TREATMENT OF ENDOMETRIAL CANCERS WITH TUMOR INFILTRATING LYMPHOCYTE THERAPIES

I. CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 63/596,588, filed November 6, 2023, and U.S. Provisional Application No. 63/694,763, filed September 13, 2024, and U.S. Provisional Application No. 63/699,700, filed September 26, 2024, the disclosures of which are herein incorporated by reference in their entireties.

II. SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML file format and is hereby incorporated by reference in its entirety. Said XML file, created on November 4, 2024, is named 116983-5130-WO_Sequence_Listing.XML and is 311,296 bytes in size.

III. BACKGROUND OF THE INVENTION

[0003] Treatment of endometrial cancer remains challenging, particularly for patients that do not respond to commonly-used initial lines of therapy, including nivolumab monotherapy, pembrolizumab monotherapy, therapy using a combination of nivolumab and ipilimumab, ipilimumab monotherapy, and various combinations of the foregoing and other immunotherapies and chemotherapy regimens. Adoptive cell therapy using autologous tumor-infiltrating lymphocytes (TIL) has shown durable responses in a subset of patients with metastatic melanoma (Sarnaik AA et al., *J Clin Oncol* 2021), cervical carcinoma (Jazaeri AA et al., ASCO 2019 #182), non-small-cell lung cancer, and other epithelial malignancies.

[0004] It is understood that overexpression of different cytokines can modify the tumor microenvironment, that can further promote survival, activity and/or longevity of administered TILs. For example, overexpression of IL-15 can improve homeostatic maintenance of long-lived CD8+ memory T-cells, inhibits AICD and reverses T-cell energy. Similarly, overexpression of IL-18 induces production of IFNγ and acute Th1 response. Likewise, overexpression of IL21 supports T-cell survival in absence of IL-2, favoring CM/EM phenotype and decreasing PD1 expression. Additionally, constitutive co-expression of IL-15 and IL-21 may support high expansion levels in in vivo (and probably in vitro), upon administration of the TILs, and should restrict signaling to TILs and allow them to persist, decrease toxicity. The decrease in toxicity may, for example, enable adoptive cell therapy without nonmyeloablative lymphodepletion.

IV. BRIEF SUMMARY OF THE INVENTION

[0005] In an embodiment, the invention provides methods and compositions for the treatment of endometrial cancer using tumor infiltrating lymphocyte therapies. In an embodiment, the invention provides methods and compositions for the treatment of uterine cancer using tumor infiltrating lymphocyte therapies.

[0006] In an embodiment, the invention provides methods and compositions for the treatment of endometrial cancer using tumor infiltrating lymphocyte therapies, wherein the endometrial cancer is resected and processed to prepare tumor infiltrating lymphocytes.

[0007] Embodiments disclosed herein provide a method of treating a subject with endometrial cancer, the method comprising administering expanded tumor infiltrating lymphocytes (TILs) comprising:

(a) adding a tumor digest or tumor fragments from an endometrial cancer into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from the subject;
(b) 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 (b) to step (c) occurs without opening the system;
(c) performing a second expansion by supplementing additional cell culture medium comprising 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 (b) to step (c) occurs without opening the system;
(d) harvesting the third population of TILs obtained from step (c), wherein the transition from step (c) to step (d) occurs without opening the system;
(e) transferring the harvested third TIL population from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system;
(f) cryopreserving the infusion bag comprising the harvested TIL population from step (e) using a cryopreservation process; and
(g) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (f) to the subject.

[0008] In some embodiments, the endometrial cancer is metastatic or unresectable. In some embodiments, the subject was refractory to or progressed following prior treatment with a PD-1 or

