1 and 3, and TPS ≥ 1% for Cohort 2).

[002762] Have received a single line of systemic therapy that included CPI and chemotherapy concurrently, with documented radiographic disease progression on or following this single line of systemic therapy.

[002763] Prior systemic therapy in the adjuvant or neoadjuvant setting, or as part of definitive chemoradiotherapy was not counted as a line of therapy if the disease had not progressed during or within 12 months of the completion of such therapy. Prior TIL treatment on this protocol did not count as a line of therapy for Cohort 4 (retreatment) patients.

[002764] Had documented exercise tolerance no less than 85% of their age-expected normal range and no signs or symptoms of ischemia or clinically significant arrhythmias.

[002765] Had Eastern Cooperative Oncology Group (ECOG) performance status of 0 or 1 and an estimated life expectancy of > 6 months, in the Investigator's opinion.

[002766] Cohorts 1 and 2: Must have had at least one resectable lesion (or aggregate lesions) of a minimum 1.5 cm in diameter for TIL production.

[002767] Cohort 3 only: Patients must have had a single RECIST 1.1 measurable lesion and no additional lesion available for surgical harvest, or be unable to safely undergo a surgical harvest for TIL generation, but able to safely have tumor harvest via radiology guided core biopsy sufficient for TIL generation.

[002768] Cohort 4: Followed either paradigm.

[002769] All Cohorts: If the lesion considered for harvest was within a previously irradiated field, the lesion must have demonstrated radiographic progression prior to harvest and the irradiation must have been completed at least 3 months prior to enrollment. Patients must have an adequate histopathology specimen for protocol-required testing.

[002770] Following tumor harvest for TIL manufacturing, all patients must have had at least one remaining measurable lesions, as defined by RECIST 1.1, with the following considerations:

- Lesions in previously irradiated areas were not selected as target lesions unless there had been demonstrated progression in those lesions and the irradiation has been completed at least 3 months prior to enrollment.

- Cohorts 1 and 2 only: Lesions that were surgically partially resected for TIL generation that were still measurable per RECIST v1.1 could be selected as nontarget lesions but could not serve as a target lesion for response assessment.

- Cohort 3 only: If no other lesion was available for core biopsy for TIL generation, the single RECIST v1.1 measurable lesion may have served as both, the harvest site for the core biopsies, and the lesion for response monitoring.

- Cohort 4: May follow either paradigm but must have had at least 1 RECIST v1.1 measurable lesion to follow for response.

Efficacy Assessment:

[002771] The following efficacy parameters for TIL-based immunotherapy as a single therapy in patients with NSCLC were investigated in each cohort: ORR, CR rate, DOR, DCR, PFS, and OS.

Statistical Considerations:

[002772] The statistical analyses were based on the estimation of efficacy and safety parameters and will be performed by cohort. No formal statistical comparisons were applied between cohorts.

[002773] The primary efficacy endpoint was ORR as assessed per RECIST v1.1 by the IRC (Cohorts 1 and 2) or by the Investigator (Cohorts 3 and 4).

[002774] The ORR, CR rates, and the DCRs were summarized using point estimates and 2-sided 95% confidence limits based on the Clopper-Pearson exact method. Kaplan-Meier methods were used to summarize time-to-event efficacy endpoints, such as DOR, PFS, and OS. DOR analyses were performed for patients who achieve objective responses.

[002775] The safety analyses were descriptive and based on the summarization of TEAEs, SAEs, and AEs leading to discontinuation from the study, vital signs, and clinical laboratory tests.

Sample Size Determination:

[002776] The total number of planned patients infused with TIL-based immunotherapy in Cohorts 1, 2 and 3 was approximately 95.

[002777] Cohort 1 and 2: Approximately 40 patients in each cohort. For each cohort, Simon's two-stage design (Simon, 1989) with minimax was used to test the null hypothesis of ≤10% ORR against the alternative hypothesis of ORR >10%. In the first stage, twenty-five patients were accrued. If there are 2 or fewer patients responding to the therapy in these 25 patients, the cohort could be terminated. Otherwise, expansion into Stage 2 to a total of 40 patients occurred concurrently with the analysis of Stage 1. At the end of the second stage, if at least 7 patients respond to therapy among the total of 40 patients, the null hypothesis was rejected. This 2-stage design provided 70% power to reject the null hypothesis of 10% ORR based on an assumption of 20% ORR for TIL-based immunotherapy at a one-sided alpha level of 0.1.

[002778] Cohort 3: Approximately 15 patients were planned, which provided an estimated ORR with a half-width 90% confidence interval (CI) of <0.23 by the Clopper-Pearson exact method.

[002779] Cohort 4: Retreatment cohort: Patients who had been previously treated with TIL-based immunotherapy in Cohort 1, 2 or 3 of this study.

EXAMPLE 17: COMPLETE RESPONSE (CR) TO IOVANCE TUMOR INFILTRATING LYMPHOCYTES (TIL) ALONE ADMINISTERED TO A PATIENT WITH RELAPSED NON-SMALL CELL LUNG CANCER (NSCLC): CASE REPORT

Introduction

[002780] NSCLC is the most common and lethal cancer with a world-wide prevalence of over 2 million and 1.7 million deaths annually. Treatment options are limited, and prognosis remains poor for patients with relapsed metastatic NSCLC (mNSCLC) after failing standard of care therapies including platinum-doublet chemotherapy and checkpoint inhibitors (CPI). There remains a significant unmet medical need in NSCLC for patients who progress after CPI.

[002781] Adoptive cell therapy with tumor infiltrating lymphocytes (TIL) has demonstrated responses in various malignancies including, melanoma, cervical cancer, NSCLC and HNSCC alone or in combination with checkpoint inhibitors (CPI).

[002782] The safety and efficacy of TIL therapy, in a case study of a mNSCLC heavily pre-treated patient with PD-L1 expression level less than< 1%, is presented.

Methods

[002783] We report on a 72-year-old female, never-smoker with metastatic NSCLC diagnosed after presenting with cough and cold symptoms. The workup included a chest computer tomography (CT) showing a 135 mm lung mass. Staging identified pulmonary, splenic and nodular lymphatic lesions (T4N1M1b; Stage IVB), PD-L1 <1%). Biopsy confirmed a basaloid squamous cell carcinoma. Therapy was initiated with carboplatin and +Nab paclitaxel but was discontinued after 3 cycles due to an allergic reaction and poor tolerability. The second-line of therapy consisted of was nivolumab which was, discontinued after 4 cycles due to disease progression. The patient had a PD-L1 level of less than 1%. A third-line regimen of gemcitabine and cisplatin doublet therapy was then administered. Cisplatin was discontinued after 4 cycles and gemcitabine was completed after 6 cycles. After an initial response, disease progression was observed.

[002784] Approximately 4 months after completing gemcitabine, with disease progressing rapidly below the diaphragm, the patient enrolled in (NCT03645928), a prospective, open-label, multi-cohort,

non-randomized, multicenter phase 2 study evaluating ACT with TIL. The patient had an ECOG performance status of 1, baseline target lesion sum-of-diameters SOD of 50 mm and had an increase of 127% in her SOD from screening to baseline on study prior to receiving TIL. The patient underwent tumor resection for TIL generation and received TIL as a single therapy and a one-time treatment. Preconditioning chemotherapy consisted of cyclophosphamide/fludarabine, then TIL followed by 3 doses of 600,000 IU/kg IL-2 (*i.e.*, aldesleukin). Treatment tolerability and safety were assessed on an ongoing basis along with efficacy evaluation by the Investigator using RECIST v1.1.

Results

[002785] Adverse events were consistent with the known toxicities of the lymphodepletion and IL-2. Treatment emergent adverse events were acute, self-limiting, manageable, and short in duration. Adverse events ≥ G3 were limited to G4 pancytopenia, and G3 hypotension and bacteremia. The patient experienced no serious adverse events.

[002786] At week 6, a partial response with PR (44% decrease) in target lesions was observed at the patient's first assessment. At 7 months after administration of TIL, when reduction of sum of diameters (SODs) was at a 48% decrease, a positron-emission tomography (PET) CT was conducted and showed no metabolic activity within the residual CT lesion. The patient is considered a complete response (CR) by PET-CT. The examination was ongoing at 15 months post TIL administration and total SOD reduction reached 60%. The patient has required no other anti-cancer therapy to be administered since the TIL administration.

Conclusions

[002787] This case presentation demonstrates that treatment with TILs as described in the present application can offer a therapeutic option for patients with metastatic NSCLC who have disease progression on mNSCLC after multiple lines of standard of care therapies, including CPI. Enrollment is ongoing and studies to continue to monitor and evaluate impact of TIL in NSCLC patients.

EXAMPLE 18: EXEMPLARY PRODUCTION OF A CRYOPRESERVED TIL CELL THERAPY

[002788] This example describes an exemplarty cGMP manufacture of TIL Cell Therapy Process in G-REX Flasks according to current Good Tissue Practices and current Good Manufacturing Practices.

Table 54 - Process Expansion Examplary Plan

Estimated Day (post-seed)	Activity	Target Criteria	Anticipated Vessels	Estimated Total Volume (mL)
0	Tumor Dissection	≤ 50 desirable tumor fragments per G-REX100MCS	G-REX100MCS 1 flask	≤1000
11	REP Seed	5 – 200 × 10^6 viable cells per G-REX500MCS	G-REX500MCS 1 flasks	≤5000
16	REP Split	1 × 10^9 viable cells per G-REX500MCS	G-REX500MCS ≤5 flasks	≤25000
22	Harvest	Total available cells	3-4 CS-750 bags	≤530

Table 55 - Flask Volumes

Flask Type	Working Volume/Flask
G-REX100MCS	1000
G-REX500MCS	5000

PROCESS INFORMATION - PRIMARY

Day 0 CM1 Media Preparation

[002789] In the BSC added reagents to RPMI 1640 Media bottle. Added the following reagents t Added per bottle: Heat Inactivated Human AB Serum (100.0 mL); GlutaMax (10.0 mL); Gentamicin sulfate, 50 mg/mL (1.0 mL); 2-mercaptoethanol (1.0 mL)

[002790] Removed unnecessary materials from BSC. Passed out media reagents from BSC, left Gentamicin Sulfate and HBSS in BSC for Formulated Wash Media preparation.

[002791] Thawed IL-2 aliquot. Thawed one 1.1 mL IL-2 aliquot (6x106 IU/mL) (BR71424) until all ice had melted. Recorded IL-2: Lot # and Expiry

[002792] Transferred IL-2 stock solution to media. In the BSC, transferred 1.0 mL of IL-2 stock solution to the CM1 Day 0 Media Bottle prepared. Added CM1 Day 0 Media 1 bottle and IL-2 (6x106 IU/mL) 1.0 mL.

[002793] Passed G-REX100MCS into BSC. Aseptically passed G-REX100MCS (W3013130) into the BSC.

[002794] Pumped all Complete CM1 Day 0 Media into G-REX100MCS flask. Tissue Fragments Conical or GRex100MCS .

Day 0 Tumor Wash Media Preparation

[002795] In the BSC, added 5.0 mL Gentamicin (W3009832 or W3012735) to 1 × 500 mL HBSS Media (W3013128) bottle. Added per bottle: HBSS (500.0 mL); Gentamicin sulfate, 50 mg/mL (5.0 mL). Filtered HBSS containing gentamicin prepared through a 1L 0.22-micron filter unit (W1218810).

Day 0 Tumor Processing

[002796] Obtained Tumor. Obtained tumor specimen from QAR and transferred into suite at 2-8ºC immediately for processing.

[002797] Aliquoted Tumor Wash Media.

[002798] Tumor Wash 1 Using 8" forceps (W3009771), removed the tumor from the specimen bottle and transferred to the "Wash 1" dish prepared. Followed by Tumor Wash 2 and Tumor Wash 3.

[002799] Measured Tumor. Assessed Tumor. Assessed whether > 30% of entire tumor area observed to be necrotic and/or fatty tissue. If applicable: Clean-Up Dissection. If tumor was large and >30% of tissue exterior was observed to be necrotic/fatty, performed "clean up dissection" by removing necrotic/fatty tissue while preserving tumor inner structure using a combination of scalpel and/or forceps.

[002800] Dissect Tumor Using a combination of scalpel and/or forceps, cut the tumor specimen into even, appropriately sized fragments (up to 6 intermediate fragments). Transferred intermediate tumor fragments. Dissected Tumor Fragmentsinto pieces approximately 3x3x3mm in size. Stored Intermediate Fragments to Prevent Drying.

[002801] Repeated Intermediate Fragment Dissection. Determined number of pieces collected. If desirable tissue remains, selected additional Favorable Tumor Pieces from the "favorable intermediate fragments" 6-well plate to fill the drops for a maximum of 50 pieces.

[002802] Prepared Conical Tube. Transferred Tumor Pieces to 50mL Conical Tube. Prepared BSC for G- REX100MCS. Removed G-REX100MCS from Incubator. Aseptically passed G-REX100MCS flask into the BSC. Added tumor fragments to G-REX100MCS flask. Evenly distributed pieces.

[002803] Incubated G-REX100MCS at the following parameters: Incubated G-REX flask: Temperature LED Display: 37.0±2.0 ºC; CO2 Percentage: 5.0±1.5 %CO2. Calculations: Time of incubation; lower limite = time of incubation + 252 hours; upper limit = time of incubation + 276 hours.

[002804] After process was complete, discarded any remaining warmed media and thawed aliquots of IL-2.

Day 11 – Media Preparation

[002805] Monitored Incubator. Monitored Incubator. Incubator parameters: Temperature LED Display: 37.0±2.0 ºC; CO2 Percentage: 5.0±1.5 %CO2.

[002806] Warmed 3x 1000 mL RPMI 1640 Media (W3013112) bottles and 3x 1000 mL AIM-V (W3009501) bottles in an incubator for ≥ 30 minutes. Removed RPMI 1640 Media from incubator. Prepared RPMI 1640 Media. Filter Media. Thawed 3 × 1.1mL aliquots of IL-2 (6x106 IU/mL) (BR71424). Removed AIM-V Media from the incubator. Add IL-2 to AIM-V. Aseptically transferred a 10L Labtainer Bag and a repeater pump transferr set into the BSC.

[002807] Prepared 10L Labtainer media bag. Prepared Baxa pump. Prepared 10L Labtainer media bag. Pumped media into 10L Labtainer. Removed pumpmatic from Labtainer bag.

[002808] Mixed media. Gently massaged the bag to mix. Sample media per sample plan. Removed 20.0mL of media and place in a 50mL conical tube.

[002809] Prepared Cell Count Dilution Tubes In the BSC, added 4.5mL of AIM-V Media that had been labelled with "For Cell Count Dilutions" and lot number to four 15mL conical tubes. Transferred reagents from the BSC to 2-8°C. Prepared 1L Transfer Pack. Outside of the BSC weld (per Process Note 5.11) a 1L Transfer Pack to the transfer set attached to the "Complete CM2 Day 11 Media" bag prepared. Prepared feeder cell transfer pack. Incubated Complete CM2 Day 11 Media.

Day 11 - TIL Harvest

[002810] Preprocessing table. Incubator parameters: Temperature LED Display: 37.0±2.0 ºC; CO2 Percentage: 5.0±1.5 %CO2. Removed G-REX100MCS from incubator. Prepared 300mL Transfer Pack. Welded transfer packs to G-REX100MCS.

[002811] Prepare flask for TIL Harvest and nitiation of TIL Harvest. TIL Harvested. Using the GatheRex, transferred the cell suspension through the blood filter into the 300mL transfer pack. Inspect membrane for adherent cells.

[002812] Rinsed flask membrane. Closed clamps on G-REX100MCS. Ensured all clamps are closed. Heat sealed the TIL and the "Supernatant" transfer pack. Calculated volume of TIL suspension. Prepared Supernatant Transfer Pack for Sampling.

[002813] Pulled Bac-T Sample. In the BSC, draw up approximately 20.0 mL of supernatant from the 1L "Supernatant" transfer pack and dispense into a sterile 50mL conical tube.

[002814] Inoculated BacT per Sample Plan. Removed a 1.0 mL sample from the 50mL conical labeled BacT prepared using an appropriately sized syringe and inoculated the anaerobic bottle.

[002815] Incubated TIL. Placed TIL Transfer Pack in incubator until needed. Performed cell counts and calculations. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Viability ÷ 2. Viable Cell Concentration ÷ 2. Determined Upper and Lower Limit for counts. Lower Limit: Average of Viable Cell Concentration × 0.9. Upper Limit: Average of Viable Cell Concentration × 1.1. Confirmed both counts within acceptable limits. Determined an average Viable Cell Concentration from all four counts performed.

[002816] Adjusted Volume of TIL Suspension. Calculate the adjusted volume of TIL suspension after removal of cell count samples. Total TIL Cell Volume (A). Volume of Cell Count Sample Removed (4.0 ml) (B) Adjusted Total TIL Cell Volume C=A-B.

[002817] Calculated Total Viable TIL Cells. Average Viable Cell Concentraion*: Total Volume; Total Viable Cells: C = A × B.

[002818] Calculation for flow cytometry: if the Total Viable TIL Cell count from was ≥ $4.0x10^7$, calculated the volume to obtain $1.0x10^7$ cells for the flow cytometry sample.

[002819] Total viable cells required for flow cytometry: $1.0x10^7$ cells. Volume of cells required for flow cytometry: Viable cell concentration divived by $1.0x10^7$ cells A.

[002820] Calculated the volume of TIL suspension equal to $2.0x10^8$ viable cells. As needed, calculated the excess volume of TIL cells to remove and removed excess TIL and placed TIL in incubator as needed. Calculated total excess TIL removed, as needed.

[002821] Calculated amount of CS-10 media to add to excess TIL cells with the target cell concentration for freezing is 1.0×10^8 cells/mL. Centrifuged excess TILs, as needed. Observed conical tube and added CS-10.

[002822] Filled Vials. Aliquoted 1.0mL cell suspension, into appropriately sized cryovials.Aliquoted residual volume into appropriately sized cryovial per SOP-00242. If volume is ≤0.5mL, add CS10 to vial until volume is 0.5mL.

[002823] TIL Cryopreservation of Sample

[002824] Calculated the volume of cells required to obtain $1x10^7$ cells for cryopreservation. Removed sample for Cryopreservation. Placed TIL in Incubator.

Cryopreservation of sample.

[002825] Observed conical tube and added CS-10 slowly and record volume of 0.5mL of CS10 added.

Day 11 - Feeder Cells

[002826] Obtained feeder cells. Obtained 3 bags of feeder cells with at least two different lot numbers from LN2 freezer. Kept cells on dry ice until ready to thaw. Prepared waterbath or Cryotherm. Thawed Feeder Cells at 37.0 ± 2.0°C water bath or cytotherm for ~3-5 minutes or until ice has just disappeared. Removed media from incubator. Pooled thawed feeder cells. Added feeder cells to transfer pack. Dispensed the feeder cells from the syringe into the transfer pack. Mixed pooled feeder cells and labeled transfer pack.

[002827] Calculated total volume of feeder cell suspension in Transfer Pack

[002828] Removed cell count samples. Using a separate 3mL syringe for each sample, pulled 4x1.0mL cell count samples from Feeder Cell Suspension Transfer Pack using the needless injection port. Aliquoted each sample into the cryovials labeled. Performed Cell Counts and Determine Multiplication FactorSelected protocols and entered multiplication factors. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Determined Upper and Lower Limit for counts and confirm within limits.

[002829] Adjusted Volume of Feeder Cell Suspension. Calculated the adjusted volume of Feeder Cell suspension after removal of cell count samples. Calculated Total Viable Feeder Cells. Obtained additional Feeder Cells as needed. Thawed Additional Feeder Cells as needed. Placed the 4th Feeder Cell bag into a zip top bag and thaw in a 37.0 ± 2.0°C water bath or cytotherm for ~3-5 minutes and pooled additional feeder cells. Measured Volume. Measured the volume of the feeder cells in the syringe and recorded below (B). Calculated the new total volume of feeder cells. Added Feeder Cells to Transfer Pack.

[002830] Prepared dilutions as needed, adding 4.5mL of AIM-V Media to four 15mL conical tubes. Prepared cell counts. Using a separate 3mLsyringe for each sample, removed 4 × 1.0mL cell count samples from Feeder Cell Suspension transfer pack, using the needless injection port. Performed cell counts and calculations. Determined an average Viable Cell Concentration from all four counts performed. Adjusted Volume of Feeder Cell suspension and calculated the adjusted volume of Feeder Cell suspension after removal of cell count samples. Total Feeder Cell Volume minues 4.0 mL removed. Calculated the volume of Feeder Cell Suspension that was required to obtain $5x10^9$ viable feeder cells. Calculated excess feeder cell volume. Calculated the volume of excess feeder cells to remove. Removed excess feeder cells.

[002831] Using a 1.0mL syringe and 16G needle, drew up 0.15mL of OKT3 and added OKT3. Heat sealed the Feeder Cell Suspension transfer pack.

Day 11 G-REX Fill and Seed

[002832] Set up G-REX500MCS. Removed "Complete CM2 Day 11 Media", from incubator and pumped media into G-REX500MCS. Pumped 4.5L of media into the G-REX500MCS, filling to the line marked on the flask. Heat sealed and incubated flask as needed. Welded the Feeder Cell suspension transfer pack to the G-REX500MCS. Added Feeder Cells to G-REX500MCS. Heat sealed. Welded the TIL Suspension transfer pack to the flask. Added TIL to G-REX500MCS. Heat sealed. Incubated G-REX500MCS at 37.0±2.0 ºC, CO2 Percentage: 5.0±1.5 %CO2.

[002833] Calculated incubation window. Performed calculations to determine the proper time to remove G-REX500MCS from incubator on Day 16. Lower limit: Time of incubation + 108 hours. Upper limit: Time of incubation + 132 hours.

Day 11 Excess TIL Cryopreservation

[002834] Applicable: Froze Excess TIL Vials. Verified the CRF has been set up prior to freeze. Perform Cryopreservation. Transferred vials from Controlled Rate Freezer to the appropriate storage. Upon completion of freeze, transfer vials from CRF to the appropriate storage container. Transferred vials to appropriate storage. Recorded storage location in LN2.

Day 16 Media Preparation

[002835] Pre-warmed AIM-V Media. Calculated time Media was warmed for media bags 1, 2, and 3. Ensured all bags have been warmed for a duration between 12 and 24 hours. Setup 10L Labtainer for Supernatant. Attached the larger diameter end of a fluid pump transfer set to one of the female ports of a 10L Labtainer bag using the Luer connectors. Setup 10L Labtainer for Supernatant and label. Setup 10L Labtainer for Supernatant. Ensure all clamps were closed prior to removing from the BSC. NOTE: Supernatant bag was used during TIL Harvest, which may be performed concurrently with media preparation.

[002836] Thawed IL-2. Thawed 5x1.1mL aliquots of IL-2 ($6x10^6$ IU/mL) (BR71424) per bag of CTS AIM V media until all ice had melted. Aliquoted 100.0mL GlutaMax. Added IL-2 to GlutaMax. Prepared CTS AIM V media bag for formulation. Prepared CTS AIM V media bag for formulation. Stage Baxa Pump. Prepared to formulate media. Pumped GlutaMax +IL-2 into bag. Monitored parameters: Temperature LED Display: 37.0±2.0 ºC, CO2 Percentage: 5.0±1.5 %CO2. Warmed Complete CM4 Day 16 Media. Prepared Dilutions.

Day 16 REP Spilt

[002837] Monitored Incubator parameters: Temperature LED Display: 37.0±2.0 ºC, CO2 Percentage: 5.0±1.5 %CO2. Removed G-REX500MCS from the incubator. Prepared and labeled 1L Transfer Pack as TIL Suspension and weighed 1L.

[002838] Volume Reduction of G-REX500MCS. Transferred ~4.5L of culture supernatant from the G-REX500MCS to the 10L Labtainer per SOP-01777.

[002839] Prepared flask for TIL Harvest. After removal of the supernatant, closed all clamps to the red line.

[002840] Initiation of TIL Harvest. Vigorously tap flask and swirl media to release cellsensure all cells have detached.

[002841] TIL Harvest. Released all clamps leading to the TIL suspension transfer pack. Using the GatheRex transferred the cell suspension into the TIL Suspension transfer pack. NOTE: Be sure to maintain the tilted edge until all cells and media are collected. Inspected membrane for adherent cells. Rinsed flask membrane. Closed clamps on G-REX500MCS. Heat sealed the Transfer Pack containing the TIL. Heat sealed the 10L Labtainer containing the supernatant. Recorded weight of Transfer Pack with cell suspension and calculate the volume suspension. Prepared transfer pack for sample removal. Removed testing samples from cell supernatant.

[002842] Sterility & BacT Testing Sampling: removed a 1.0mL sample from the 15 mL conical labeled BacT prepared. Removed Cell Count Samples. In the BSC, using separate 3mL syringes for each sample, removed 4x1.0 mL cell count samples from "TIL Suspension" transfer pack.

[002843] Removed Mycoplasma Samples. Using a 3mL syringe, removed 1.0 mL from TIL Suspension transfer pack and place into 15 mL conical labeled "Mycoplasma diluent" prepared.

[002844] Prepared Transfer Pack for Seeding. Placed TIL in Incubator. Removed cell suspension from the BSC and place in incubator until needed. Performed cell counts and calculations. Diluted cell count samples initially by adding 0.5mL of cell suspension into 4.5mL of AIM-V media prepared which gave a 1:10 dilution. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Determined Upper and Lower Limit for counts. NOTE: Dilution may be adjusted according based off the expected concentration of cells. Determined an average Viable Cell Concentration from all four counts performed. Adjusted Volume of TIL Suspension. Calculated the adjusted volume of TIL suspension after removal of cell count samples. Total TIL Cell Volume minus 5.0 mL removed for testing.

[002845] Calculated Total Viable TIL Cells. Calculated the total number of flasks to seed. NOTE: The maximum number of G-REX500MCS flasks to seed was five. If the calculated number of flasks to seed exceeded five, only five were seeded USING THE ENTIRE VOLUME OF CELL SUSPENSION AVAILABLE.

[002846] Calculate number of flasks for subculture. Calculated the number of media bags required in addition to the bag prepared. Prepared one 10L bag of "CM4 Day 16 Media" for every two

G-REX-500M flask needed as calculated. Proceeded to seed the first GREX-500M flask(s) while additional media is prepared and warmed. Prepared and warmed the calculated number of additional media bags determined. Filled G-REX500MCS. Prepared to pump media and pumped 4.5L of media into G-REX500MCS. Heat Sealed. Repeated Fill. Incubated flask. Calculated the target volume of TIL suspension to add to the new G-REX500MCS flasks. If the calculated number of flasks exceeds five only five will be seeded, USING THE ENTIRE VOLUME OF CELL SUSPENSION. Prepared Flasks for Seeding. Removed G-REX500MCS from the incubator. Prepared G-REX500MCS for pumping. Closed all clamps on except large filter line. Removed TIL from incubator. Prepared cell suspension for seeding. Sterile welded (per Process Note 5.11) "TIL Suspension" transfer pack to pump inlet line. Placed TIL suspension bag on a scale.

[002847] Seeded flask with TIL Suspension. Pump the volume of TIL suspension calculated into flask. Heat sealed. Filled remaining flasks.

[002848] Monitored Incubator. Incubator parameters: Temperature LED Display: 37.0±2.0 °C, CO2 Percentage: 5.0±1.5 %CO2. Incubated Flasks.

[002849] Determined the time range to remove G-REX500MCS from incubator on Day 22.

Day 22 Wash Buffer Preparation

[002850] Prepared 10 L Labtainer Bag. In BSC, attach a 4" plasma transfer set to a 10L Labtainer Bag via luer connection. Prepared 10 L Labtainer Bag. Closed all clamps before transferring out of the BSC. NOTE: Prepared one 10L Labtainer Bag for every two G-REX500MCS flasks to be harvested. Pumped Plasmalyte into 3000mL bag and removed air from 3000mL Origen bag by reversing the pump and manipulating the position of the bag. Added Human Albumin 25% to 3000mL Bag. Obtain a final volumeof 120.0 mL of Human Albumin 25%.

[002851] Prepared IL-2 Diluent. Using a 10mL syringe, removed 5.0 mL of LOVO Wash Buffer using the needleless injection port on the LOVO Wash Buffer bag. Dispensed LOVO wash buffer into a 50mL conical tube.

[002852] CRF Blank Bag LOVO Wash Buffer Aliquotted. Using a 100mL syringe, drew up 70.0 mL of LOVO Wash Buffer from the needleless injection port.

[002853] Thawed IL-2. Thawed one 1.1mL of IL-2 (6x106 IU/mL)), until all ice has melted. IL-2 Preparation. Added 50µL IL-2 stock (6x106 IU/mL) to the 50mL conical tube labeled "IL-2 Diluent."

[002854] Cryopreservation Prep. Placed 5 cryo-cassettes at 2-8°C to precondition them for final product cryopreservation.

[002855] Prepared Cell Count Dilutions. In the BSC, added 4.5mL of AIM-V Media that has been labelled with lot number and "For Cell Count Dilutions" to 4 separate 15mL conical tubes. Prepared Cell Counts. Labeled 4 cryovials with vial number (1-4). Kept vials under BSC to be used.

Day 22 TIL Harvest

[002856] Monitored Incubator. Incubator Parameters Temperature LED display: 37 ± 2.0°C, CO2 Percentage: 5%±1.5%. Removed G-REX500MCS Flasks from Incubator. Prepared TIL collection bag and labeled. Sealed off extra connections. Volume Reduction: Transferred ~4.5L of supernatant from the G-REX500MCS to the Supernatant bag.

[002857] Prepared flask for TIL Harvest. Initiated collection of TIL. Vigorously tap flask and swirl media to release cells. Eusure all cells have detached. Initiated collection of TIL. Released all clamps leading to the TIL suspension collection bag. TIL Harvest. Using the GatheRex, transferred the TIL suspension into the 3000mL collection bag. Inspect membrane for adherent cells. Rinsed flask membrane. Closed clamps on G- Rex500MCS and ensured all clamps are closed. Transferred cell suspension into LOVO source bag. Closed all clamps. Heat Sealed. Removed 4x1.0mL Cell Counts Samples

[002858] Performed Cell Counts. Performed cell counts and calculations utilizing NC-200 and Process Note 5.14. Diluted cell count samples initially by adding 0.5mL of cell suspension into 4.5mL of AIM-V media prepared. This gave a 1:10 dilution. Determined the Average Viability, Viable Cell Concentration, and Total Nucleated Cell concentration of the cell counts performed. Determined Upper and Lower Limit for counts. Determined the Average Viability, Viable Cell Concentration, and Total Nucleated Cell concentration of the cell counts performed. Weighed LOVO Source Bag. Calculated Total Viable TIL Cells. Calculated Total Nucleated Cells.

[002859] Prepared Mycoplasma Diluent. Removed 10.0 mL from one supernatant bag via luer sample port and placed in a 15mL conical.

LOVO

[002860] Performed "TIL G-REX Harvest" protocoland determined the final product target volume. Loaded disposable kit. Removed filtrate bag. Entered Filtrate capacity. Placed Filtrate container on benchtop. Attached PlasmaLyte. Verified that the PlasmaLyte was attached and observed that the PlasmaLyte is moving. Attached Source container to tubing and verified Source container was attached. Confirmed PlasmaLyte was moving.

Final Formulation and Fill

[002861] Target volume/bag calculation. Calculated volume of CS-10 and LOVO wash buffer to formulate blank bag. Prepared CRF Blank.

[002862] Calculated the volume of IL-2 to add to the Final Product. Final IL-2 Concentration desired (IU/mL) – 300IU/mL. IL-2 working stock: 6×10^4 IU/mL. Assembled Connect apparatus. Sterile welded a 4S-4M60 to a CC2 Cell Connection. Sterile welded (per Process Note 5.11) the CS750 Cryobags to the harness prepared. Welded CS-10 bags to spikes of the 4S-4M60.Prepared TIL with IL-2. Using an appropriately sized syringe, removed amount of IL-2 determined from the "IL-2 $6x10^4$" aliquot. Labeled Forumlated TIL Bag. Added the Formulated TIL bag to the apparatus. Added CS10. Switched Syringes. Drew ~10mL of air into a 100mL syringe and replaced the 60mL syringe on the apparatus. Added CS10. Prepared CS-750 bags. Dispensed cells.

[002863] Removed air from final product bags and take retain. Once the last final product bag was filled, closed all clamps. Drew 10mL of air into a new 100mL syringe and replace the syringe on the apparatus. Dispensed retain into a 50mL conical tube and label tube as "Retain" and lot number. Repeat air removal step for each bag.

[002864] Prepared final product for cryopreservation, incuding visual inspection. Held the cryobags on cold pack or at 2-8°C until cryopreservation.

[002865] Removed Cell Count Sample. Using an appropriately sized pipette, remove 2.0 mL of retain and place in a 15mL conical tube to be used for cell counts. Performed cell counts and calculations. NOTE: Diluted only one sample to appropriate dilution to verify dilution is sufficient. Diluted additional samples to appropriate dilution factor and proceed with counts. Determined the Average of Viable Cell Concentration and Viability of the cell counts performed. Determined Upper and Lower Limit for counts. NOTE: Dilution may be adjusted according based off the expected concentration of cells. Determined the Average of Viable Cell Concentration and Viability. Determined Upper and Lower Limit for counts. Calculated IFN-γ. Heat Sealed Final Product Bags.

[002866] Labeled and Collected Samples per exemplary Sample Plan below.

Table 56: Sample Plan

Sample	Number of Containers	Sample Volume to Add to Each	Container Type
*Mycoplasma	1	1.0 mL	15 mL Conical
Endotoxin	2	1.0 mL	2 mL Cryovial
Gram Stain	1	1.0 mL	2 mL Cryovial
IFN-g	1	1.0 mL	2 mL Cryovial

Flow Cytometry	1	1.0 mL	2 mL Cryovial
**Bac-T Sterility	2	1.0 mL	Bac-T Bottle
QC Retain	4	1.0 mL	2 mL Cryovial
Satellite Vials	10	0.5 mL	2 mL Cryovial

[002867] Sterility & BacT. Testing Sampling. In the BSC, remove a 1.0mL sample from the retained cell suspension collected using an appropriately sized syringe and inoculate the anaerobic bottle. Repeat the above for the aerobic bottle

Final Product Cryopreservation

[002868] Prepared Controlled Rate Freezer. Verified the CRF had been set up. Set up CRF probes. Placed final product and samples in CRF. Determined the time needed to reach 4 °C ± 1.5 °C and proceed with the CRF run. CRF Completed and Stored. Stopped the CRF after the completion of the run. Remove cassettes and vials from CRF. Transferred cassettes and vials to vapor phase LN2 for storage. Recorded storage location

POST PROCESSING SUMMARY

Post-Processing: Final Drug Product

[002869] (Day 22) Determination of CD3+ Cells on Day 22 REP by Flow Cytometry

[002870] (Day 22) Gram Staining Method (GMP)

[002871] (Day 22) Bacterial Endotoxin Test by Gel Clot LAL Assay (GMP)

[002872] (Day 16) BacT Sterility Assay (GMP)

[002873] (Day 16) Mycoplasma DNA Detection by TD-PCR (GMP)

[002874] Acceptable Appearance Attributes

[002875] (Day 22) BacT Sterility Assay (GMP)(Day 22)

[002876] (Day 22) IFN-gamma Assay

EXAMPLE 19: FIRST PHASE 2 RESULTS OF AUTOLOGOUS TUMOR-INFILTRATING LYMPHOCYTE MONOTHERAPY IN PATIENTS WITH ADVANCED, IMMUNE CHECKPOINT INHIBITOR-TREATED, NON-SMALL CELL LUNG CANCER (NSCLC)

Introduction

Background

[002877] A majority of patients with advanced NSCLC develop disease progression with first-line ICI ± chemotherapy[1].

[002878] In the setting of ICI resistance, effective strategies to provide deep and durable responses are urgently needed.

[002879] Gen 2 process TILs are centrally manufactured autologous TIL cell products that have demonstrated activity in advanced melanoma, cervical cancer, and head and neck carcinoma[2–5].

[002880] TIL + nivolumab has demonstrated safety and efficacy in ICI-naïve patients with advanced NSCLC in a phase 1 trial[6].

[002881] This example demonstrates first safety and efficacy data for single-agent Gen 2 process TIL cell therapy in patients with advanced NSCLC from a multicenter phase 2 study.

Methods

Study Design

[002882] Reported is a prospective, phase 2, multicenter, multicohort, open-label study evaluating autologous TIL cell therapy in multiple settings and indications.

[002883] Provided here is data from Cohort 3B, investigating TIL monotherapy in patients with advanced or metastatic NSCLC.

Cohort 3B Patients

[002884] Eligibility required age ≥18 years, 1–3 prior lines of systemic therapy including either ICI or oncogene-directed therapy, ECOG performance status 0–1, ≥1resectable lesion (~1.5 cm in diameter) for TIL manufacturing, and ≥1 measurable lesion post-resection for response assessment.

Endpoints

[002885] Primary

[002886] Efficacy, defined as investigator-assessed ORR per RECIST v1.1.

[002887] Safety, as measured by incidence of Grade ≥3 TEAEs (defined as AEs that occur from the time of TIL infusion, up to 30 days after TIL infusion or start of a new anticancer therapy).

[002888] Exploratory

[002889] Biomarker analyses, including TCR repertoire of the TIL product using RNA sequencing (HTBIvc assay, iRepertoire, Inc., Huntsville, AL); clones present above the limits of detection in each individual patient TIL product lot were counted and their proportion estimated to assess TIL clonality and diversity.

[002890] The patient journey and central Gen 2 GMP manufacturing of TIL product is depicted in Fig. 37.

[002891] The cohort 3B patient treatment schema is depicted in Fig. 38.

Results

[002892] Patient disposition is presented in Fig. 39.

[002893] Full analysis set includes all patients who received TIL therapy infusion within specifications.

[002894] Efficacy-evaluable set includes all patients who received TIL therapy within specifications and had ≥1 efficacy evaluation.

[002895] Translational set includes all patients who received TIL therapy infusion and had TIL available from the final drug-product for translational analysis.

[002896] TABLE 57. Baseline Patient Characteristics (FAS)

Characteristic	**COM-202 Cohort 3B (N=28)**
Sex, n (%)	
Male	14 (50.0)
Female	14 (50.0)
Median (min, max) age, y	61.0 (40, 74)
Smoker (current or former), n (%)	24 (85.7)
Histologic cell type, n (%)	

Adenocarcinoma	22 (78.6)
Squamous	5 (17.9)
Other	1 (3.6)
Tumor PD-L1 expression, n (%)*	
TPS <1%	4 (14.3)
TPS 1%–49%	10 (35.7)
TPS ≥50%	8 (28.6)
Median (min, max) number of target and non-target lesions	4.5 (2, 11)
Median (min, max) target lesion sum of diameters, mm	79.0 (22, 179)
Prior brain metastases, n (%)	10 (35.7)
Median (min, max) number of prior systemic therapies	2.0 (1, 6)
Prior systemic therapies, n (%)	
Anti–PD-1 and/or anti–PD-L1	28 (100)
Chemotherapy	27 (96.4)
Anti–PD-1	23 (82.1)
Anti–PD-L1	7 (25.0)
Anti–VEGF	6 (21.4)
Anti–CTLA-4	6 (21.4)
EGFR inhibitor	1 (3.6)
Tyrosine kinase inhibitor	1 (3.6)
Other	3 (10.7)

[002897] Per central laboratory from tumor harvest specimen; tumor PD-L1 expression data were missing for 6 patients.

[002898] All patients received prior ICI.

[002899] TILs were most commonly harvested from lung metastases (60.7%).

[002900] TABLE 58. Treatment-Emergent Adverse Events* (≥30%, FAS)

	COM-202 Cohort 3B (N=28)		
TEAE, n (%)	**Any Grade**	**Grade 3/4**	**Grade 5**
Any event	28 (100)	27 (96.4)	2 (7.1)[‡]
Thrombocytopenia	20 (71.4)	19 (67.9)	0
Anemia	19 (67.9)	14 (50.0)	0
Hypotension	17 (60.7)	7 (25.0)	0
Chills	16 (57.1)	1 (3.6)	0
Pyrexia	16 (57.1)	1 (3.6)	0
Hypoxia	13 (46.4)	5 (17.9)	0
Diarrhea	10 (35.7)	3 (10.7)	0
Neutropenia[†]	10 (35.7)	6 (21.4)	0
Peripheral edema	10 (35.7)	0	0
Alopecia	9 (32.1)	0	0
Decreased appetite	9 (32.1)	3 (10.7)	0
Dyspnea	9 (32.1)	3 (10.7)	0
Fatigue	9 (32.1)	4 (14.3)	0

[002901] TEAEs include AEs that occurred from the time of TIL infusion, up to 30 days after TIL infusion or start of a new anticancer therapy.

[002902] Only laboratory abnormalities considered clinically significant were reported as AEs.

[002903] One Grade 5 event each was reported for chronic cardiac failure and multiple organ dysfunction syndrome.

[002904] Safety was consistent with the underlying advanced disease and known safety profiles of NMA-LD and IL-2.

[002905] Any-grade tumor harvest-related AEs were reported for 16 (41.0%) patients, most commonly procedural pain, n=7 (17.9%) and hypoxia, n=4 (10.3%).

[002906] Majority of tumor harvest-related AEs were Grade 1 or 2.

[002907] Adverse Events Over Time (FAS) are depicted in Fig. 40.

[002908] Most AEs occurred prior to or within the first 2 weeks after TIL infusion.

[002909] Median number of IL-2 doses: 5.5.

[002910] TABLE 59a. Efficacy

	COM-202 Cohort 3B (N=28)	
Response	**n/N**	**% (95% CI)**
Full-Analysis Set (FAS)		
ORR	6/28	21.4 (8.3, 41.0)
CR	1/28	3.6
PR	5/28	17.9
SD	12/28	42.9
PD	6/28	21.4
DCR	18/28	64.3 (44.1, 81.4)
NE*	4/28	14.3
Efficacy-Evaluable Set		
ORR	6/24	25.0 (9.8, 46.7)
DCR	18/24	75.0 (53.3, 90.2)

[002911] *Excluded from efficacy-evaluable set due to death prior to first assessment.

[002912] TABLE 59b. Efficacy

	Median	
Duration, months	**(95% CI)**	**Min, Max**
Study follow-up (FAS)	9.8 (5.8, 14.5)	0.1+, 22.1

[002913] ORR: 21.4% in the FAS; 25.0% in the efficacy-evaluable set.

[002914] All responders received ≥2 prior lines of systemic therapy.

[002915] Median number of TIL infused was 20.9×10^9. Median time from resection to infusion was 35.0 days. Median time from infusion to BOR was 2.2 months.

[002916] Best percentage change from baseline in target lesion sum of diameters (efficacy-evaluable set) data are depicted in Fig. 41. For patient 2, the overall response of CR was based on investigator assessment of a complete metabolic response via negative FDG-PET scan.

[002917] Time to first response, duration of response, and time on efficacy assessment for confirmed responders who achieved PR or better are depicted in Fig. 42. Per central laboratory from tumor harvest specimen, except for patient 2, who had TPS assessed locally using archival tumor sample. Patient 25 had PD due to new lesion; patients 26 and 22 had unequivocal PD of non-target disease.

[002918] One patient had a complete metabolic response, ongoing at 20.7 months.

[002919] 2 responses, including the CR, occurred in patients with TPS <1%.

[002920] Percentage change from baseline in target lesion sum of diameters (FAS) data are depicted in Fig. 43.

[002921] The overall response of CR is based on a negative FDG-PET scan.

[002922] TABLE 60. TIL TCR Repertoire Analyses

	COM-202 Cohort 3B, Translational Set (N=27)	
TIL Product Parameter	**Median***	**Min, Max**
Unique TCR clones	4396	865, 17,317
Shannon Entropy Index (TCR clone diversity)†	7.18	3.55, 11.66
Simpson Clonality Index (TCR clonality)‡	0.20	0.02, 0.60

[002923] Comparison with prior published datasets[7,8] using the limit of detection applied to this dataset. Unique TCR clones: 5596 for melanoma and 6874 for cervical. Shannon Entropy Index: 7.60 for melanoma and 7.11 for cervical. Simpson Clonality Index: 0.18 for melanoma and 0.20 for cervical.

[002924] A larger Shannon Entropy Index indicates a more diverse CDR3 population. Values can range from 0 (monoclonal sample) to log2(R) (evenly distributed, polyclonal sample with R unique clones).

[002925] Simpson Clonality Index reflects mono- or poly-clonality of a sample and is inversely related to diversity (Shannon Entropy Index). Values can range from 0 (evenly distributed, polyclonal sample) to 1 (monoclonal sample).

[002926] 27 patients had TIL available from the final drug-product for TCR repertoire analysis; analyses of correlation with clinical outcome are ongoing.

Conclusions

[002927] This signal-finding study demonstrated the feasibility of tumor harvest, TIL manufacturing, and TIL treatment in patients with advanced NSCLC.

[002928] Patients tolerated surgical resection, including pulmonary lesions. TIL manufacturing was feasible for most patients. One-time TIL treatment with conditioning regimen was well-tolerated.

[002929] The TCR repertoire of TILs generated from NSCLC tumors demonstrated a similar number of unique TCR clones, as well as measures of diversity and clonality, as previously published for lifileucel for melanoma[7] and TIL therapy for cervical cancer[8].

[002930] Despite multiple prior lines of therapy, 6 patients experienced responses, including 2 with durable responses, consistent with published experience including durable CRs extending beyond 1 year[6].

Abbreviations

AE, adverse event; BOR, best overall response; CR, complete response; CTLA-4, cytotoxic T lymphocyte antigen-4; CY, cyclophosphamide; ECOG, Eastern Cooperative Oncology Group; EGFR, epidermal growth factor receptor; EOA, end of assessment; EOS, end of study; EOT, end of treatment; FAS, full-analysis set; FDG-PET, fluorodeoxyglucose-positron emission tomography; FLU, fludarabine; GMP, good manufacturing practices; ICI, immune checkpoint inhibitors; IL-2, interleukin-2; NA, not assessed; ND, none detected; NMA-LD, nonmyeloablative lymphodepletion; NSCLC, non-small cell lung cancer; ORR, objective response rate; PD, progressive disease; PR, partial response; Pt, patient; PD-1, programmed cell death protein-1; PD-L1, programmed death ligand-1; RECIST, Response Evaluation Criteria in Solid Tumors; SD, stable disease; TCR, T-cell receptor; TEAEs, treatment-emergent adverse events; TIL, tumor-infiltrating lymphocytes; TPS, tumor proportion score.

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EXAMPLE 20: A PHASE 2 MULTICENTER STUDY OF AUTOLOGOUS TUMOR-INFILTRATING LYMPHOCYTE (TIL) CELL THERAPY IN PATIENTS WITH METASTATIC NON-SMALL CELL LUNG CANCER (MNSCLC)

[002931] Background

[002932] Patients with metastatic non-small lung cancer (mNSCLC) without actionable driver mutations have limited second-line (2L) options after progression on concurrent or sequential front-line immune checkpoint inhibitors (ICI) + chemotherapy ± bevacizumab.

[002933] Autologous tumor-infiltrating lymphocyte (TIL) cell therapies have demonstrated efficacy and second-line (2L) treatment options[1] after progression on first-line treatment with concurrent safety in several patient populations with unmet medical need, including unresectable and metastatic melanoma; relapsed, refractory or persistent cervical cancer; metastatic head and neck squamous cell carcinoma; and mNSCLC[3-5].

[002934] Early clinical experience with TILs in heavily pretreated patients with mNSCLC has demonstrated feasibility, safety, and a 21.4% objective response rate (ORR), including 2 of 6 responders with PD-L1–negative tumors (Schoenfeld AJ, SITC 2021 [abs 458])[6].

[002935] TIL cell therapy has also shown evidence of efficacy in mNSCLC in a Phase 1 study in combination with nivolumab[7].

[002936] To address the urgent need for better 2L therapeutic options, the ongoing clinical trial has been amended to clarify allowed prior therapies and allow patient enrollment for tumor harvest and TIL generation prior to disease progression and minimize the time between prior therapy and initiation of TIL therapy as well as cost of TIL production.

[002937] Study overview

[002938] This study is an open-label, multi-cohort, multicenter Phase 2 study evaluating adoptive cell therapy with autologous TIL in patients with metastatic stage IV NSCLC without *EGFR*, *ALK*, or *ROS* genomic alterations, who have progressed on or following prior therapy, including concurrent or sequential ICI + platinum-based chemotherapy ± bevacizumab, or targeted therapies.

[002939] Patients may be enrolled for tumor harvest and generation prior to disease progression, with the intent to proceed with TIL treatment upon progression.

[002940] As illustrated in Figure 45, patients with metastatic NSCLC with no EGFR, ALK, or ROS genomic alterations, who have disease progression on or after prior ICI + chemotherapy ± bevacizumab, or targeted therapiesare, are dividied into 4 cohorts as follows:

[002941] Cohort 1 - TPS <1% prior to ICI or with no historical TPS (n=40).

[002942] Cohort 2 - TPS ≥1% prior to ICI (n=40).

[002943] Cohort 3 - 16-day Gen 3 manufacturing using image-guided core tumor biopsy for patients unable to undergo surgical tumor resection (any TPS) (n=15).

[002944] Cohort 4 - Retreatment (prior responders to TILs or patients with unconfirmed PD from cohorts 1–3) (n not specified).

[002945] Approximately 95 patients are planned to be infused with TILs in Cohorts 1, 2, and 3.

[002946] Primary endpoint of the study aims to evaluate ORR per RECIST 1.1 as assessed by IRC (Cohorts 1 and 2) or by investigator (Cohorts 3 and 4).

[002947] Secondary endpoints include assess safety and additional efficacy parameters, and percentage of successful TIL products generated from core biopsies (Cohort 3).

[002948] Exploratory endpoints of the study include analyses of predictive and pharmacodynamic biomarkers of clinical activity of TILs.

[002949] Key eligibility criteria include mNSCLC with no EGFR, ALK, or ROS1 genomic alterations, progressing after ≤2 prior lines of therapy (if concurrent ICI + chemotherapy; ≤3 prior lines if sequential), including targeted therapy in those with actionable mutations (eg, MET, HER2, RET, BRAF, KRAS); in those without actionable mutations, progression after 1 prior concurrent ICI + chemotherapy (≤2 prior lines if sequential); ≥1.5-cm lesion(s) for TIL generation; ≥1 remaining RECIST-measurable lesion(s) after tumor harvest; and ECOG PS of 0 or 1. Tumor harvest and TIL manufacturing can occur before or after confirmed progression. TILs are generated at centralized

GMP facilities, and the final cryopreserved infusion product is shipped to the sites. Upon progression, patients receive a conditioning regimen of nonmyeloablative lymphodepletion with 2 doses of cyclophosphamide (60 mg/kg) and 5 doses of fludarabine (25 mg/m2), followed by one-time infusion of TILs (1–150 × 10^9 cells), and ≤6 doses of IL-2 (600,000 IU/kg).

[002950] Key Inclusion Criteria for Enrollment

- Patients must have confirmed histologic or pathologic diagnosis of NSCLC.
- Metastatic Stage IV NSCLC without *EGFR*, *ALK*, or *ROS* genomic alterations with documented radiographic disease progression on or following first-line therapy including ICI and platinum-based chemotherapy ± bevacizumab, or targeted therapy
- For patients without actionable mutations: ≤1 prior line of therapy if concurrent ICI and platinum-based chemotherapy, or ≤2 prior lines if sequential
- For patients with actionable mutations (other than *EGFR, ALK or ROS*): 1 additional line of appropriate targeted therapy will be allowed
- For patients with pre-progression tumor harvest and TIL generation: Presence of residual resectable disease after platinum-based chemotherapy component of either concurrent or sequential ICI and platinum-based chemotherapy
- Cohorts 1 and 2: ≥1 resectable lesion and ≥1 measurable lesion; Cohort 3: able to undergo tumor harvest for TIL generation via image-guided core biopsy and have sufficient remaining lesion(s) to serve as target lesion(s)
- ECOG performance status of 0 or 1, and an estimated life expectancy of ≥6 months
- LVEF > 45%, New York Heart Association Class 1
- FEV_1 > 50% or FEV_1/FVC > 70%

[002951] Key Exclusion Criteria for Enrollment

- Known actionable *EGFR*, *ALK*, or *ROS* driver mutations
- Symptomatic and/or untreated brain metastases
- Organ allograft or prior cell transfer within the past 20 years
- Systemic steroid therapy ≥10 mg/day of prednisone or another steroid equivalent
- Any form of primary immunodeficiency

- Live or attenuated vaccination within 28 days prior to the start of treatment
- Active medical illness(es) that pose increased risk
- Participation in another interventional clinical study within 21 days of the initiation of treatment

[002952] Abbreviations

[002953] 2L, second line; CY, cyclophosphamide; FLU, fludarabine; ECOG, Eastern Cooperative Oncology Group; EOA, end of assessment; EOS, end of study; EOT, end of treatment; FEV1, forced expiratory volume in 1 second; FVC, forced vital capacity; GMP, good manufacturing practice; ICI, immune checkpoint inhibitor; IL-2, interleukin-2; IRC, independent review committee; LVEF, left ventricular ejection fraction; NMA-LD, nonmyeloablative lymphodepletion; mNSCLC, metastatic non-small lung cancer; ORR, objective response rate; PD, progressive disease; RECIST, Response Evaluation Criteria in Solid Tumors; TIL, tumor infiltrating lymphocytes; TPS, tumor proportion score (measure of tumor PD-L1 expression)

[002954] References

1. Horvath L, et al. *Mol Cancer.* 2020; 19:141.

2. Socinski M et al. N Engl J Med. 2018; 378: 2288- 2301.

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7. Creelan B, et al. *Nat Med.* 2021;27: 1410-1481.

[002955] The examples set forth above are provided to give those of ordinary skill in the art a complete disclosure and description of how to make and use the embodiments of the compositions, systems and methods of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Modifications of the above-described modes for carrying out the invention that are obvious to persons of skill in the art are intended to be within the scope of the following claims. All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains.

[002956] All headings and section designations are used for clarity and reference purposes only and are not to be considered limiting in any way. For example, those of skill in the art will appreciate the usefulness of combining various aspects from different headings and sections as appropriate according to the spirit and scope of the invention described herein.

[002957] All references cited herein are hereby incorporated by reference herein in their entireties and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

[002958] Many modifications and variations of this application can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments and examples described herein are offered by way of example only, and the application is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which the claims are entitled.

WHAT IS CLAIMED IS:

1. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naive to a cancer treatment, the method comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

wherein the patient subsequently receives an ICI treatment and/or a standard of care treatment;

optionally wherein the first population of TILs is further expanded into a therapeutic population of TILs if the patient exhibits progressive disease on or after the ICI and/or standard of care treatment.

2. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

wherein the patient subsequently resumes the maitnainence therapy;

optionally wherein the first population of TILs is further expanded into a therapeutic population of TILs if the patient exhibits progressive disease on or after the resumption of the maintenance therapy.

3. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naïve to a cancer treatment, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first

population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

4. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naïve to a cancer treatment, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the

first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

5. The method of claim 4, wherein the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

6. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells

(APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

7. A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable

surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

8. The method of any one of the preceding claims, wherein the cancer patient is naïve to any cancer treatment.

9. The method of any one of the preceding claims, wherein the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

10. The method of any one of the preceding claims, wherein the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after step (a).

11. The method of claim 10, wherein the patient is in a washout period at initiation of step (a).

12. The method of claim 10, wherein step of thawing and the subsequent steps are performed after the patient receives the cancer treatment or resumes the maintenance therapy and the patient exhibits progressive disease.

13. The method of any one of the preceding claims, wherein the patient exhibits progressive disease at least about 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 month, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 25 months, 26 months, 27 months, 28 months, 29 months, 30 months, 31 months, 32 months, 33 months, 34 months, 35 months, 36 months, after the step (b) of cryopreserving.

14. The method of any one of the preceding claims, wherein the patient receives or is going to receive a first-line ICI treatment and/or standard treatment.

15. The method of any one of the preceding claims, wherein the patient receives or is going to receive a second-line ICI treatment and/or standard treatment.

16. The method of any one of the preceding claims, wherein the patient is diagnosed with NSCLC.

17. The method of any one of the preceding claims, wherein the patient is diagnosed with metastatic stage IV NSCLC.

18. The method of any one of the preceding claims, wherein the subject or patient has at least one of:

i) a predetermined tumor proportion score (TPS) of PD-L1 of < 1%,

ii) a TPS score of PD-L1 of 1%-49%, or

iii) a predetermined absence of one or more driver mutations.

19. The method of any of the preceding claims, wherein the patient or subject has a TPS of PD-L1 of 1%-49%.

20. The method of any of the preceding claims, wherein the patient or subject has a TPS of PD-L1 of < 1% and has a predetermined absence of one or more driver mutations.

21. The method of any of the preceding claims, wherein the one or more driver is selected from the group consisting of an EGFR mutation, an EGFR insertion, EGFR exon20, a KRAS mutation, a BRAF-mutation, a BRAF V600 mutation, an ALK-mutation, a c-ROS-mutation (ROS1-mutation), a ROS1 fusion, a RET mutation, a RET fusion, an ERBB2 mutation, an ERBB2 amplification, a BRCA mutation, a MAP2K1 mutation, PIK3CA, CDKN2A, a PTEN mutation, an UMD mutation, an NRAS mutation, a KRAS mutation, an NF1 mutation, a MET mutation, a MET splice and/or altered MET signaling, a TP53 mutation, a CREBBP mutation, a KMT2C mutation, a KMT2D mutation, an ARID1A mutation, a RB1 mutation, an ATM mutation, a SETD2 mutation, a FLT3 mutation, a PTPN11 mutation, a FGFR1 mutation, an EP300 mutation, a MYC mutation, an EZH2 mutation, a JAK2 mutation, a FBXW7 mutation, a CCND3 mutation, and a GNA11 mutation.

22. The method of any of the preceding claims, wherein the patient or subject has a TPS of < 1% and has a NSCLC that is not indicated for treatment by an EGFR inhibitor, a BRAF inhibitor, an ALK inhibitor, a c-Ros inhibitor, a RET inhibitor, an ERBB2 inhibitor, BRCA inhibitor, a MAP2K1 inhibitor, PIK3CA inhibitor, CDKN2A inhibitor, a PTEN inhibitor, an UMD inhibitor, an NRAS inhibitor, a KRAS inhibitor, an NF1 inhibitor, MET inhibitor a TP53 inhibitor, a CREBBP inhibitor, a KMT2C inhibitor, a KMT2D mutation, an ARID1A mutation, a RB1 inhibitor, an ATM inhibitor, a SETD2 inhibitor, a FLT3 inhibitor, a PTPN11 inhibitor, a FGFR1 inhibitor, an EP300 inhibitor, a MYC inhibitor, an EZH2 inhibitor, a JAK2 inhibitor, a FBXW7 inhibitor, a CCND3 inhibitor, and a GNA11 inhibitor.

23. The method of claim 20, wherein the one or more driver mutations comprises a genomic alteration of EGFR, ALK, or ROS.

24. The method of claim 20, wherein the one or more driver mutations consists of a genomic alteration of EGFR, ALK, or ROS.

25. The method of any of the preceding claims, wherein the NSCLC has low or no expression of PD-L1.

26. The method of any of the preceding claims, wherein the patient has a predetermined absence of one or more driver mutations.

27. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to treatment with a chemotherapeutic agent.

28. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to treatment with a VEGF-A inhibitor.

29. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent but is not being currently treated with a chemotherapeutic agent.

30. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent but is not being currently treated with a chemotherapeutic agent and has a TPS of < 1%.

31. The method of any of the preceding claims, wherein the NSCLC has been treated with a VEGF-A inhibitor but is not being currently treated with a VEGF-A inhibitor.

32. The method of any of the preceding claims, wherein the NSCLC has been treated with a VEGF-A inhibitor but is not being currently treated with a VEGF-A inhibitor and has a TPS of < 1%.

33. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor, but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

34. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor and has a TPS of < 1%.

35. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody.

36. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor.

37. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

38. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a VEGF-A

inhibitor but is not being currently treated with a VEGF-A inhibitor.

39. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

40. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has low or no expression of PD-L1.

41. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or a VEGF-A inhibitor and has a TPS of < 1%.

42. The method of any of the preceding claims, wherein the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 and/or anti-PD-L2 antibody.

43. The method of any of the preceding claims, wherein the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has been previously treated a chemotherapeutic agent and/or a VEGF-A inhibitor.

44. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to treatment with an anti-PD-1 and/or anti-PD-L1 antibody.

45. The method of any of the preceding claims, wherein the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-1 and/or anti-PD-L1 antibody treatment.

46. The method of any of the preceding claims, wherein the NSCLC has been previously treated with an anti-PD-L1 antibody and the tumor proportion score was determined prior to the anti-PD-L1 antibody treatment, or the NSCLC has been previously treated with an anti-PD-1 antibody and the tumor proportion score was determined prior to the anti-PD-1 antibody treatment.

47. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent and/or a VEGF-A inhibitor.

48. The method of any of the preceding claims, wherein the NSCLC has not been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has bulky disease at baseline.

49. The method of any of the preceding claims, wherein the NSCLC has been previously treated with an anti-PD-1 and/or anti-PD-L1 antibody and has bulky disease at baseline.

50. The method of any of the preceding claims, wherein the NSCLC has been treated with a

chemotherapeutic agent and has bulky disease at baseline.

51. The method of any of the preceding claims, wherein the NSCLC has been treated with a chemotherapeutic agent and/or VEGF-A inhibitor but is not being currently treated with a chemotherapeutic agent and/or VEGF-A inhibitor and has bulky disease at baseline.

52. The method of any of the preceding claims, wherein bulky disease is indicated where the maximal tumor diameter is greater than 7 cm measured in either the transverse or coronal plane or swollen lymph nodes with a short-axis diameter of 20 mm or greater.

53. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to at least two prior systemic treatment courses, not including neo-adjuvant or adjuvant therapies.

54. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to an anti-PD-1 or an anti-PD-L1 antibody selected from the group consisting of nivolumab, pembrolizumab, JS001, TSR-042, pidilizumab, BGB-A317, SHR-1210, REGN2810, MDX-1106, PDR001, anti-PD-1 from clone: RMP1-14, anti-PD-1 antibodies disclosed in U.S. Patent No. 8,008,449, durvalumab, atezolizumab, avelumab, and fragments, derivatives, variants, as well as biosimilars thereof.

55. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to pembrolizumab or a biosimilar thereof.

56. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to nivolumab or a biosimilar thereof.

57. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to an anti-CTLA-4 antibody.

58. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to an anti- CTLA -4 antibody and pembrolizumab or a biosimilar thereof.

59. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to an anti- CTLA -4 antibody, and nivolumab or a biosimilar thereof.

60. The method of any of the preceding claims, wherein the anti-CTLA-4 antibody is ipilimumab or a biosimilar thereof.

61. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to durvalumab or a biosimilar thereof.

62. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to atezolizumab or a biosimilar thereof.

63. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to

avelumab or a biosimilar thereof.

64. The method of any of the preceding claims, wherein the chemotherapeutic agent is a platinum doublet chemotherapeutic agent(s).

65. The method of Claim 64, wherein the platinum doublet chemotherapeutic agent therapy comprises:

i) a first chemotherapeutic agent selected from the group consisting of cisplatin and carboplatin,

ii) and a second chemotherapeutic agent selected from the group consisting of vinorelbine, gemcitabine and a taxane (including for example, paclitaxel, docetaxel or nab-paclitaxel).

66. The method of any of the preceding claims, wherein the chemotherapeutic agent, including the first and/or second chemotherapeutic agent, is in combination with pemetrexed.

67. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, and cisplatin.

68. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to a combination therapy comprising carboplatin, paclitaxel, pemetrexed, cisplatin, nivolumab, and ipilimumab.

69. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to a VEGF-A inhibitor.

70. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to a VEGF-A inhibitor selected from the group consisting of bevacizumab, ranibizumab, and icrucumab.

71. The method of any of the preceding claims, wherein the NSCLC is refractory or resistant to bevacizumab.

72. The method of any of the preceding claims, wherein the NSCLC has been analyzed for the absence or presence of one or more driver mutations.

73. The method of any of the preceding claims, wherein one or more driver mutations are not present.

74. The method of any of the preceding claims, wherein the NSCLC treatment is independent of the presence or absence of one or more driver mutations.

75. The method of any of the preceding claims, wherein the one or more driver mutations is selected from the group consisting of an EGFR mutation, an EGFR insertion, a KRAS mutation, a BRAF-mutation, an ALK-mutation, a c-ROS-mutation a c-ROS-mutation, EML4-ALK, and MET mutation.

76. The method of Claim 75, wherein the EGFR mutation results in tumor transformation from NSCLC to small cell lung cancer (SCLC).

77. The method of any of the preceding claims, wherein the NSCLC treatment is independent of the presence or absence of high-tumor mutational burden (high-TMB) and/or microsatellite instability-high (MSI-high) status.

78. The method of any of the preceding claims, wherein the NSCLC exhibits high-TMB and/or MSI-high status.

79. A method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(f) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step

(g) using a cryopreservation process.

80. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is on maintenance therapy that is interrupted, comprising:

(a) prior to the resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(f) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (e) to step (f) occurs without opening the system;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

81. A method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(f) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

82. The method of claim 81, wherein the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

83. A method of making a cryopreserved population of TILs from a cancer patient, comprising:

(a) prior to the patient receives a cancer treatment, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of

TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) waiting for the patient to exhibit progressive disease on or after the cancer treatment;

(d) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(e) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(f) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(g) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (f) to step (g) occurs without opening the system; and

(h) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (g) to (h) occurs without opening the system; and

(i) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

84. The method of any of the preceding claims, wherein the patient is naïve to any cancer treatment.

85. The method of any of the preceding claims, wherein the patient receives a first-line ICI treatment and/or standard treatment.

86. The method of any of the preceding claims, wherein the patient receives a second-line ICI treatment and/or standard treatment.

87. The method of any of the preceding claims, wherein step (b) comprises flash freezing of the tumor fragments or tumor digest.

88. The method of any of the preceding claims, wherein the flash freezing comprises:

i) incubating the tumor fragments or tumor digest in a cryopreservation medium; optionally incubating for about 30 minutes to about 60 minutes at about 2°C to about 8°C in a cryopreservation medium comprising 10% v/v DMSO, and

ii) freezing the tumor wherein the freezing is flash freezing using the vapor phase of liquid nitrogen.

89. The method of any of the preceding claims, wherein step (b) comprises controlled-rate freezing of the tumor fragments or tumor digest.

90. The method of any of the preceding claims, wherein the controlled-rate freezing comprises:

i) adding cryopreservation medium to a closable vessel;

ii) pre-cooling the closable vessel in a controlled-rate freezing device;

iii) placing the tumor in the closable vessel comprising cryopreservation medium and closing the vessel;

iv) incubating the closed vessel comprising the tumor and cryopreservation medium at a temperature of about 2-8C for a time period of about 30 to 60 minutes; and

v) slow-freezing the vessel in a controlled-rate freezing device.

91. The method of any of the preceding claims, wherein the cancer patient is naïve to any cancer treatment.

92. The method of any of the preceding claims, wherein the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

93. The method of any of the preceding claims, wherein the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after step (a).

94. The method of any of the preceding claims, wherein the patient receives a first-line ICI treatment and/or standard treatment.

95. The method of any of the preceding claims, wherein the patient receives a second-line ICI treatment and/or standard treatment.

96. The method of any of the preceding claims, wherein the patient is diagnosed with NSCLC.

97. The method of any of the preceding claims, wherein the patient is diagnosed with metastatic stage IV NSCLC.

98. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system;

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process;

99. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-14 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-14 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

100. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining a first population of TILs from a tumor resected from a subject by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second

population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

101. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a tumor in the subject or patient,

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs, and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

102. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, resecting a tumor from the subject or patient, the tumor comprising a first population of TILs, optionally from surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from a tumor;

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and adding the first population of TILs into a closed system;

(d) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-11 days to obtain the second population of TILs and wherein the transition from step (c) to step (d) occurs without opening the system;

(e) performing a second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and antigen presenting cells (APCs), to produce a third population of TILs, wherein the second expansion is performed for about 7-11 days to obtain the third population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, and wherein the transition from step (d) to step (e) occurs without opening the system;

(f) harvesting the third population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system;

(g) transferring the harvested third TIL population from step (e) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

103. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor resected from the subject or patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;

(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;

(c) thawing the cryopreserved tumor fragments or tumor digest and adding the first population of TILs into a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (e), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (f) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

104. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from surgical resection, needle biopsy, core biopsy, small

biopsy, or other means for obtaining a sample that contains a mixture of tumor and TIL cells from the subject or patient;

(b) cryopreserving the sample comprising the first population of TILs from step (a) to produce cryopreserved sample;

(c) thawing the cryopreserved sample and contacting the first population of TILs with a first cell culture medium in a closed system;

(d) performing a priming first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs) to produce a second population of TILs, wherein the priming first expansion is performed in a container comprising a first gas-permeable surface area, wherein the priming first expansion is performed for first period of about 1 to 7/8 days to obtain the second population of TILs, wherein the second population of TILs is greater in number than the first population of TILs;

(e) performing a rapid second expansion by supplementing the cell culture medium of the second population of TILs with additional IL-2, OKT-3, and APCs, to produce a third population of TILs, wherein the number of APCs added in the rapid second expansion is at least twice the number of APCs added in step (b), wherein the rapid second expansion is performed for a second period of about 1 to 11 days to obtain the third population of TILs, wherein the third population of TILs is a therapeutic population of TILs, wherein the rapid second expansion is performed in a container comprising a second gas-permeable surface area;

(f) harvesting therapeutic population of TILs obtained from step (f), wherein the transition from step (e) to step (f) occurs without opening the system; and

(g) transferring the harvested TIL population from step (g) to an infusion bag, wherein the transfer from step (f) to (g) occurs without opening the system; and

(h) cryopreserving the infusion bag comprising the harvested TIL population from step (g) using a cryopreservation process.

105. The method of claim 104, wherein the rapid expansion can proceed for 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid expansion.

106. The method of any of the preceding claims, wherein the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL in the first cell culture medium, when present.

107. The method of any of the preceding claims, wherein the IL-2 is present at an initial concentration of between 1000 IU/mL and 6000 IU/mL and the OKT-3 antibody is present at an

initial concentration of about 30 ng/mL in the second wherein the initial expansion, when present, is performed using a gas permeable container.

108. The method of any of the preceding claims, wherein the rapid expansion, when present, is performed using a gas permeable container.

109. The method of any of the preceding claims, wherein the first cell culture medium, when present, further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof.

110. The method of any of the preceding claims, wherein the second cell culture medium, when present, further comprises a cytokine selected from the group consisting of IL-4, IL-7, IL-15, IL-21, and combinations thereof.

111. The method according to any of the preceding claims, wherein the harvested population of TILs comprises a therapeutically effective population of TILs, and wherein a therapeutically effective population of TILs comprises from about 2.3×10^{10} to about 13.7×10^{10} TILs.

112. The method of any of the preceding claims, wherein the initial expansion is performed over a period of 21 days or less.

113. The method of any of the preceding claims, wherein the initial expansion is performed over a period of 7 days or less.

114. The method of any of the preceding claims, wherein the rapid expansion is performed over a period of 7 days or less.

115. The method of any of the preceding claims, wherein the first expansion and the second expansion are each individually performed within a period of 11 days.

116. The method of any of the preceding claims, wherein step of performing the first expansion through the setp of harvesting are performed in about 10 days to about 24 days.

117. The method of any of the preceding claims, wherein step of performing the first expansion through the setp of harvesting are performed in about 10 days to about 22 days.

118. The method of any of the preceding claims, further comprising a step of modifying a portion of the TILs at any time prior to the harvesting such that each of the modified TILs comprises an immunomodulatory composition associated with its surface membrane.

119. The method of any of the preceding claims, wherein the step of modifying comprises gene-editing the TILs to effect transfer of at least one gene editing system selected from the group consisting of a TALEN system, a CRISPR system and zinc finger system, into the modified TILs.

120. The method of any of the preceding claims, wherein during the step of modifying the cell

membranes of the modified TILs are temporarily disrupted to effect transfer of the at least one gene editing system by using a microfluidic platform or sterile electroporation.

121. The method of Claim 120, wherein the microfluidic platform is a SQZ platform.

122. The method of any of the preceding claims, wherein immunomodulatory composition comprises one or more membrane anchored immunomodulatory fusion proteins each comprising one or more immunomodulatory agents and a cell membrane anchor moiety.

123. The method of any of the preceding claims, wherein the immunomodulatory composition comprises two or more different membrane anchored immunomodulatory fusion proteins, wherein each of the different membrane anchored immunomodulatory fusion proteins each comprises a different immunomodulatory agent.

124. The method of any of the preceding claims, wherein immunomodulatory composition comprises a fusion protein comprising one or more immunomodulatory agents linked to a TIL surface antigen binding domain.

125. The method of any of the preceding claims, wherein immunomodulatory composition comprises a nanoparticle comprising a plurality of immunomodulatory agents.

126. The method of any of the preceding claims, wherein the immunomodulatory agents comprise one or more cytokines.

127. The method of claim 126, wherein the one or more cytokines comprise IL-2, IL-6, IL-7, IL-9, IL-12, IL-15, IL-18, IL-21, IL-23, IL-27, IFN gamma, TNFa, IFN alpha, IFN beta, GM-CSF, or GCSF or a variant thereof.

128. The method of any of the preceding claims, wherein the immunomodulatory agents comprise a CD40 agonist.

129. The method of any of the preceding claims, wherein the membrane anchored immunomodulatory fusion protein is according to the formula, from N- to C-terminus: S-IA-L-C, wherein S is a signal peptide, IA is an immunomodulatory agent, L is a linker and C is a cell membrane anchor moiety.

130. The method of any of the preceding claims, wherein the cell membrane anchor moiety comprises a CD8a transmembrane-intracellular domain, a B7-1 transmembrane domain, a B7-2 transmembrane domain, or a CD8a transmembrane domain.

131. The method of any of the preceding claims, wherein the one or more immunomodulatory agents comprise one or more cytokines.

132. The method of any of the preceding claims, wherein the one or more cytokines comprises IL-

2, IL-6, IL-7, IL-9, IL-12, IL-15, IL-18, IL-21, IL-23, IL-27, IFN gamma, TNFa, IFN alpha, IFN beta, GM-CSF, or GCSF or a variant thereof.

133. The method of any of the preceding claims, wherein the TIL surface antigen binding domain comprises an antibody variable heavy domain and variable light domain.

134. The method of any of the preceding claims, wherein the TIL surface antigen binding domain comprises an antibody or fragment thereof.

135. The method of any of the preceding claims, wherein the TIL surface antigen binding domain exhibits an affinity for one or more of following TIL surface antigens: CD45, CD4, CD8, CD3, CDlla, CDllb, CDllc, CD18, CD25, CD127, CD19, CD20, CD22, HLA-DR, CD197, CD38, CD27, CD196, CXCR3, CXCR4, CXCR5, CD84, CD229, CCR1, CCR5, CCR4, CCR6, CCR8, CCR10, CD 16, CD56, CD 137, OX40, or GITR.

136. The method of any of the preceding claims, wherein the nanoparticle is a liposome, a protein nanogel, a nucleotide nanogel, a polymer nanoparticle, or a solid nanoparticle.

137. The method of claim 136, wherein the nanoparticle is a nanogel.

138. The method of any of the preceding claims, wherein the nanoparticle further comprises an antigen binding domain that binds to one or more of the following antigens: CD45, CDlla (integrin alpha- L), CD 18 (integrin beta-2), CD1lb, CD1lc, CD25, CD8, or CD4.

139. The method of any of the preceding claims, wherein the modifying comprises introducing a heterologous nucleic acid encoding the fusion protein into the portion of TILs and expressing the fusion protein on the surface of the modified TILs.

140. The method of claim 139, wherein the heterologous nucleic acid is introduced into the genome of the modified TIL using one or more methods selected from a CRISPR method, a TALE method, a zinc finger method, and a combination thereof.

141. The method of any of the preceding claims, wherein the modifying comprises incubating the fusion protein with the portion of TILs under conditions to permit the binding of the fusion protein to the portion of TILs.

142. The method of any of the preceding claims, wherein the modifying comprises attaching the immunomodulatory composition to the surface of the portion of TILs.

143. The method according to any of the preceding claims, wherein the modifying is carried out on TILs from the first expansion, or TILs from the second expansion, or both.

144. The method according to any of the preceding claims, wherein the modifying is carried out on

TILs from the priming first expansion, or TILs from the rapid second expansion, or both.

145. The method according to any of the preceding claims, wherein the modifying is carried out after the first expansion and before the second expansion.

146. The method according to any of the preceding claims, wherein the modifying is carried out after the priming first expansion and before the rapid second expansion, or both.

147. The method according to any of the preceding claims, wherein the modifying is carried out after the second expansion.

148. The method according to any of the preceding claims, wherein the modifying is carried out after the rapid second expansion.

149. The method according to any of the preceding claims, wherein the modifying is carried out after the harvesting.

150. The method according to any of the preceding claims, wherein the modified TILs further comprise a genetic modification that causes expression of one or more immune checkpoint genes to be silenced or reduced in at least a portion of the therapeutic population of TILs.

151. The method according to claim 150, wherein said one or more immune checkpoint genes is/are selected from the group comprising PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

152. The method according to claim 150, wherein said one or more immune checkpoint genes is/are selected from the group comprising PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, and PKA.

153. The method according to any of the preceding claims, wherein the modified TILs further comprises a genetic modification that causes expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs, the immune checkpoint gene(s) being selected from the group comprising CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, IL-2, IL-4, IL-7, IL-10, IL-15, IL-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

154. The method according to any of the preceding claims, wherein the genetic modification is produced using a programmable nuclease that mediates the generation of a double-strand or single-strand break at said one or more immune checkpoint genes.

155. The method according to any of the preceding claims, wherein the genetic modification is produced using one or more methods selected from a CRISPR method, a TALE method, a zinc finger method, and a combination thereof.

156. The method of any of any of the preceding claims, wherein the modified TILs are modified to transiently express the immunomodulatory composition on the cell surface.

157. The method of claim 156, wherein the immunomodulatory composition comprises one or more membrane anchored immunomodulatory fusion proteins, wherein each fusion protein comprises one or more immunomodulatory agents and a cell membrane anchor moiety.

158. The method of any of the preceding claims, wherein the modified TILs are modified by transfecting the TILs with a nucleic acid encoding the fusion protein.

159. The method of claim 158, wherein the nucleic acid is an RNA.

160. The method of claim 159, wherein the RNA is a mRNA.

161. The method of claim 160, wherein the TILs are transfected with the mRNA by a SQZ platform or electroporation.

162. The method of claim 161, wherein the TILs are transfected with the mRNA by a SQZ platform or electroporation after the first expansion and before the second expansion.

163. The method of claim 161, wherein the TILs are transfected with the mRNA by a SQZ platform or electroporation before the first expansion.

164. The method of claim 160, wherein the modified TILs are transfected with the nucleic acid encoding the fusion protein using a microfluidic device to temporarily disrupt the cell membranes of the TILs, thereby allowing transfection of the nucleic acid.

165. The method of any of the preceding claims, wherein the method further comprises activating the TILs by incubation with an anti-CD3 agonist before transfecting the TILs with the mRNA.

166. The method of claim 165, wherein the anti-CD3 agonist is OKT-3.

167. The method of claim 165 or 166, wherein the TILs are activated by incubating the TILs with the anti-CD3 agonist for about 1 to 3 days before transfecting the TILs with the mRNA.

168. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;
(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and
(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

169. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;
(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;
(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;
(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and
(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

170. The method of any of the preceding claims, wherein the enzymatic media comprises a DNase.

171. The method of any of the preceding claims, wherein the enzymatic media comprises a collagenase.

172. The method of any of the preceding claims, wherein the enzymatic media comprises a neutral protease.

173. The method of any of the preceding claims, wherein the enzymatic media comprises a hyaluronidase.

174. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(g) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide an expanded number of TILs.

175. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;

(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3-9 days to produce a second population of TILs;

(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;

(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and

(h) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide an expanded number of TILs.

176. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;

(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;

(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and

(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

177. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;
(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;
(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and
(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

178. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;
(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;
(e) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and
(f) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

179. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;
(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 and OKT-3 for about 3-9 days to produce a second population of TILs;
(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs;
(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and
(g) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

180. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;
(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and
(f) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

181. A method of making a cryopreserved population of TILs from a cancer patient, wherein the

patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;
(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;
(e) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;
(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs; and
(g) culturing the fourth population of TILs in a third cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 5-15 days, to produce an expanded number of TILs.

182. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;
(d) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;
(f) culturing the third population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fourth population of TILs; and

(g) splitting the culture of the fourth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-7 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

183. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor tissue to produce a tumor digest;
(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and culturing the first population of TILs in a first cell culture medium comprising IL-2 for about 3 days to produce a second population of TILs;
(e) culturing the second population of TILs in a second cell culture medium comprising IL-2 and OKT-3 for 2-4 days to produce a third population of TILs;
(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;
(g) culturing the fourth population of TILs in a second cell culture medium comprising antigen presenting cells (APCs), OKT-3, and IL-2 for about 1-7 days, to produce a culture of a fifth population of TILs; and
(h) splitting the culture of the fifth population of TILs into a plurality of subcultures, culturing each of the plurality of subcultures in a third cell culture medium comprising IL-2 for about 3-6 days, and combining the plurality of subcultures to provide a fifth population of TILs comprising an expanded number of TILs.

184. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and performing an initial expansion (or priming

first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 8 days;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-6 days, to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;
(f) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

185. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) subsequent to the cancer progression, performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), wherein the priming first expansion occurs for a period of about 3 to 8 days;

(d) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and
(e) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about

1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

186. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 8 days;

(e) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or anti-CD3 agonist and anti-CD28 agonist beads or antibodies, for 1-6 days, to produce a third population of TILs;
(f) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;
(g) performing a rapid second expansion of the fourth population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

187. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a tumor tissue resected from a subject or patient;
(b) digesting in an enzyme media the tumor fragments to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs from step (a) to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and performing an initial expansion (or priming first expansion) of the first population of TILs in a first cell culture medium to obtain a second population of TILs, wherein the first cell culture medium comprises IL-2, optionally OKT-3, and optionally antigen presenting cells (APCs), where the priming first expansion occurs for a period of about 1 to 8 days;

(e) gene-editing at least a portion of the second population of TILs, to produce a third population of TILs; and
(f) performing a rapid second expansion of the third population of TILs in a second cell culture medium to obtain an expanded number of TILs, wherein the second cell culture medium comprises IL-2, OKT-3, and APCs; and wherein the rapid expansion is performed over a period of 14 days or less, optionally the rapid second expansion can proceed for about 1 day, 2 days, 3 days, 4, days, 5 days, 6 days, 7 days, 8 days, 9 days or 10 days after initiation of the rapid second expansion.

188. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;
(b) cryopreserving the tumor tissue comprising the first population of TILs from step (a) to produce a cryopreserved tumor tissue;
(c) thawing the cryopreserved tumor tissue and adding the tumor tissue into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or CD3 agonist and CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;

(f) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the fifth population of TILs, wherein the second expansion is performed in a closed container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(g) harvesting the therapeutic population of TILs obtained from step (f), wherein each of steps (c) to (g) is performed in a closed, sterile system, and wherein the transition from step (c) to step (d), the transition from step (d) to step (e), the transition from step (e) to step (f) and/or the transition from step (f) to step (g) occurs without opening the system.

189. A method of making a cryopreserved population of TILs from a cancer patient, wherein the patient is naive to a cancer treatment or on a maintaience therapy that is interrupted, the method comprising:

(a) prior to the cancer treatment or resumption of the maintenance therapy, obtaining and/or receiving a first population of TILs from a sample of tumor tissue produced by surgical resection, needle biopsy, core biopsy, small biopsy, or other means for obtaining tumor tissue from a patient or subject;
(b) digesting the sample of tumor tissue in an enzymatic media to produce a tumor digest;

(c) cryopreserving the tumor digest comprising the first population of TILs to produce a cryopreserved tumor digest;
(d) thawing the cryopreserved tumor digest and adding the tumor digest into a closed system and performing a first expansion by culturing the first population of TILs in a first cell culture medium comprising IL-2 to produce a second population of TILs, wherein the first expansion is performed in a closed container providing a first gas-permeable surface area, wherein the first expansion is performed for about 3-9 days to obtain the second population of TILs;

(d) activating the second population of TILs using anti-CD3 agonist beads or antibodies, or CD3 agonist and CD28 agonist beads or antibodies, for 1-7 days, to produce a third population of TILs;
(e) gene-editing at least a portion of the third population of TILs, to produce a fourth population of TILs;
(f) performing a second expansion by culturing the fourth population of TILs in a second cell culture medium comprising IL-2, OKT-3, and antigen presenting cells (APCs), to produce a fifth population of TILs, wherein the second expansion is performed for about 5-15 days to obtain the fifth population of TILs, wherein the second expansion is performed in a closed

container providing a second gas-permeable surface area, wherein the fifth population of TILs is a therapeutic population of TILs; and

(g) harvesting the therapeutic population of TILs obtained from step (f), wherein each of steps (d) to (g) is performed in a closed, sterile system, and wherein the transition from step (d) to step (e), the transition from step (e) to step (f), and/or the transition from step (f) to step (g) occurs without opening the system.