PD-L1 inhibitor. In some embodiments, the subject was refractory to or progressed following prior treatment with chemotherapy. In some embodiments, the chemotherapy is a platinum chemotherapy and a taxane. In some embodiments, the platinum chemotherapy is selected from the group consisting of cisplatin, carboplatin, and oxaliplatin. In some embodiments, the taxane is selected from the group consisting of paclitaxel, albumin-bound paclitaxel, and docetaxel. In some embodiments, the endometrial cancer is microsatellite instability high (MSI-H). In some embodiments, the endometrial cancer is mismatch repair deficient (dMMR). In some embodiments, the endometrial cancer is microsatellite stable (MSS). In some embodiments, the endometrial cancer is mismatch repair proficient (pMMR). In some embodiments, the subject is treatment naïve. In some embodiments, the method comprises the additional step of administering a therapeutically effective dosage of a PD-1 or PD-L1 inhibitor. In some embodiments, the anti-PD-1 or anti-PD-L1 antibody is selected from the group consisting of dostarlimab, nivolumab, pembrolizumab, JS001, TSR-042, pidilizumab, BGB-A317, SHR-1210, REGN2810, MDX-1106, PDR001, anti-PD-l from clone: RMP1-14, an anti-PD-l 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 method further comprises the step of treating the subject with a non-myeloablative lymphodepletion regimen prior to administering the therapeutic population of TILs to the subject. 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. In some embodiments, the method further comprises the step of treating the subject with an IL-2 regimen starting on the day after administration of the therapeutic population of TILs to the subject. In some embodiments, 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.

[0009] In some embodiments, the first expansion is performed over a period of 12 days or less. In some embodiments, the second expansion is performed over a period of 12 days or less. In some embodiments, steps (a) through (d) are performed in about 10 days to about 22 days. In some embodiments, steps (a) through (d) are performed in about 15 days to about 22 days. In some embodiments, steps (a) through (d) are performed in about 20 days to about 22 days. 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. 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 cell culture medium. 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.

[0010] Some embodiments disclosed herein provide a method of expanding tumor infiltrating lymphocytes (TILs) comprising:

(a) adding a tumor digest or tumor fragments from an endometrial cancer into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from a subject;
(b) 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 (b) to step (c) occurs without opening the system;
(c) performing a second expansion by supplementing additional cell culture medium comprising 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 (b) to step (c) occurs without opening the system;
(d) harvesting the third population of TILs obtained from step (c), wherein the transition from step (c) to step (d) occurs without opening the system;
(e) transferring the harvested third TIL population from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system; and
(f) cryopreserving the infusion bag comprising the harvested TIL population from step (e) using a cryopreservation process.

[0011] In some embodiments, the tumor digest in step (a) was prepared by incubating a sample of the tumor that was resected from the subject in an enzymatic media. In some embodiments, the method further comprises disrupting the tumor sample mechanically so as to dissociate the tumor sample. In some embodiments, the method further comprises purifying the disassociated tumor sample using a density gradient separation. In some embodiments, the enzymatic media comprises DNase. In some embodiments, the enzymatic media comprises 30 units/mL of DNase. In some embodiments, the enzymatic media comprises collagenase. In some embodiments, the enzymatic media comprises 1.0 mg/mL of collagenase. In some embodiments, the medium in the first expansion and/or the second expansion is free of human serum.

[0012] In some embodiments, the first expansion is performed over a period of 12 days or less. In some embodiments, the second expansion is performed over a period of 12 days or less. In some embodiments, steps (a) through (d) are performed in about 10 days to about 22 days. In some embodiments, steps (a) through (d) are performed in about 15 days to about 22 days. In some

embodiments, steps (a) through (d) are performed in about 20 days to about 22 days. 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. 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 cell culture medium. 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. In some embodiments, the APCs are peripheral blood mononuclear cells (PBMCs). In some embodiments, the PBMCs are supplemented at a ratio of about 1:25 TIL:PBMCs.

[0013] Some embodiments disclosed herein provide a cryopreserved therapeutic population of tumor infiltrating lymphocytes (TILs) produced by a method comprising:

(a) adding a tumor digest or tumor fragments into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from a subject having endometrial cancer;

(b) 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 a first period of about 3 to 11 days to obtain the second population of TILs, and wherein the transition from step (a) to step (b) occurs without opening the system;

(c) performing a second expansion by supplementing the cell culture medium 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 a second period of about 7 to 11 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 (b) to step (c) occurs without opening the system;

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

(e) transferring the harvested therapeutic population of TILs from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system; and

(f) cryopreserving the infusion bag comprising the harvested therapeutic population of TILs from step (e) using a cryopreservation process.