190. The method of any of the preceding claims, wherein the rapid second expansion is performed by culturing the third or fourth population of TILs in the second cell culture medium for a first period of about 1-7 days, at the end of the first period the culture is split into a plurality of subcultures, each of the plurality of subcultures is cultured in a third culture medium comprising IL-2 for a second period of about 3-6 days, and at the end of the second period the plurality of subcultures are combined to provide the expanded number of TILs.

191. The method of any of the preceding claims, wherein the step of gene-editing at least a portion of the second or third population of TILs comprises performing a sterile electroporation step or a SQZ microfluidic membrane disruption step on the second or third population of TILs, wherein the sterile electroporation step or the SQZ microfluidic membrane disruption step mediates the transfer of at least two gene editors.

192. The method of claim 191, wherein the electroporation step or the SQZ microfluidic membrane disruption step consists of a single event that mediates the transfer of the at least two gene editors.

193. The method of any of the preceding claims, wherein in the electroporation step or the SQZ microfluidic membrane disruption step each of the at least two gene editors is transferred individually by an event independently of the transfer of any other gene editor.

194. The method of any of the preceding claims, wherein the electroporation step further comprises a rest period after each event.

195. The method of any of the preceding claims, wherein the electroporation step or the SQZ microfluidic membrane disruption step comprises a first event that mediates the transfer of a first gene editor for modulating expression of a first protein, a first rest period, a second event that mediates the transfer of a second gene editor for modulating expression of a second protein, and a second rest period, wherein the first and second rest periods are the same or different.

196. The method of any of the preceding claims, wherein the first and second rest periods comprise incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

197. The method of any of the preceding claims, wherein the first and second rest periods comprise incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

198. The method of any of the preceding claims, wherein the first and second rest periods are independently about 10 hours to 5 days.

199. The method of any of the preceding claims, wherein the first and second rest periods are independently about 10 hours to 3 days.

200. The method of any of the preceding claims, wherein the first rest period is about 1 to 3 days.

201. The method of any of the preceding claims, wherein the first rest period is about 3 days.

202. The method of any of any of the preceding claims, wherein the second rest period is about 10 hours to 1 day.

203. The method of any of any of the preceding claims, wherein the second rest period is about 12 hours to 24 hours.

204. The method of any of any of the preceding claims, wherein the second rest period is about 15 hours to about 18 hours.

205. The method of any of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

206. The method of any of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

207. The method of any of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

208. The method of claim 207, wherein the first rest period is about 3 days and the second rest period is about 10 to 16 hours.

209. The method of any of the preceding claims, wherein the at least two gene editors comprise a first gene editor comprising a first TALE nuclease system for modulating expression of a first protein and a second gene editor comprising a second TALE nuclease system for modulating expression of a second protein.

210. The method of any of the preceding claims, wherein the electroporation step or the SQZ microfluidic membrane disruption step comprises a first event that mediates the transfer of the first TALE nuclease system, a first rest period, a second event that mediates the transfer of the second TALE nuclease system, and a second rest period, wherein the first and second rest periods are the same or different.

211. The method of any of the preceding claims, wherein the first and second rest periods comprise incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

212. The method of any of the preceding claims, wherein the first and second rest periods comprise incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

213. The method of any of the preceding claims, wherein the first and second rest periods are independently about 10 hours to 5 days.

214. The method of any of the preceding claims, wherein the first and second rest periods are independently about 10 hours to 3 days.

215. The method of any of the preceding claims, wherein the first rest period is about 1 to 3 days.

216. The method of any of the preceding claims, wherein the first rest period is about 3 days.

217. The method of any of the preceding claims, wherein the second rest period is about 10 hours to 1 day.

218. The method of any of the preceding claims, wherein the second rest period is about 12 hours to 24 hours.

219. The method of any of the preceding claims, wherein the second rest period is about 15 hours to about 18 hours.

220. The method of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

221. The method of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

222. The method of any of the preceding claims, wherein the second rest period comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

223. The method of any of the preceding claims, wherein the first rest period is about 3 days and the second rest period is about 10 to 16 hours.

224. The method of any of the preceding claims, wherein the step of gene-editing at least a portion of the second or third population of TILs comprises performing a sterile electroporation step or a SQZ microfluidic membrane disruption step on the second or third population of TILs, wherein the sterile electroporation step or the SQZ microfluidic membrane disruption step mediates the transfer of at least one gene editor.

225. The method of any of the preceding claims, wherein the gene editor is a TALE nuclease system for modulating the expression of at least one protein.

226. The method of any of the preceding claims, wherein the TALE nuclease system modulates expression of PD-1, CTLA-4, TIGIT, CBL-B and/or LAG-3.

227. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CTLA-4.

228. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and LAG-3.

229. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CISH.

230. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and CBL-B.

231. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1 and TIGIT.

232. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and LAG-3.

233. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and CISH.

234. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4 and CBL-B.

235. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CISH and CBL-B.

236. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CISH and TIGIT.

237. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of PD-1.

238. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CTLA-4.

239. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of LAG-3.

240. The method of any of the preceding claims, wherein the gene editor comprises a TALE

nuclease system that modulates expression of CISH.

241. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of CBL-B.

242. The method of any of the preceding claims, wherein the gene editor comprises a TALE nuclease system that modulates expression of TIGIT.

243. The method of any of the preceding claims, wherein the method further comprises the step of resting the third or fourth population of TILs after the gene-editing step and before the step of culturing the third or fourth population of TILs.

244. The method of any of the preceding claims, wherein the resting step comprises incubating the third or fourth population of TILs at about 30-40 °C with about 5% CO2.

245. The method of any of the preceding claims, wherein the method further comprises the step of resting the third or fourth population of TILs for about one day after the gene-editing step and before the step of culturing the third or fourth population of TILs.

246. The method of any of the preceding claims, wherein the method further comprises the step of resting the third or fourth population of TILs for about 12 hours to 24 hours after the gene-editing step and before the step of culturing the third or fourth population of TILs.

247. The method of any of the preceding claims, wherein the step of resting the third or fourth population of TILs comprises resting the third or fourth population of TILs for about 15 hours to 18 hours.

248. The method of any of the preceding claims, wherein the step of resting the third or fourth population of TILs comprises resting the third or fourth population of TILs for about 15 hours.

249. The method of any of the preceding claims, wherein the step of resting the third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2.

250. The method of any of the preceding claims, wherein the step of resting the third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about 15 hours to 23 hours at about 30°C.

251. The method of any of the preceding claims, wherein the step of resting third or fourth population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to 23 hours at about 30°C.

252. The method of any of the preceding claims, wherein the step of resting the third or fourth

population of TILs comprises incubating the third or fourth population of TILs in a cell culture medium comprising IL-2 for about one hour at 37°C followed by about 15 hours to 22 hours at about 30°C.

253. The method of any of the preceding claims, wherein the first protein and the second protein are independently selected from the group consisting of PD-1, CTLA-4, LAG-3, CISH, TIGIT and CBL-B, with the proviso that the first protein and the second protein are different.

254. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of PD-1 and CTLA-4.

255. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of PD-1 and LAG-3.

256. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of PD-1 and CISH.

257. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of PD-1 and CBL-B.

258. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of PD-1 and TIGIT.

259. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of CTLA-4 and LAG-3.

260. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of CTLA-4 and CISH.

261. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of CTLA-4 and CBL-B.

262. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of LAG-3 and CISH.

263. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of LAG-3 and CBL-B.

264. The method of any of the preceding claims, wherein the first protein and the second protein are selected from the group consisting of CISH and CBL-B.

265. The method of any of the preceding claims, wherein the first protein is PD-1 and the second protein is CTLA-4.

266. The method of any of the preceding claims, wherein the first protein is CTLA-4 and the second protein is PD-1.

267. The method of any of the preceding claims, wherein the first protein is PD-1 and the second protein is LAG-3.

268. The method of any of the preceding claims, wherein the first protein is LAG-3 and the second protein is PD-1.

269. The method of any of the preceding claims, wherein the first protein is PD-1 and the second protein is CISH.

270. The method of any of the preceding claims, wherein the first protein is CISH and the second protein is PD-1.

271. The method of any of the preceding claims, wherein the first protein is PD-1 and the second protein is CBL-B.

272. The method of any of the preceding claims, wherein the first protein is CBL-B and the second protein is PD-1.

273. The method of any of the preceding claims, wherein the first protein is PD-1 and the second protein is TIGIT.

274. The method of any of the preceding claims, wherein the first protein is TIGIT and the second protein is PD-1.

275. The method of any of the preceding claims, wherein the first protein is CTLA-4 and the second protein is LAG-3.

276. The method of any of the preceding claims, wherein the first protein is LAG-3 and the second protein is CTLA-4.

277. The method of any of the preceding claims, wherein the first protein is CTLA-4 and the second protein is CISH.

278. The method of any of the preceding claims, wherein the first protein is CISH and the second protein is CTLA-4.

279. The method of any of the preceding claims, wherein the first protein is CTLA-4 and the second protein is CBL-B.

280. The method of any of the preceding claims, wherein the first protein is CBL-B and the second protein is CTLA-4.

281. The method of any of the preceding claims, wherein the first protein is LAG-3 and the second protein is CISH.

282. The method of any of the preceding claims, wherein the first protein is CISH and the second

protein is LAG-3.

283. The method of any of the preceding claims, wherein the first protein is LAG-3 and the second protein is CBL-B.

284. The method of any of the preceding claims, wherein the first protein is CBL-B and the second protein is LAG-3.

285. The method of any of the preceding claims, wherein the first protein is CISH and the second protein is CBL-B.

286. The method of any of the preceding claims, wherein the first protein is CBL-B and the second protein is CISH.

287. The method of any of the preceding claims, wherein the first protein or the second protein is PD-1.

288. The method of any of the preceding claims, wherein the first protein or the second protein is CTLA-4.

289. The method of any of the preceding claims, wherein the first protein or the second protein is LAG-3.

290. The method of any of the preceding claims, wherein the first protein or the second protein is CISH.

291. The method of any of the preceding claims, wherein the first protein or the second protein is CBL-B.

292. The method of any of the preceding claims, wherein the first protein or the second protein is TIGIT.

293. The method of any of the preceding claims, wherein the first gene editor downregulates expression of the first protein and the second gene editor downregulates expression of the second protein.

294. The method of any of the preceding claims, wherein the expanded number of TILs comprises a therapeutic population of TILs.

295. The method of any of the preceding claims, wherein the antigen presenting cells (APCs) are PBMCs.

296. The method of any of the preceding claims, wherein the PBMCs are irradiated and allogeneic.

297. The method according to any of the preceding claims, wherein the antigen-presenting cells are artificial antigen-presenting cells.

298. The method according to any of the preceding claims, wherein the IL-2 concentration is about 10,000 IU/mL to about 5,000 IU/mL.

299. The method according to any of the preceding claims, wherein the first cell culture medium and/or the second cell culture medium further comprises a 4-1BB agonist and/or an OX40 agonist.

300. The method of any of the preceding claims, wherein the patient is naïve to an ICI treatment, an anti-VEGF treatment, a chemotherapeutic treatment, or combinations thereof.

301. The method of any of the preceding claims, wherein the patient is naïve to any cancer treatment.

302. The method of any of the preceding claims, wherein the patient receives a first-line ICI treatment and/or standard treatment.

303. The method of any of the preceding claims, wherein the patient receives a second-line ICI treatment and/or standard treatment.

304. The method of any of the preceding claims, wherein step of thawing and the subsequent steps are performed after the patient receives the cancer treatment or resumes the maintenance therapy and exhibits progressive disease.

305. The method of any of the preceding claims, wherein the patient is in a washout period at initiation of step (a).

306. A method of treating a cancer patient by administering a population of tumor infiltrating lymphocytes (TILs) to the cancer patient in need thereof, wherein the cancer patient has received at least one prior therapy and has exhibited cancer progression on or after the at least one prior therapy, wherein obtaining the population of the TILs comprises multilesional sampling, wherein the population of TILs was made from a tumor sample harvested before the cancer patient receives the at least one prior therapy; and wherein the population of TILs is administered to the subject or patient after the cancer patient has exhibited cancer progression on or after the at least one prior therapy.

307. A method of treating a cancer patient by administering a population of tumor infiltrating lymphocytes (TILs) to the cancer patient in need thereof, wherein the cancer patient has received at least one prior therapy and has exhibited cancer progression on or after the at least one prior therapy, wherein obtaining the population of the TILs comprises multilesional sampling,

wherein the population of TILs was made before the cancer patient receives the at least one prior therapy according to any of the preceding claims;

and wherein the population of TILs is administered to the subject or patient after the cancer

patient has exhibited cancer progression on or after the at least one prior therapy.

308. The method of any of the preceding claims, wherein at the time of harvesting the tumor sample, the cancer patient is naïve to any cancer treatment.

309. The method of any of the preceding claims, wherein at the time of harvesting the tumor sample, the patient is naïve to ICI treatment, anti-VEGF treatment, or chemotherapeutic treatment.

310. The method of any of the preceding claims, wherein at the time of harvesting the tumor sample, the patient is on maintenance therapy that is interrupted at the time of step (a), and the maintenance therapy is resumed after step (a).

311. The method of any of the preceding claims, wherein at the time of harvesting the tumor sample, the patient is in a washout period at initiation of step (a).

312. The method of any of the preceding claims, wherein the patient receives or is going to receive a first-line ICI treatment and/or standard treatment.

313. The method of any of the preceding claims, wherein the patient receives or is going to receive a second-line ICI treatment and/or standard treatment.

314. The method of any of the preceding claims, further comprising administering an ICI to the cancer patient.

315. The method of any of the preceding claims, wherein the ICI is an inhibitor of a gene selected from the group consisting of PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

316. The method of any of the preceding claims, further comprising the step of treating the patient with a non-myeloablative lymphodepletion regimen prior to administering the population of TILs to the patient.

317. The method of any of the preceding claims, wherein the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

318. The method of any of the preceding claims, wherein the non-myeloablative lymphodepletion regimen comprises the steps of administration of cyclophosphamide at a dose of 60 mg/m^2/day

and fludarabine at a dose of 25 mg/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for three days.

319. The method of any of the preceding claims, wherein the cyclophosphamide is administered with mesna.

320. The method of any of the preceding claims, further comprising the step of treating the patient with an IL-2 regimen starting on the day after administration of the population of TILs to the patient.

321. The method of any of the preceding claims, further comprising the step of treating the patient with an IL-2 regimen starting on the same day as administration of the population of TILs to the patient.

322. The method of any of the preceding claims, wherein the IL-2 regimen is a high-dose IL-2 regimen comprising 600,000 or 720,000 IU/kg of aldesleukin, or a biosimilar or variant thereof, administered as a 15-minute bolus intravenous infusion every eight hours until tolerance.

323. An expanded number of tumor infiltrating lymphocytes (TILs) or a therapeutic population of TILs manufactured by the method of any of the preceding claims.

324. A pharmaceutical composition comprising the expanded number of TILs or therapeutic population of TILs of any of the preceding claims and a pharmaceutically acceptable carrier.

325. A population of TILs manufactured using the method of any of the preceding claims.

326. A pharmaceutical composition comprising the population of TILs of claim 325.

327. The pharmaceutical composition of claim 326, further comprising an ICI.

328. The pharmaceutical composition of claim 327, wherein the ICI is an inhibitor of a gene selected from the group consisting of PD-1, CTLA-4, LAG-3, HAVCR2 (TIM-3), Cish, TGFβ, PKA, CBL-B, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, BTLA, CD160, TIGIT, TET2, BAFF (BR3), CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244, TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, TOX, SOCS1, ANKRD11, and BCOR.

329. A method of treating a cancer patient by administering the population of TILs of any of the preceding claims or the pharmaceutical composition of any of the preceding claims to the cancer patient, wherein the cancer patient has received at least one prior therapy, and the cancer patient exhibits cancer progression on or after the at least one prior therapy.

Process 2A: about 22 days from Steps A - E

1. **STEP A**

Obtain Patient Tumor Sample

2. **STEP B**

Fragmentation and First Expansion

3 days to 14 days

3. **STEP C**

First Expansion to Second Expansion Transition

No Storage and Closed System

4. **STEP D**

Second Expansion

IL-2, OKT-3, and antigen-presenting feeder cells

Closed System

5. **STEP E**

Harvest TILS from Step D

Closed System

6. **STEP F**

Final Formulation and/or Transfer to Infusion Bag

(optionally cryopreserve)

Figure 1

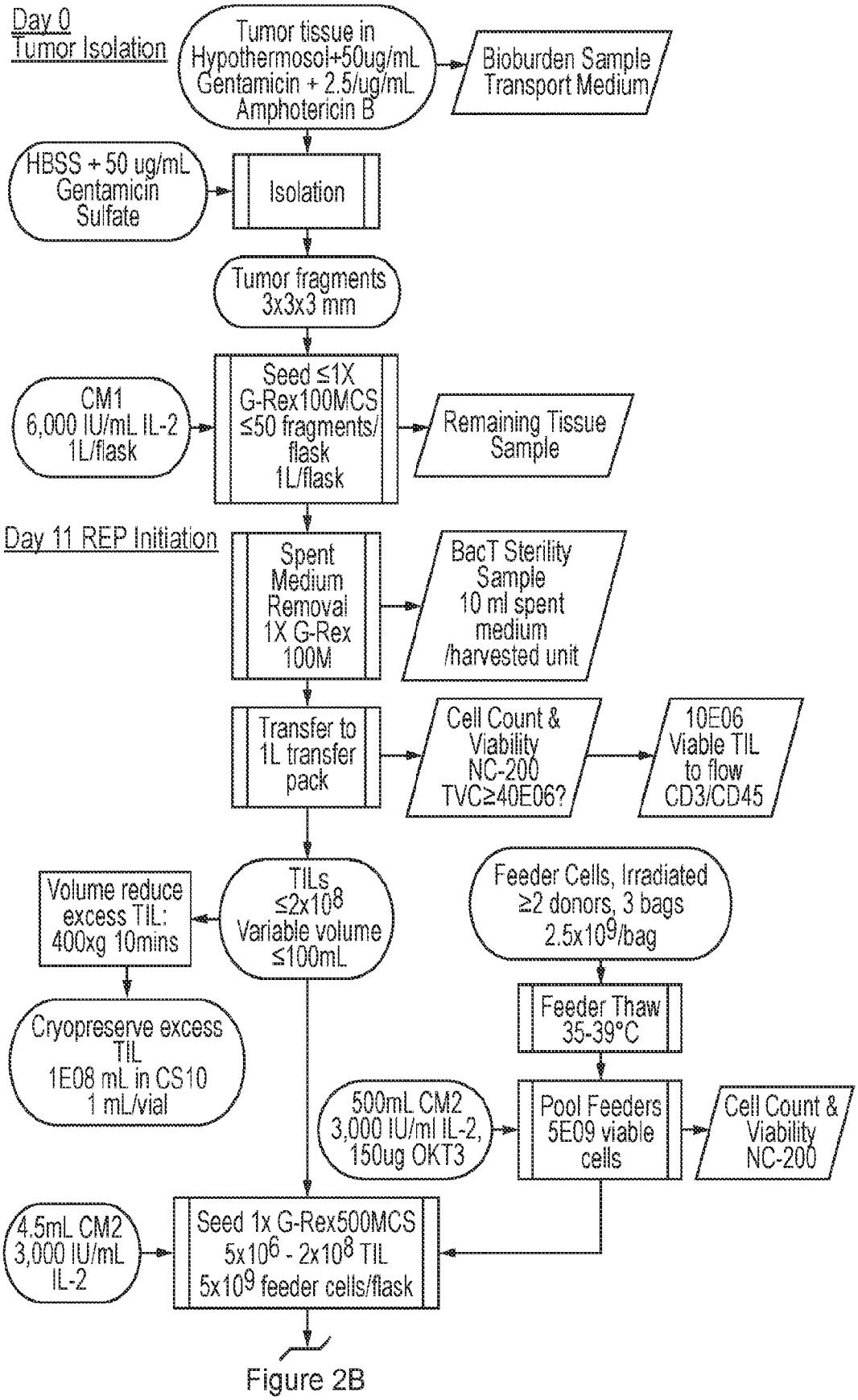

Day 0
Tumor Isolation
Tumor tissue in Hypothermosol+50ug/mL Gentamicin + 2.5/ug/mL Amphotericin B
Bioburden Sample Transport Medium
HBSS + 50 ug/mL Gentamicin Sulfate
Isolation
Tumor fragments 3x3x3 mm
CM1 6,000 IU/mL IL-2 1L/flask
Seed ≤1X G-Rex100MCS ≤50 fragments/ flask 1L/flask
Remaining Tissue Sample
Day 11 REP Initiation
Spent Medium Removal 1X G-Rex 100M
BacT Sterility Sample 10 ml spent medium /harvested unit
Transfer to 1L transfer pack
Cell Count & Viability NC-200 TVC≥40E06?
10E06 Viable TIL to flow CD3/CD45
Volume reduce excess TIL: 400xg 10mins
TILs ≤2x10^8 Variable volume ≤100mL
Feeder Cells, Irradiated ≥2 donors, 3 bags 2.5x10^9/bag
Feeder Thaw 35-39°C
Cryopreserve excess TIL 1E08 mL in CS10 1 mL/vial
500mL CM2 3,000 IU/ml IL-2, 150ug OKT3
Pool Feeders 5E09 viable cells
Cell Count & Viability NC-200
4.5mL CM2 3,000 IU/mL IL-2
Seed 1x G-Rex500MCS 5x10^6 - 2x10^8 TIL 5x10^9 feeder cells/flask
Figure 2B

Figure 2A

Figure 2A

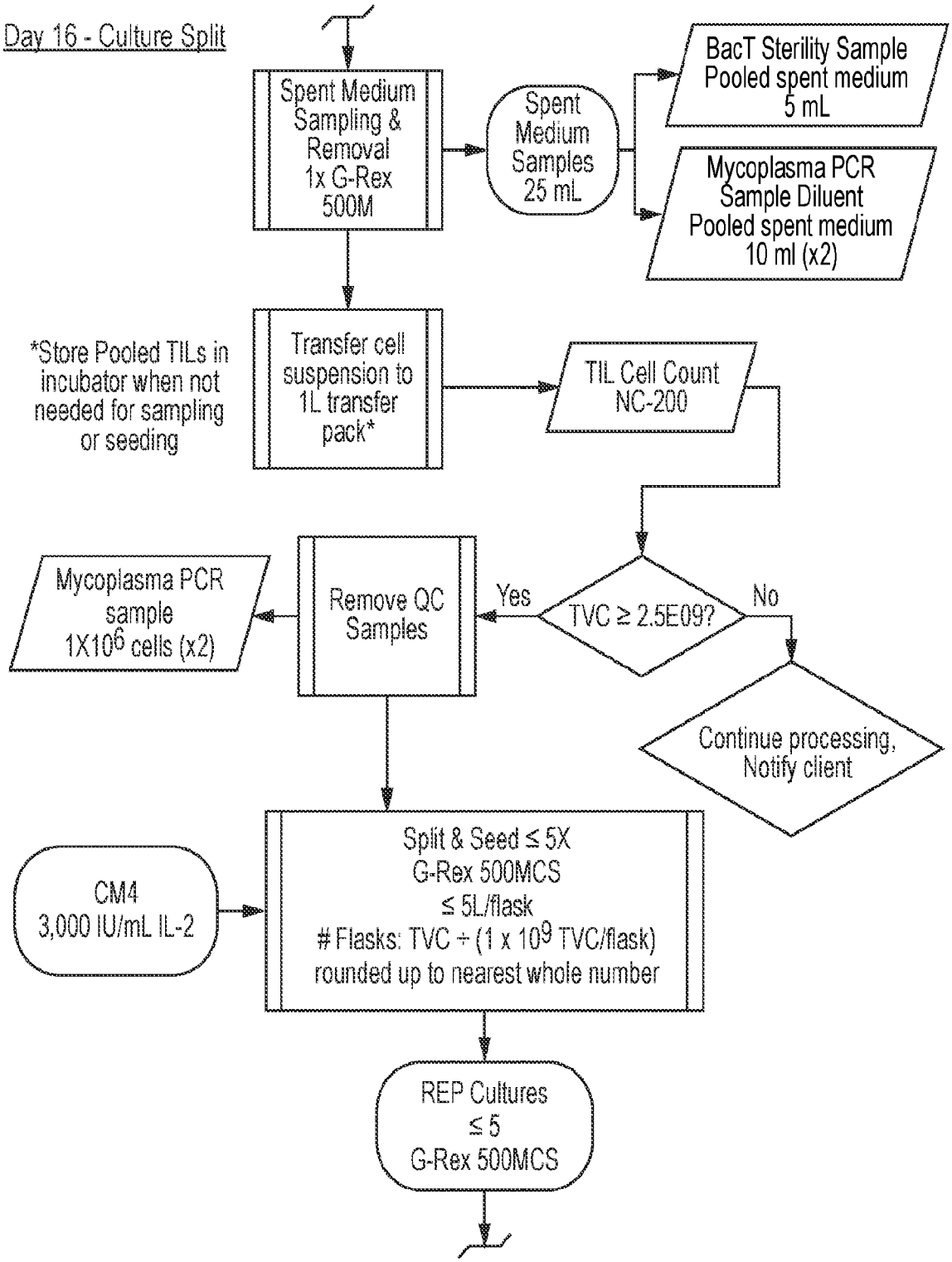


Figure 2C

Figure 2B

Figure 2B

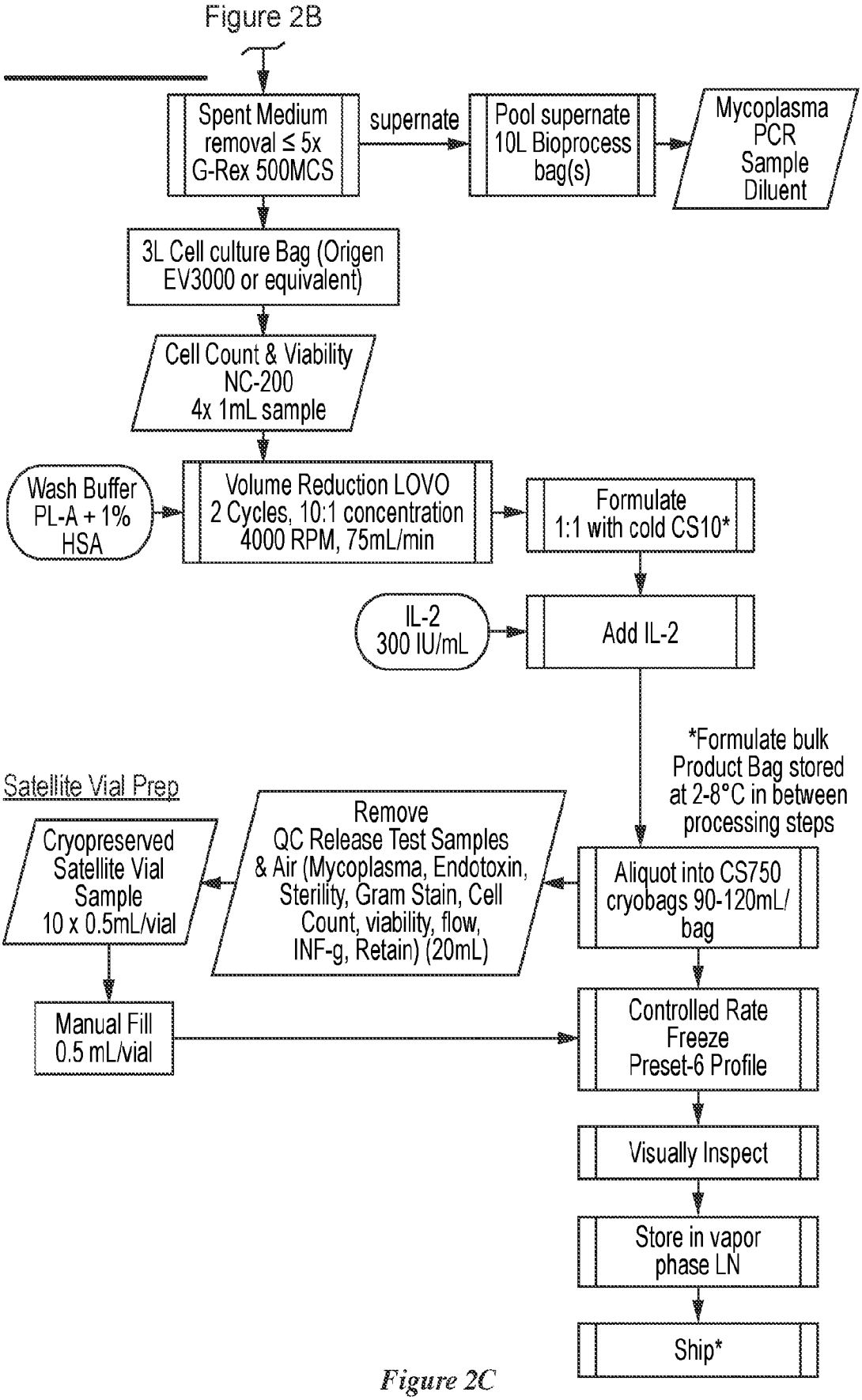


Figure 2C

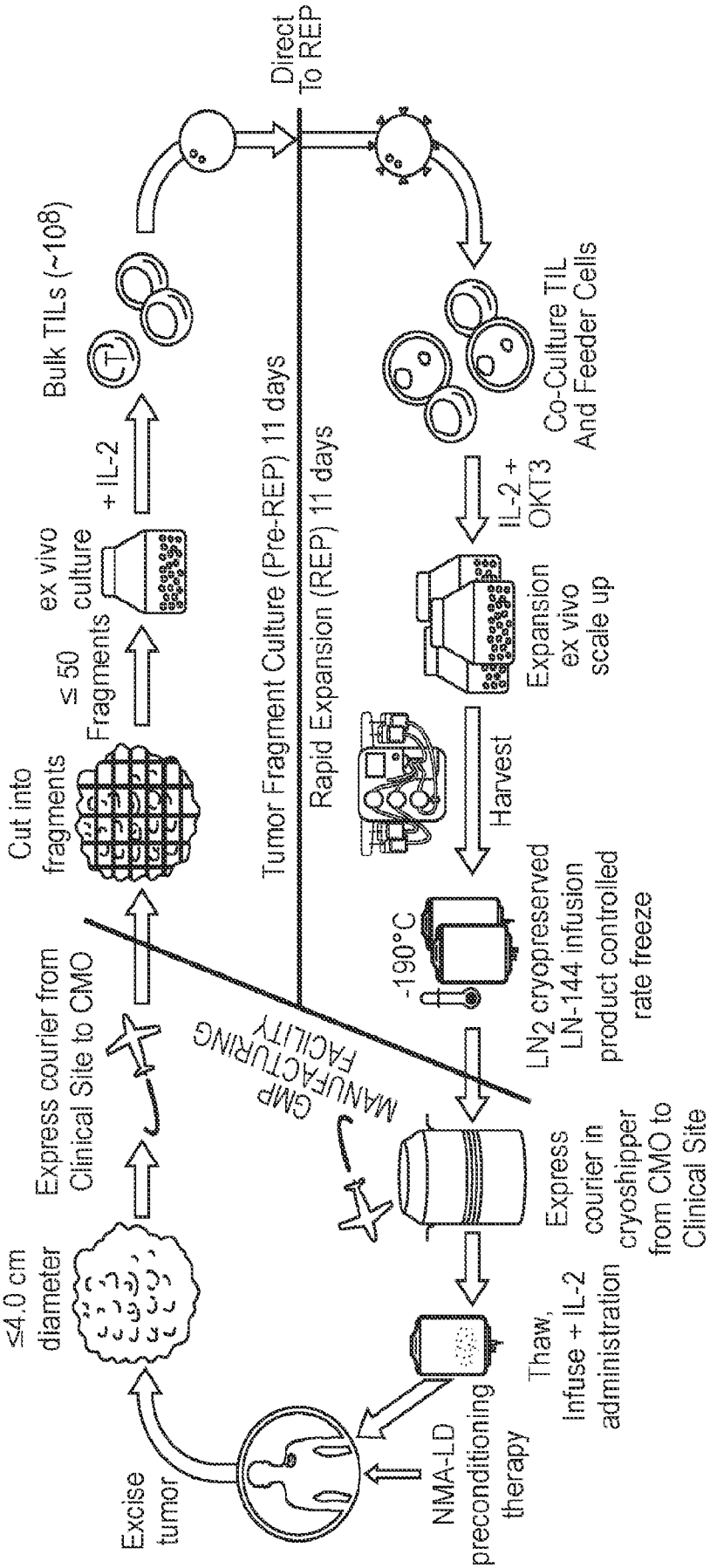

Direct To REP
Bulk TILs (~10^8)
+ IL-2
ex vivo culture
≤ 50 Fragments
Cut into fragments
Tumor Fragment Culture (Pre-REP) 11 days
Rapid Expansion (REP) 11 days
Co-Culture TIL And Feeder Cells
IL-2 + OKT3
Expansion ex vivo scale up
Harvest
-190°C
LN2 cryopreserved LN-144 infusion product controlled rate freeze
GMP MANUFACTURING FACILITY
Express courier from Clinical Site to CMO
≤4.0 cm diameter
Express courier in cryoshipper from CMO to Clinical Site
Thaw, Infuse + IL-2 administration
NMA-LD preconditioning therapy
Excise tumor

Figure 3

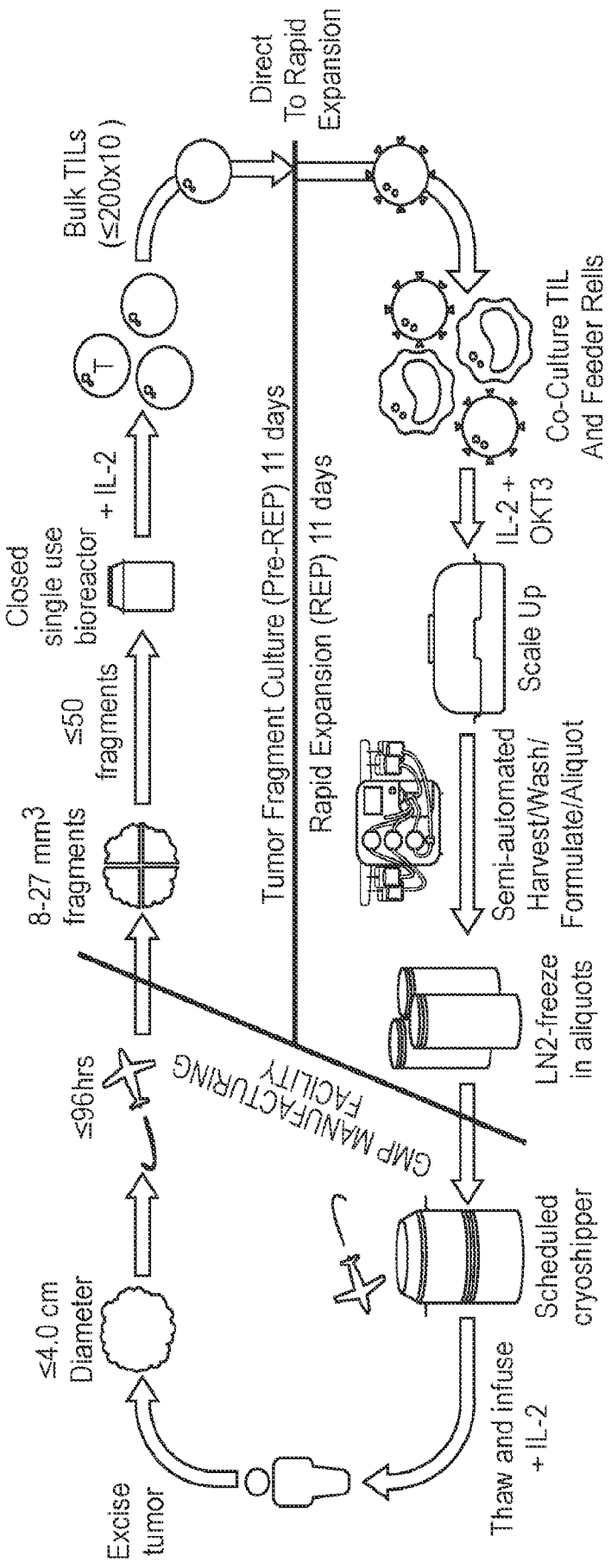

Excise tumor
≤4.0 cm Diameter
≤96hrs
GMP MANUFACTURING FACILITY
8-27 mm3 fragments
≤50 fragments
Closed single use bioreactor
+ IL-2
Bulk TILs (≤200x10)
Direct To Rapid Expansion
Tumor Fragment Culture (Pre-REP) 11 days
Rapid Expansion (REP) 11 days
Co-Culture TIL And Feeder Rells
IL-2 + OKT3
Scale Up
Semi-automated Harvest/Wash/ Formulate/Aliquot
LN2-freeze in aliquots
Scheduled cryoshipper
Thaw and infuse + IL-2

Figure 4

Process 1C: 43-55 Days for Steps A - E	Process 2A: about 22 days from Steps A - E
1. **STEP A** Obtain Patient Tumor Sample	1. **STEP A** Obtain Patient Tumor Sample
2. **STEP B** Fragmentation and First Expansion 11 days to 21 days	2. **STEP B** Fragmentation and First Expansion 3 days to 14 days
3. **STEP C** First Expansion to Second Expansion Transition Optional Storage until Selection	3. **STEP C** First Expansion to Second Expansion Transition No Storage and Closed System
4. **STEP D** Second Expansion IL-2, OKT-3, antigen-presenting feeder cells Optionally repeat one or more times	4. **STEP D** Second Expansion IL-2, OKT-3, antigen-presenting feeder cells Closed System
5. **STEP E** Harvest TILs from Step D	5. **STEP E** Harvest TILs from Step D Closed System
6. **STEP F** Final Formulation and/or Transfer to Infusion Bag	6. **STEP F** Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)

Figure 5

Process Step	Process 1C Embodiment	Process 2A Embodiment	Advantages
Pre-REP	• 4 fragments per 10 GREX-10 flasks • 11-21 day duration	• 40 fragments per 1 GREX-100M flask • 11 day duration	• Increased tumor fragments per flask • Shortened culture time • Reduced number of steps • Amenable to closed system
Pre-REP to REP Transition	• Pre-REP TIL are frozen until phenotyped for selection then thawed to proceed to the REP (-day 30) • REP requires >40x10^6 TIL	• Pre-REP TIL directly move to REP on day 11 • REP requires 25-200x10^6 TIL	• Shortened pre-REP-to-REP process • Reduced number of steps • Eliminated phenotyping selection • Amenable to closed system
REP	• 6 GREX-100M flasks on REP day 0 • 5x10^6 TIL and 5x10^8 PBMC feeders per flask on REP day 0 • Split to 18-36 flasks on REP day 7 • 14 day duration	• 1 GREX-500M flask on day 11 • 25-200x10^6 TIL and 5x10^9 PBMC feeders on day 11 • Split to ≤ 6 GREX-500M flasks on day 16 • 11 day duration	• Reduced number of steps • Shorter REP duration • Closed system transfer of TIL between flasks • Closed system media exchanges
Harvest	• TIL harvested via centrifugation	• TIL harvested via LOVO automated cell washing system	• Reduced number of steps • Automated cell washing • Closed system • Reduced loss of product during wash
Final Formulation	• Fresh product in Hypothermosol • Single infusion bag • Limited shipping stability	• Cryopreserved product in PlasmaLyte-A + 1% HSA and CS10 stored in LN_2 • Multiple aliquots • Longer shipping stability	• Shipping flexibility • Flexible patient scheduling • More timely release testing
Overall Estimated Process Time	• 43 -55 days	• 22 days	• Faster turnaround to patient

Figure 6

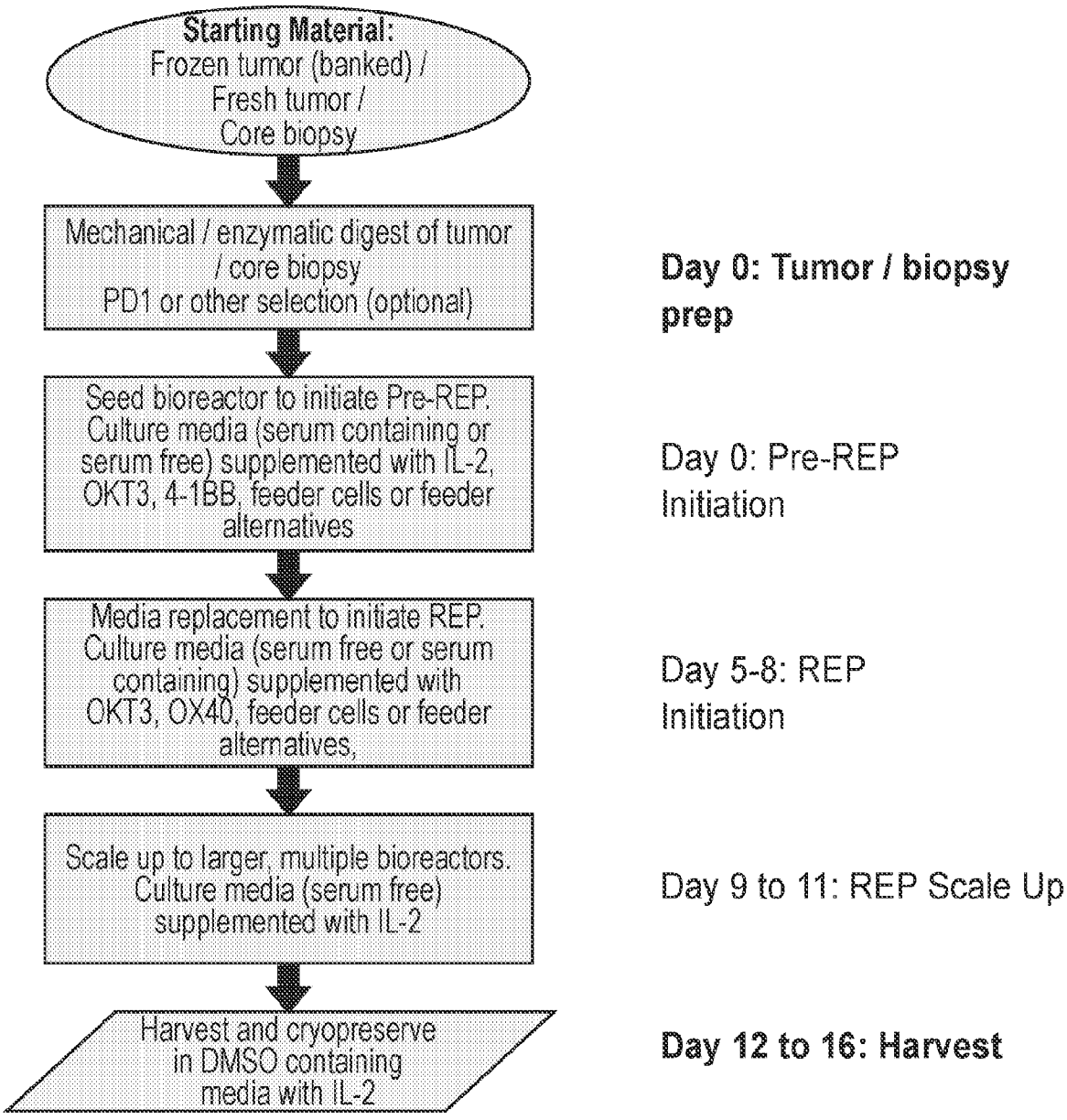

Starting Material:
Frozen tumor (banked) /
Fresh tumor /
Core biopsy
Mechanical / enzymatic digest of tumor / core biopsy
PD1 or other selection (optional)
Seed bioreactor to initiate Pre-REP. Culture media (serum containing or serum free) supplemented with IL-2, OKT3, 4-1BB, feeder cells or feeder alternatives
Media replacement to initiate REP. Culture media (serum free or serum containing) supplemented with OKT3, OX40, feeder cells or feeder alternatives,
Scale up to larger, multiple bioreactors. Culture media (serum free) supplemented with IL-2
Harvest and cryopreserve in DMSO containing media with IL-2
Day 0: Tumor / biopsy prep
Day 0: Pre-REP Initiation
Day 5-8: REP Initiation
Day 9 to 11: REP Scale Up
Day 12 to 16: Harvest

Figure 7

Process 2A: about 22 days from Steps A-E	Process GEN3: about 14-18 days from Steps A-E
STEP A Obtain Patient Tumor Sample (optionally can be frozen before Step B)	**STEP A** Obtain Patient Tumor Sample (optionally can be frozen before Step B)
STEP B First Expansion (physical fragmentation to at least 40 fragments per container grown for about 3 days to 14 days with media comprising IL-2)	**STEP B** Priming First Expansion (physical fragmentation of up to 60 fragments per container grown for about 1 days to 7 days with media comprising IL-2, OKT-3, and antigen-presenting feeder cells)
STEP C First Expansion to Second Expansion Transition (Step B TILs directly move to Step D, optionally on Step B day 11)	**STEP C** Priming First Expansion to Rapid Second Expansion Transition (Step B TILs directly move to Step D on day 7)
STEP D Second Expansion (TILs grown in growth media medium comprising IL-2, OKT-3, and antigen-presenting feeder cells in a closed container)	**STEP D** Rapid Second Expansion (TILs grown in growth media medium comprising IL-2, OKT-3, and 2X antigen-presenting feeder cells; Days 10-11 scale up and add additional IL-2)
STEP E Harvest TILS from Step D (TILs harvested via closed system)	**STEP E** Harvest TILS from Step D
STEP F Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)	**STEP F** Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)

Figure 8A

Process GEN 3: about 14-18 days from Steps A-E

STEP A
Obtain Patient Tumor Sample
(optionally can be frozen before Step B)

STEP B
Priming First Expansion
(physical fragmentation of up to 60 fragments per container grown for about 1 days to 7 days with media comprising IL-2, OKT-3, and antigen-presenting feeder cells)

STEP C
Priming First Expansion to Rapid Second Expansion Transition
(Step B TILs directly move to Step D on day 7)

STEP D
Rapid Second Expansion
(TILs grown in growth media medium comprising IL-2, OKT-3, and 2X antigen-presenting feeder cells; Days 10-11 scale up and add additional IL-2)

STEP E
Harvest TILS from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag
(optionally cryopreserve)

Figure 8B

Embodiment GEN 3.0: about 14-18 days from Steps A - E	Embodiment GEN 3.1 control: about 14-18 days from Steps A - E	Embodiment GEN 3.1 Test/F: about 14-18 days from Steps A - E
STEP A Obtain Patient Tumor Sample (optionally can be frozen before Step B)	**STEP A** Obtain Patient Tumor Sample (optionally can be frozen before Step B)	**STEP A** Obtain Patient Tumor Sample (optionally can be frozen before Step B)
STEP B Priming First Expansion (physical fragmentation of up to 60 fragments per container grown for about 1 days to 7/8 days with media comprising IL-2)	**STEP B** Priming First Expansion (physical fragmentation of up to 60 fragments per container grown for about 1 days to 7/8 days with media comprising IL-2, and OKT-3)	**STEP B** Priming First Expansion (physical fragmentation of up to 60 fragments per container grown for about 1 days to 7/8 days with media comprising IL-2, OKT-3, and antigen-presenting feeder cells)
STEP C Priming First Expansion to Rapid Second Expansion Transition (Step B TILs directly move to Step D on day 7/8)	**STEP C** Priming First Expansion to Rapid Second Expansion Transition (Step B TILs directly move to Step D on day 7/8)	**STEP C** Priming First Expansion to Rapid Second Expansion Transition (Step B TILs directly move to Step D on day 7/8)
STEP D Rapid Second Expansion (TILs grown in growth media medium comprising IL-2, OKT-3, and antigen-presenting feeder cells; Days 10-11 scale up and add additional IL-2)	**STEP D** Rapid Second Expansion (TILs grown in growth media medium comprising IL-2, OKT-3, and 2X antigen-presenting feeder cells; Days 10-11 scale up and add additional IL-2)	**STEP D** Rapid Second Expansion (TILs grown in growth media medium comprising IL-2, OKT-3, and 2X antigen-presenting feeder cells; Days 10-11 scale up and add additional IL-2)
STEP E Harvest TILS from Step D	**STEP E** Harvest TILS from Step D	**STEP E** Harvest TILS from Step D
STEP F Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)	**STEP F** Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)	**STEP F** Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)

Figure 8C

Modified Gen 2-like Process: about 22 days from Steps A - E

STEP A
Obtain Patient Tumor Sample
(optionally can be frozen before Step B;
optionally tumor sample can be a core/small biopsy)

STEP B1
Initial Culture
physical fragmentation of up to 60 tumor fragments or up to 10 cores/small biopsies per container, TILs grown for 3 days in growth medium comprising IL-2

STEP B2
Priming First Expansion
TILs grown for 8 days in growth medium comprising IL-2, OKT-3, and antigen-presenting feeder cells)

STEP C
Priming First Expansion to Rapid Second Expansion Transition
(Step B TILs directly move to Step D on day 11)

STEP D
Rapid Second Expansion
(volume reduced; TILs grown in growth media medium comprising IL-2, OKT-3, and 50X antigen-presenting feeder cells; Day 16 scale up and add additional IL-2)

STEP E
Harvest TILS from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag
(optionally cryopreserve)

Figure 8D

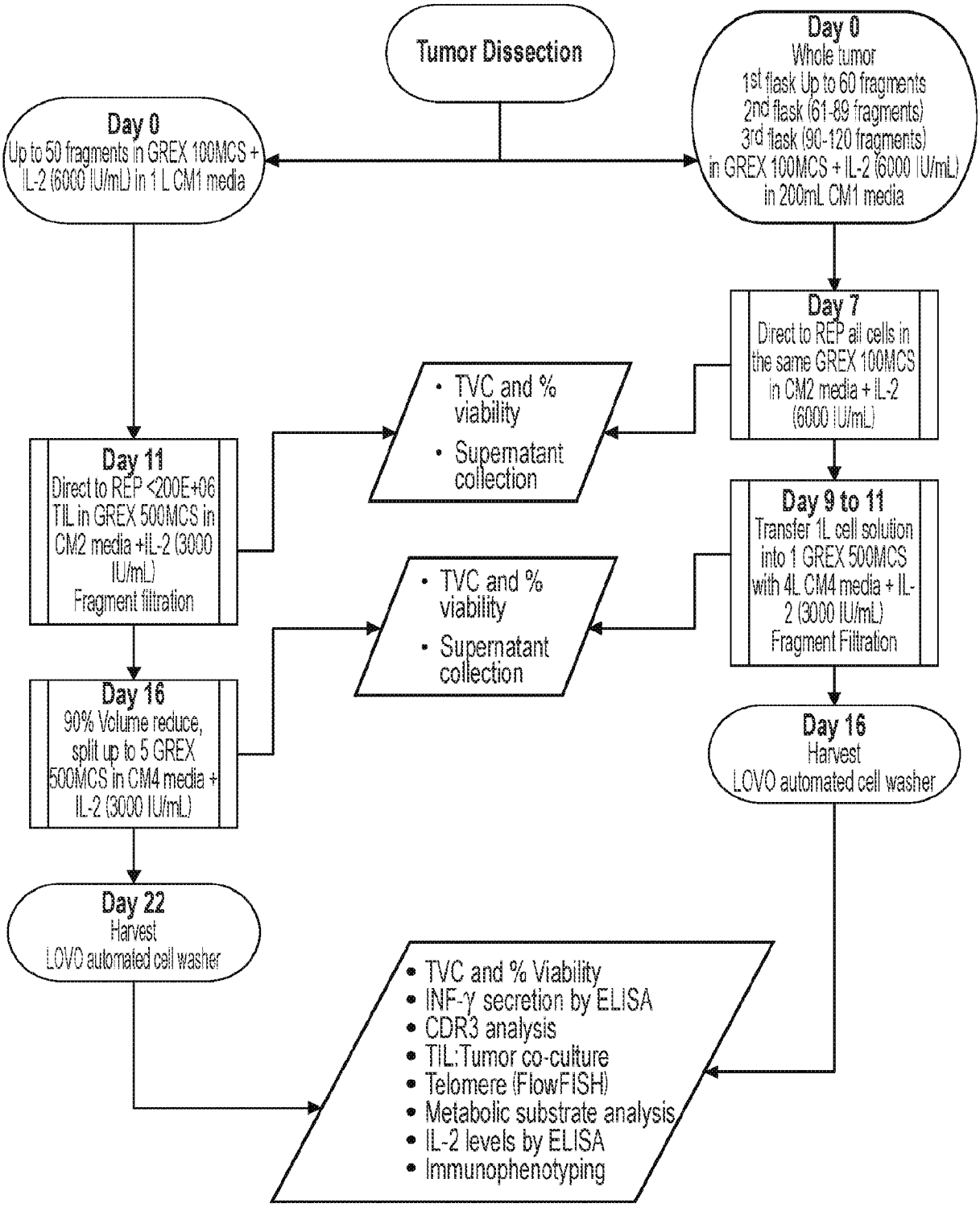

Tumor Dissection
Day 0
Whole tumor
1st flask Up to 60 fragments
2nd flask (61-89 fragments)
3rd flask (90-120 fragments)
in GREX 100MCS + IL-2 (6000 IU/mL)
in 200mL CM1 media
Day 0
Up to 50 fragments in GREX 100MCS + IL-2 (6000 IU/mL) in 1 L CM1 media
Day 7
Direct to REP all cells in the same GREX 100MCS in CM2 media + IL-2 (6000 IU/mL)
• TVC and % viability
• Supernatant collection
Day 11
Direct to REP <200E+06 TIL in GREX 500MCS in CM2 media +IL-2 (3000 IU/mL)
Fragment filtration
Day 9 to 11
Transfer 1L cell solution into 1 GREX 500MCS with 4L CM4 media + IL-2 (3000 IU/mL)
Fragment Filtration
• TVC and % viability
• Supernatant collection
Day 16
90% Volume reduce, split up to 5 GREX 500MCS in CM4 media + IL-2 (3000 IU/mL)
Day 16
Harvest
LOVO automated cell washer
Day 22
Harvest
LOVO automated cell washer
• TVC and % Viability
• INF-γ secretion by ELISA
• CDR3 analysis
• TIL:Tumor co-culture
• Telomere (FlowFISH)
• Metabolic substrate analysis
• IL-2 levels by ELISA
• Immunophenotyping

Figure 9

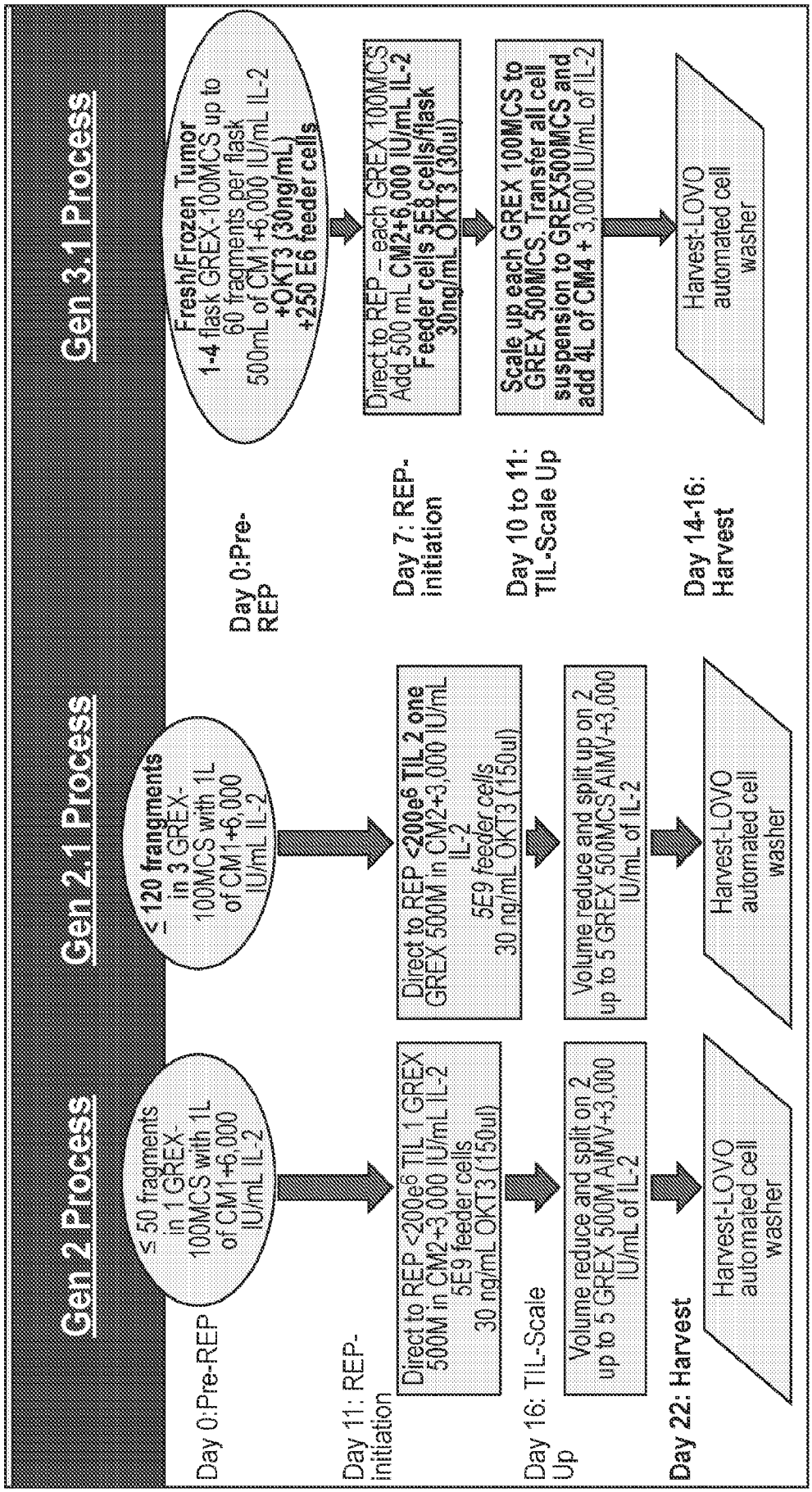

Gen 2 Process
Gen 2.1 Process
Gen 3.1 Process
Day 0:Pre-REP
≤ 50 fragments in 1 GREX-100MCS with 1L of CM1+6,000 IU/mL IL-2
Day 11: REP-initiation
Direct to REP <200e6 TIL 1 GREX 500M in CM2+3,000 IU/mL IL-2 5E9 feeder cells 30 ng/mL OKT3 (150ul)
Day 16: TIL-Scale Up
Volume reduce and split on 2 up to 5 GREX 500M AIMV+3,000 IU/mL of IL-2
Day 22: Harvest
Harvest-LOVO automated cell washer
≤ 120 frangments in 3 GREX-100MCS with 1L of CM1+6,000 IU/mL IL-2
Direct to REP <200e6 TIL 2 one GREX 500M in CM2+3,000 IU/mL IL-2 5E9 feeder cells 30 ng/mL OKT3 (150ul)
Volume reduce and split up on 2 up to 5 GREX 500MCS AIMV+3,000 IU/mL of IL-2
Harvest-LOVO automated cell washer
Fresh/Frozen Tumor 1-4 flask GREX-100MCS up to 60 fragments per flask 500mL of CM1+6,000 IU/mL IL-2 +OKT3 (30ng/mL) +250 E6 feeder cells
Day 0:Pre-REP
Direct to REP – each GREX 100MCS Add 500 mL CM2+6,000 IU/mL IL-2 Feeder cells 5E8 cells/flask 30ng/mL OKT3 (30ul)
Day 7: REP-initiation
Scale up each GREX 100MCS to GREX 500MCS. Transfer all cell suspension to GREX500MCS and add 4L of CM4 + 3,000 IU/mL of IL-2
Day 10 to 11: TIL-Scale Up
Harvest-LOVO automated cell washer
Day 14-16: Harvest

Figure 10

STEP	Gen 2	Gen 2.1	Gen 3.0 Optimized
Pre REP- day 0	≤ 50 fragments/ 1 G-Rex 100MCS - **11 days**	≤ 180 fragments/ 3 G-Rex, Pre-formulated CM1 warmed media 100MCS - **11 days**	***Fresh or Frozen Tumor*** Whole tumor with ≤ 30 fragments up to 60 fragments per 1 G-Rex. 100MCS (up to 4 G-Rex), preformulated warmed media - **7 days. Pre REP, Feeders 2.5 E8 cells + OKT-3 (30ng/mL)**
REP Initiation	Direct to REP- Day 11- **<200 E6 TIL** 1 G-Rex 500MCS	Direct to REP- Day 11- **<200 E6 TIL** Pre-formulated CM2 warmed media in one G-Rex 500MCS	Direct to REP - Day **7-all cells TIL- same G-Rex 100MCS (100MCS up to 4 GREX), Standard media or Defined Media (Serum free). Addition Feeders 5 E8 cells +OKT-3 (30ng/mL)**
TIL propagation or Scale up	1 to 5 G-REX 500MCS **Split day 16**	2 to 5 G-REX 500MCS Pre-formulated CM4 warmed media **Split day 16**	From G-REX 100MCS transfer TIL suspension to G-REX 500MCS, up to 4 GREX 500 MCS- Standard media or Defined Media (Serum Free) **Scale up on day 10 or 11**
Harvest	**Harvest day 22,** LOVO-automated cell washer	**Harvest day 22,** LOVO-automated cell washer (5 wash cycle)	**Harvest day 14 or 16** LOVO- automated cell washer (5 wash cycle)
Final formulation	Cryopreserved Product 300IU/ml IL2- CS10 in LN_2, multiple aliquots	Cryopreserved Product 300IU/ml IL2- CS10 in LN_2, multiple aliquots	Cryopreserved product 300IU/ml IL-2- CS10 in LN_2 multiple aliquots
Process time	**22 days**	**22 days**	**16 days**

Figure 11

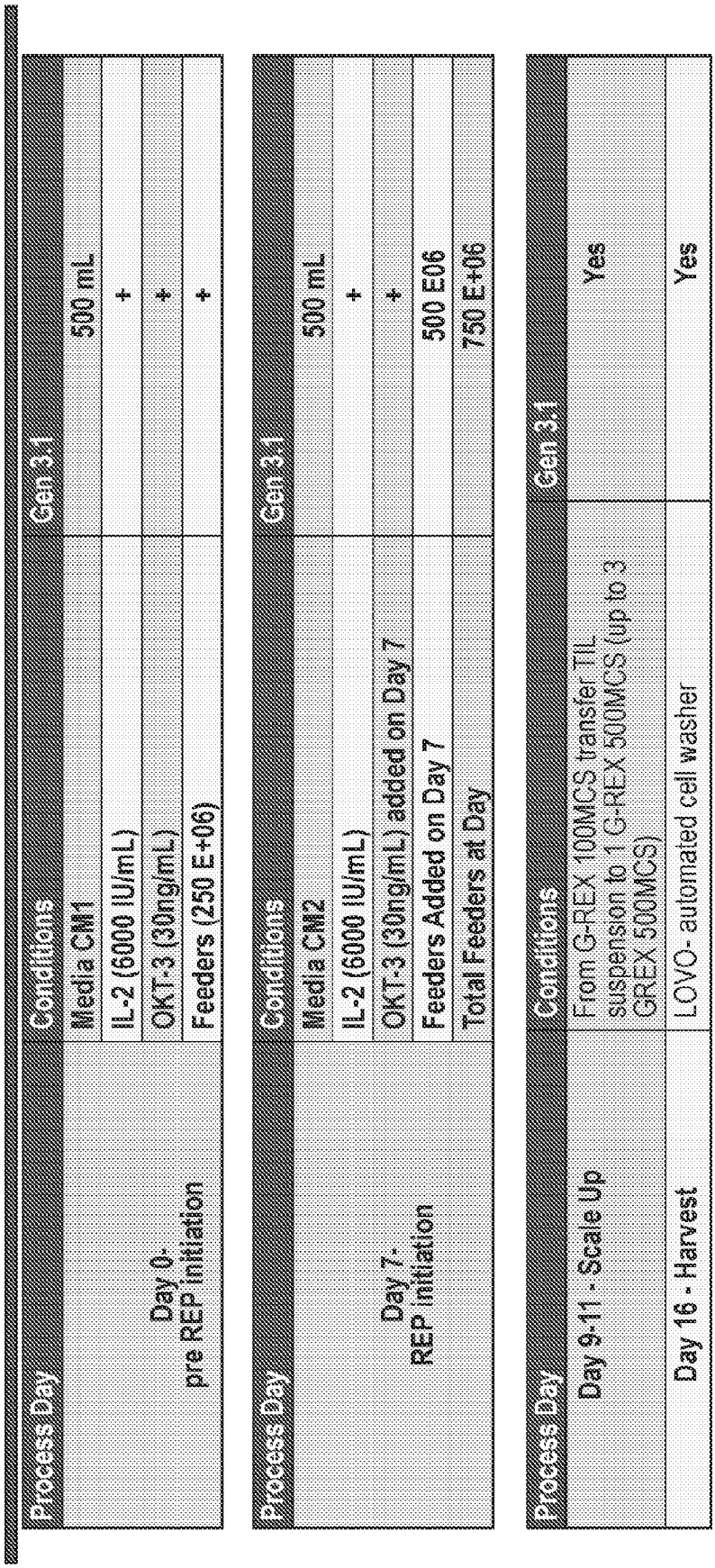

Process Day
Conditions
Gen 3.1
Day 0-
pre REP initiation
Media CM1
500 mL
IL-2 (6000 IU/mL)
+
OKT-3 (30ng/mL)
+
Feeders (250 E+06)
+
Process Day
Conditions
Gen 3.1
Day 7-
REP initiation
Media CM2
500 mL
IL-2 (6000 IU/mL)
+
OKT-3 (30ng/mL) added on Day 7
+
Feeders Added on Day 7
500 E06
Total Feeders at Day
750 E+06
Process Day
Conditions
Gen 3.1
Day 9-11 - Scale Up
From G-REX 100MCS transfer TIL suspension to 1 G-REX 500MCS (up to 3 GREX 500MCS)
Yes
Day 16 - Harvest
LOVO- automated cell washer
Yes

Figure 12

Process Comparison	Key Process Changes	Benefit
Gen 2 : Gen 2.1	• Initiate process with two flasks instead of one flask • Divide REP initiation feeder layer between 2 G-Rex500MCS Flasks • Pre-formulate media and warm prior to use	• Potential doubling of final cell count (dose) with increased TIL repertoire. • Process redundancy throughout process
Gen 2.1 : Gen 3.1	• Fresh or Frozen tumor • 14-16 day process (from 22 day) • Reduce total feeder layer on process • Feeder layer and OKT3 present at Day 0 • REP initiated with fragments • 100MCS scales to 500MCS • Scales to multiple pre-REP flasks • Standard Media and Defined Media (Serum Free)	• Increased potency • Improved phenotype • Decreased process time • Reduced reagent testing • Decreased process variability • Defined reagents • Increased repertoire • Reduce impurities (feeder) • Comparable or Higher Dose.

Figure 13

Process Comparison	Key Process Changes	Desired Improvement	Criteria for Success	Outcome
Gen 2 : Gen 3.0	• 14-16 days • Initiate REP with fragments up to 4 flask. • 100MCS scales to 500MCS	• Increased potency • Improved phenotype • Decreased process time	• Increase potency as measured by INF-g ✓ • Comparable phenotype ✓ • Comparable Dose ✓ • Comparable purity (feeder cell) ✓ • Maintain clonal diversity ✓	• Potency increased over Gen2 • Improved expression of CD28 on CD8 cells • Maximum capacity of flask reached by day 16 on Gen 3.1 • Reduced feeder cell usage • Increased diversity

Figure 14

Process	Gen 2	Gen 3
L4054	Standard Media	Standard Media
L4055	Standard Media	Standard Media
M1085T	Standard Media	Standard Media

Standard Media:
Pre REP: CM1
REP initiation : CM2
Split or Scale up : CM4

Process	Gen 3	Gen 3.1 Control	Gen 3.1
L4063	Standard Media	Standard Media	Standard Media
L4064	Defined Media	Defined Media	Defined Media

Defined Media:
CTS Optimizer (Serum Free Media) in each day of the process

Figure 15

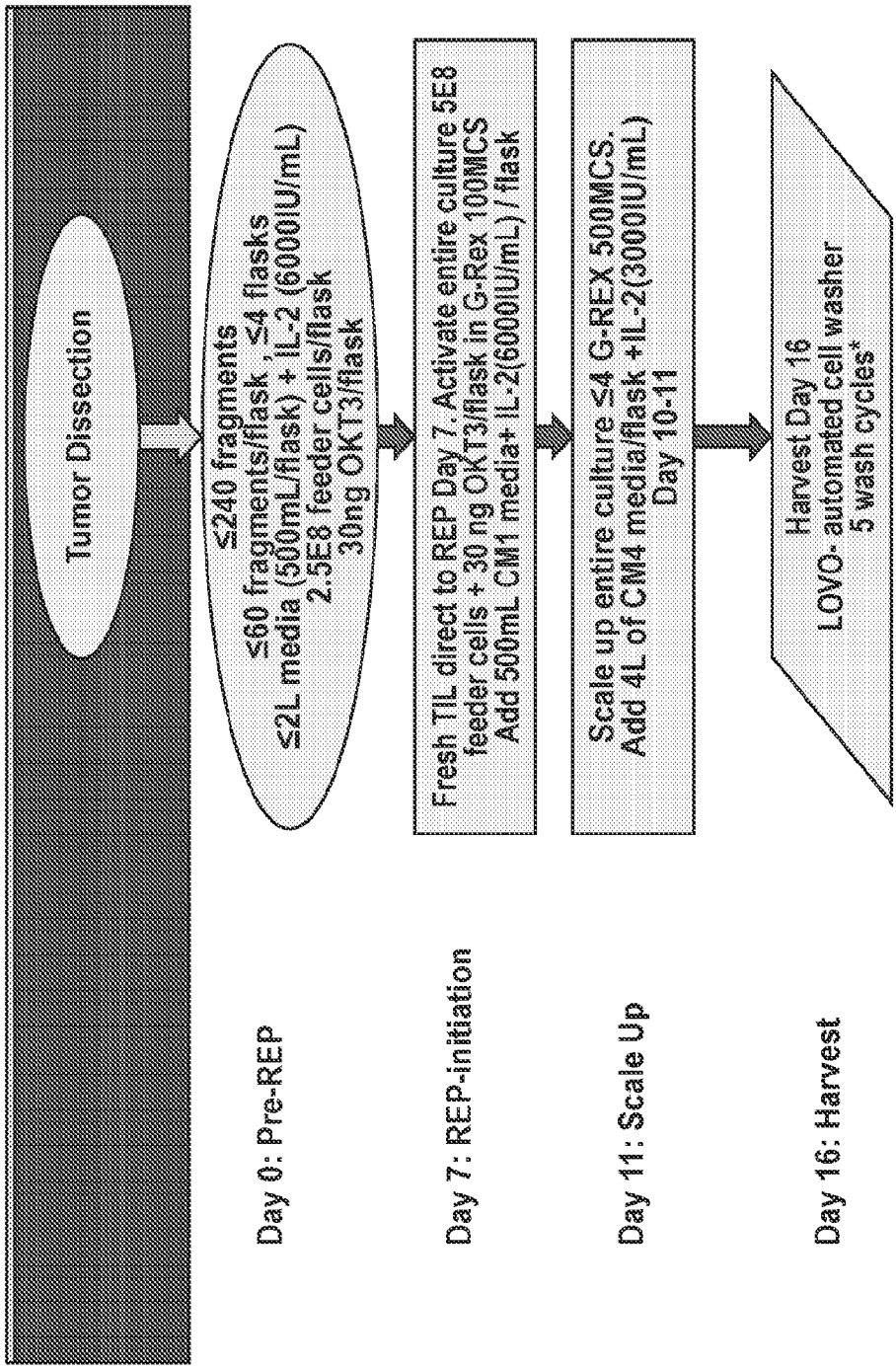

Tumor Dissection
≤240 fragments
≤60 fragments/flask , ≤4 flasks
≤2L media (500mL/flask) + IL-2 (6000IU/mL)
2.5E8 feeder cells/flask
30ng OKT3/flask
Fresh TIL direct to REP Day 7. Activate entire culture 5E8 feeder cells + 30 ng OKT3/flask in G-Rex 100MCS
Add 500mL CM1 media+ IL-2(6000IU/mL) / flask
Scale up entire culture ≤4 G-REX 500MCS.
Add 4L of CM4 media/flask +IL-2(3000IU/mL)
Day 10-11
Harvest Day 16
LOVO- automated cell washer
5 wash cycles*
Day 0: Pre-REP
Day 7: REP-initiation
Day 11: Scale Up
Day 16: Harvest

Figure 16

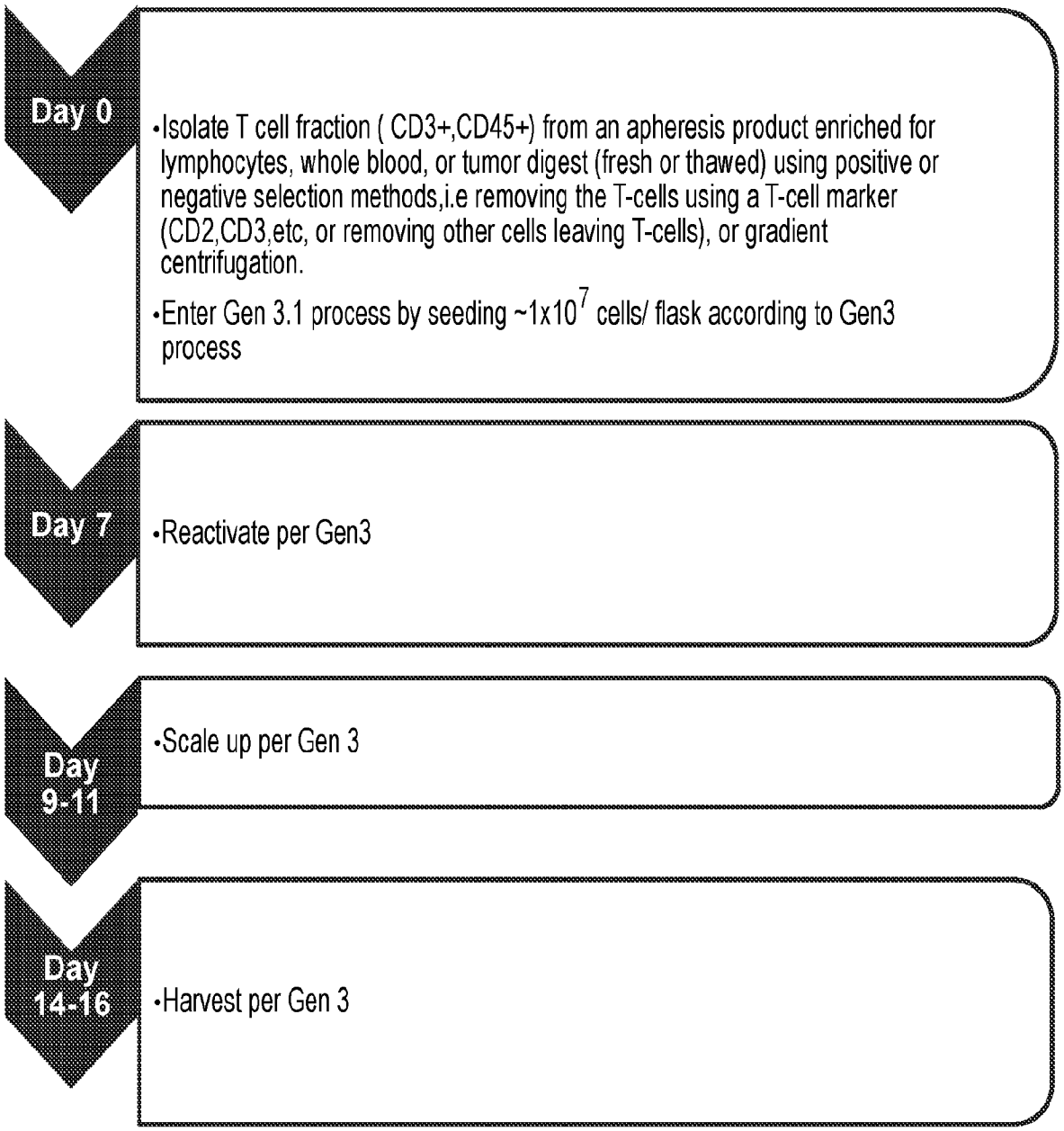

Day 0
•Isolate T cell fraction (CD3+,CD45+) from an apheresis product enriched for lymphocytes, whole blood, or tumor digest (fresh or thawed) using positive or negative selection methods,i.e removing the T-cells using a T-cell marker (CD2,CD3,etc, or removing other cells leaving T-cells), or gradient centrifugation.
•Enter Gen 3.1 process by seeding ~1x10^7 cells/ flask according to Gen3 process
Day 7
•Reactivate per Gen3
Day 9-11
•Scale up per Gen 3
Day 14-16
•Harvest per Gen 3

Figure 17

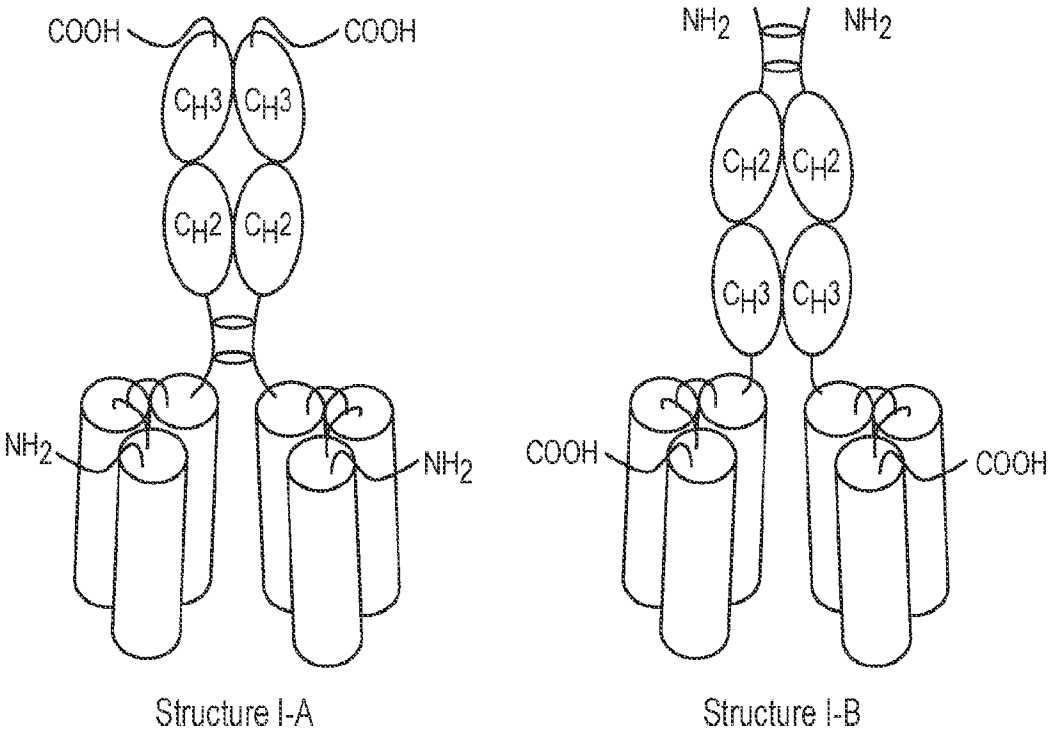

COOH
COOH
CH3
CH3
CH2
CH2
NH2
NH2
Structure I-A
NH2
NH2
CH2
CH2
CH3
CH3
COOH
COOH
Structure I-B

Figure 18

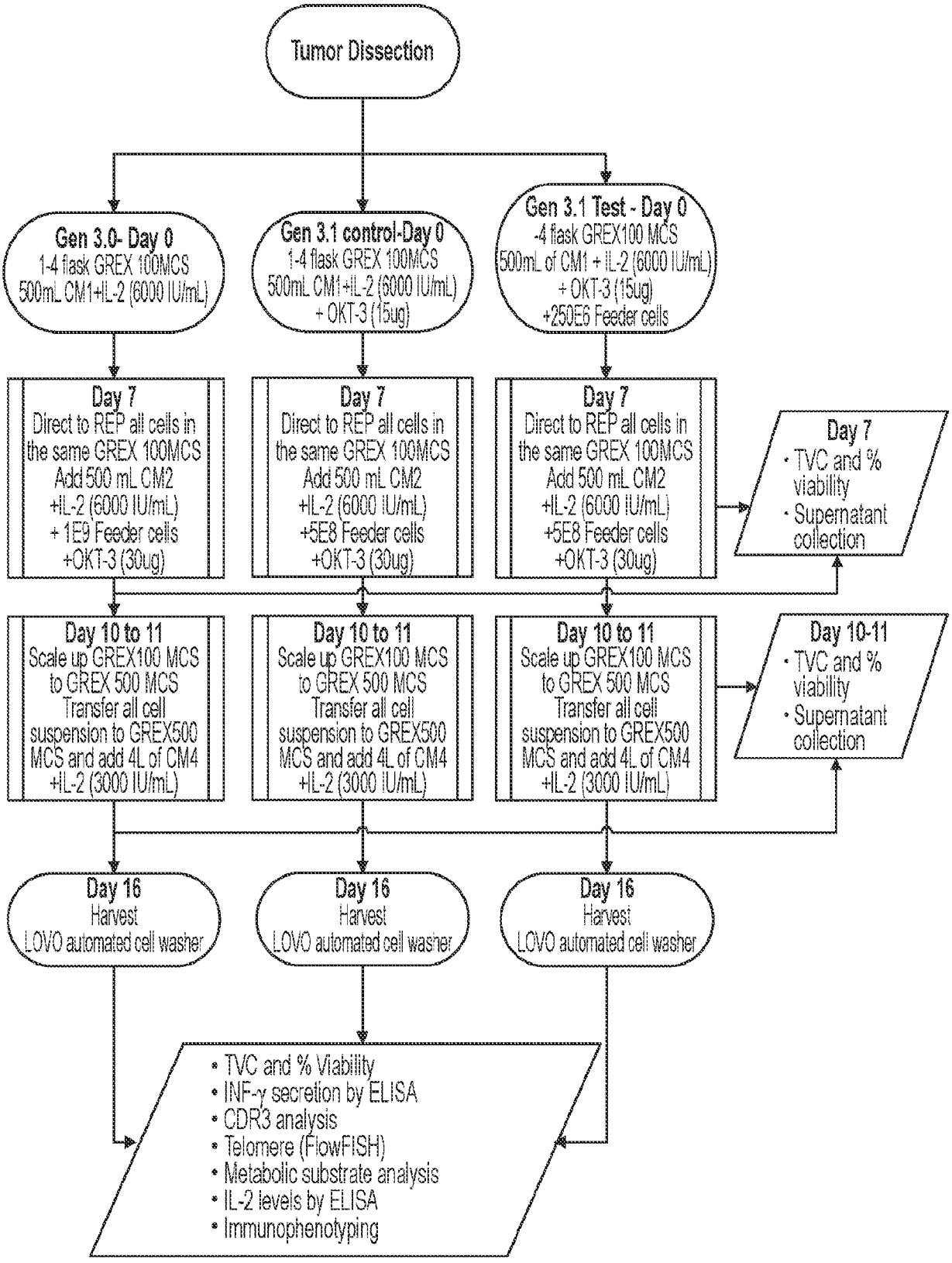
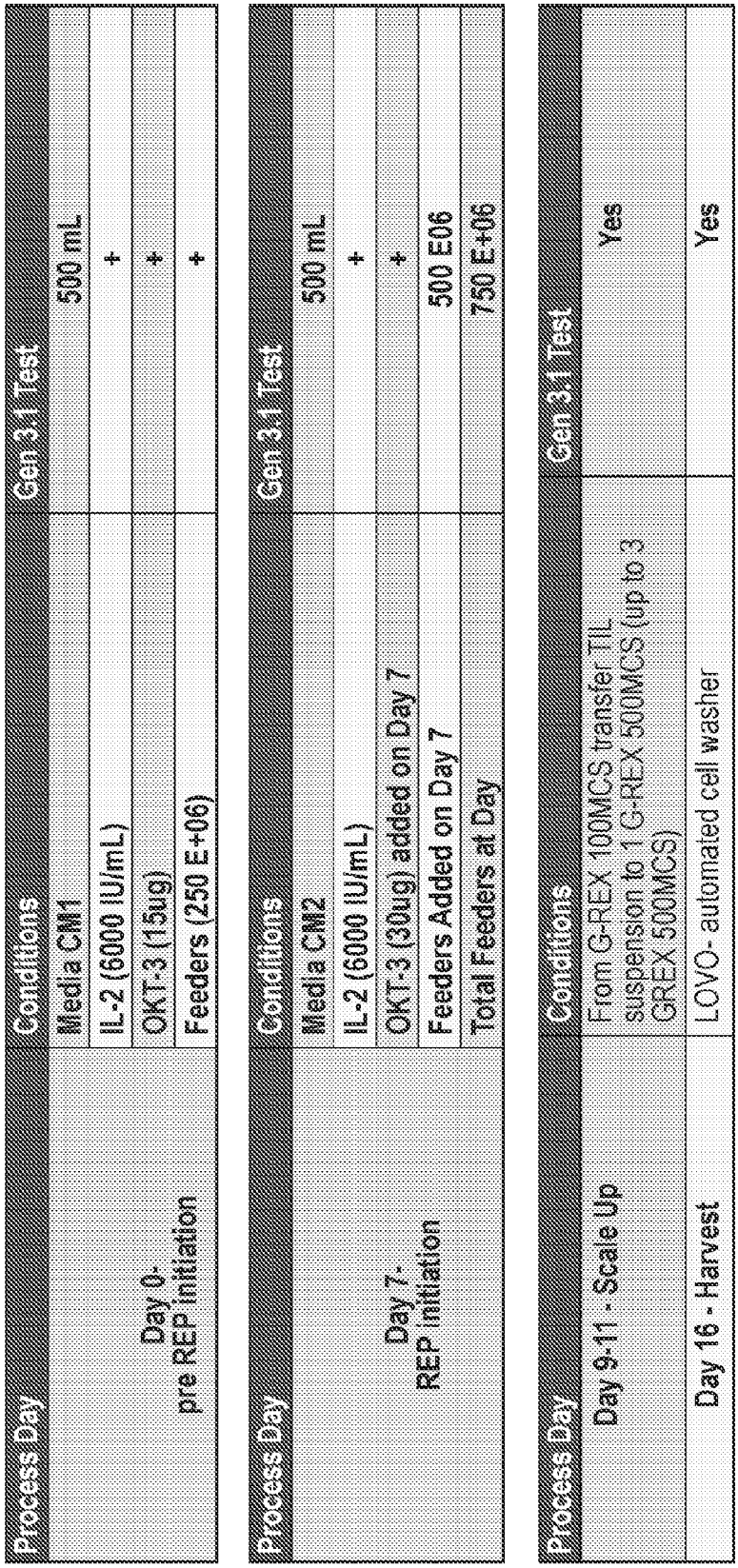