[0014] In some embodiments, the tumor digest in step (a) was prepared by incubating a sample of the tumor that was resected from the subject in an enzymatic media. In some embodiments, the method further comprises disrupting the tumor sample mechanically so as to dissociate the tumor sample. In some embodiments, the method further comprises purifying the disassociated tumor sample using a density gradient separation. In some embodiments, the enzymatic media comprises DNase. In some embodiments, the enzymatic media comprises 30 units/mL of DNase. In some embodiments, the enzymatic media comprises collagenase. In some embodiments, the enzymatic media comprises 1.0 mg/mL of collagenase. In some embodiments, the medium in the first expansion and/or the second expansion is free of human serum.

[0015] In some embodiments, the therapeutic population of TILs harvested in step (d) comprises sufficient TILs for use in administering a therapeutically effective dosage to a subject. In some embodiments, the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^9 to about 5×10^9. In some embodiments, the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^9 to about 9×10^{10}. In some embodiments, the number of TILs sufficient for administering a therapeutically effective dosage is from about 5×10^9 to about 1×10^{10}. In some embodiments, the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^{10} to about 5×10^{10}. the therapeutic population of TILs harvested in step (d) exhibits an increased subpopulation of CD8+ cells relative to the first and/or second population of TILs

[0016] In some embodiments, the first expansion is performed over a period of 12 days or less. In some embodiments, the second expansion is performed over a period of 12 days or less. In some embodiments, steps (a) through (d) are performed in about 10 days to about 22 days. In some embodiments, steps (a) through (d) are performed in about 15 days to about 22 days. In some embodiments, steps (a) through (d) are performed in about 20 days to about 22 days. 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. 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 cell culture medium. 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. In some embodiments, the APCs are peripheral blood mononuclear cells (PBMCs). In some embodiments, the PBMCs are supplemented at a ratio of about 1:25 TIL:PBMCs. In some embodiments, the tumor digest is a cryopreserved tumor digest.

V. BRIEF DESCRIPTION OF THE DRAWINGS

[0017] Figure 1: Exemplary Gen 2 (process 2A) chart providing an overview of Steps A through F.

[0018] Figures 2A-2C: Process flow chart of an embodiment of Gen 2 (process 2A) for TIL manufacturing.

[0019] Figure 3: Shows a diagram of an embodiment of a cryopreserved TIL exemplary manufacturing process (~22 days).

[0020] Figure 4: Shows a diagram of an embodiment of Gen 2 (process 2A), a 22-day process for TIL manufacturing.

[0021] Figure 5: Comparison table of Steps A through F from exemplary embodiments of process 1C and Gen 2 (process 2A) for TIL manufacturing.

[0022] Figure 6: Detailed comparison of an embodiment of process 1C and an embodiment of Gen 2 (process 2A) for TIL manufacturing.

[0023] Figure 7: 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.

[0024] Figures 8A-8B: A) shows an example of structure and synthesis of lipid click molecule having a BCN group. B) shows an example of structure and synthesis of an anchoring molecule having a PEG-azide molecule tagged thereto.

[0025] Figures 9A-9B: Phenotype of endometrial TIL.

[0026] Figures 10A-10C: NeoTCR8 analysis of endometrial TIL.

[0027] Figures 11A-11B: Enhanced TIL cell activation after co-culture with autologous tumor digest.

[0028] Figures 12A-12B: Increased cytokine production after co-culture with autologous tumor digest.

[0029] Figure 13: TIL-mediated autologous anti-tumor killing using MOS. Abbreviations: ANOVA, analysis of variance; MOS, micro-organospheres; NIR, near-infrared spectroscopy. ****, $p<0.0001$.

[0030] Figure 14: Study diagram of a Phase 2, open-label, single-arm, multicenter study of the lifileucel regimen in participants with advanced endometrial cancer. Abbreviations: CY = cyclophosphamide; EOA = end of assessment; EOS = end of study; EOT = end of treatment; FLU = fludarabine; IL=2 = interleukin-2; NMA-LD = nonmyeloablative lymphodepletion; Q3M = every 3 months; Q6W = every 6 weeks.

VI. BRIEF DESCRIPTION OF THE SEQUENCE LISTING

[0031] SEQ ID NO:1 is the amino acid sequence of the heavy chain of muromonab.

[0032] SEQ ID NO:2 is the amino acid sequence of the light chain of muromonab.

[0033] SEQ ID NO:3 is the amino acid sequence of a recombinant human IL-2 protein.

[0034] SEQ ID NO:4 is the amino acid sequence of aldesleukin.

[0035] SEQ ID NO:5 is an IL-2 form.