Tumor Dissection
Gen 3.0- Day 0
1-4 flask GREX 100MCS
500mL CM1+IL-2 (6000 IU/mL)
Gen 3.1 control-Day 0
1-4 flask GREX 100MCS
500mL CM1+IL-2 (6000 IU/mL)
+ OKT-3 (15ug)
Gen 3.1 Test - Day 0
-4 flask GREX100 MCS
500mL of CM1 + IL-2 (6000 IU/mL)
+ OKT-3 (15ug)
+250E6 Feeder cells
Day 7
Direct to REP all cells in the same GREX 100MCS
Add 500 mL CM2
+IL-2 (6000 IU/mL)
+ 1E9 Feeder cells
+OKT-3 (30ug)
Day 7
Direct to REP all cells in the same GREX 100MCS
Add 500 mL CM2
+IL-2 (6000 IU/mL)
+5E8 Feeder cells
+OKT-3 (30ug)
Day 7
Direct to REP all cells in the same GREX 100MCS
Add 500 mL CM2
+IL-2 (6000 IU/mL)
+5E8 Feeder cells
+OKT-3 (30ug)
Day 7
• TVC and % viability
• Supernatant collection
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10-11
• TVC and % viability
• Supernatant collection
Day 16
Harvest
LOVO automated cell washer
Day 16
Harvest
LOVO automated cell washer
Day 16
Harvest
LOVO automated cell washer
• TVC and % Viability
• INF-γ secretion by ELISA
• CDR3 analysis
• Telomere (FlowFISH)
• Metabolic substrate analysis
• IL-2 levels by ELISA
• Immunophenotyping

Figure 19



Process Day	Conditions	Gen 3.1 Test
Day 0- pre REP initiation	Media CM1	500 mL
	IL-2 (6000 IU/mL)	+
	OKT-3 (15ug)	+
	Feeders (250 E+06)	+

Process Day	Conditions	Gen 3.1 Test
Day 7- REP initiation	Media CM2	500 mL
	IL-2 (6000 IU/mL)	+
	OKT-3 (30ug) added on Day 7	+
	Feeders Added on Day 7	500 E06
	Total Feeders at Day	750 E+06

Process Day	Conditions	Gen 3.1 Test
Day 9-11 - Scale Up	From G-REX 100MCS transfer TIL suspension to 1 G-REX 500MCS (up to 3 GREX 500MCS)	Yes
Day 16 - Harvest	LOVO- automated cell washer	Yes

Figure 20

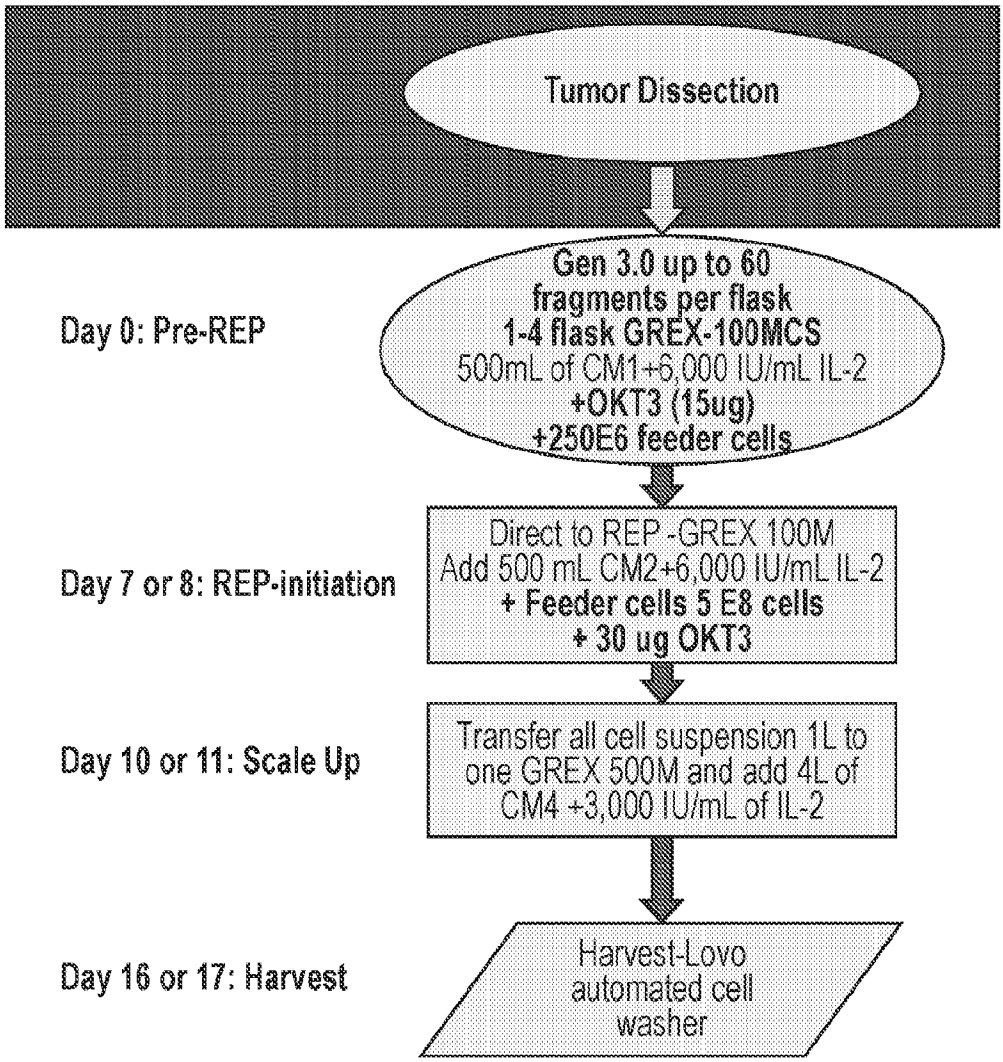

Tumor Dissection
Day 0: Pre-REP
Gen 3.0 up to 60 fragments per flask
1-4 flask GREX-100MCS
500mL of CM1+6,000 IU/mL IL-2
+OKT3 (15ug)
+250E6 feeder cells
Day 7 or 8: REP-initiation
Direct to REP -GREX 100M
Add 500 mL CM2+6,000 IU/mL IL-2
+ Feeder cells 5 E8 cells
+ 30 ug OKT3
Day 10 or 11: Scale Up
Transfer all cell suspension 1L to one GREX 500M and add 4L of CM4 +3,000 IU/mL of IL-2
Day 16 or 17: Harvest
Harvest-Lovo automated cell washer

Figure 21

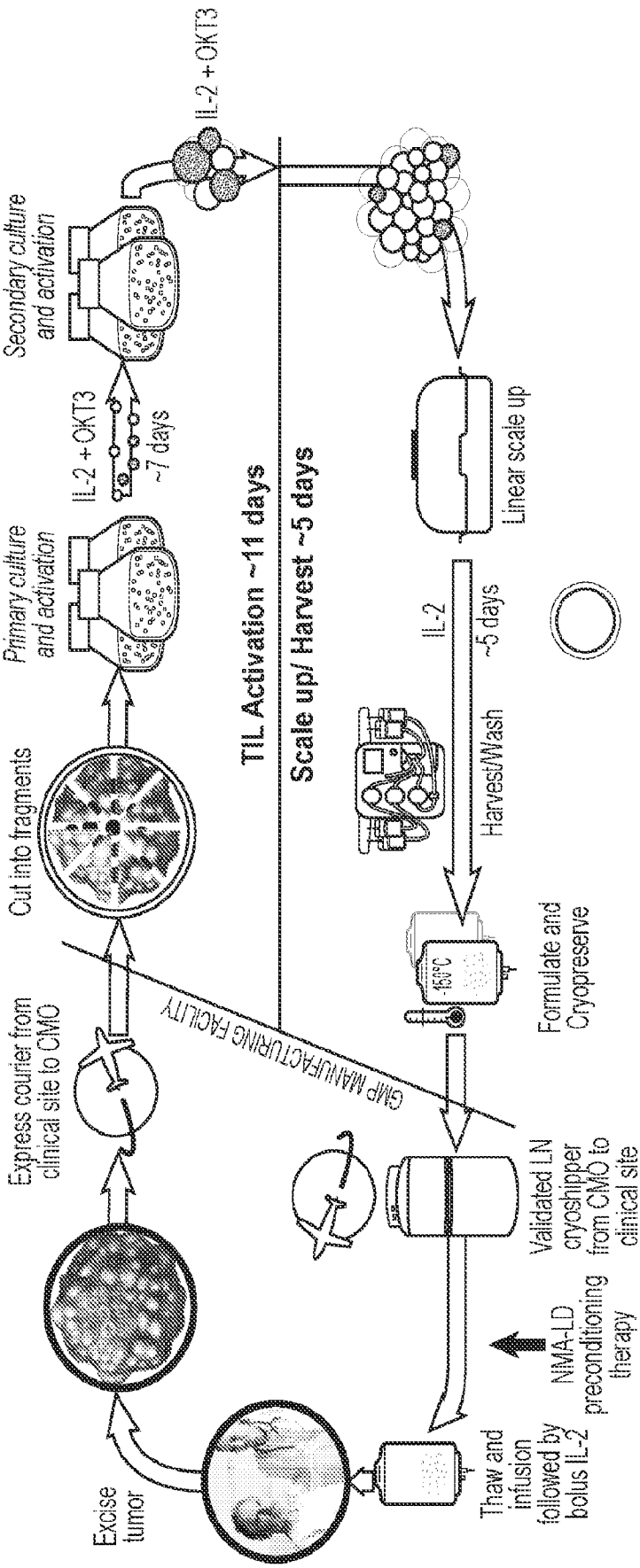

Excise tumor
Thaw and infusion followed by bolus IL-2
NMA-LD preconditioning therapy
Validated LN cryoshipper from CMO to clinical site
Express courier from clinical site to CMO
GMP MANUFACTURING FACILITY
Cut into fragments
Primary culture and activation
IL-2 + OKT3
~7 days
Secondary culture and activation
IL-2 + OKT3
TIL Activation ~11 days
Scale up/ Harvest ~5 days
Linear scale up
IL-2
~5 days
Harvest/Wash
-150°C
Formulate and Cryopreserve

Figure 22

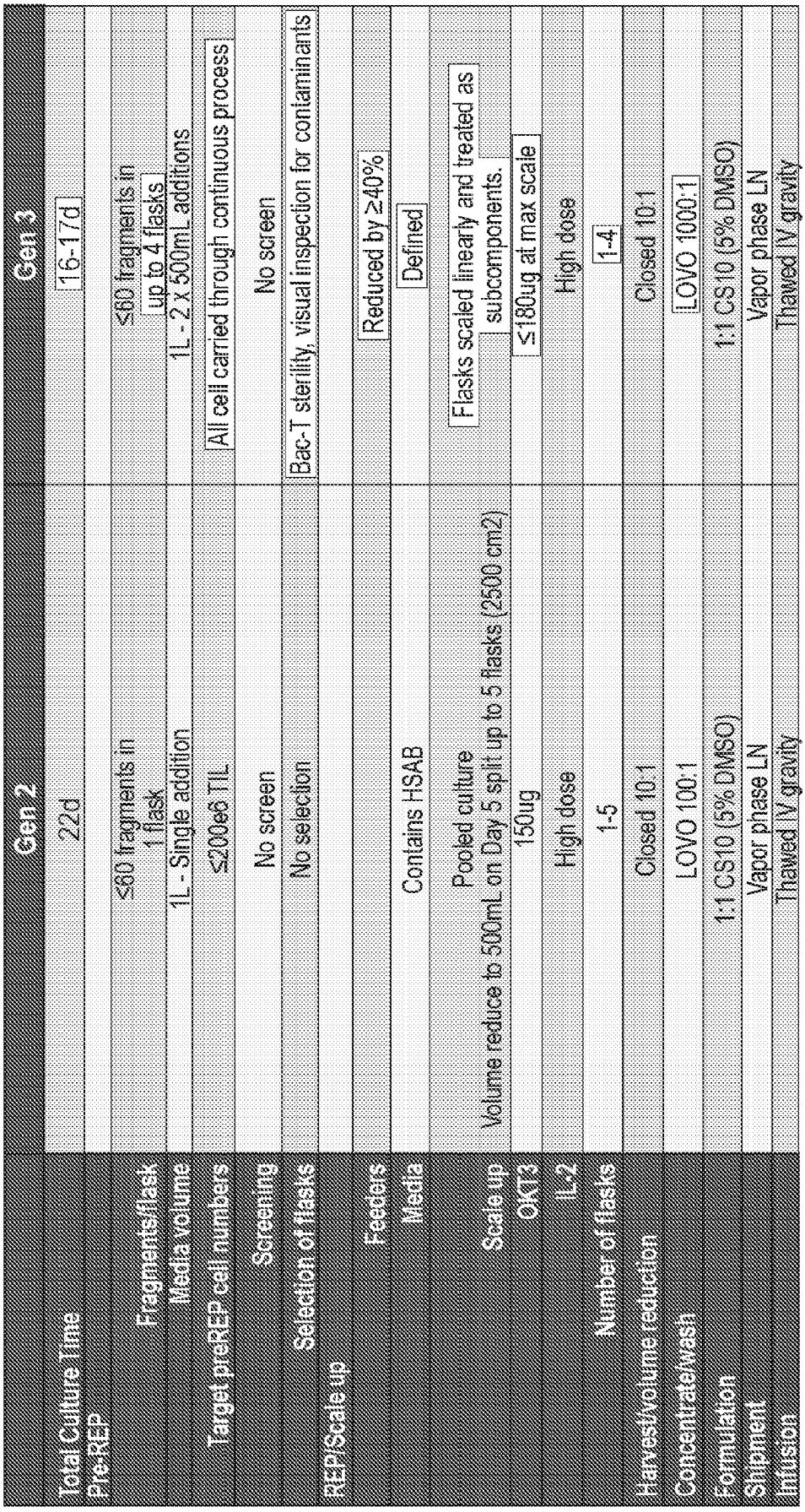

Gen 2
Gen 3
Total Culture Time
22d
16-17d
Pre-REP
Fragments/flask
≤60 fragments in 1 flask
≤60 fragments in up to 4 flasks
Media volume
1L - Single addition
1L - 2 x 500mL additions
Target preREP cell numbers
≤200e6 TIL
All cell carried through continuous process
Screening
No screen
No screen
Selection of flasks
No selection
Bac-T sterility, visual inspection for contaminants
REP/Scale up
Feeders
Reduced by ≥40%
Media
Contains HSAB
Defined
Scale up
Pooled culture
Volume reduce to 500mL on Day 5 split up to 5 flasks (2500 cm2)
Flasks scaled linearly and treated as subcompcnents.
OKT3
150ug
≤180ug at max scale
IL-2
High dose
High dose
Number of flasks
1-5
1-4
Harvest/volume reduction
Closed 10:1
Closed 10:1
Concentrate/wash
LOVO 100:1
LOVO 1000:1
Formulation
1:1 CS10 (5% DMSO)
1:1 CS10 (5% DMSO)
Shipment
Vapor phase LN
Vapor phase LN
Infusion
Thawed IV gravity
Thawed IV gravity

Figure 23A

	Gen 2	Gen 3
Total Culture Time	22d	16-17d
PreREP		
Fragments/flask	≤60 fragments in 1 flask	≤60 fragments in up to 4 flasks
Media Volume	1L - Single addition	1L - 2 x 500mL additions
Target preREP cell numbers	≤200e6 TIL	All cell carried through continuous process
Screening	No screen	No screen
Selection of flasks	No selection	Bac-T sterility, visual inspection for contaminants
REP/Scale up		
Feeders		Reduced by ≥40%
Media	Contains HSAB	Defined
Scale up	Pooled culture Volume reduce to 500mL on Day 5 split up to 5 flasks (2500 cm2)	Flasks scaled linearly and treated as subcomponents.
OKT3	150ug	≤180ug at max scale
IL-2	High dose	High dose
Number of flasks	1-5	1-4
Harvest/Volume reduction	Closed 10:1	Closed 10:1
Concentrate/wash	LOVO 100:1	LOVO 1000:1
Formulation	1:1 CS10 (5% DMSO)	1:1 CS10 (5% DMSO)
Shipment	Vapor phase LN	Vapor phase LN
Infusion	Thawed IV gravity	Thawed IV gravity

Figure 23B

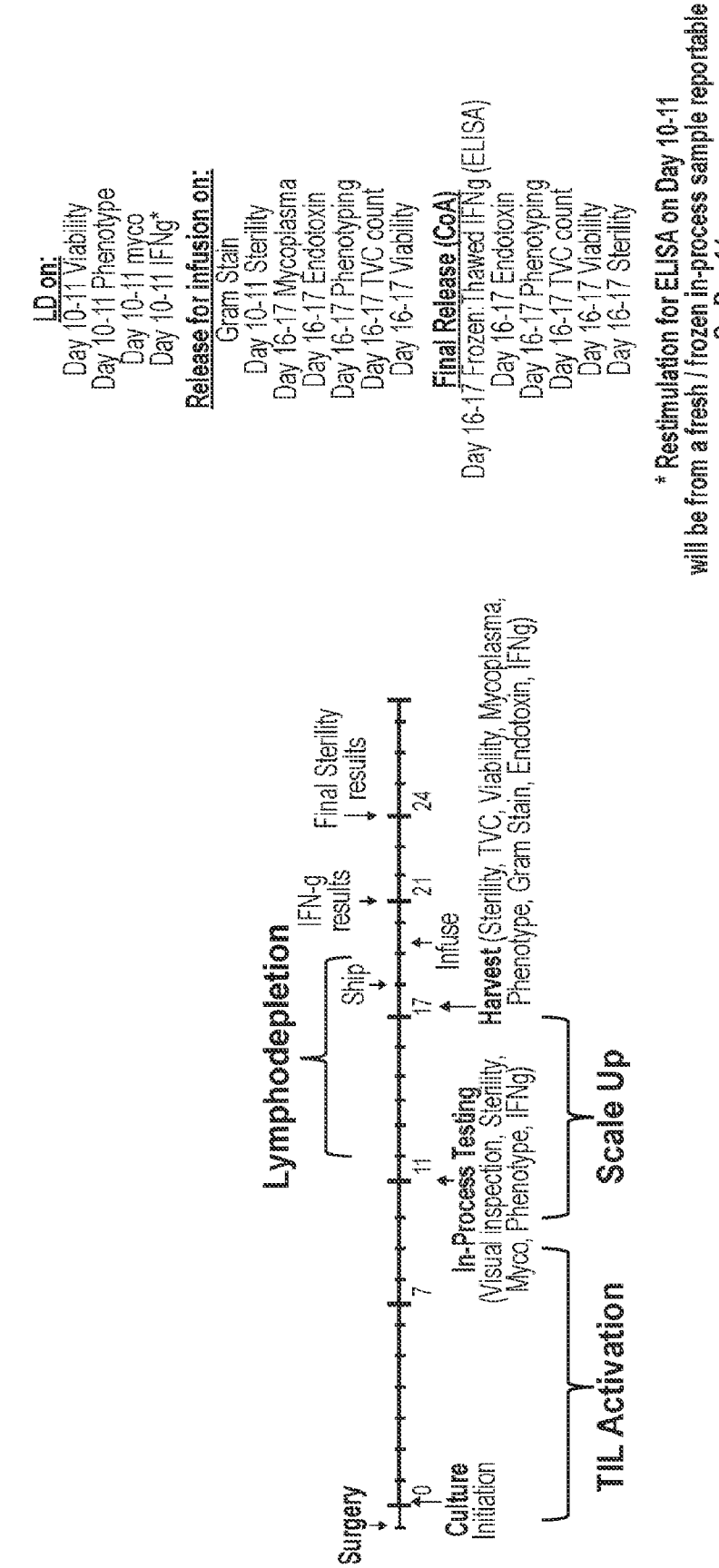

LD on:
Day 10-11 Viability
Day 10-11 Phenotype
Day 10-11 myco
Day 10-11 IFNg*
Release for infusion on:
Gram Stain
Day 10-11 Sterility
Day 16-17 Mycoplasma
Day 16-17 Endotoxin
Day 16-17 Phenotyping
Day 16-17 TVC count
Day 16-17 Viability
Final Release (CoA)
Day 16-17 Frozen: Thawed IFNg (ELISA)
Day 16-17 Endotoxin
Day 16-17 Phenotyping
Day 16-17 TVC count
Day 16-17 Viability
Day 16-17 Sterility
* Restimulation for ELISA on Day 10-11
will be from a fresh / frozen in-process sample reportable
On Day 14
Lymphodepletion
IFN-g results
Ship
Final Sterility results
Surgery
Culture Initiation
In-Process Testing
(Visual inspection, Sterility, Myco, Phenotype, IFNg)
Harvest (Sterility, TVC, Viability, Mycoplasma, Phenotype, Gram Stain, Endotoxin, IFNg)
Infuse
0
7
11
17
21
24
TIL Activation
Scale Up

Figure 24

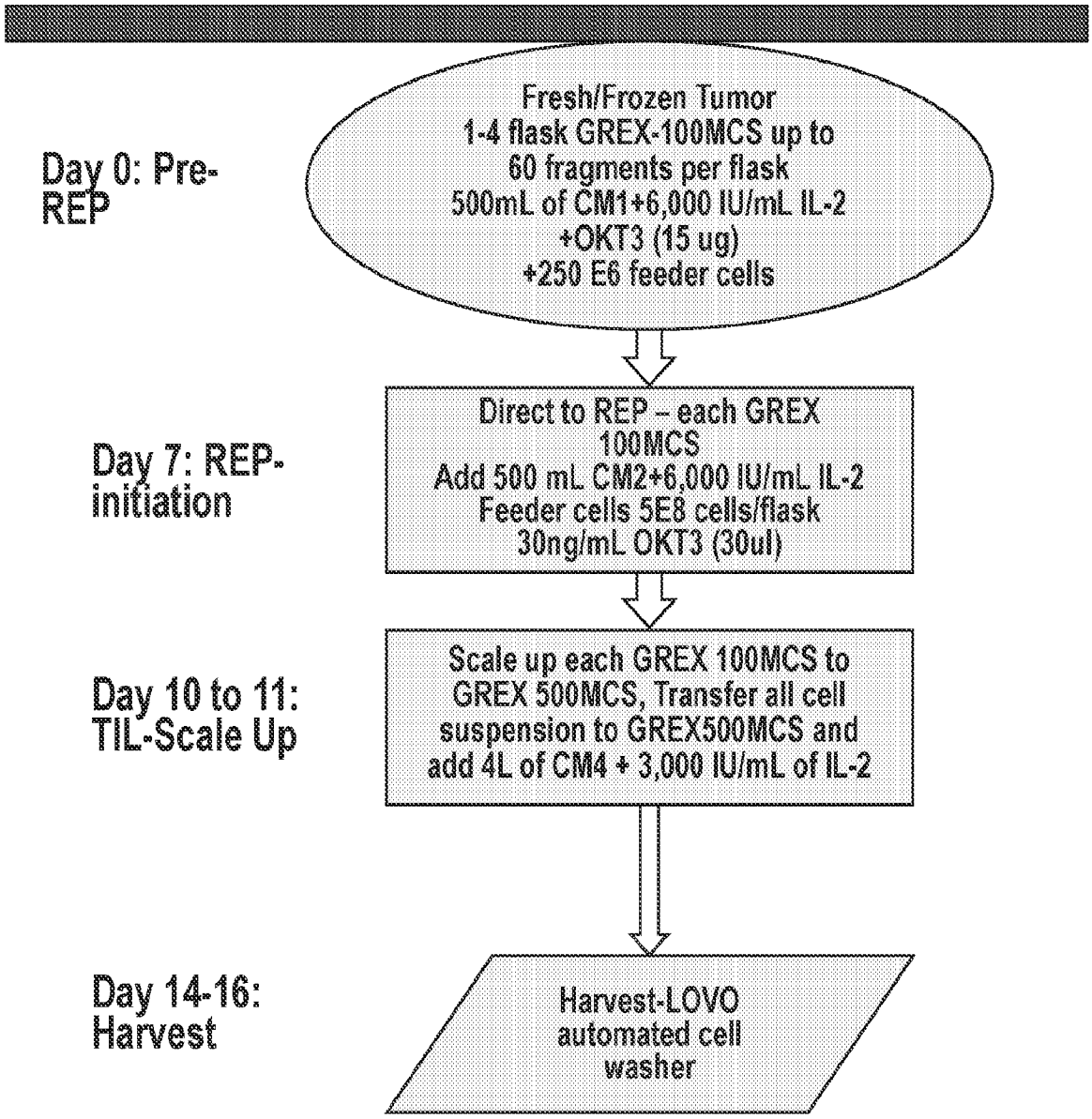

Day 0: Pre-REP
Fresh/Frozen Tumor
1-4 flask GREX-100MCS up to
60 fragments per flask
500mL of CM1+6,000 IU/mL IL-2
+OKT3 (15 ug)
+250 E6 feeder cells
Day 7: REP-initiation
Direct to REP – each GREX 100MCS
Add 500 mL CM2+6,000 IU/mL IL-2
Feeder cells 5E8 cells/flask
30ng/mL OKT3 (30ul)
Day 10 to 11: TIL-Scale Up
Scale up each GREX 100MCS to GREX 500MCS, Transfer all cell suspension to GREX500MCS and add 4L of CM4 + 3,000 IU/mL of IL-2
Day 14-16: Harvest
Harvest-LOVO automated cell washer

Figure 25

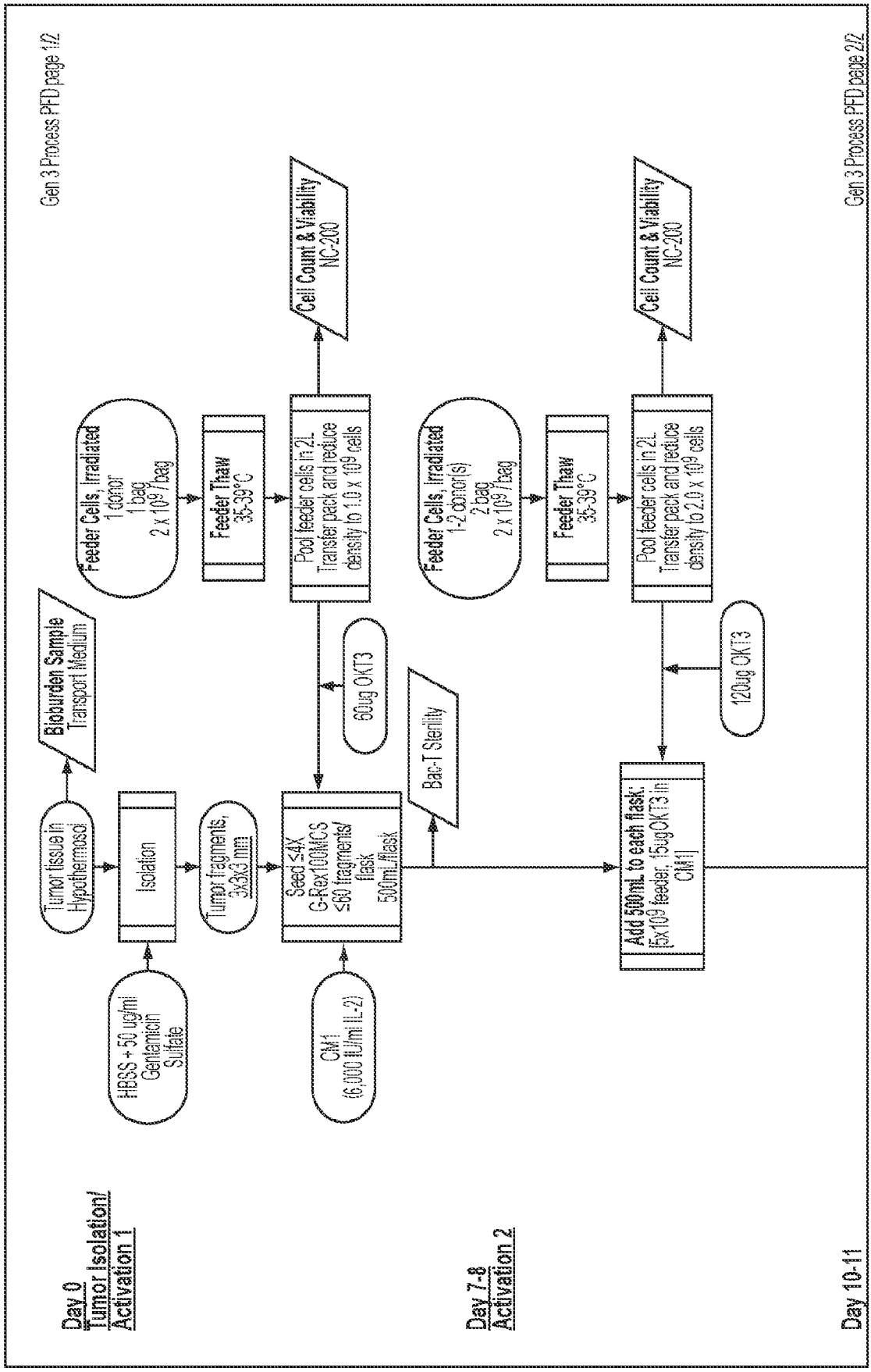

Gen 3 Process PFD page 1/2
Gen 3 Process PFD page 2/2
Day 0
Tumor Isolation/
Activation 1
Day 7-8
Activation 2
Day 10-11
Tumor tissue in Hypothermosol
Bioburden Sample Transport Medium
HBSS + 50 ug/ml Gentamicin Sulfate
Isolation
Tumor fragments, 3x3x3 mm
CM1 (6,000 IU/ml IL-2)
Seed ≤4X G-Rex100MCS ≤60 fragments/ flask 500mL/flask
60ug OKT3
Bac-T Sterility
Feeder Cells, Irradiated 1 donor 1 bag 2 x 10^9 /bag
Feeder Thaw 35-39°C
Pool feeder cells in 2L Transfer pack and reduce density to 1.0 x 10^9 cells
Cell Count & Viability NC-200
Add 500mL to each flask: (5x 10^9 feeder, 15ug OKT3 in CM1)
120ug OKT3
Feeder Cells, Irradiated 1-2 donor(s) 2 bag 2 x 10^9 /bag
Feeder Thaw 35-39°C
Pool feeder cells in 2L Transfer pack and reduce density to 2.0 x 10^9 cells
Cell Count & Viability NC-200

Figure 26A

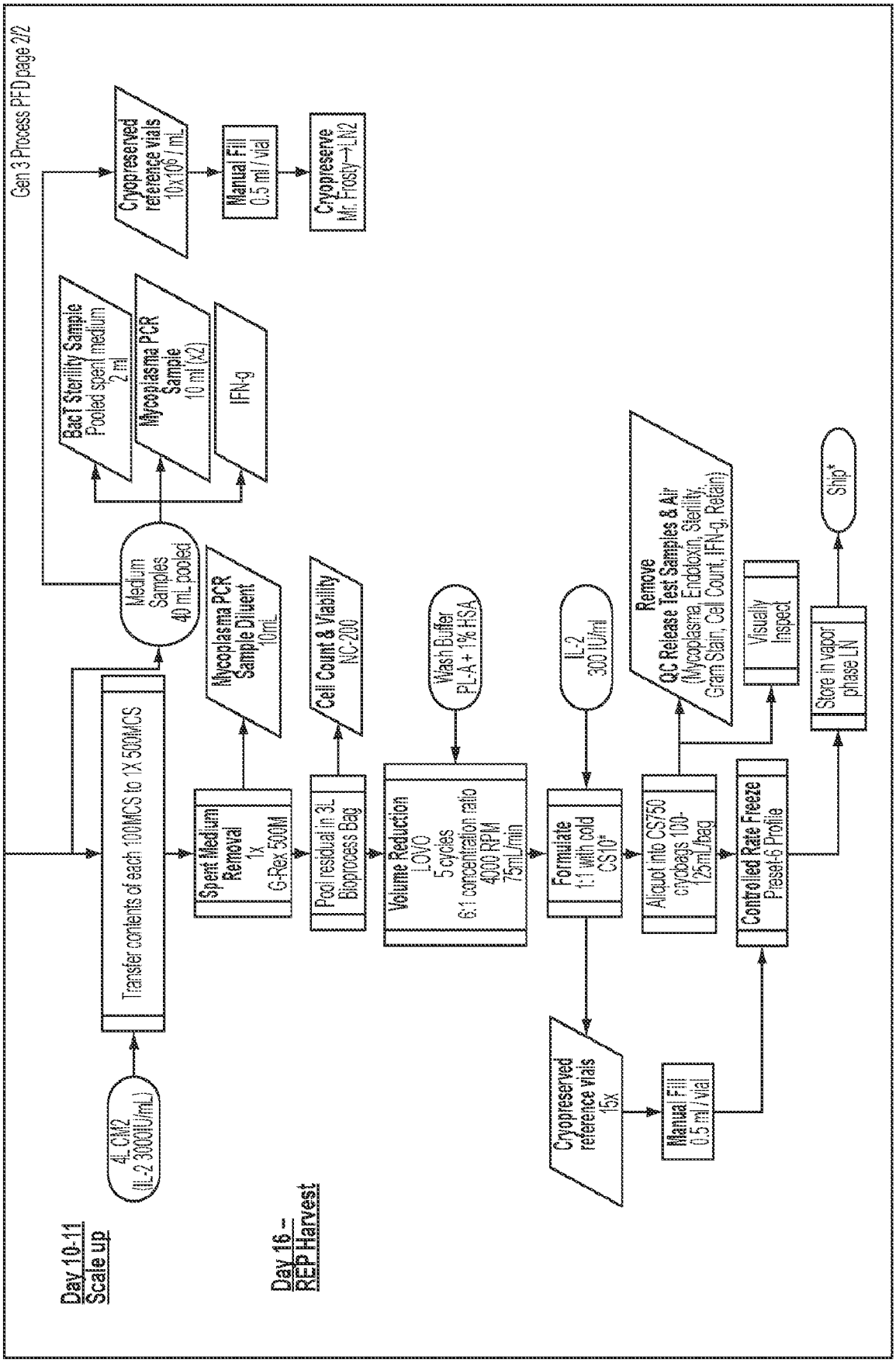

Gen 3 Process PFD page 2/2
Day 10-11
Scale up
4L CM2
(IL-2 3000IU/mL)
Transfer contents of each 100MCS to 1X 500MCS
Day 16 –
REP Harvest
Spent Medium
Removal
1x
G-Rex 500M
Pool residual in 3L
Bioprocess Bag
Volume Reduction
LOVO
5 cycles
6:1 concentration ratio
4000 RPM
75mL/min
Formulate
1:1 with cold
CS10*
Aliquot into CS750
cryobags 100-
125mL/bag
Controlled Rate Freeze
Preset-6 Profile
Store in vapor
phase LN
Ship*
Visually
Inspect
Remove
QC Release Test Samples & Air
(Mycoplasma, Endotoxin, Sterility,
Gram Stain, Cell Count, IFN-g, Retain)
Cryopreserved
reference vials
15x
Manual Fill
0.5 ml / vial
Wash Buffer
PL-A + 1% HSA
IL-2
300 IU/ml
Medium
Samples
40 mL pooled
Mycoplasma PCR
Sample Diluent
10mL
Cell Count & Viability
NC-200
Bact Sterility Sample
Pooled spent medium
2 ml
Mycoplasma PCR
Sample
10 ml (x2)
IFN-g
Cryopreserved
reference vials
10x10^6 / mL
Manual Fill
0.5 ml / vial
Cryopreserve
Mr. Frosty→LN2

Figure 26B

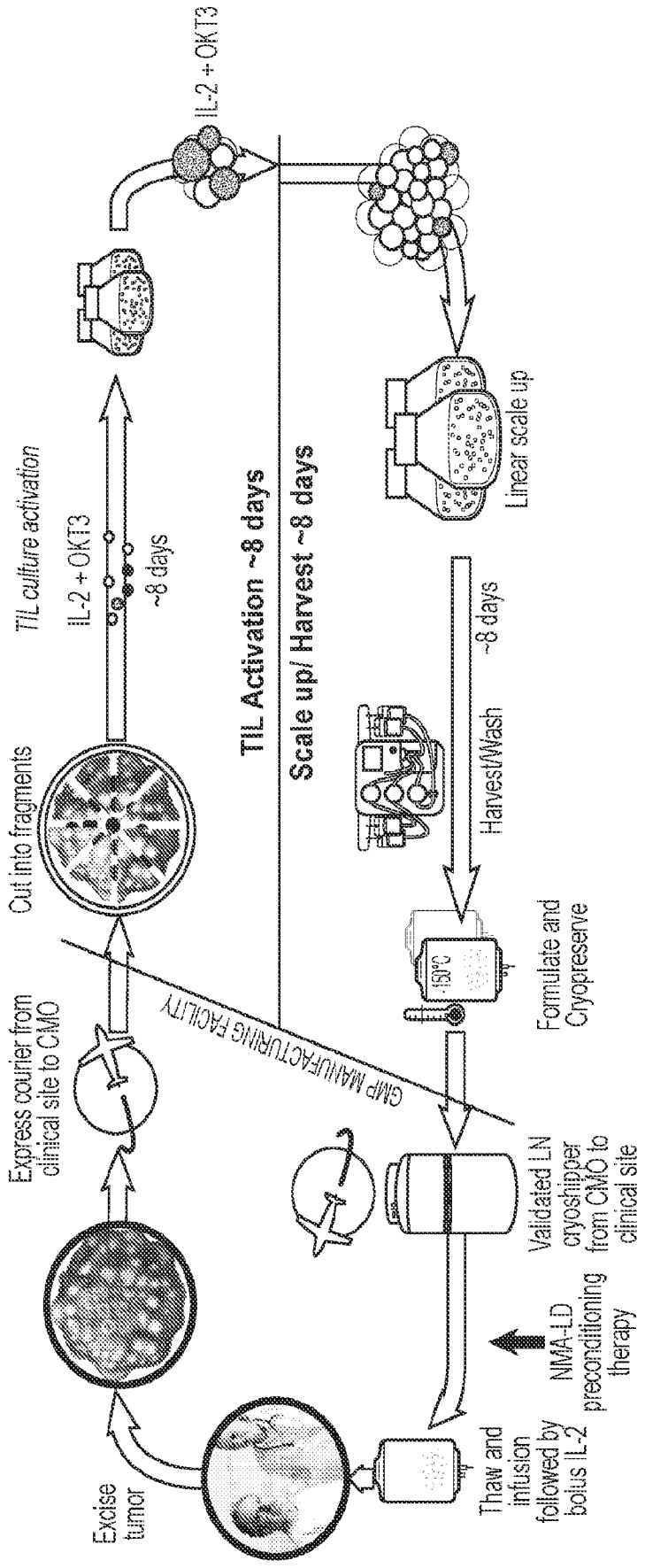

IL-2 + OKT3
TIL culture activation
IL-2 + OKT3
~8 days
Cut into fragments
Express courier from clinical site to CMO
Excise tumor
TIL Activation ~8 days
Scale up/ Harvest ~8 days
Linear scale up
~8 days
Harvest/Wash
Formulate and Cryopreserve
GMP MANUFACTURING FACILITY
Validated LN cryoshipper from CMO to clinical site
NMA-LD preconditioning therapy
Thaw and infusion followed by bolus IL-2

Figure 27

STEP	Gen 2	Gen 2.1	Gen 3.0
Pre REP- day 0	≤ 50 fragments/ 1 G-Rex 100MCS - **11 days**	≤ 180 fragments/ 3 G-Rex, Pre-formulated CM1 warmed media 100MCS - **11 days**	***Fresh or Frozen Tumor*** Whole tumor with ≤ 30 fragments up to 60 fragments per 1 G-Rex. 100MCS (up to 4 G-Rex), preformulated warmed media - **7 days. Pre REP, Feeders 250e^6 cells + OKT-3 (15ug)**
REP Initiation	Direct to REP- Day 11- **<200e^6 TIL** 1 G-Rex 500MCS	Direct to REP- Day 11- **<200e^6 TIL** Pre-formulated CM2 warmed media in one G-Rex 500MCS	Direct to REP - Day **7-all cells TIL- same G-Rex 100MCS (100MCS up to 4 GREX), Standard media or Defined Media (Serum free). Addition Feeders 500e^6 cells +OKT-3 (30ug)**
TIL propagation or Scale up	1 to 5 G-REX 500MCS **Split day 16**	2 to 5 G-REX 500MCS Pre-formulated CM4 warmed media **Split day 16**	From G-REX 100MCS transfer TIL suspension to G-REX 500MCS, up to 4 GREX 500 MCS- Standard media or Defined Media (Serum Free) **Scale up on day 10 or 11**
Harvest	**Harvest day 22,** LOVO-automated cell washer	**Harvest day 22,** LOVO-automated cell washer (5 wash cycle)	**Harvest day 14 or 16** LOVO- automated cell washer (5 wash cycle)
Final formulation	Cryopreserved Product 300IU/ml IL2- CS10 in LN_2, multiple aliquots	Cryopreserved Product 300IU/ml IL2- CS10 in LN_2, multiple aliquots	Cryopreserved product 300IU/ml IL-2- CS10 in LN_2 multiple aliquots
Process time	**22 days**	**22 days**	**16 days**

Figure 28

Process Comparison	Process Changes	Differences
Gen 2 : Gen 2.1	• Initiate process with two flasks instead of one flask • Divide REP initiation feeder layer between 2 G-Rex500MCS Flasks • Pre-formulate media and warm prior to use	• Potential doubling of final cell count (dose with increased TIL repertoire. • Process redundancy throughout process
Gen 2.1 : Gen 3.1	• Fresh or Frozen tumor • 14-16 day process (from 22 day) • Reduce total feeder layer on process • Feeder layer and OKT3 present at Day 0 • REP initiated with fragments • 100MCS scales to 500MCS • Scales to multiple pre-REP flasks • Standard Media and Defined Media (Serum Free)	• Increased potency • Improved phenotype • Decreased process time • Reduced reagent testing • Decreased process variability • Defined reagents • Increased repertoire • Reduce impurities (feeder) • Comparable or Higher Dose.