[0036] SEQ ID NO:6 is the amino acid sequence of nemvaleukin alfa.

[0037] SEQ ID NO:7 is an IL-2 form.

[0038] SEQ ID NO:8 is a mucin domain polypeptide.

[0039] SEQ ID NO:9 is the amino acid sequence of a recombinant human IL-4 protein.

[0040] SEQ ID NO:10 is the amino acid sequence of a recombinant human IL-7 protein.

[0041] SEQ ID NO:11 is the amino acid sequence of a recombinant human IL-15 protein.

[0042] SEQ ID NO:12 is the amino acid sequence of a recombinant human IL-21 protein.

[0043] SEQ ID NO:13 is an IL-2 sequence.

[0044] SEQ ID NO:14 is an IL-2 mutein sequence.

[0045] SEQ ID NO:15 is an IL-2 mutein sequence.

[0046] SEQ ID NO:16 is the HCDR1_IL-2 for IgG.IL2R67A.H1.

[0047] SEQ ID NO:17 is the HCDR2 for IgG.IL2R67A.H1.

[0048] SEQ ID NO:18 is the HCDR3 for IgG.IL2R67A.H1.

[0049] SEQ ID NO:19 is the HCDR1_IL-2 kabat for IgG.IL2R67A.H1.

[0050] SEQ ID NO:20 is the HCDR2 kabat for IgG.IL2R67A.H1.

[0051] SEQ ID NO:21 is the HCDR3 kabat for IgG.IL2R67A.H1.

[0052] SEQ ID NO:22 is the HCDR1_IL-2 clothia for IgG.IL2R67A.H1.

[0053] SEQ ID NO:23 is the HCDR2 clothia for IgG.IL2R67A.H1.

[0054] SEQ ID NO:24 is the HCDR3 clothia for IgG.IL2R67A.H1.

[0055] SEQ ID NO:25 is the HCDR1_IL-2 IMGT for IgG.IL2R67A.H1.

[0056] SEQ ID NO:26 is the HCDR2 IMGT for IgG.IL2R67A.H1.

[0057] SEQ ID NO:27 is the HCDR3 IMGT for IgG.IL2R67A.H1.

[0058] SEQ ID NO:28 is the VH chain for IgG.IL2R67A.H1.

[0059] SEQ ID NO:29 is the heavy chain for IgG.IL2R67A.H1.

[0060] SEQ ID NO:30 is the LCDR1 kabat for IgG.IL2R67A.H1.

[0061] SEQ ID NO:31 is the LCDR2 kabat for IgG.IL2R67A.H1.

[0062] SEQ ID NO:32 is the LCDR3 kabat for IgG.IL2R67A.H1.

[0063] SEQ ID NO:33 is the LCDR1 chothia for IgG.IL2R67A.H1.

[0064] SEQ ID NO:34 is the LCDR2 chothia for IgG.IL2R67A.H1.

[0065] SEQ ID NO:35 is the LCDR3 chothia for IgG.IL2R67A.H1.

[0066] SEQ ID NO:36 is a VL chain.

[0067] SEQ ID NO:37 is a light chain.

[0068] SEQ ID NO:38 is a light chain.

[0069] SEQ ID NO:39 is a light chain.

[0070] SEQ ID NO:40 is the amino acid sequence of human 4-1BB.

[0071] SEQ ID NO:41 is the amino acid sequence of murine 4-1BB.

[0072] SEQ ID NO:42 is the heavy chain for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0073] SEQ ID NO:43 is the light chain for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0074] SEQ ID NO:44 is the heavy chain variable region (VH) for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0075] SEQ ID NO:45 is the light chain variable region (VL) for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0076] SEQ ID NO:46 is the heavy chain CDR1 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0077] SEQ ID NO:47 is the heavy chain CDR2 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0078] SEQ ID NO:48 is the heavy chain CDR3 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0079] SEQ ID NO:49 is the light chain CDR1 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0080] SEQ ID NO:50 is the light chain CDR2 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0081] SEQ ID NO:51 is the light chain CDR3 for the 4-1BB agonist monoclonal antibody utomilumab (PF-05082566).

[0082] SEQ ID NO:52 is the heavy chain for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0083] SEQ ID NO:53 is the light chain for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0084] SEQ ID NO:54 is the heavy chain variable region (VH) for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0085] SEQ ID NO:55 is the light chain variable region (VL) for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0086] SEQ ID NO:56 is the heavy chain CDR1 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0087] SEQ ID NO:57 is the heavy chain CDR2 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0088] SEQ ID NO:58 is the heavy chain CDR3 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0089] SEQ ID NO:59 is the light chain CDR1 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0090] SEQ ID NO:60 is the light chain CDR2 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0091] SEQ ID NO:61 is the light chain CDR3 for the 4-1BB agonist monoclonal antibody urelumab (BMS-663513).

[0092] SEQ ID NO:62 is an Fc domain for a TNFRSF agonist fusion protein.

[0093] SEQ ID NO:63 is a linker for a TNFRSF agonist fusion protein.

[0094] SEQ ID NO:64 is a linker for a TNFRSF agonist fusion protein.

[0095] SEQ ID NO:65 is a linker for a TNFRSF agonist fusion protein.

[0096] SEQ ID NO:66 is a linker for a TNFRSF agonist fusion protein.

[0097] SEQ ID NO:67 is a linker for a TNFRSF agonist fusion protein.

[0098] SEQ ID NO:68 is a linker for a TNFRSF agonist fusion protein.

[0099] SEQ ID NO:69 is a linker for a TNFRSF agonist fusion protein.

[00100] SEQ ID NO:70 is a linker for a TNFRSF agonist fusion protein.

[00101] SEQ ID NO:71 is a linker for a TNFRSF agonist fusion protein.

[00102] SEQ ID NO:72 is a linker for a TNFRSF agonist fusion protein.

[00103] SEQ ID NO:73 is an Fc domain for a TNFRSF agonist fusion protein.

[00104] SEQ ID NO:74 is a linker for a TNFRSF agonist fusion protein.

[00105] SEQ ID NO:75 is a linker for a TNFRSF agonist fusion protein.

[00106] SEQ ID NO:76 is a linker for a TNFRSF agonist fusion protein.

[00107] SEQ ID NO:77 is a 4-1BB ligand (4-1BBL) amino acid sequence.

[00108] SEQ ID NO:78 is a soluble portion of 4-1BBL polypeptide.

[00109] SEQ ID NO:79 is a heavy chain variable region (VH) for the 4-1BB agonist antibody 4B4-1-1 version 1.

[00110] SEQ ID NO:80 is a light chain variable region (VL) for the 4-1BB agonist antibody 4B4-1-1 version 1.

[00111] SEQ ID NO:81 is a heavy chain variable region (VH) for the 4-1BB agonist antibody 4B4-1-1 version 2.

[00112] SEQ ID NO:82 is a light chain variable region (VL) for the 4-1BB agonist antibody 4B4-1-1 version 2.

[00113] SEQ ID NO:83 is a heavy chain variable region (VH) for the 4-1BB agonist antibody H39E3-2.

[00114] SEQ ID NO:84 is a light chain variable region (VL) for the 4-1BB agonist antibody H39E3-2.

[00115] SEQ ID NO:85 is the amino acid sequence of human OX40.

[00116] SEQ ID NO:86 is the amino acid sequence of murine OX40.

[00117] SEQ ID NO:87 is the heavy chain for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00118] SEQ ID NO:88 is the light chain for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00119] SEQ ID NO:89 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00120] SEQ ID NO:90 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00121] SEQ ID NO:91 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00122] SEQ ID NO:92 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00123] SEQ ID NO:93 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00124] SEQ ID NO:94 is the light chain CDR1 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00125] SEQ ID NO:95 is the light chain CDR2 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00126] SEQ ID NO:96 is the light chain CDR3 for the OX40 agonist monoclonal antibody tavolixizumab (MEDI-0562).

[00127] SEQ ID NO:97 is the heavy chain for the OX40 agonist monoclonal antibody 11D4.

[00128] SEQ ID NO:98 is the light chain for the OX40 agonist monoclonal antibody 11D4.

[00129] SEQ ID NO:99 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 11D4.

[00130] SEQ ID NO:100 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 11D4.

[00131] SEQ ID NO:101 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody 11D4.

[00132] SEQ ID NO:102 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody 11D4.

[00133] SEQ ID NO:103 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody 11D4.

[00134] SEQ ID NO:104 is the light chain CDR1 for the OX40 agonist monoclonal antibody 11D4.