Figure 29

Table 2. Description of Gen 3 optimization conditions.

Process Day	Conditions	Gen 3.0	Gen 3.1 control	Gen 3.1 Test
Day 0 : Tumor Fragment Isolation and Activation	Media (*)	500 mL	500 mL	500 mL
	IL-2	6000 IU/mL	6000 IU/mL	6000 IU/mL
	OKT-3	-	15 ug	15 ug
	Feeders	-	-	2.5E+06
Process Day	**Conditions**	**Gen 3.0**	**Gen 3.1 control**	**Gen 3.1 Test**
Day 7 - 8 : TIL Culture Reactivation	Media (*)	500 mL	500 mL	500 mL
	IL-2	6000 IU/mL	6000 IU/mL	6000 IU/mL
	OKT-3	30 ug	30 ug	30 ug
	Feeders	1 E+09	500 E+06	500E+06
	Total Feeders added through Day 7	1 E+09	500 E+06	750E+06
Process Day	**Conditions**	**Gen 3.0**	**Gen 3.1 control**	**Gen 3.1 Test**
Day 10-11 : Culture Scale Up	From GREX 100 transfer whole TIL suspension to 1 GREX 500 containing 4L media with IL-2 (3000 IU/mL)			
Process Day	**Conditions**	**Gen 3.0**	**Gen 3.1 control**	**Gen 3.1 Test**
Day 16-17: Harvest/Wash/Formulate	LOVO automated cell washer and cryopreservation with CS10.			

(*) Media can be standard media or CTS serum free media.

Figure 30

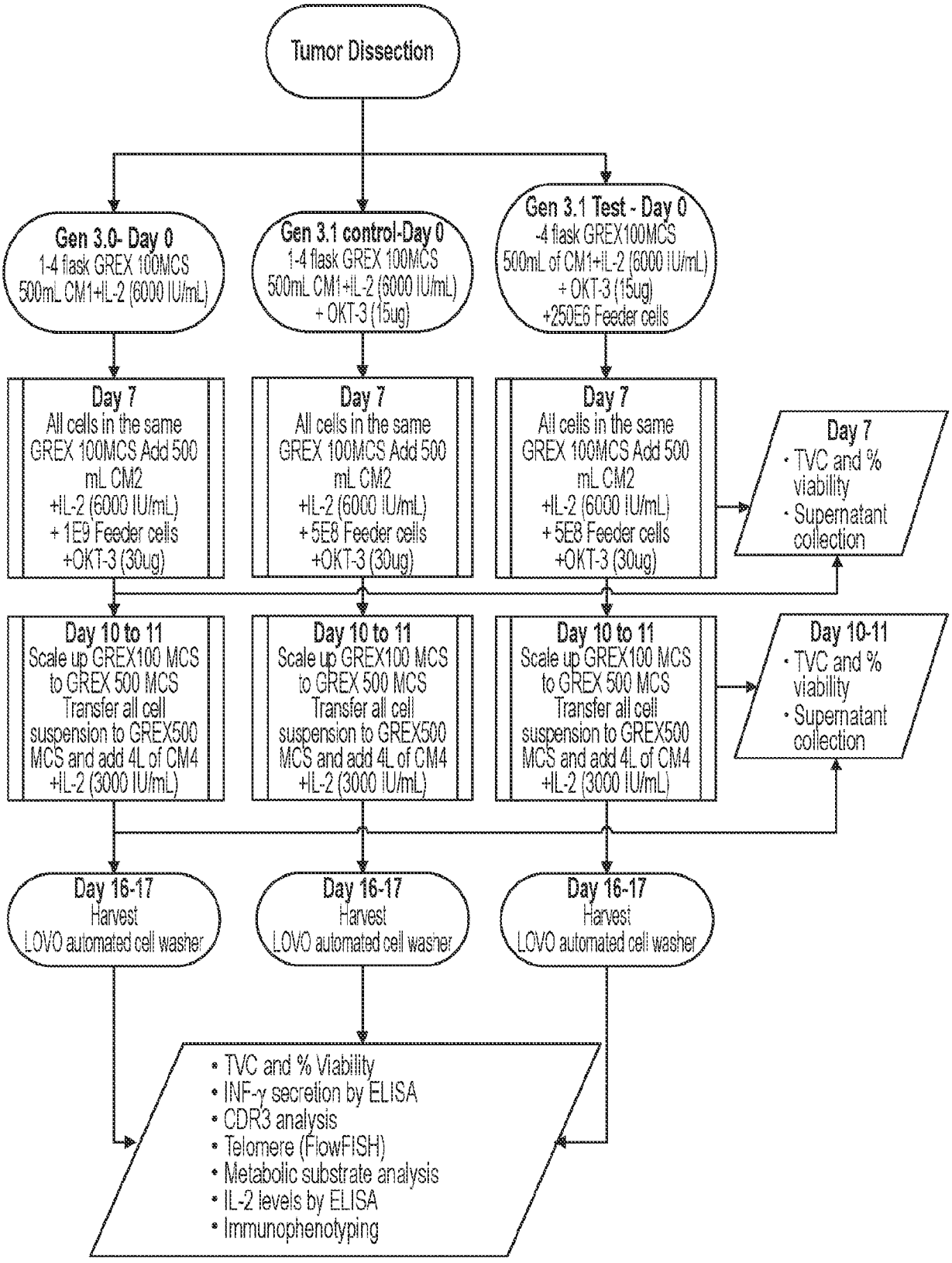

Tumor Dissection
Gen 3.0- Day 0
1-4 flask GREX 100MCS
500mL CM1+IL-2 (6000 IU/mL)
Gen 3.1 control-Day 0
1-4 flask GREX 100MCS
500mL CM1+IL-2 (6000 IU/mL)
+ OKT-3 (15ug)
Gen 3.1 Test - Day 0
-4 flask GREX100MCS
500mL of CM1+IL-2 (6000 IU/mL)
+ OKT-3 (15ug)
+250E6 Feeder cells
Day 7
All cells in the same GREX 100MCS Add 500 mL CM2
+IL-2 (6000 IU/mL)
+ 1E9 Feeder cells
+OKT-3 (30ug)
Day 7
All cells in the same GREX 100MCS Add 500 mL CM2
+IL-2 (6000 IU/mL)
+ 5E8 Feeder cells
+OKT-3 (30ug)
Day 7
All cells in the same GREX 100MCS Add 500 mL CM2
+IL-2 (6000 IU/mL)
+ 5E8 Feeder cells
+OKT-3 (30ug)
Day 7
• TVC and % viability
• Supernatant collection
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10 to 11
Scale up GREX100 MCS to GREX 500 MCS
Transfer all cell suspension to GREX500 MCS and add 4L of CM4
+IL-2 (3000 IU/mL)
Day 10-11
• TVC and % viability
• Supernatant collection
Day 16-17
Harvest
LOVO automated cell washer
Day 16-17
Harvest
LOVO automated cell washer
Day 16-17
Harvest
LOVO automated cell washer
• TVC and % Viability
• INF-γ secretion by ELISA
• CDR3 analysis
• Telomere (FlowFISH)
• Metabolic substrate analysis
• IL-2 levels by ELISA
• Immunophenotyping

Figure 31

Step	Process Gen 3-Optimized
Day 0 Tumor isolation and Activation	≤240 fragments ≤60 fragments/flask ≤4 flasks ≤2L media (500mL/flask) IL-2 (6000IU/mL) $2.5x10^8$ feeder cells/flask 15ug OKT3/flask
Day 7 - 8 Reactivation	Fresh TIL direct to REP Activate entire culture $5x10^8$ feeder cells 30 ug OKT3/flask G-Rex 100MCS Add 500mL media+ IL-2(6000IU/mL)
Day 10 - 11 Scale up or TIL Sub-culture	≤4 G-REX 500MCS Scale up entire culture transferring 1L from GREX 100MCS into GREX 500MCS and add 4L of media +IL-2 (3000 IU/mL) /flask
Day 16 - 17 Harvest	Harvest LOVO- automated cell washer Cryopreservation on Plasmalyte 1% HSA: CS10

Figure 32

Test	Acceptance Criteria	Gen 3.1 Test vs Gen 3.0 Process
Cell Count (TVC)	Gen 3.1 > 30% to Process Gen 3.0	Met
% Viability	≥70% Viability	Met
Immunophenotyping (%CD3+/ %CD45+)	≤5% difference between Gen 3.1 and Gen 3.0 process	Met
IFNγ secretion	Gen 3.1 ≥ to Process Gen 3.0	Met

Figure 33

FIG. 34

Figure 1 Diagram of Study Design

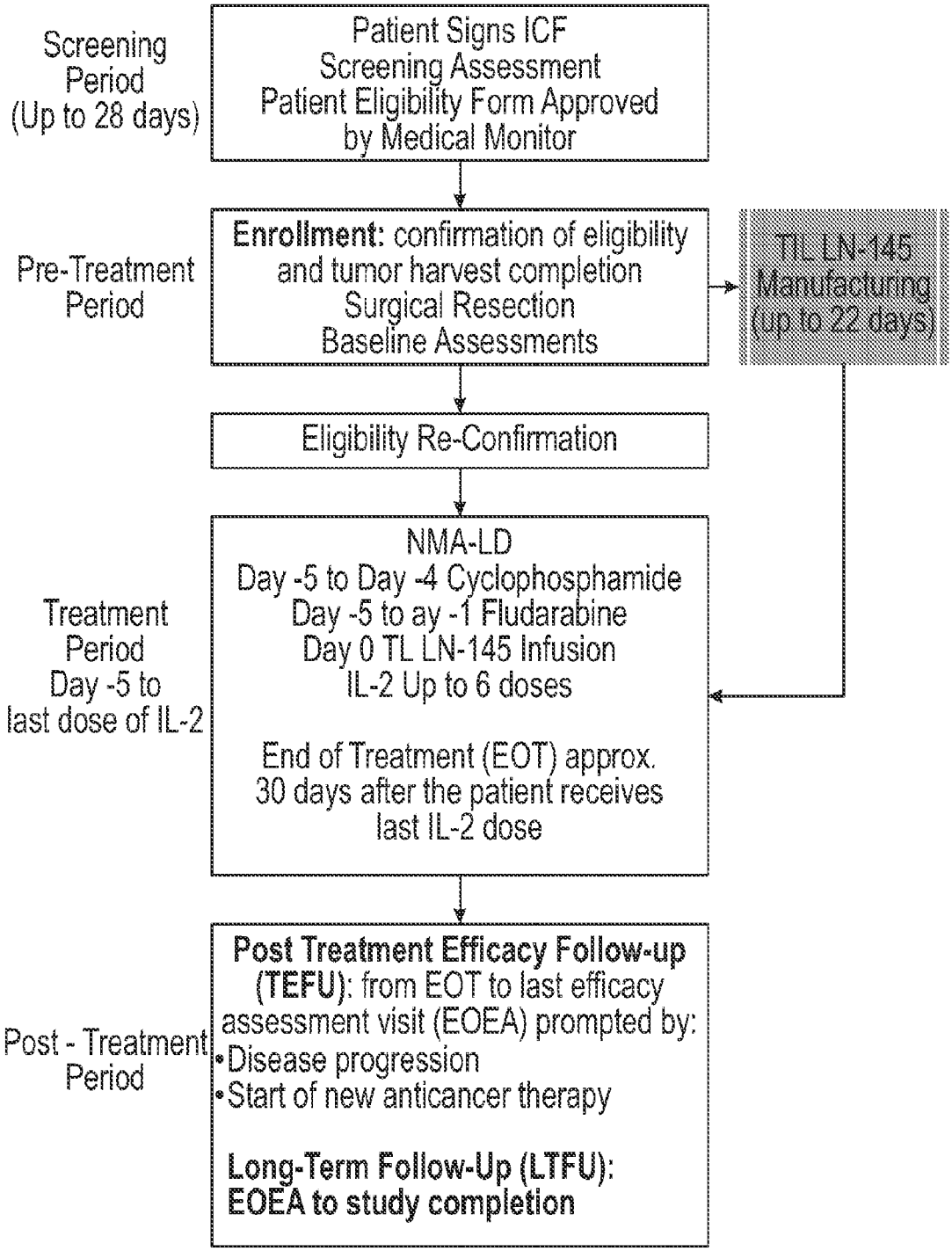


FIG. 35

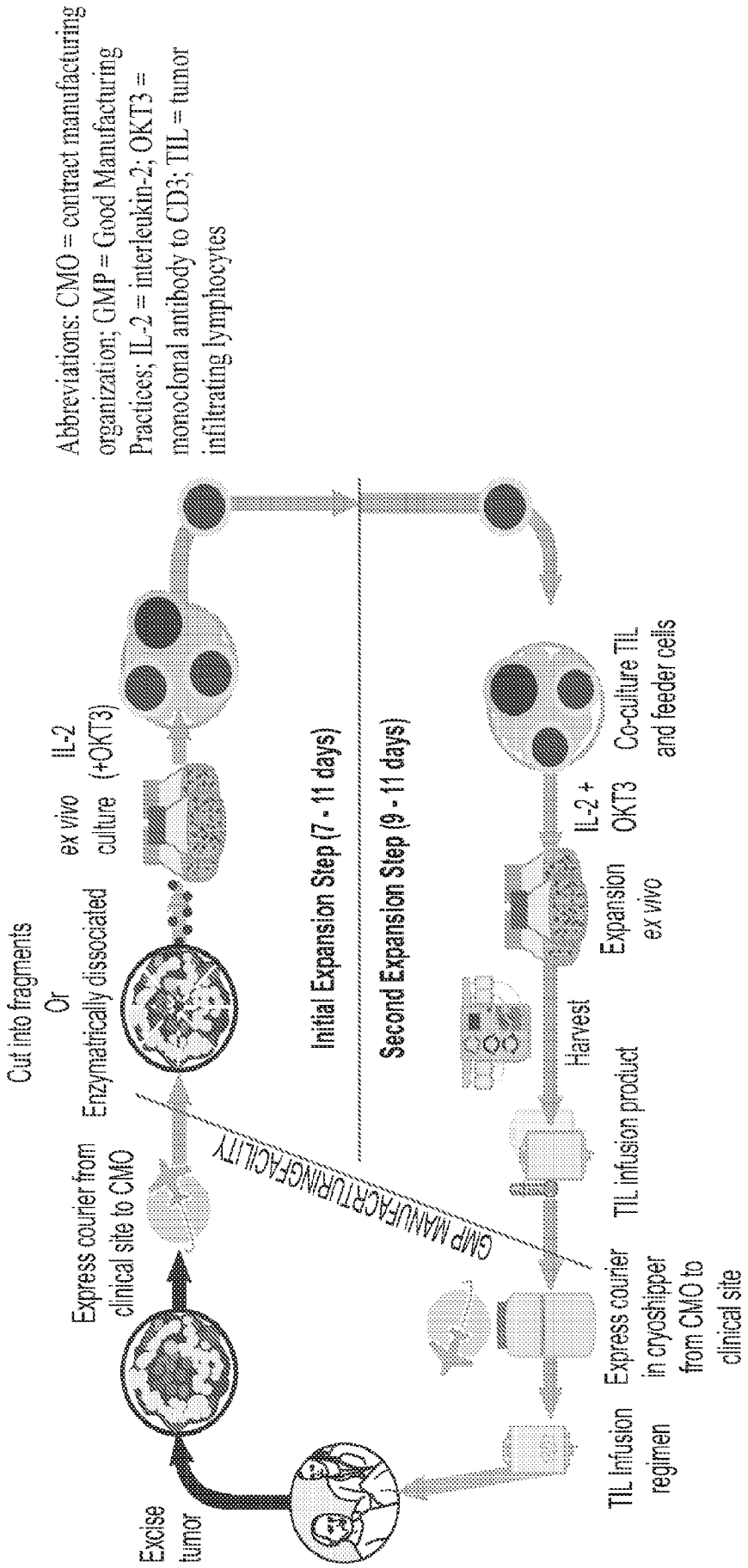

Abbreviations: CMO = contract manufacturing organization; GMP = Good Manufacturing Practices; IL-2 = interleukin-2; OKT3 = monoclonal antibody to CD3; TIL = tumor infiltrating lymphocytes
Excise tumor
Express courier from clinical site to CMO
Cut into fragments Or Enzymatically dissociated
ex vivo culture IL-2 (+OKT3)
Initial Expansion Step (7 - 11 days)
Second Expansion Step (9 - 11 days)
GMP MANUFACTURING FACILITY
Harvest
TIL infusion product
Express courier in cryoshipper from CMO to clinical site
TIL Infusion regimen
IL-2 + OKT3 Expansion ex vivo
Co-culture TIL and feeder cells

FIG. 36

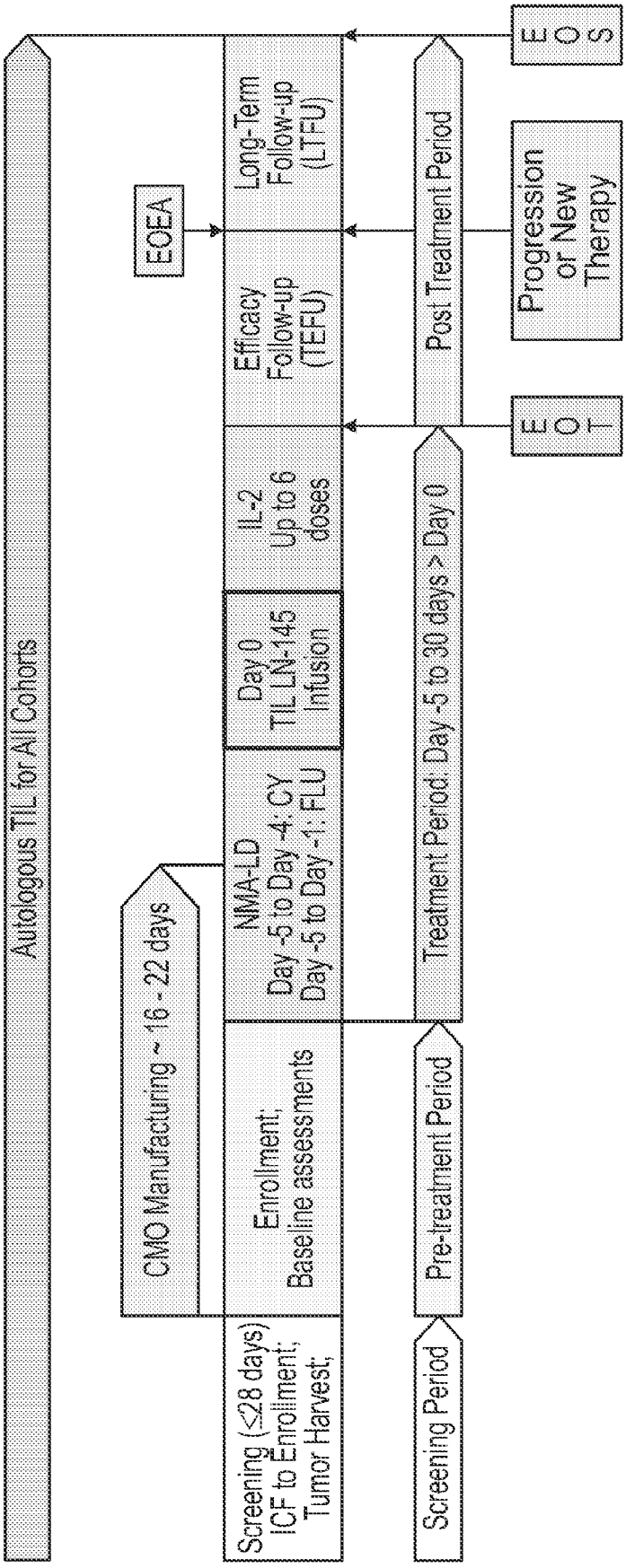

Autologous TIL for All Cohorts
CMO Manufacturing ~ 16 - 22 days
Screening (≤28 days)
ICF to Enrollment;
Tumor Harvest;
Enrollment;
Baseline assessments
Screening Period
NMA-LD
Day -5 to Day -4: CY
Day -5 to Day -1: FLU
Day 0
TIL LN-145
Infusion
IL-2
Up to 6
doses
Pre-treatment Period
Treatment Period: Day -5 to 30 days > Day 0
EOEA
Efficacy
Follow-up
(TEFU)
Long-Term
Follow-up
(LTFU)
Post Treatment Period
EOT
Progression
or New
Therapy
EOS

FIG. 37

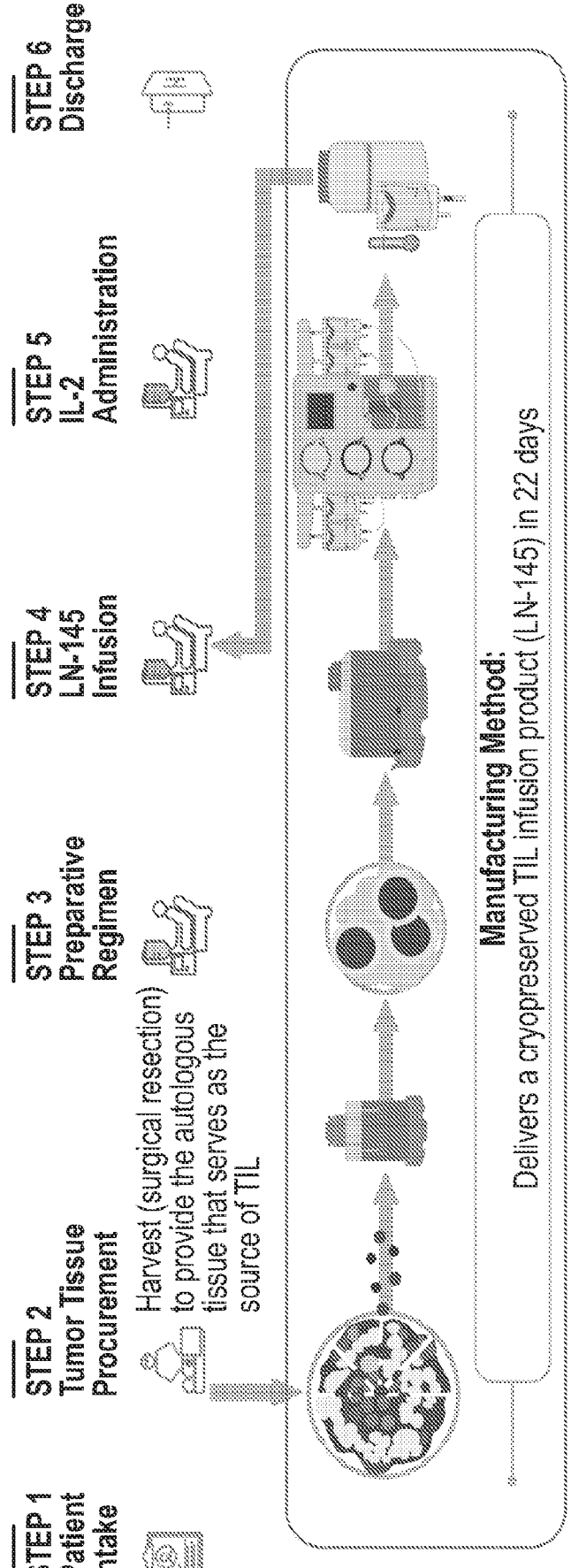

STEP 1
Patient
Intake
STEP 2
Tumor Tissue
Procurement
Harvest (surgical resection)
to provide the autologous
tissue that serves as the
source of TIL
STEP 3
Preparative
Regimen
STEP 4
LN-145
Infusion
STEP 5
IL-2
Administration
STEP 6
Discharge
Manufacturing Method:
Delivers a cryopreserved TIL infusion product (LN-145) in 22 days

FIG. 38

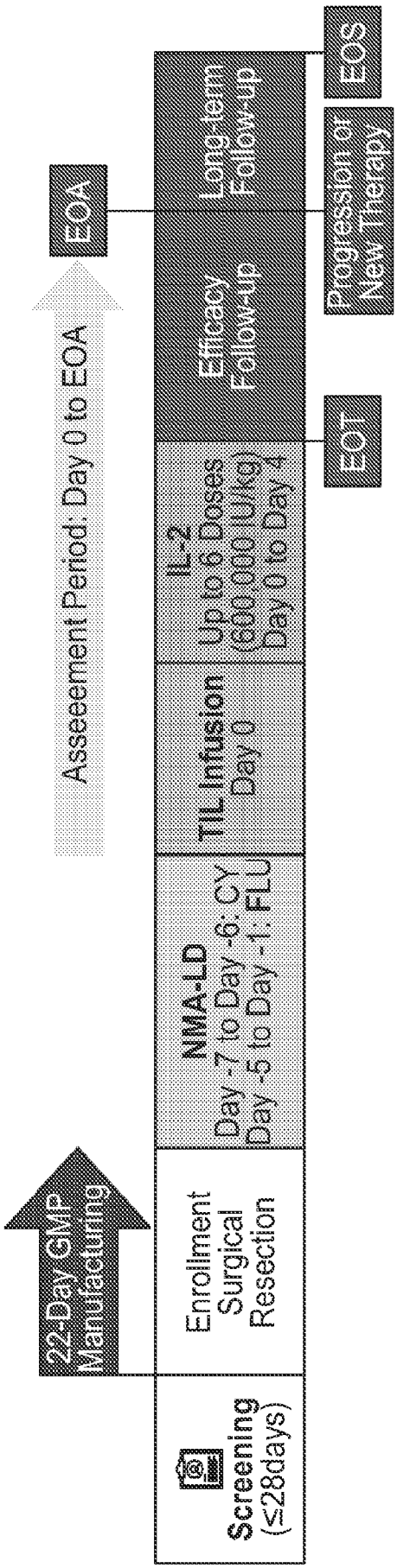
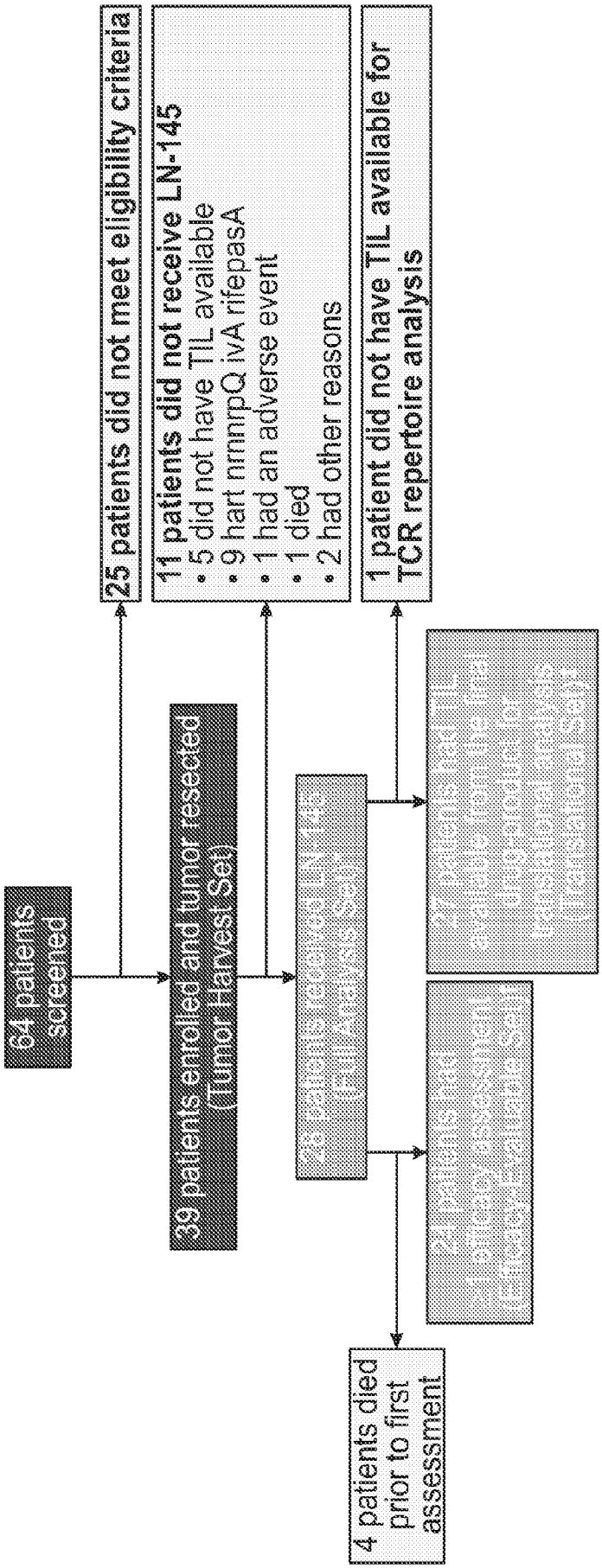

Screening (≤28days)
22 Day CMP Manufacturing
Enrollment Surgical Resection
NMA-LD Day -7 to Day -6: CY Day -5 to Day -1: FLU
TIL Infusion Day 0
IL-2 Up to 6 Doses (600,000 IU/kg) Day 0 to Day 4
Efficacy Follow-up
Long-term Follow-up
EOT
EOA
EOS
Progression or New Therapy
Assessment Period: Day 0 to EOA

FIG. 39



*Full analysis set includes all patients who received LN- 145 infusion within specifications.
†Efficacy-evaluable set includes all patients who received LN-145 within specifications and had ≥1 efficacy evaluation
‡Translational set includes all patients who received LN-145 infusion and had TIL available from the final drug-product for translational analysis.

FIG. 40

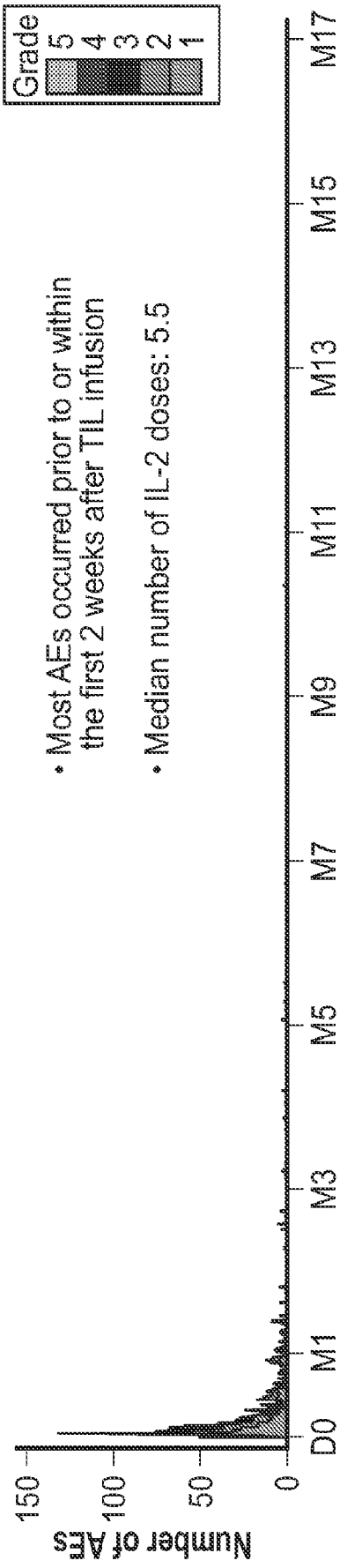
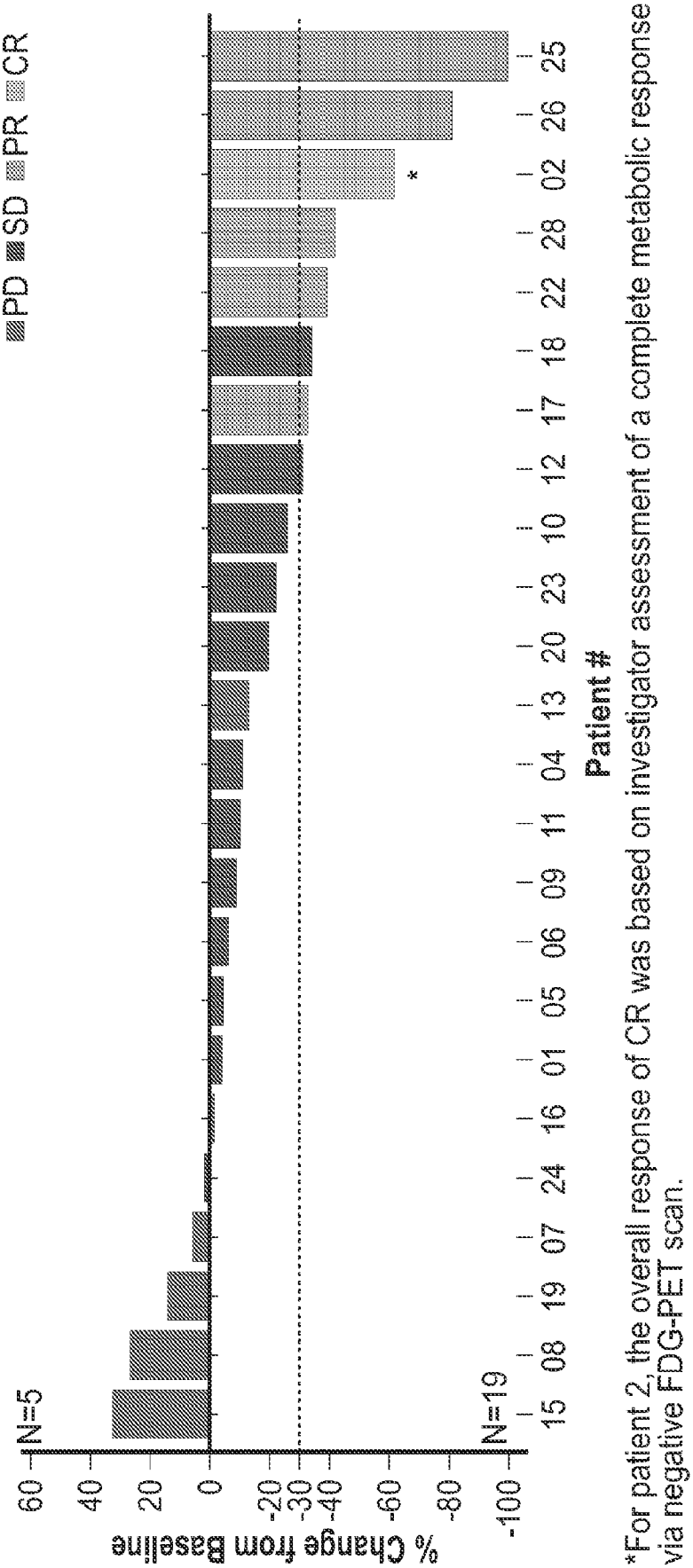
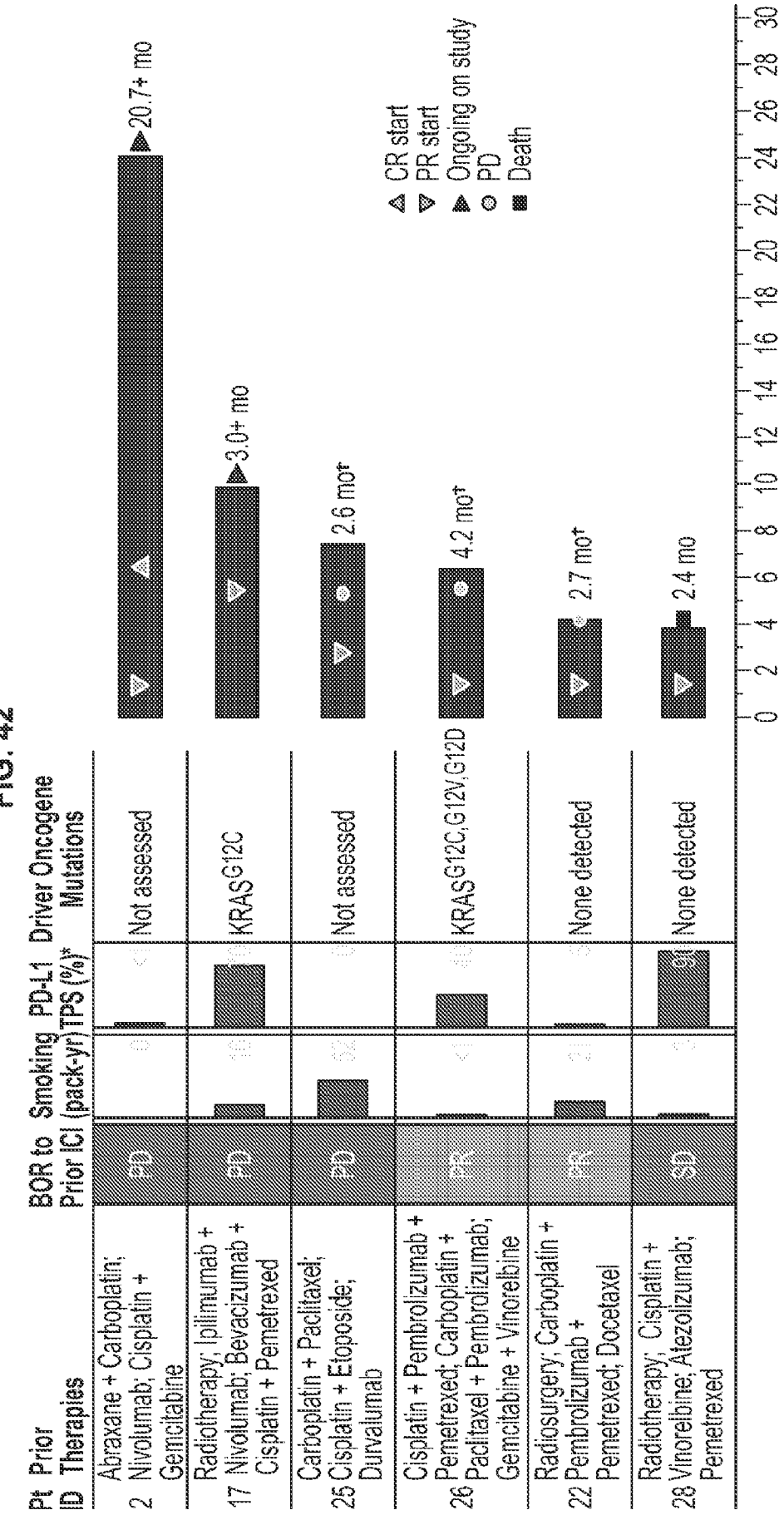

Grade
5
4
3
2
1
• Most AEs occurred prior to or within the first 2 weeks after TIL infusion
• Median number of IL-2 doses: 5.5
Number of AEs
150
100
50
0
D0
M1
M3
M5
M7
M9
M11
M13
M15
M17
Time from TIL Dose

FIG. 41



*For patient 2, the overall response of CR was based on investigator assessment of a complete metabolic response via negative FDG-PET scan.

FIG. 42



*Per central laboratory from tumor harvest specimen, except for patient 2, who had TPS assessed locally using archival tumor sample.
†Patient 25 had PD due to new lesion; patients 26 and 22 had unequivocal PD of non-target disease.

FIG. 43

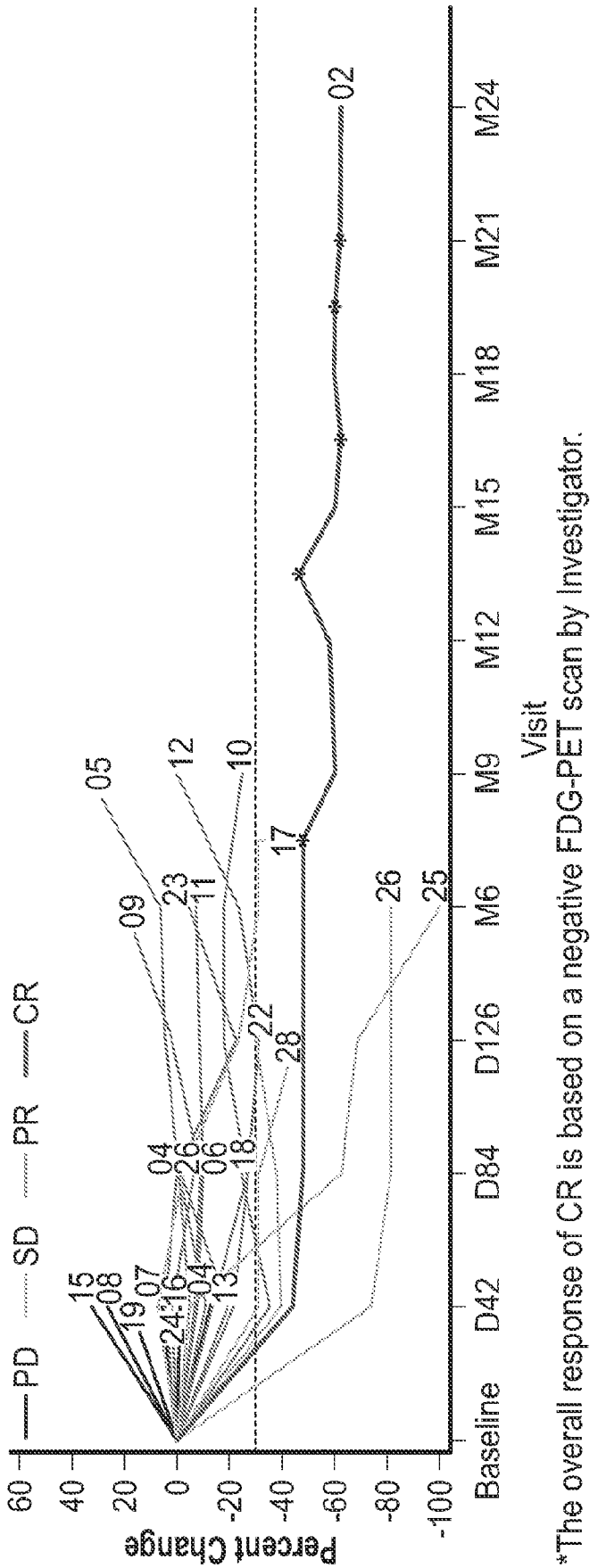

PD
SD
PR
CR
Percent Change
60
40
20
0
-20
-40
-60
-80
-100
Baseline
D42
D84
D126
M6
M9
M12
M15
M18
M21
M24
Visit
*The overall response of CR is based on a negative FDG-PET scan by Investigator.