[00135] SEQ ID NO:105 is the light chain CDR2 for the OX40 agonist monoclonal antibody 11D4.

[00136] SEQ ID NO:106 is the light chain CDR3 for the OX40 agonist monoclonal antibody 11D4.

[00137] SEQ ID NO:107 is the heavy chain for the OX40 agonist monoclonal antibody 18D8.

[00138] SEQ ID NO:108 is the light chain for the OX40 agonist monoclonal antibody 18D8.

[00139] SEQ ID NO:109 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 18D8.

[00140] SEQ ID NO:110 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 18D8.

[00141] SEQ ID NO:111 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody 18D8.

[00142] SEQ ID NO:112 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody 18D8.

[00143] SEQ ID NO:113 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody 18D8.

[00144] SEQ ID NO:114 is the light chain CDR1 for the OX40 agonist monoclonal antibody 18D8.

[00145] SEQ ID NO:115 is the light chain CDR2 for the OX40 agonist monoclonal antibody 18D8.

[00146] SEQ ID NO:116 is the light chain CDR3 for the OX40 agonist monoclonal antibody 18D8.

[00147] SEQ ID NO:117 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody Hu119-122.

[00148] SEQ ID NO:118 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody Hu119-122.

[00149] SEQ ID NO:119 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody Hu119-122.

[00150] SEQ ID NO:120 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody Hu119-122.

[00151] SEQ ID NO:121 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody Hu119-122.

[00152] SEQ ID NO:122 is the light chain CDR1 for the OX40 agonist monoclonal antibody Hu119-122.

[00153] SEQ ID NO:123 is the light chain CDR2 for the OX40 agonist monoclonal antibody Hu119-122.

[00154] SEQ ID NO:124 is the light chain CDR3 for the OX40 agonist monoclonal antibody Hu119-122.

[00155] SEQ ID NO:125 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody Hu106-222.

[00156] SEQ ID NO:126 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody Hu106-222.

[00157] SEQ ID NO:127 is the heavy chain CDR1 for the OX40 agonist monoclonal antibody Hu106-222.

[00158] SEQ ID NO:128 is the heavy chain CDR2 for the OX40 agonist monoclonal antibody Hu106-222.

[00159] SEQ ID NO:129 is the heavy chain CDR3 for the OX40 agonist monoclonal antibody Hu106-222.

[00160] SEQ ID NO:130 is the light chain CDR1 for the OX40 agonist monoclonal antibody Hu106-222.

[00161] SEQ ID NO:131 is the light chain CDR2 for the OX40 agonist monoclonal antibody Hu106-222.

[00162] SEQ ID NO:132 is the light chain CDR3 for the OX40 agonist monoclonal antibody Hu106-222.

[00163] SEQ ID NO:133 is an OX40 ligand (OX40L) amino acid sequence.

[00164] SEQ ID NO:134 is a soluble portion of OX40L polypeptide.

[00165] SEQ ID NO:135 is an alternative soluble portion of OX40L polypeptide.

[00166] SEQ ID NO:136 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 008.

[00167] SEQ ID NO:137 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 008.

[00168] SEQ ID NO:138 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 011.

[00169] SEQ ID NO:139 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 011.

[00170] SEQ ID NO:140 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 021.

[00171] SEQ ID NO:141 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 021.

[00172] SEQ ID NO:142 is the heavy chain variable region (VH) for the OX40 agonist monoclonal antibody 023.

[00173] SEQ ID NO:143 is the light chain variable region (VL) for the OX40 agonist monoclonal antibody 023.

[00174] SEQ ID NO:144 is the heavy chain variable region (VH) for an OX40 agonist monoclonal antibody.

[00175] SEQ ID NO:145 is the light chain variable region (VL) for an OX40 agonist monoclonal antibody.

[00176] SEQ ID NO:146 is the heavy chain variable region (VH) for an OX40 agonist monoclonal antibody.

[00177] SEQ ID NO:147 is the light chain variable region (VL) for an OX40 agonist monoclonal antibody.

[00178] SEQ ID NO:148 is the heavy chain variable region (VH) for a humanized OX40 agonist monoclonal antibody.

[00179] SEQ ID NO:149 is the heavy chain variable region (VH) for a humanized OX40 agonist monoclonal antibody.

[00180] SEQ ID NO:150 is the light chain variable region (VL) for a humanized OX40 agonist monoclonal antibody.

[00181] SEQ ID NO:151 is the light chain variable region (VL) for a humanized OX40 agonist monoclonal antibody.

[00182] SEQ ID NO:152 is the heavy chain variable region (VH) for a humanized OX40 agonist monoclonal antibody.

[00183] SEQ ID NO:153 is the heavy chain variable region (VH) for a humanized OX40 agonist monoclonal antibody.

[00184] SEQ ID NO:154 is the light chain variable region (VL) for a humanized OX40 agonist monoclonal antibody.

[00185] SEQ ID NO:155 is the light chain variable region (VL) for a humanized OX40 agonist monoclonal antibody.

[00186] SEQ ID NO:156 is the heavy chain variable region (VH) for an OX40 agonist monoclonal antibody.

[00187] SEQ ID NO:157 is the light chain variable region (VL) for an OX40 agonist monoclonal antibody.

[00188] SEQ ID NO:158 is the heavy chain amino acid sequence of the PD-1 inhibitor nivolumab.

[00189] SEQ ID NO:159 is the light chain amino acid sequence of the PD-1 inhibitor nivolumab.

[00190] SEQ ID NO:160 is the heavy chain variable region (VH) amino acid sequence of the PD-1 inhibitor nivolumab.

[00191] SEQ ID NO:161 is the light chain variable region (VL) amino acid sequence of the PD-1 inhibitor nivolumab.

[00192] SEQ ID NO:162 is the heavy chain CDR1 amino acid sequence of the PD-1 inhibitor nivolumab.

[00193] SEQ ID NO:163 is the heavy chain CDR2 amino acid sequence of the PD-1 inhibitor nivolumab.

[00194] SEQ ID NO:164 is the heavy chain CDR3 amino acid sequence of the PD-1 inhibitor nivolumab.

[00195] SEQ ID NO:165 is the light chain CDR1 amino acid sequence of the PD-1 inhibitor nivolumab.

[00196] SEQ ID NO:166 is the light chain CDR2 amino acid sequence of the PD-1 inhibitor nivolumab.

[00197] SEQ ID NO:167 is the light chain CDR3 amino acid sequence of the PD-1 inhibitor nivolumab.

[00198] SEQ ID NO:168 is the heavy chain amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00199] SEQ ID NO:169 is the light chain amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00200] SEQ ID NO:170 is the heavy chain variable region (VH) amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00201] SEQ ID NO:171 is the light chain variable region (VL) amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00202] SEQ ID NO:172 is the heavy chain CDR1 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00203] SEQ ID NO:173 is the heavy chain CDR2 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00204] SEQ ID NO:174 is the heavy chain CDR3 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00205] SEQ ID NO:175 is the light chain CDR1 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00206] SEQ ID NO:176 is the light chain CDR2 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00207] SEQ ID NO:177 is the light chain CDR3 amino acid sequence of the PD-1 inhibitor pembrolizumab.

[00208] SEQ ID NO:178 is the heavy chain amino acid sequence of the PD-L1 inhibitor durvalumab.

[00209] SEQ ID NO:179 is the light chain amino acid sequence of the PD-L1 inhibitor durvalumab.

[00210] SEQ ID NO:180 is the heavy chain variable region (VH) amino acid sequence of the PD-L1 inhibitor durvalumab.

[00211] SEQ ID NO:181 is the light chain variable region (VL) amino acid sequence of the PD-L1 inhibitor durvalumab.

[00212] SEQ ID NO:182 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00213] SEQ ID NO:183 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00214] SEQ ID NO:184 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00215] SEQ ID NO:185 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00216] SEQ ID NO:186 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00217] SEQ ID NO:187 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor durvalumab.

[00218] SEQ ID NO:188 is the heavy chain amino acid sequence of the PD-L1 inhibitor avelumab.

[00219] SEQ ID NO:189 is the light chain amino acid sequence of the PD-L1 inhibitor avelumab.

[00220] SEQ ID NO:190 is the heavy chain variable region (VH) amino acid sequence of the PD-L1 inhibitor avelumab.

[00221] SEQ ID NO:191 is the light chain variable region (VL) amino acid sequence of the PD-L1 inhibitor avelumab.