FIG. 44

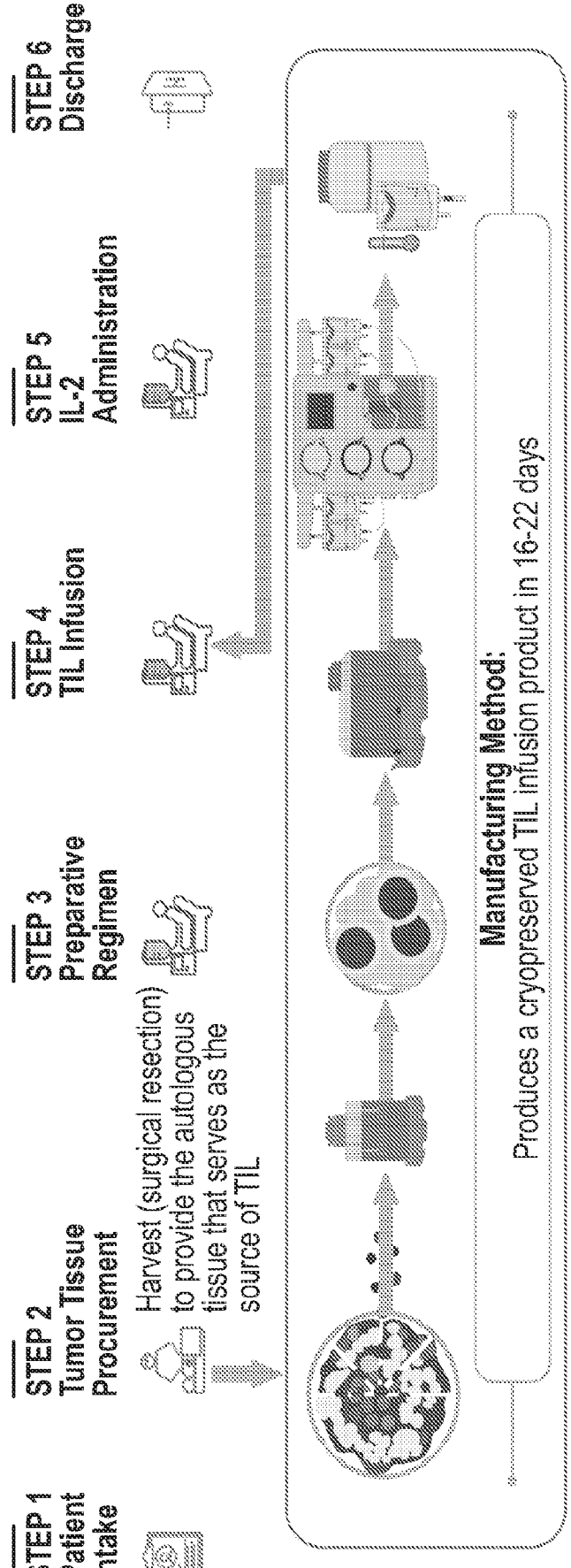
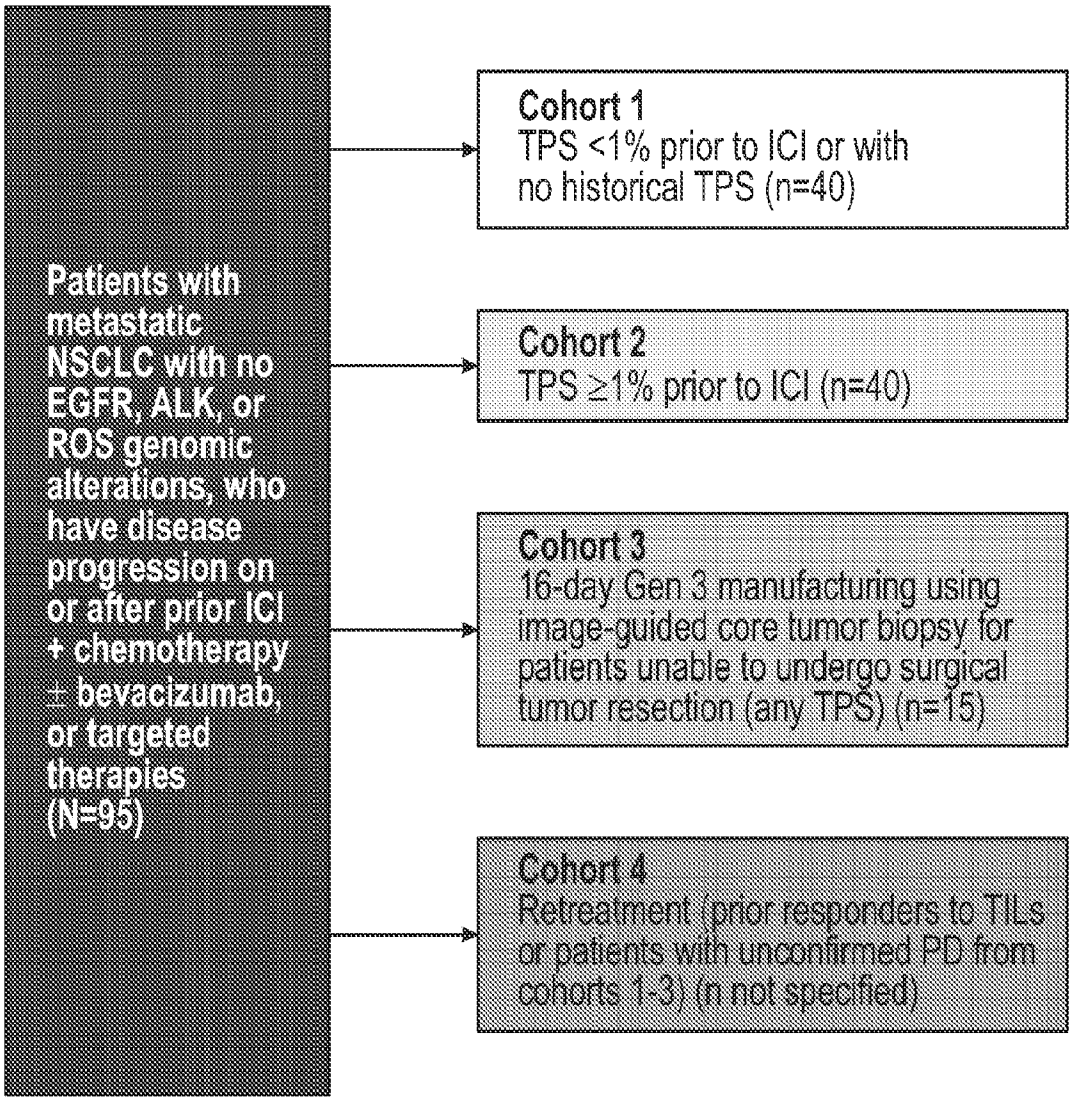

STEP 1
Patient Intake
STEP 2
Tumor Tissue Procurement
Harvest (surgical resection) to provide the autologous tissue that serves as the source of TIL
STEP 3
Preparative Regimen
STEP 4
TIL Infusion
STEP 5
IL-2 Administration
STEP 6
Discharge
Manufacturing Method:
Produces a cryopreserved TIL infusion product in 16-22 days

FIG. 45


Patients with metastatic NSCLC with no EGFR, ALK, or ROS genomic alterations, who have disease progression on or after prior ICI + chemotherapy ± bevacizumab, or targeted therapies (N=95)
Cohort 1
TPS <1% prior to ICI or with no historical TPS (n=40)
Cohort 2
TPS ≥1% prior to ICI (n=40)
Cohort 3
16-day Gen 3 manufacturing using image-guided core tumor biopsy for patients unable to undergo surgical tumor resection (any TPS) (n=15)
Cohort 4
Retreatment (prior responders to TILs or patients with unconfirmed PD from cohorts 1-3) (n not specified)

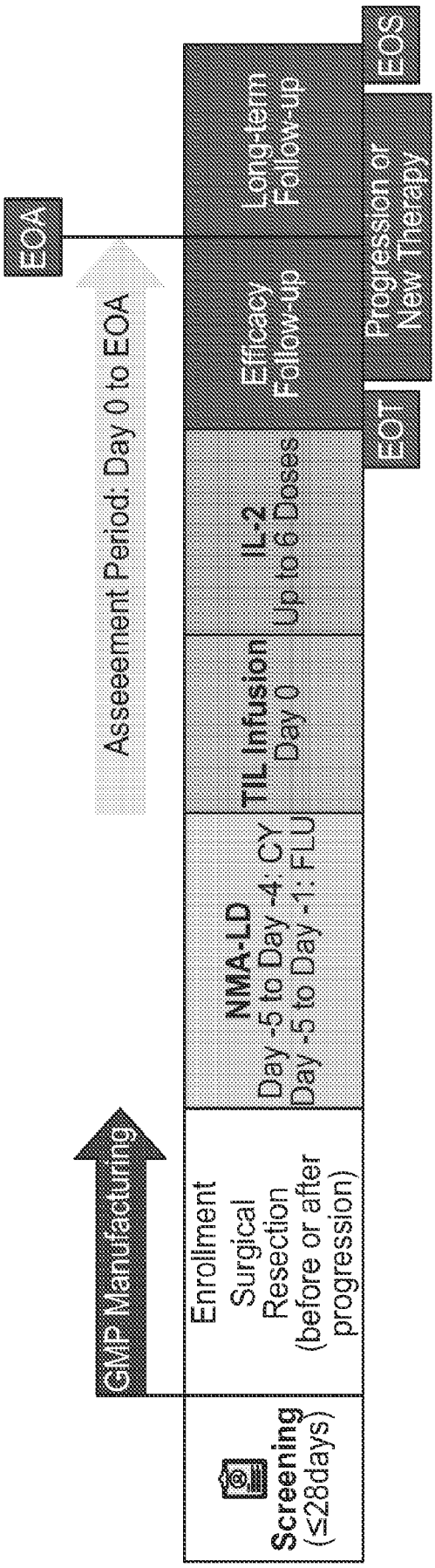

Screening (≤28days)
CMP Manufacturing
Enrollment
Surgical Resection (before or after progression)
NMA-LD
Day -5 to Day -4: CY
Day -5 to Day -1: FLU
TIL Infusion
Day 0
IL-2
Up to 6 Doses
EOT
Efficacy Follow-up
Progression or New Therapy
Long-term Follow-up
EOS
EOA
Asseeement Period: Day 0 to EOA

FIG. 46

FIG. 47

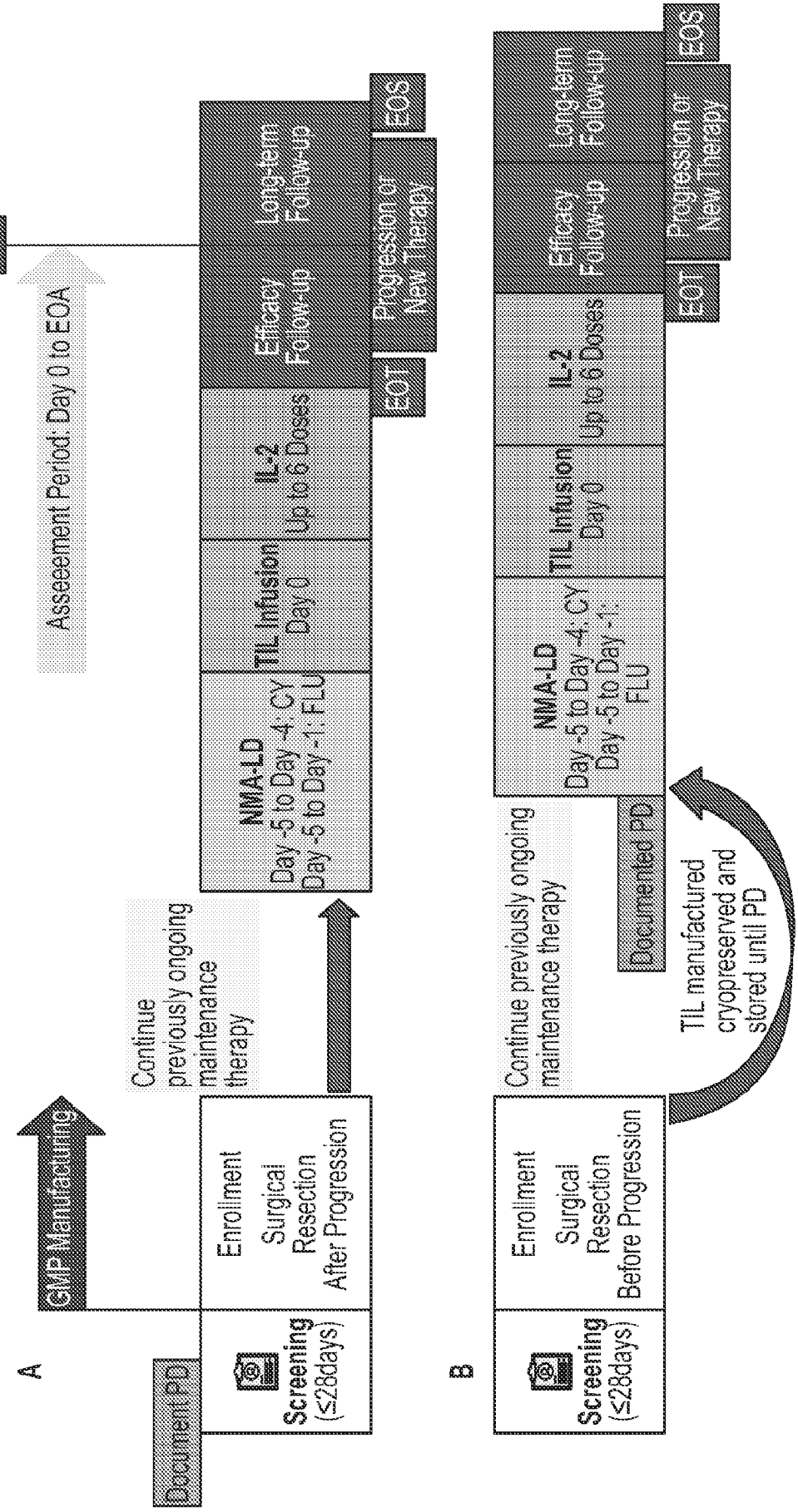

A
Document PD
Screening (≤28days)
Enrollment
Surgical Resection After Progression
CMP Manufacturing
Continue previously ongoing maintenance therapy
NMA-LD Day -5 to Day -4: CY Day -5 to Day -1: FLU
TIL Infusion Day 0
IL-2 Up to 6 Doses
Efficacy Follow-up
Long-term Follow-up
EOT
Progression or New Therapy
EOS
EOA
Assessment Period: Day 0 to EOA
B
Screening (≤28days)
Enrollment
Surgical Resection Before Progression
Documented PD
TIL manufactured cryopreserved and stored until PD
Continue previously ongoing maintenance therapy
NMA-LD Day -5 to Day -4: CY Day -5 to Day -1: FLU
TIL Infusion Day 0
IL-2 Up to 6 Doses
EOT
Efficacy Follow-up
Long-term Follow-up
Progression or New Therapy
EOS

FIG. 48A

STEP A
Obtain Patient Tumor Sample (optionally can be frozen before Step B)

STEP B
First Expansion (physical fragmentation and/or enzymatic digest; culture TILs in medium comprising IL-2 for about 3-9 days)

STEP C
Activation, Gene Editing (culture TILs in medium comprising anti-CP3 and anti-CD38 beads for about 1-7 days; electroporate TILs with TALEN mRNAs; rest for about 1 day)

STEP D
Rapid Second Expansion (culture TILs in medium comprising APCs, OKT-3, and IL-2 for about 5-15 days)

STEP E
Harvest TILs from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve

FIG. 48B

STEP A
Obtain Patient Tumor Sample (optionally can be frozen before Step B)

STEP B
First Expansion (physical fragmentation and/or enzymatic digest; culture TILs in medium comprising IL -2 for about 3-9 days)

STEP C
Activation, Gene Editing (culture TILs in medium comprising anti-CD3 and anti-CD38 beads for about 1-7 days; electroporate TILs with TALEN mRNAs; rest for about 1 day)

STEP D
Rapid Second Expansion (culture TILs in medium comprising APCs, OKT-3, and IL-2 for about 1-7 days; scale up and add culture in medium comprising IL -2 for about 3-6 days)

STEP E
Harvest TILs from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)

FIG. 48C

STEP A
Obtain Patient Tumor Sample (optionally can be frozen before Step B)

STEP B
First Expansion (physical fragmentation and/or enzymatic digest; culture TILs in medium comprising IL -2 and OKT-3 for about 3-9 days)

STEP C
Gene Editing (electroporate TILs with TALEN mRNAs; rest for about 1 day)

STEP D
Rapid Second Expansion (culture TILs in medium comprising APCs, OKT-3, and IL-2 for about 5-15 days)

STEP E
Harvest TILs from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve

FIG. 48D

STEP A
Obtain Patient Tumor Sample (optionally can be frozen before Step B)

STEP B
First Expansion (physical fragmentation and/or enzymatic digest; culture TILs in medium comprising IL -2 and OKT-3 for about 3-9 days)

STEP C
Gene Editing (electroporate TILs with TALEN mRNAs; rest for about 1 day)

STEP D
Rapid Second Expansion (culture TILs in medium comprising APCs, OKT-3, and IL-2 for about 1-7 days; scale up and add culture in medium comprising IL -2 for about 3-6 days)

STEP E
Harvest TILs from Step D

STEP F
Final Formulation and/or Transfer to Infusion Bag (optionally cryopreserve)

FIG. 49

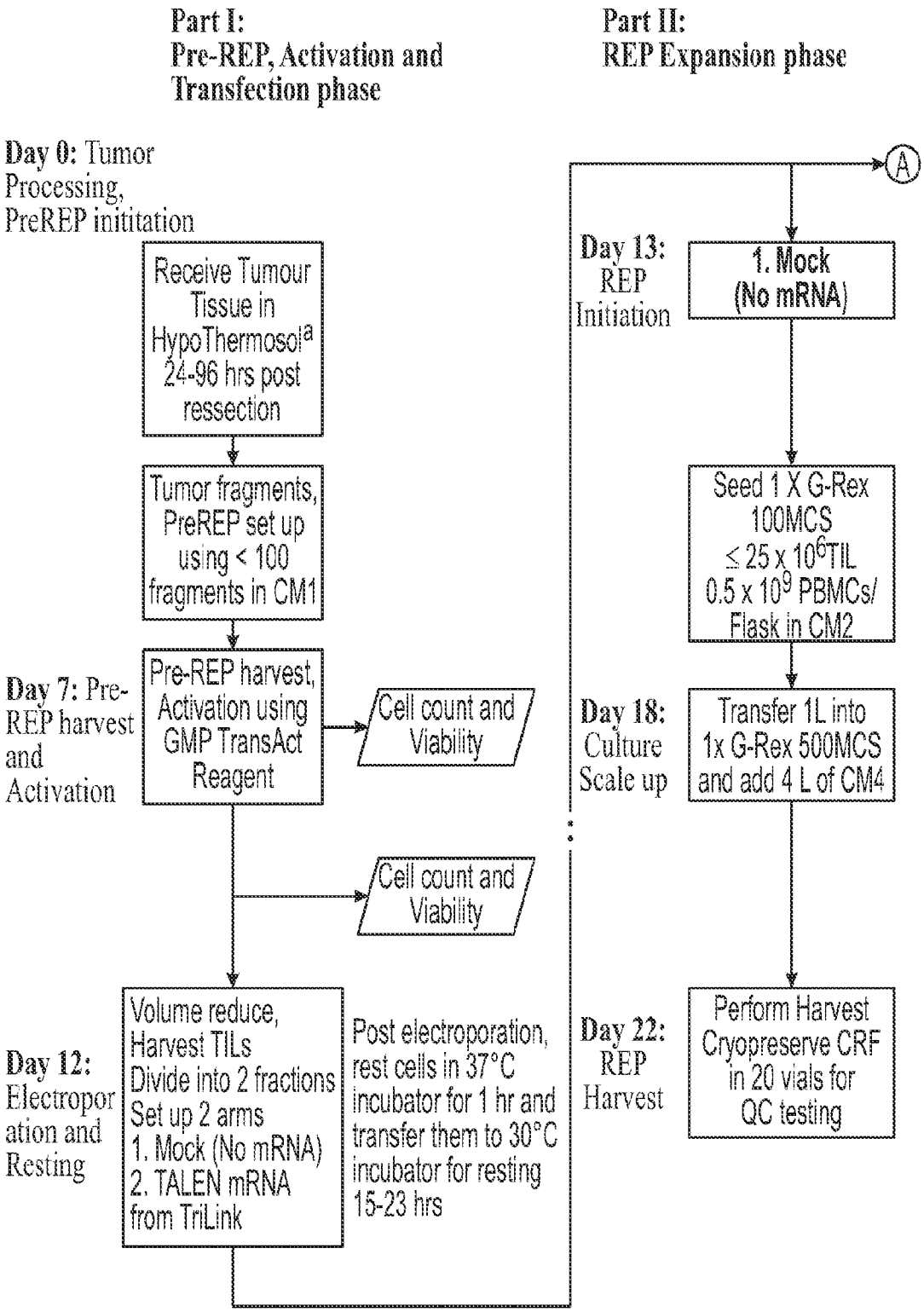

Part I:
Pre-REP, Activation and Transfection phase
Part II:
REP Expansion phase
Day 0: Tumor Processing, PreREP inititation
Receive Tumour Tissue in HypoThermosol[a] 24-96 hrs post ressection
Tumor fragments, PreREP set up using < 100 fragments in CM1
Day 7: Pre-REP harvest and Activation
Pre-REP harvest, Activation using GMP TransAct Reagent
Cell count and Viability
Cell count and Viability
Day 12: Electroporation and Resting
Volume reduce, Harvest TILs Divide into 2 fractions Set up 2 arms 1. Mock (No mRNA) 2. TALEN mRNA from TriLink
Post electroporation, rest cells in 37°C incubator for 1 hr and transfer them to 30°C incubator for resting 15-23 hrs
A
Day 13: REP Initiation
1. Mock (No mRNA)
Seed 1 X G-Rex 100MCS ≤ 25 x 10^6 TIL 0.5 x 10^9 PBMCs/ Flask in CM2
Day 18: Culture Scale up
Transfer 1L into 1x G-Rex 500MCS and add 4 L of CM4
Day 22: REP Harvest
Perform Harvest Cryopreserve CRF in 20 vials for QC testing

FIG. 49
(Continued)

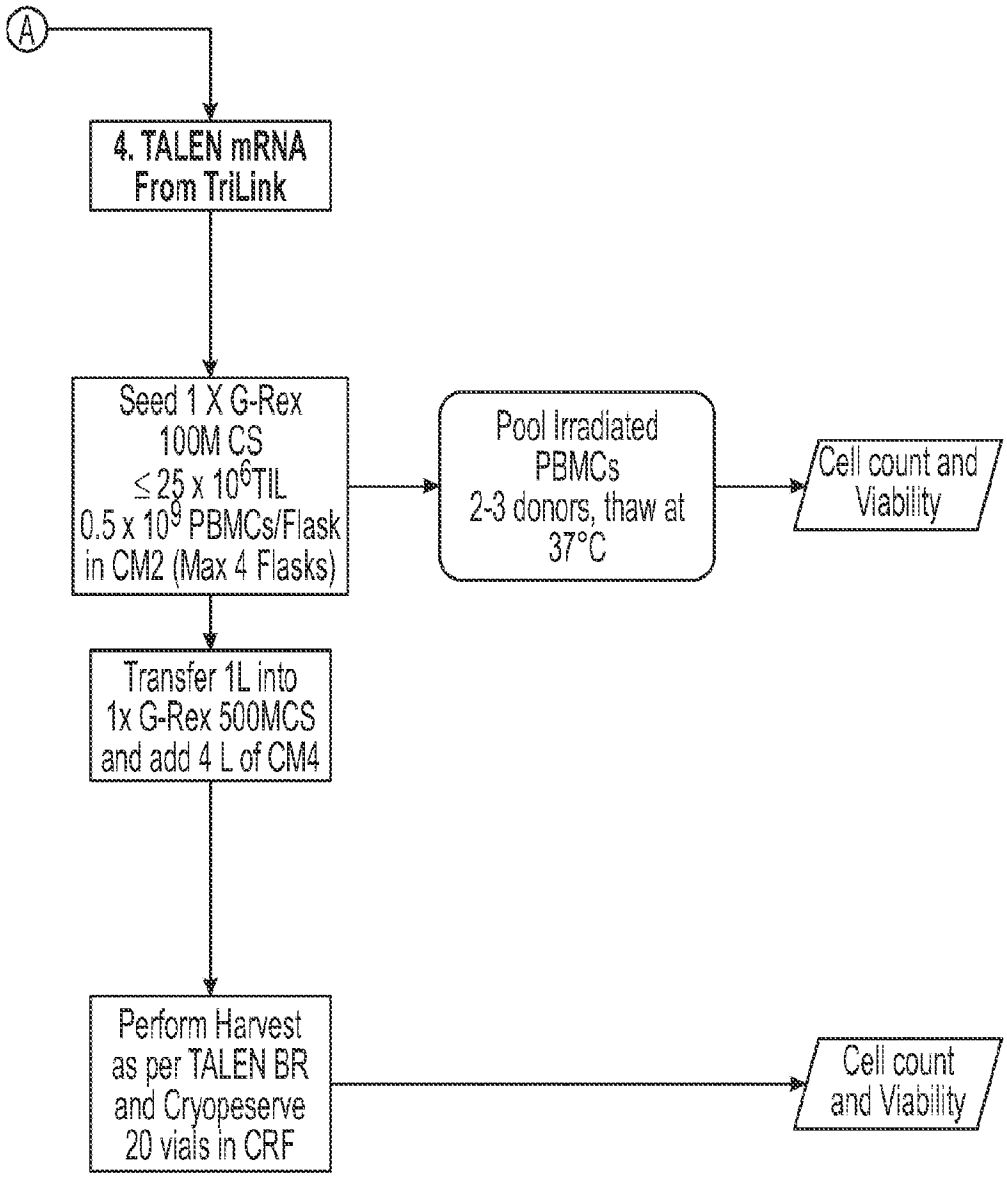


FIG. 50

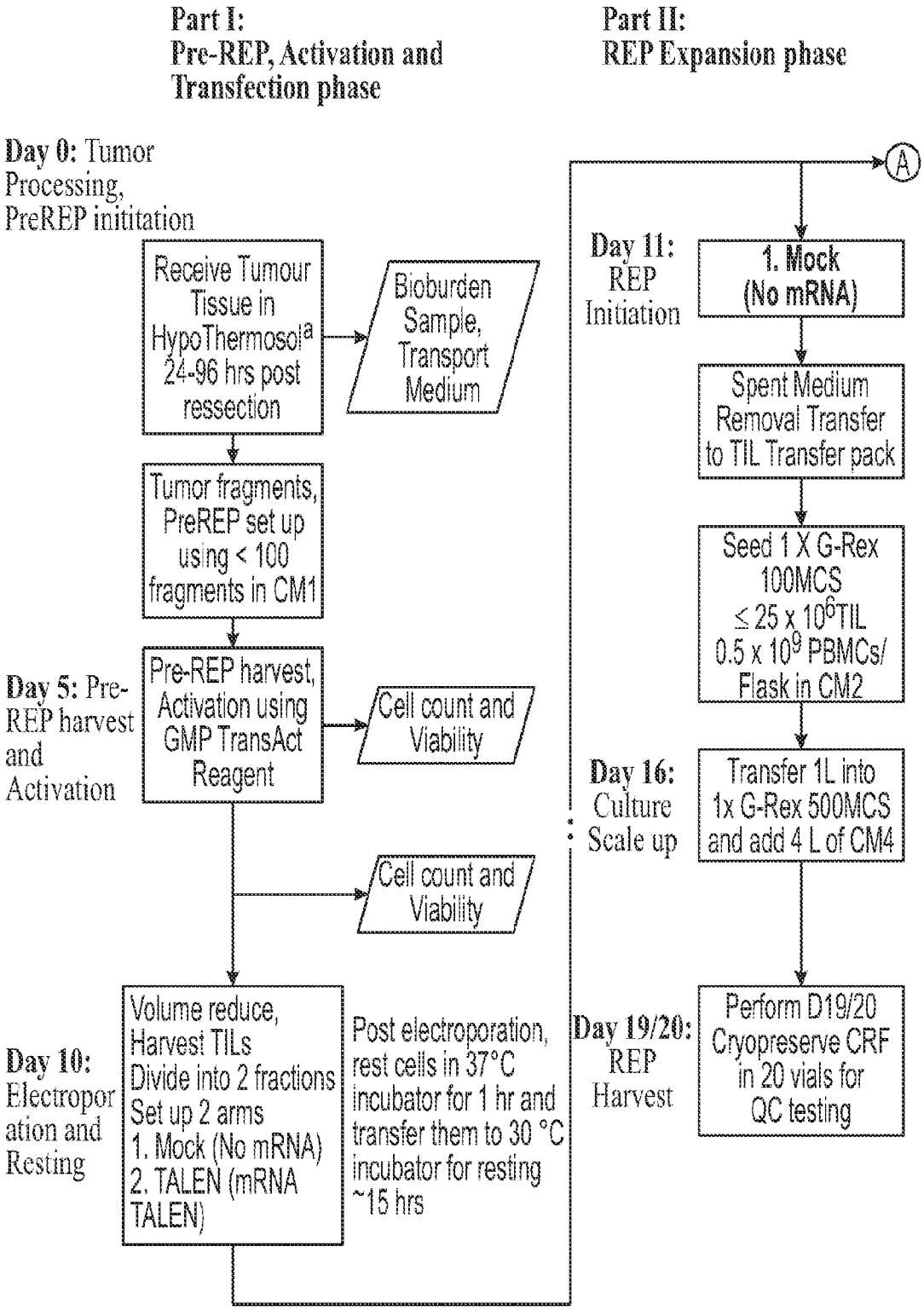

Part I:
Pre-REP, Activation and Transfection phase
Part II:
REP Expansion phase
Day 0: Tumor Processing, PreREP inititation
Receive Tumour Tissue in HypoThermosol[a] 24-96 hrs post ressection
Bioburden Sample, Transport Medium
Tumor fragments, PreREP set up using < 100 fragments in CM1
Day 5: Pre-REP harvest and Activation
Pre-REP harvest, Activation using GMP TransAct Reagent
Cell count and Viability
Cell count and Viability
Day 10: Electroporation and Resting
Volume reduce, Harvest TILs Divide into 2 fractions Set up 2 arms 1. Mock (No mRNA) 2. TALEN (mRNA TALEN)
Post electroporation, rest cells in 37°C incubator for 1 hr and transfer them to 30 °C incubator for resting ~15 hrs
A
Day 11: REP Initiation
1. Mock (No mRNA)
Spent Medium Removal Transfer to TIL Transfer pack
Seed 1 X G-Rex 100MCS ≤ 25 x 10^6 TIL 0.5 x 10^9 PBMCs/ Flask in CM2
Day 16: Culture Scale up
Transfer 1L into 1x G-Rex 500MCS and add 4 L of CM4
Day 19/20: REP Harvest
Perform D19/20 Cryopreserve CRF in 20 vials for QC testing

FIG. 50
(Continued)

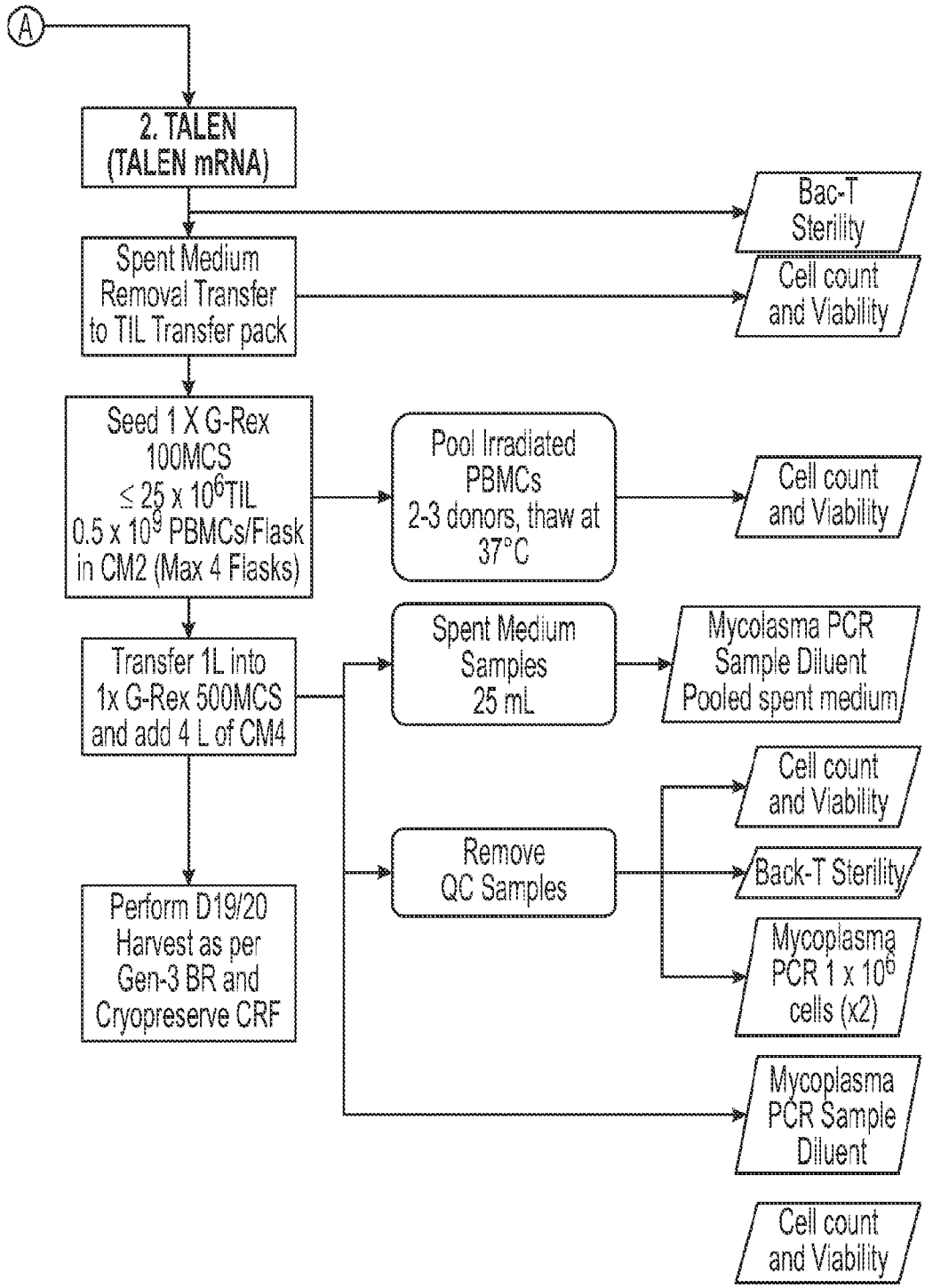


FIG. 51A

Signal Sequence: MDWTWILFLVAAATRVHS (SEQ ID NO:252)
Linker (Lr1): SGGGSGGGGSGGGGSGGGGSLQ (SEQ ID NO:246)
Anchor (Ar2):(human B7.1 transmembrane-intracellular amino acid sequence)
LLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:239)
FurinA-P2A sequence: RAKRSGSGATNFSLLKQAGDVEENPGP (SEQ ID NO:251)

Tethered IL-12-Lr1-Ar2

MDWTWILFLVAAATRVHSIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKT
LTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTT
ISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYE
NYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTS
ATVICRKNASISVRAQDRYYSSSWSEWASVPCSGGGGGSGGRNLPVATPDPGMFPCLHHSQNLLRAVSNML
QKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYE
DLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF
RIRAVTIDRVMSYLNASIGGGGSGGGGSGGGGSGGGGSGGGGSLQLLPSWAITLISVNGIFVICCLTYCFAPRC
RERRRNERLRRESVRPV (SEQ ID NO:303)

Tethered IL-12-Lr1-Ar2

ATGGATTGGACCTGGATTCTGTTCCTCGTGGCCGCCGCTACCCGCGTGCACTCCATCTGGGAGCTGAAGAAAGAC
GTGTACGTGGTGGAATTGGATTGGTACCCCGACGCCCCAGGCGAGATGGTGGTCCTGACTTGCGACACGCCGGA
GGAGGACGGCATCACCTGGACGCTGGACCAGAGCAGCGAAGTGCTGGGCTCTGGTAAGACCTTAACCATCCAGG
TCAAGGAGTTCGGTGATGCAGGACAGTACACGTGTCACAAGGGCGGGGAGGTCTTGTCCCATAGCCTGCTGCTCC
TGCACAAGAAGGAAGACGGCATCTGGTCTACGGATATCCTTAAAGACCAGAAGGAGCCCAAGAACAAAACCTTCC
TGCGATGCGAGGCTAAGAATTACTCCGGGGCGCTTTACCTGTTGGTGGCTCACAACCATCTCGACCGACCTGACCTT
CTCCGTGAAGTCTTCCAGGGGATCTTCTGATCCGCAAGGCGTTACCTGCGGGGCCGCTACCCTGTCGGCTGAGCGC
GTCCGTGGTGACAACAAGGAGTACGAGTACTCGGTGGAATGCCAGGAGGACAGCGCCTGCCCAGCGGCCGAAGA
GTCCTTGCCCATCGAGGTGATGGTGGACGCTGTACACAAGCTCAAGTACGAGAACTACACCTCCTCCTTCTTTATAC
GCGACATCATCAAGCCTGACCCCCCTAAAAACCTGCAGCTGAAGCCCCTTAAAAACTCTCGACAGGTCGAGGTATC
CTGGGAGTACCCCGACACCTGGTCTACTCCTCATTCGTATTTCAGCCTGACCTTCTGCGTGCAGGTGCAGGGCAAG
TCCAAGCGCGAGAAGAAGGACCGCGTGTTCACCGACAAAACCAGCGCGACTGTCATTTGTCGGAAGAACGCGAG
CATCTCCGTACGGGCACAGGATCGCTATTACTCCAGCAGTTGGTCAGAGTGGGCTTCGGTTCCGTGTTCTGGAGGA
GGTGGCGGCGGCTCACGCAACCTGCCCGTGGCGACGCCGGACCCGGGTATGTTCCTTGTCTGCACCACTCTCAG
AACTTGCTCCGTGCCGTCTCGAATATGCTGCAGAAGGCCCGCCAGACTCTGGAGTTCTATCCATGCACTAGTGAGG
AGATCGATCATGAGGACATCACCAAGGACAAGACATCCACCGTGGAGGCTTGTCTGCCGCTGGAGTTGACAAAGA
ACGAGAGCTGCCTCAATAGCCGCGAGACTTCCTTCATCACCAACGGCTCCTGCCTCGCGAGCCGTAAGACCTCCTT
TATGATGGCGCTGTGCCTGTCAAGTATCTACGAAGATCTGAAAATGTATCAGGTGGAGTTCAAAACTATGAACGC
AAAACTCCTGATGGATCCCAAGCGCCAAATTTTCTTGGACCAGAACATGCTTGCCGTGATCGACGAGCTGATGCAG
GCCCTGAACTTCAACTCCGAGACCGTCCCTCAGAAGTCGTCTCTGGAGGAACCCGACTTTTACAAGACAAAGATCA
AGCTGTGCATCCTGCTACACGCGTTCCGCATTCGGGCCGTGACCATTGACCGCGTGATGTCCTACCTGAATGCCTC
GTCCGGCGGGGGGGGCTCCGGTGGGGGCGGCTCTGGCGGAGGCGGCTCAGGTGGCGGCGGCTCCGGCGGAGG
TTCGCTTCAGCTTCTGCCCAGTTGGGCAATCACTCTGATTTCCGTCAACGGAATCTTCGTCATCTGCTGCCTGACCTA
CTGCTTTGCTCCCAGATGTAGAGAGCGCCGCCGCAACGAGCGCCTGCGTCGTGAGAGCGTGAGGCCTGTG (SEQ
ID NO:304)

FIG. 51B

Tethered IL-18-Lr1-Ar2

MDWTWILFLVAAATRVHSYFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDS
QPRGMAVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEKE
RDLFKLILKKEDELGDRSIMFTVQNEDGGGGSGGGGSGGGGSGGGGSGGGSLQLLPSWALTLISVNGIFVIC
CLIYCFAPRCRERRKNERLRRESVRPV (SEQ ID NO:305)

Tethered IL-18-Lr1-Ar2

ATGGATTGGACCTGGATTTTGTTCCTGGTGGCTGCAGCCACTCGGGTCCACAGCTACTTCGGCAAGCTG
GAGAGTAAACTTTCCGTGATCCGCAACCTCAACGACCAAGTGCTGTTCATTGACCAGGGCAACCGCCCC
CTCTTTGAAGACATGACCGACAGCGATTGTCGTGACAATGCGCCCCGCACCATCTTTATAATTTCCATGT
ACAAGGATAGCCAGCCGCGGGGAATGGCGGTAACGATCTCGGTGAAGTGTGAAAAAATCTCGACCCTG
TCATGCGAGAACAAGATCATTTCCTTCAAAGAGATGAATCCACCCGACAACATCAAGGACACCAAGTCC
GACATCATCTTCTTCCAGCGGCAGCGTGCCTGGGCATGACAACAAGATGCAGTTCGAGAGCTCGTCTTAC
GAGGGCTATTTCCTGGCCTGCGAGAAGGAGCGTGACCTGTTCAAGCTTATCCTGAAGAAGGAGGACGA
GCTGGGGGACCGCAGCATCATGTTTACAGTGCAGAACGAGGATTCTGGTGGCGGCGGTAGCGGGGGC
GGGGGTTCTGGCGGCGGAGGCTCCGGTGGAGGAGGCTCCGGCGGCGGTTCGTTGCAGCTGCTGCCCA
GTTGGGCCATCACTCTAATCTCCGTCAACGGCATCTTCGTCATCTGTTGCCTGACCTACTGCTTTGCTCCG
AGGTGTAGAGAGCGACGCCGCAACGAGCGCCTCCGCCGTGAGTCCGTGCGCCCTGTT (SEQ ID
NO:306)

Tethered DR-IL-18 (6-27 variant)-Lr1-Ar2 (yellow highlight: mutated residues)

MDWTWILFLVAAATRVHSYFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISKYSDS
SERGMAVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFSRVPGHSNKSQFESSSYEGYFLACEKERDL
FKLILKKEDELGDRSIMFTVQNEDSGGGGSGGGGSGGGGSGGGGSGGGSLQLLPSWALTLISVNGIFVICCLI
YCFAPRCRERKRNERLRRESVRPV (SEQ ID NO:307)

Tethered DR-IL-18 (6-27 variant)-Lr1-Ar2

ATGGATTGGACCTGGATCCTGTTCCTGGTGGCGGCGGCAACTCGCGTACATAGCTATTTCGGCAAGCTG
GAGAGCAAACTATCAGTGATCCGCAACCTCAACGACCAGGTCTTGTTTATTGACCAGGGCAACCGCCCC
CTGTTCGAAGACATGACAGACAGCGATTGTCGCGACAATGCTCCTCGCACCATCTTTATCATCTCCAAGT
ACTCCGATTCTCGAGCCAGAGGTCTCGCCGTGACCATCTCCGTGAAGTGCGAGAAGATATCCACTCTTTC
ATGCGAGAACAAGATCATTTCCTTCAAGGAGATGAATCCACCCGACAACATCAAGGACACCAAGTCCGA
CATCATCTTCTTCGCTCGTGTGCCTGGCCACGGCCGCAAGACCCAGTTCGAGAGTTCCAGCTACGAGGG
CTACTTCCTGGCCTGTGAGAAAGAGCGGGACCTTTTCAAATTGATTCTGAAGAAGGAGGACGAGCTGG
GCGACCGTAGCATCATGTTTACGGTGCAGAACGAGGATTCTGGCGGGGGCGGTTCTGGAGGGGGTGG
GTCGGGCGGTGGTGGCTCCGGGGGAGGCGGCTCCGGAGGAGGCTCGCTGCAGCTGCTGCCCAGTTGG
GCCATCACGCTCATTTCTGTCAACGGCATCTTCGTCATCTGTTGCCTGACCTACTGCTTTGCTCCGAGGTG
TAGGGAACGTCGTCGCAACGAGCGCCTGCGCCGCGAGTCTGTTCGGCCGGTG (SEQ ID NO:308)

FIG. 51C

Tethered IL-12/IL-15

MDWTWILFLVAAATRVHSIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKT
LTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTT
ISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYE
NYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTS
ATVICRKNASISVRAQDRYYSSSWSEWASVPCSGGGGGGSRVIPVATPDPGMFPCLHHSQNLLRAVSNML
QKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYE
DLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAF
RIRAVTIDRVMSYLNASSGGGGSGGGGSGGGGSGGGGSLQLIPSWAITLISVNGIFVICLTYCFAPRC
KERRRNERLRRESVRPVRAKRSGSGATNFSLLKQAGDVEENPGPNLWTWILFLVAAATRVHSNWVNVISD
LKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESG
CKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGGSGGGGSGGGGSGGGGSLQLIPSWAITLISVNGIF
VICLTYCFAPRCKERRRNERLRRESVRPV (SEQ ID NO:309)

Tethered IL-12/IL-15

ATGGATTGGACCTGGATTCTGTTTTTGGTGGCGGCCGCCACCCGCGTCCATTCCATATGGGAATTAAAGAAGGACGTGTACGT
GGTGGAGCTTGACTGGTACCCTGACGCTCCCGGCGAGATGGTGGTCCTGACCTGCGATACCCCCGAGGAGGACGGCATCACC
TGGACCCTGGACCAGAGCTCCGAGGTGCTGCGAAGCGGTAAAACCCTCACCATACAGGTGAAGGAGTTCGGTGATGCTGGCC
AGTACACCTGTCACAAAGGCGGGGAGGTACTTTCCCATTCGCTGCTCCTGCTTCACAAGAAGGAAGACGGCATTTGGTCGACC
GATATTCTGAAGGACCAGAAGGAACCAAAAAACAAGACCTTTTTGCGTTCCGAGGCCAAGAACTATTCCGGCCGCTTCACCTG
CTGGTGGCTAACGACCATCTCAACCGACCTGACCTTCTCCGTTAAGTCTAGCCGTGGTAGCTCCGACCCTCAGGGGGTAACCTG
CGGGGCTGCGACCCTGAGTGCGGAGCGGGTACGCGGCGACAACAAGGAGTACGAGTACTCCGTGGAATGTCAGGAGGATA
GTGCCTGCCCAGCGGCCGAGGAGTCCCTGCCCATCGAGGTAATGGTGGACGCCGTCCACAAGCTGAAGTACGAGAACTACAC
TAGCTCCTTCTTTATTAGAGACATCATCAAGCCCGACCCGCCTAAGAACCTGCAGCTGAAACCTCTCAAAAACTCCCGCCAGGT
TGAAGTGTCGTGGGAGTACCCTGACACCTGGTCTACACCGCACAGCTATTTCTCGCTTACATTCTGCGTGCAGGTGCAGGCCA
AATCCAAGCGCGAGAAGAAAGACCGCGTGTTCACCGACAAAACCTCTGCTACAGTGATCTGCCGAAAGAATGCTTCTATCTCC
GTGCGTGCTCAGGACCGCTACTACTCATCAAGCTGGAGTGAGTGGGCCTCCGTGCCATGTTCCGGGGGGGGCGGCGGTGGCT
CCCGCAACCTGCCCGTTGCAACGCCCGACCCGGGTATGTTCCCATGCCTGCACCACTCCCAGAATCTGTTACGTGCTGTAAGCA
ATATGCTTCAGAAGGCTCGCCAGACTCTGGAGTTCTACCCCTGCACTTCGGAGGAGATCGACCACGAAGACATCACCAAGGAC
AAGACATCCACCGTGGAGGCGTGCCTCCCTTTGGAGCTCACAAAGAACGAGTCCTGTCTAAACTCAAGGGAGACTAGCTTCAT
CACTAATGGATCGTGTCTGGCGTCGCGCAACACCTCTTTCATGATGGCCCTGTGCCTGTCCAGCATCTATGAGGACCTTAAAAT
GTATCAGGTCGAGTTCAAGACTATGAACGCAAAGCTGCTGATGGATCCCAAGCGGCAAATTTTCCTGGACCAGAACATGCTGG
CGGTGATCGACGAGCTGATGCAGGCCCTCAACTTCAACAGCGAAACTGTTCCTCAGAAGTCCTCCCTGGAGGAGCCGGACTTT
TACAAGACCAAGATCAAGCTATGTATTTTGTTACACGCCTTCCGCATCCGCGCTGTCACTATTGACCGCGTGATGTCTTACCTGA
ACGCATCTAGTGCGGGCCGGAGGTTCCGGGGGAGGCGGCTCTGGCGGTGGCGGCTCTGGCGGTGGTGGTTCAGGAGGCGGG
TCCCTTCAGCTGCTCCCGTCGTGGGCCATCACACTGATCTCTGTGAACGCCATCTTCGTCATCTGTTGTCTTACTTACTGCTTTGC
CCCCAGGTGTAGGGAGAGACGCCGCAATGAACGGCTGAGGCGTGAGAGCGTGCGCCCGGTGAGGGCTAAGCGCAGCGGCT
CCGGCGCGACCAACTTTTCGCTGCTGAAGCAGGCCGGGGACGTGGAGGAGAATCCAGGCCCCATGGATTGGACCTGGATCCT
GTTCTTGGTGGCCGCGGCTACTCGGGTGCACTCTAATTGGGTCAACGTGATCTCCGACTTGAAAAAGATCGAGGATCTGATCC
AGAGCATGCATATCGACGCCACGCTGTACACCGAGAGCGATGTGCACCCCTCTTGCAAGGTGACCGCCATGAAGTGCTTTCTG
CTGGAGCTGCAGGTCATCTCTCTTGAGTCGGGCGATGCATCTATTCATGACACCGTCGAGAACCTAATCATCCTGGCCAACAAC
TCACTGTCTTCAAACGGCAACGTGACGGAGTCTGGGTGCAAGGAATGTGAGGAATTGGAGGAGAAAAACATCAAGGAGTTCC
TGCAGTCCTTCGTCCACATCGTGCAGATGTTTATTAACACGAGTAGTGGCGGAGGTGGCAGCGGAGGCGGGGGCTCCGGCGG
TGGAGGAAGTGGAGGCGGCGGCTCTGGTGGCGGTTCCCTACAATTGCTTCCCTCTTGGGCTATCACCCTCATCAGCGTCAACG
GTATCTTCGTCATCTGTTGTCTGACCTACTGCTTTGCCCCTCGATGCCGAGAGCGCCGTCGCAACGAGCGCCTGCGCCGGGAGT
CCGTGCGCCCCGTT (SEQ ID NO:310)

FIG. 51D

Tethered IL-18/IL-15

MDNTWILFLVAAATRVHSYFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDS
QPRGMAVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFESSSYEGYFLACEKE
RDLFKLILKKEDELGDRSIMFTVQNEDGGGGSGGGGSGGGGSGGGGSLQLLPSWATLLISVNGIFVIC
CLIYCFAPRCRERRRNERLRRESVRPVRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFLVAAATRVH
SNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSGGGGSGGGGSGGGGSGGGGSLQLLPSN
AITLISVNGIFVICCLIYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:311)

Tethered IL-18/IL-15

ATGGATTGGACCTGGATCCTTTTCTTGGTGGCGGCTGCAACCCGGGTTCATAGCTATTTCGGCAAGCTG
GAGTCCAAGCTCTCCGTGATCCGCAACCTCAACGACCAGGTGCTGTTCATCGACCAGGGCAACCGCCCC
CTGTTTGAGGACATGACAGATTCTGATTGCCGCGACAACGCGCCGCGCACCATCTTCATTATCTCTATGT
ACAAGGACTCCCAGCCACGTGGTATGGCCGTCACGATCAGCGTGAAGTGCGAGAAGATTTCTACCCTGT
CCTGCGAGAACAAGATCATCTCGTTCAAGGAGATGAACCCTCCCGACAATATCAAGGACACCAAGTCCG
ACATCATCTTCTTCCAGCGATCAGTGCCAGGCCACGACAACAAGATGCAGTTCGAGAGCAGCAGCTACG
AGGGCTACTTCCTTGCGTGCGAGAAAGAGCGCGATCTGTTCAAACTGATCCTCAAGAAGGAAGACGAG
CTCGGGGACCGCAGCATCATGTTTACCGTACAGAACGAGGACAGCGGCGGCGGCGGCTCCGGTGGAG
GCGGTAGTGGCGGAGGCGGCTCAGGCGGCGGCGGCTCCGGAGGTGGGTCGTTGCAGCTCTTGCCGAG
TTGGGCTATCACTCTTATCTCCGTAAACGGCATCTTCGTGATATGCTGCCTGACGTACTGTTTTGCTCCTA
GGTGTCGCGAGCGCCGCCGGAACGAGAGACTGCGACGGGAATCCGTGCGCCCGGTCCGCGCGAAGCG
TAGTGGCTCCGGTGCTACCAACTTTTCTCTGCTGAAGCAGGCCGGCGACGTGGAGGAGAATCCCGGCCC
TATGGACTGGACATGGATCCTGTTCCTGGTGGCTGCGGCCACCCGCGTCCACTCAAATTGGGTCAATGT
GATTTCTGACCTGAAGAAAATTGAGGATCTCATCCAGTCCATGCACATTGACGCCACTCTGTACACCGAG
AGCGATGTTCACCCCTCTTGTAAGGTGACCGCCATGAAATGTTTCCTGTTGGAGCTGCAGGTCATTTCGC
TCGAGTCTGGCGACGCATCGATCCATGACACCGTGGAGAACCTGATTATCCTGGCCAACAACTCCCTTTC
TTCAAATGGCAACGTGACTGAAAGCGGGTGCAAAGAGTGTGAGGAGCTGGAAGAAAAGAACATCAAA
GAGTTCCTGCAATCTTTCGTCCACATTGTGCAGATGTTTATTAACACGTCCTCGGGTGGCGGGGGGTCG
GGCGGGGGTGGTTCCGGCGGAGGCGGGTCCGGAGGAGGGGGCTCTGGTGGGGGATCCCTACAGCTA
CTGCCCTCTTGGGCCATCACCCTTATCTCCGTCAACGGTATCTTCGTGATCTGTTGCCTGACTTACTGCTTT
GCCCCGAGATGTCGTGAGCGTAGGAGGAACGAGCGCCTGCGCCGCGAGAGCGTGCGTCCCGTG (SEQ
ID NO:312)

FIG. 51E

Tethered anti-CD40scFV (APX005M)

MDWTWILFLVAAATRVHSQVQLVESGGGVVQPGRSLRLSCAASGFSFSSTYVCWVRQAPGKGLEWIACIYT
GDGTNYSASWAKGRFTISKDSSKNTVYLQMNSLRAEDTAVYFCARPDITYGFAINFWGPGTLVTVSSGGGGS
GGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIKCQASQSISSRLAWYQQKPGKPPKLLIYRASTLASG
VPSRFSGSGSGTDFTLTISSLQPEDVATYYCQCTGYGISWPIGGGTKVEIKSGGGGSGGGGSGGGGSGGGGS
GGGSLQLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:313)

Tethered anti-CD40scFV (APX005M)

ATGGATTGGACCTGGATCCTGTTCCTGGTGGCGGCCGCTACACGAGTCCACAGCCAGGTCCAGCTCGTG
GAGAGCGGAGGCGGCGTGGTGCAGCCAGGCCGCTCGCTGCGCCTGTCATGCGCAGCGTCCGGTTTCTC
CTTCTCGTCCGACCTACGTGTGCTGGGTCCGCCAGGCCCCTGGCAAAGGCCTGGAGTGGATTGCTTGTAT
TTATACCGGCGACGGCACCAACTACAGCGCAAGTTGGGCCAAGGGCCGTTTCACCATCTCCAAGGATAG
TAGCAAGAACACGGTATACCTGCAGATGAACTCTCTTCGCGCCGAGGACACCGCCGTGTATTTCTGTGCC
CGGCCCGACATCACTTATGGCTTCGCGATTAACTTTTGGGGCCCTGGAACCCTGGTGACCGTGTCCTCCG
GCGGCGGTGGCTCTGGGGGGGGCGGGTCCGGCGGAGGCGGCAGCGGAGGCGGCGGCTCCGACATCC
AGATGACCCAGTCGCCCAGTTCTTTGTCCGCTTCCGTGGGGGACAGGGTCACCATAAAGTGCCAGGCTT
CTCAGAGCATCTCGTCCCGCCTGGCGTGGTACCAGCAGAAGCCCGGGAAGCCCCCAAAGCTGCTCATCT
ACCGGGCTTCCACTCTGGCCAGCGGTGTCCTTCCCGCTTCTCTGGCTCCGGGTCGGGCACTGACTTTAC
ATTGACGATCTCTTCGCTTCAGCCGGAAGATGTAGCTACTTACTACTGTCAATGCACTGGCTACGGCATC
AGTTGGCCCATCGGTGGAGGCACCAAGGTGGAGATCAAAAGCGGGGGAGGCGGTTCTGGCGGTGGAG
GGTCTGGCGGGGGTGGCTCCGGGGGCGGTGGTAGCGGTGGTGGATCCCTACAGCTGCTGCCCTCTTGG
GCCATCACGCTCATTTCAGTTAATGGCATCTTCGTCATCTGCTGCCTGACCTACTGCTTTGCGCCGAGGTG
TAGAGAGCGGCGTCGCAACGAGCGCCTGCGTCGCGAGAGCGTGCGCCCGGTG (SEQ ID NO:314)

FIG. 51F

Tethered anti-CD40scFV (Dacetuzumab)

MDWTWILFLVAAATRVHSEVQLVESGGGLVQPGGSLRLSCAASGYSFTGYYIHWVRQAPGKGLEWVARVI
PNAGGTSYNQKFKGRFTLSVDNSKNTAYLQMNSLRAEDTAVYYCAREGIYWWGQGTLVTVSSGGGGSGG
GGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTFLHWYQQKPGKAPKLLIYTVSN
RFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCSQTTHVPWTFGQGTKVEIKGGGGSGGGGSGGGGSGG
GGSGGGSLQSLLPSWAITLISVNGIFVICCLTYCFAPRCKERRRNERLRRESVRPV (SEQ ID NO:315)

Tethered anti-CD40scFV (Dacetuzumab)

ATGGATTGGACCTGGATCCTGTTCCTGGTGGCGGCGGCTACACGTGTGCACTCCGAGGTGCAGTTGGTG
GAGAGCGGCGGTGGTCTGGTGCAGCCGGGCGGGAGCCTGCGCCTGTCGTGCGCCGCTTCCGGCTACTC
CTTCACCGGTTATTACATCCACTGGGTGCGACAGGCCCCGGGCAAAGGCCTGGAGTGGGTCGCTCGCGT
AATTCCTAACGCGGGTGGCACCAGCTACAACCAGAAATTTAAGGGCAGATTCACCCTCAGCGTTGACAA
CTCCAAGAACACGGCCTACCTGCAGATGAACTCCCTTCGCGCCGAGGACACCGCCGTGTACTACTGTGCT
CGCGAGGGCATCTATTGGTGGGGCCAGGGAACTCTAGTTACCGTGTCCTCCGGCGGCGGCGGCTCGGG
CGGCGGGGGTTCTGGTGGGGGCGGTTCCGGAGGGGGAGGGTCCGACATCCAGATGACCCAGAGCCCC
TCTAGTCTGAGCGCATCCGTGGGGGACAGGGTCACCATCACCTGCCGCTCGTCACAATCGCTTGTCCACT
CAAATGGCAACACTTTCCTGCATTGGTACCAGCAGAAGCCCGGCAAGGCGCCCAAGCTGCTCATCTACA
CCGTGAGCAACCGCTTTTCAGGCGTGCCATCCCGCTTCTCTGGCTCCGGCTCCGGTACAGATTTCACCCTT
ACCATTAGCTCGTTGCAGCCAGAAGACTTTGCCACCTATTTCTGTTCTCAGACGACTCACGTCCCGTGGA
CCTTCGGACAGGGCACCAAGGTGGAGATCAAGAGCGGCGGAGGTGGGAGTGGAGGCGGCGGGTCCG
GAGGGGCGGTTCTGGCGGCGGTGGTTCTGGCGGAGGGTCTCTGCAGCTGCTACCCAGTTGGGCCATC
ACTCTCATTTCTGTCAACGGCATCTTCGTCATATGTTGCCTGACCTACTGCTTTGCTCCTAGGTGTCGTGA
GCGCCGCCGCAACGAGCGGTTGCGGCGTGAATCCGTGCGCCCTGTA (SEQ ID NO:316)

FIG. 51G

Tethered anti-CD40scFV (Lucatutuzumab)

MDWTWILFLVAAATRVRSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVI
SYEESNRYHADSVKGRFTISRDNSKITLYLQMNSLRTEDTAVYYCARDGGIAAPGPDYWGQGTLVTVSSGGG
GSGGGGSGGGGSGGGGSDIVMTQSPLSLTVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPQVLISL
GSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQARQTPFTFGPGTKVDIRSGGGGSGGGGSGGG
GSGGGGSGGGSLQLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:317)

Tethered anti-CD40scFV (Lucatutuzumab)

ATGGACTGGACCTGGATCCTGTTCCTGGTCGCAGCGGCCACCCGCGTACATTCTCAGGTGCAGCTGGTG
GAATCCGGGGGTGGCCTGGTGCAACCAGGCCGTAGCCTGCGCCTGAGCTGTGCTGCGTCCGGCTTTAC
TTTTTCGTCTTACGGCATGCACTGGGTGCGCCAGGCCCCGGGTAAAGGCTTGGAGTGGGTCGCGGTTAT
CACCTATGAGGAGAGCAACCGCTACCACGCGGACTCCGTGAAGGGCCGATTCACCATCTCGCGGGACA
ACTCCAAGATAACCCTGTACCTGCAGATGAACTCTCTGCGGACTGAAGACACCGCCGTGTACTACTGTGC
CCGCGATGGCGGAATCGCCGCTCCCGGGCCCGACTATTGGGGCCAGGGCACACTCGTTACCGTCTCCTC
GGGAGGCGGCGGCAGTGGTGGTGGAGGTTCCGGCGGCGGGGGCTCCGGGGGTGGCGGCTCTGACAT
CGTGATGACGCAGAGCCCTTTGAGCCTAACAGTTACCCCCGGGGAGCCCGCTTCGATTTCATGCCGCTCC
TCCCAGAGCCTGCTGTACTCAAATGGCTACAACTACCTGGACTGGTACCTCCAGAAGCCGGGTCAGTCCC
CTCAGGTGCTCATCTCGTTGGGCAGCAACAGGGCCTCTGGCGTGCCAGACCGCTTCTCCGGATCTGGCA
GCGGAACCGATTTCACCCTGAAGATCTCTAGAGTGGAGGCTGAGGACGTGGGCGTGTATTACTGTATGC
AGCCCCGACAGACTCCCTTCACCTTCGGCCCCGGGACCAAGGTGGATATCCGCTCGGGAGGCGGCGGC
AGCGGTGGGGGAGGCAGCGGTGGTGGCGGATCCGGGGGGGGCGGCTCTGGTGGCGGATCCCTCCAG
CTGCTGCCGAGTTGGGCTATCACTCTTATTTCCGTAAATGGGATTTTCGTCATCTGCTGCCTTACCTACTG
CTTTGCACCTAGATGTCGCGAGCGTAGGCGCAACGAGCGGCTTCGTCGCGAGTCCGTCCGCCCTGTC
(SEQ ID NO:318)

FIG. 51H

Tethered anti-CD40scFV (Selicrelumab)

MDWTWILFLVAAATRVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMG
WINPDSGGTNYAQKFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCARDQPLGYCTNGVCSYFDYWGQ
GTLVTVSSAAAGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVIITCRASQGIYSWLAWYQQKPG
KAPNLLIYTASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANIFPLTFGGGTKVEIKGGGGSGGG
GSGGGGSGGGSGGGSLQLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID
NO:319)

Tethered anti-CD40scFV (Selicrelumab)

ATGGATTGGACCTGGATCCTGTTCCTGGTGGCTGCTGCCACCCGTGTGCACAGCCAGGTGCAGCTGGTG
CAATCCGGCGCCGAGGTGAAGAAGCCCGGCGCCAGCGTGAAGGTATCGTGTAAGGCTTCGGGCTACAC
GTTCACCGGCTACTACATGCATTGGGTCCGCCAGGCCCCCGGACAGGGCCTGGAGTGGATGGGCTGGA
TTAACCCCGACTCCGGCGGCACCAACTACGCGCAGAAATTTCAGGGGCGAGTGACTATGACAAGGGAC
ACTTCCATCTCCACAGCCTACATGGAGCTCAACCGCCTGCGCAGCGATGACACCGCAGTGTACTATTGTG
CTCGCGACCAGCCTCTAGGTTACTGCACTAATGGCGTATGTAGCTATTTCGACTATTGGGGCCAGGGCAC
CCTGGTCACCGTGTCCAGCGGCGGAGGGGGCTCAGGCGGAGGTGGCTCAGGAGGTGGCGGCTCGGGG
GGCGGTGGGTCCGACATTCAGATGACCCAGTCCCCGAGCTCGGTCTCTGCTTCTGTGGGAGACCGCGTG
ACGATAACCTGCCGTGCCTCCCAGGGCATCTACAGTTGGCTTGCGTGGTACCAGCAGAAGCCAGGCAAG
GCGCCAAACCTGCTGATTTACACCGCATCCACTCTTCAGTCAGGCGTTCCTTCCCGCTTCAGTGGCTCTGG
TTCTGGCACCGATTTCACGCTGACCATCTCCTCCTTGCAGCCGGAAGACTTTGCCACTTACTACTGCCAAC
AGGCCAACATCTTCCCTCTGACCTTCGGCGGTGGCACCAAGGTGGAGATCAAAGGTGGCGGAGGGGGC
TCGGGCGGGGGTGGTTCTGGCGGCGGGGGAAGTGGTGGGGGCGGATCTGGTGGTGGTAGCCTGCAG
CTCTTGCCCTCCTGGGCGATCACCCTCATCAGCGTCAATGGCATCTTCGTCATCTGTTGCCTGACCTACTG
CTTTGCGCCGAGATGTCGAGAGCGCCGGCGCAACGAGCGCCTGCGTCGGGAGTCCGTGCGCCCCGTG
(SEQ ID NO:320)

FIG. 51I

CD40L

MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHEDFVFMKTIQRCNT
GERSLSLLNCEEIKSQFEGFVKDIMLNKEETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYT
MSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQ
QSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL (SEQ ID NO:273)

CD40L

ATGATCGAGACCTACAACCAGACTTCCCCACGTAGCGCCGCCACTGGTCTACCCATCTCGATGAAAATCT
TCATGTATCTGCTGACCGTGTTCCTGATCACCCAGATGATTGGCTCCGCTCTGTTTGCCGTGTACTTGCAC
CGCCGCCTGGACAAAATTGAGGACGAGCGGAATCTGCACGAAGATTTCGTATTTATGAAGACCATCCAG
AGGTGTAACACTGGCGAGCGTTCTCTTTCGTTGCTTAACTGCGAAGAGATCAAGAGCCAGTTCGAGGGC
TTCGTCAAGGACATCATGCTCAACAAGGAGGAGACTAAGAAGGAGAACTCCTTTGAGATGCAGAAGGG
TGATCAGAACCCCCAAATTGCAGCGCATGTGATAAGCGAGGCTTCCTCCAAGACAACCAGTGTGCTGCA
GTGGGCGGAGAAGGGCTACTACACCATGTCAAATAACCTGGTGACCCTGGAGAACGGCAAGCAGCTGA
CGGTGAAGCGCCAGGGGCTCTATTACATCTACGCGCAGGTCACGTTCTGTTCGAACCGCGAAGCCTCCT
CTCAGGCTCCCTTCATCGCCTCACTGTGCCTGAAATCTCCGGGACGCTTCGAGCGAATCCTGCTCCGCGC
CGCCAACACGCACTCCTCCGCCAAGCCTTGCGGGCAGCAGAGCATCCACCTTGGTGGGGTTTTTGAGCT
GCAGCCTGGCGCGTCCGTGTTCGTCAACGTGACCGACCCGTCCCAGGTCTCTCATGGAACCGGCTTCACC
TCCTTCGGCCTGCTCAAGTTG (SEQ ID NO:321)

FIG. 51J

Tethered CD40L/IL-15

MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHEDFVFMKTIQRCNT
GERSLSLLNCEEIKSQFEGFVKDIMLNKEETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYT
MSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQ
QSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL (SEQ ID NO:322)

Tethered CD40L/IL-15

ATGATCGAAACTTACAACCAGACGAGCCCGCGCTCCGCCGCCACCGGGCTGCCCATCTCTATGAAAATCT
TCATGTATCTGCTGACCGTGTTTCTGATCACCCAGATGATCGGTTCCGCGCTGTTTGCCGTGTACCTGCAC
CGCCGCCTGGACAAGATAGAAGACGAGCGCAACCTGCACGAAGATTTCGTCTTCATGAAGACCATCCAG
CGGTGTAATACCGGCGAGAGGAGCCTGAGCTTGCTCAACTGCGAGGAGATCAAAAGTCAGTTCGAGGG
CTTCGTTAAGGACATCATGCTCAACAAGGAGGAGACCAAGAAGGAGAACTCCTTCGAGATGCAAAAGG
GGGACCAGAACCCTCAGATCGCCGCGCATGTAATTTCCGAGGCCTCATCCAAGACGACTTCTGTCCTACA
GTGGGCAGAGAAGGCCTACTACACCATGTCTAATAACCTGGTCACCCTTGAGAACGGCAAGCAACTGAC
AGTGAAGCGCCAGGGCCTCTACTACATCTACGCGCAGGTGACCTTCTGCAGCAACCGCGAGGCTTCCTC
CCAAGCTCCCTTCATCGCATCTCTGTGCCTGAAAAGCCCTGGCCGCTTCGAGCGGATTCTCCTTCGTGCA
GCAAACACTCACTCGTCCGCCAAGCCCTGTGGACAGCAGAGCATCCACCTGGGCGGCGTGTTCGAGCTG
CAGCCAGGCGCCTCCGTGTTCGTCAATGTGACCGACCCGTCCCAGGTGTCCCATGGCACTGGCTTCACCT
CCTTCGGCCTCCTCAAACTGTCCGGCGGCGGTGGCAGTGGTGGCGGGGGATCAGGTGGCGGCGGCTCC
GGAGGTGGCGGGTCCGGGGGCAGGTTCTCTTCAGCTTCTGCCTAGCTGGGCGATCACCCTGATCTCCGTT
AATGGCATCTTCGTCATTTGTTGTTTGACCTATTGCTTTGCCCCGAGATGTCGAGAGCGTAGACGCAACG
AGCGCCTGCGCCGTGAAAGCGTGCGACCTGTGCGCGCTAAGCGCAGCGGCTCCGGCGCTACCAACTTCT
CATTACTCAAGCAGGCTGGACATGTAGAGGAGAATCCAGGGCCAATGGATTGGACCTGGATCCTGTTCC
TGGTGGCCGCCGCGACTCGCGTCCACAGTAATTGGGTCAACGTGATCTCTGACCTGAAAAAGATTGAGG
ACTTGATCCAGAGCATGCACATTGACGCTACCCTGTACACGGAGAGTGACGTGCACCCCTCGTGCAAGG
TGACAGCCATGAAGTGCTTTTTGCTGGAGTTGCAGGTCATCTCTCTAGAGAGCGGTGATGCCTCCATCCA
TGACACCGTGGAGAACCTTATCATCCTGGCCAACAACAGCCTGTCGAGCAACGGCAACGTGACCGAGTC
CGGGTGCAAGGAATGTGAGGAGCTGGAGGAGAAAAACATCAAGGAGTTCCTGCAGTCGTTTGTGCACA
TCGTGCAGATGTTTATTAACACCTCTTCTGGCGGTGGGGGATCGGGGGGGGGCGGCTCCGGCGGTGGC
GGTTCTGGAGGCGGTGGTTCTGGCGGGGGATCTTTACAGCTGCTGCCCAGTTGGGCGATCACTCTCATT
TCCGTGAACGGCATTTTCGTCATTTGCTGTTTGACCTACTGCTTTGCTCCGAGGTGTCGCGAGCGTCGCC
GCAACGAGCGCCTACGGCGGGAATCGGTGAGGCCCGTG (SEQ ID NO:323)

FIG. 52A

Signal Sequence: MDWTWILFLVAAATKVHS (SEQ ID NO:252)
Signal Sequence: MYRMQLLSCIALSLALVTNS (SEQ ID NO:254)
Linker (L1): SGGGSGGGSGGGSGGGSGGGSLQ (SEQ ID NO:246)
Anchor (Ar2): (human B7.1 transmembrane-intracellular amino acid sequence)
LLPSWAITLISVNGIFVICCLTYCFAPRCRERRNERLRRESVRPV (SEQ ID NO:239)
FurinA-P2A sequence: RAKRSGSGATNFSLLKQAGDVEENPGP (SEQ ID NO:251)
)

Tethered IL-2

MYRMQLLSCIALSLALVTNSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE
ELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
SGGGSGGGSGGGSGGGSGGGSLQLLPSWAITLISVNGIFVICCLTYCFAPRCRERRNERLRRESVRPV (SEQ ID NO:324)

Tethered IL-2

ATGTATCGGATGCAGCTGCTGTCTTGTATTGCTCTATCACTGGCGCTGGTGACCAACTCCGCTCCTACTTCCAGCTC
GACCAAGAAGACCCAGCTCCAACTTGAGCACCTGCTGCTTGATCTTCAGATGATCCTGAACGGCATCAACAACTAC
AAAAACCCCAAGCTGACCCGCATGCTCACTTTCAAGTTCTACATGCCTAAAAAGGCCACCGAGCTCAAGCACTTGC
AGTGCCTGGAGGAGGAGTTGAAGCCGTTGGAAGAGGTGCTCAACCTGGCCCAGTCCAAGAATTTCCATCTAAGAC
CCCGCGACCTGATCTCTAACATCAACGTGATTGTACTGGAGCTGAAGGGCTCCGAGACCACCTTCATGTGCGAGTA
CGCGGACGAGACTGCAACCATCGTGGACTTCCTGAACCGCTGGATCACCTTCTGTCAGAGCATCATCTCGACCCTT
ACATCTGGCGGCGGGGGGTCGGGCGGTGGGGGCTCTGGAGGAGGCGGTAGTGGGGGTGGCGGCTCCGGTGGA
GGCAGCCTGCAGCTGCTCCCAAGTTGGGCCATCACCCTGATTAGCGTCAATGGCATCTTCGTCATATGTTGTCTGA
CCTACTGCTTTGCCCCCCGCTGCCGAGAACGTCGCCGCAACGAGCGGCTGCGCAGGGAGTCCGTGCGCCCGGTGT
GA(SEQ ID NO:325)

FIG. 52B

Tethered IL-12

MGWSWILFLVAAATGVHSIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF
GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGS
SDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQL
KPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEW
ASVPCSGGGGGGSRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPL
ELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELM
QALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNASGGGGSGGGGSGGGGSGGGGSGGGGSLQ
LLPSWAITLISVNGIFVICCLTYCFAPRCRERRSERLRRESVRPV (SEQ ID NO:326)

Tethered IL-12

ATGTATCGGATGCAGCTGCTGTCTTGTATTGCTCTATCACTGGCGCTGGTGACCAACTCCGCTCCTACTTCCAGCTC
GACCAAGAAGACCCAGCTCCAACTTGAGCACCTGCTGCTTGATCTTCAGATGATCCTGAACGGCATCAACAACTAC
AAAAACCCCAAGCTGACCCGCATGCTCACTTTCAAGTTCTACATGCCTAAAAAGGCCACCGAGCTCAAGCACTTGC
AGTGCCTGGAGGAGGAGTTGAAGCCGTTGGAAGAGGTGCTCAACCTGGCCCAGTCCAAGAATTTCCATCTAAGAC
CCCGCGACCTGATCTCTAACATCAACGTGATTGTACTGGAGCTGAAGGGCTCCGAGACCACCTTCATGTGCGAGTA
CGCGGACGAGACTGCAACCATCGTGGAGTTCCTGAACCGCTGGATCACGTTCTGTCAGAGCATCATCTCGACCCTT
ACATCTGGCGGCCGGGGGGTCGGGCGGTGGGGGCTCTGGAGGAGGCGGTAGTGGGGGTGGCGGCTCCGGTGGA
GGCAGCCTGCAGCTGCTCCCAAGTTGGGCCATCACCCTGATTAGCGTCAATGGCATCTTCGTCATATGTTGTCTGA
CCTACTGCTTTGCCCCCCGCTGCCGAGAACGTCGCCGCAACGAGCGGCTGCGCAGGGAGTCCGTGCGCCCGGTGT
GA (SEQ ID NO:327)

FIG. 52C

Tethered IL-15

MDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDT
VENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGGGSGGGGSGGGGSGGGGSGGGSLQ
LLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:328)

Tethered IL-15

ATGGATTGGACCTGGATCCTGTTCCTGGTGGCTGCGGCCACCCGTGTACACAGCAACTGGGTCAATGTGATCTCCG
ACCTGAAGAAGATTGAGGACCTCATCCAGTCTATGCACATTGACGCAACACTTTACACCGAGAGCGATGTGCACCC
CTCTTGCAAGGTGACTGCCATGAAATGTTTCTTGCTCGAATTGCAGGTCATCTCTCTGGAGAGTGGGGACGCTTCC
ATACATGACACCGTGGAGAACCTGATCATCCTGGCCAACAACAGCCTCTCGTCAAATGGCAACGTGACTGAGAGC
GGGTGCAAAGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTCCTGCAGAGCTTCGTCCACATCGTGCA
GATGTTTATTAACACGTCGTCCGGAGGCGGGGGCTCTGGTGGCGGCGGCTCCGGGGGAGGCGGCTCCGGTGGC
GGTGGTTCCGGCGGAGGCTCGCTACAGCTGCTGCCCAGTTGGGCCATCACCCTTATTTCTGTCAACGGCATCTTCG
TTATCTGTTGCCTGACCTACTGCTTTGCGCCGAGGTGTCGCGAGCGGCGTCGCAACGAGCGCCTGCGCCGAGAAT
CCGTGCGCCCTGTGTGA (SEQ ID NO:329)

CD40L

MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHEDFVFMKTIQRCNTGERSLSLL
NCEEIKSQFEGFVKDIMLNKEETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQ
LTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFVNV
TDPSQVSHGTGFTSFGLLKL (SEQ ID NO:273)

CD40L

ATGATCGAGACCTACAACCAGACTTCCCCACGTAGCGCCGCCACTGGTCTACCCATCTCGATGAAAATCTTCATGTA
TCTGCTGACCGTGTTCCTGATCACCCAGATGATTGGCTCCGCTCTGTTTGCCGTGTACTTGCACCGCCGCCTGGACA
AAATTGAGGACGAGCGGAATCTGCACGAAGATTTCGTATTTATGAAGACCATCCAGAGGTGTAACACTGGCGAGC
GTTCTCTTTCGTTGCTTAACTGCGAAGAGATCAAGAGCCAGTTCGAGGGCTTCGTCAAGGACATCATGCTCAACAA
GGAGGAGACTAAGAAGGAGAACTCCTTTGAGATGCAGAAGGGTGATCAGAACCCCCAAATTGCAGCGCATGTGA
TAAGCGAGGCTTCCTCCAAGACAACCAGTGTGCTGCAGTGGGCGGAGAAGGGCTACTACACCATGTCAAATAACC
TGGTGACCCTGGAGAACGGCAAGCAGCTGACGGTGAAGCGCCAGGGGCTCTATTACATCTACGCGCAGGTCACG
TTCTGTTCGAACCGCGAAGCCTCCTCTCAGGCTCCCTTCATCGCCTCACTGTGCCTGAAATCTCCGGGACGCTTCGA
GCGAATCCTGCTCCGCGCCGCCAACACGCACTCCTCCGCCAAGCCTTGCGGGCAGCAGAGCATCCACCTTGGTGG
GGTTTTTGAGCTGCAGCCTGGCGCGTCCGTGTTCGTCAACGTGACCGACCCGTCCCAGGTCTCTCATGGAACCGGC
TTCACCTCCTTCGGCCTGCTCAAGTTG (SEQ ID NO:321)

FIG. 52D

GFP

ATGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCA
CAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCAC
CGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCC
GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCA
AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTG
AAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGT
CTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCA
GCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACT
ACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGA
CCGCCGCCGGGATCACTCACGGCATGGACGAGCTGTACAAGTGA (SEQ ID NO:330)

Tethered IL-21

MDWTWILFLVAAATRVHSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQK
AQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRT
HGSEDSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSLQLLPSWAITLISVNGIFVICC
LTYCFAPRCRERRRNERLRRESVRPV (SEQ ID NO:331)

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2023/065404

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K35/17 C12N5/0783
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K C12N

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2021/123832 A1 (INSTIL BIO UK LTD [GB]) 24 June 2021 (2021-06-24) claim 42 claim 87 -----	1-305, 308-329
X	US 2021/274776 A1 (VEERAPATHRAN ANAND [US] ET AL) 9 September 2021 (2021-09-09) paragraphs [0006], [0457]; figure 1 paragraph [0018] -----	1-305, 308-329
X	WO 2018/182817 A1 (IOVANCE BIOTHERAPEUTICS INC [US]; WARDELL SETH [US] ET AL.) 4 October 2018 (2018-10-04) cited in the application claim 1 paragraph [0323] paragraph [0071] ----- -/--	1-305, 308-329

[x] Further documents are listed in the continuation of Box C.

[x] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance;; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance;; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
6 July 2023	15/09/2023

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Lanzrein, Markus

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Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2023/065404

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

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

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

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

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

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

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

see additional sheet

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

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

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

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims;; it is covered by claims Nos.:

1-305(completely); 308-329(partially)

Remark on Protest

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

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

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2023/065404

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 3 034 092 A1 (UNIVERSITÉ DE LAUSANNE [CH]) 22 June 2016 (2016-06-22) paragraph [0001] paragraph [0034] -----	1-305, 308-329

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Form PCT/ISA/210 (continuation of second sheet) (April 2005)

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International application No
PCT/US2023/065404

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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-305(completely); 308-329(partially)

A method of making a cryopreserved population of TILs from a NSCLC patient, wherein the patient is naive to a cancer treatment or in maintenance therapy, the method comprising:
(a) obtaining and/or receiving a first population of TILs from a tumor resected from the subject of patient by processing a tumor sample obtained from the subject into multiple tumor fragments or a tumor digest;
(b) cryopreserving the tumor fragments or tumor digest comprising the first population of TILs from step (a) to produce cryopreserved tumor fragments or tumor digest;
optionally expanding the TILs into a therapeutic population of TILs.

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2. claims: 306, 307(completely); 308-329(partially)

A method of treating a cancer patient by administering a population of tumor infiltrating lymphocytes (TILs) to the cancer patient in need thereof, wherein the cancer patient has received at least one prior therapy and has exhibited cancer progression on or after the at least one prior therapy, wherein obtaining the population of the TILs comprises multilesional sampling, wherein the population of TILs was made from a tumor sample harvested before the cancer patient receives the at least one prior therapy; and wherein the population of TILs is administered to the subject or patient after the cancer patient has exhibited cancer progression on or after the at least one prior therapy.