[00222] SEQ ID NO:192 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor avelumab.

[00223] SEQ ID NO:193 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor avelumab.

[00224] SEQ ID NO:194 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor avelumab.

[00225] SEQ ID NO:195 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor avelumab.

[00226] SEQ ID NO:196 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor avelumab.

[00227] SEQ ID NO:197 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor avelumab.

[00228] SEQ ID NO:198 is the heavy chain amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00229] SEQ ID NO:199 is the light chain amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00230] SEQ ID NO:200 is the heavy chain variable region (VH) amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00231] SEQ ID NO:201 is the light chain variable region (VL) amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00232] SEQ ID NO:202 is the heavy chain CDR1 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00233] SEQ ID NO:203 is the heavy chain CDR2 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00234] SEQ ID NO:204 is the heavy chain CDR3 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00235] SEQ ID NO:205 is the light chain CDR1 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00236] SEQ ID NO:206 is the light chain CDR2 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00237] SEQ ID NO:207 is the light chain CDR3 amino acid sequence of the PD-L1 inhibitor atezolizumab.

[00238] SEQ ID NO:208 is the heavy chain amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00239] SEQ ID NO:209 is the light chain amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00240] SEQ ID NO:210 is the heavy chain variable region (VH) amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00241] SEQ ID NO:211 is the light chain variable region (VL) amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00242] SEQ ID NO:212 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00243] SEQ ID NO:213 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00244] SEQ ID NO:214 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00245] SEQ ID NO:215 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00246] SEQ ID NO:216 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00247] SEQ ID NO:217 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor ipilimumab.

[00248] SEQ ID NO:218 is the heavy chain amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00249] SEQ ID NO:219 is the light chain amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00250] SEQ ID NO:220 is the heavy chain variable region (VH) amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00251] SEQ ID NO:221 is the light chain variable region (VL) amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00252] SEQ ID NO:222 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00253] SEQ ID NO:223 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00254] SEQ ID NO:224 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00255] SEQ ID NO:225 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00256] SEQ ID NO:226 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00257] SEQ ID NO:227 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor tremelimumab.

[00258] SEQ ID NO:228 is the heavy chain amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00259] SEQ ID NO:229 is the light chain amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00260] SEQ ID NO:230 is the heavy chain variable region (VH) amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00261] SEQ ID NO:231 is the light chain variable region (VL) amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00262] SEQ ID NO:232 is the heavy chain CDR1 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00263] SEQ ID NO:233 is the heavy chain CDR2 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00264] SEQ ID NO:234 is the heavy chain CDR3 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00265] SEQ ID NO:235 is the light chain CDR1 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00266] SEQ ID NO:236 is the light chain CDR2 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00267] SEQ ID NO:237 is the light chain CDR3 amino acid sequence of the CTLA-4 inhibitor zalifrelimab.

[00268] SEQ ID NO:238 is a CD8a transmembrane domain.

[00269] SEQ ID NO:239 is a B7-1 transmembrane-intracellular domain

[00270] SEQ ID NOs:240-245 are exemplary glycine-serine linkers that are useful in the immunomodulatory fusion proteins described herein.

[00271] SEQ ID NO:246 is an exemplary linker that is useful in the immunomodulatory fusion proteins described herein.

[00272] SEQ ID NO:247 is a 2A peptide C-terminus sequence.

[00273] SEQ ID NO:248 is a porcine teschovirus-1 2A peptide.

[00274] SEQ ID NO:249 is an equine rhinitis A virus 2A peptide.

[00275] SEQ ID NO:250 is a foot-and-mouth disease virus 2A peptide.

[00276] SEQ ID NO:251 is an exemplary furin-cleavable 2A peptide.

[00277] SEQ ID NOs:252 and 253 are human IgE signal peptide sequences.

[00278] SEQ ID NO:254 is a human IL-2 signal peptide sequence.

[00279] SEQ ID NO:255 is a 6X NFAT IL-2 minimal promoter.

[00280] SEQ ID NO:256 is an NFAT responsive element.

[00281] SEQ ID NO:557 is a human IL-2 promoter sequence.

[00282] SEQ ID NO:258 is human IL-15 (N72D mutant).

[00283] SEQ ID NO:259 is human IL-15R-alpha-Su/Fc domain.

[00284] SEQ ID NO:260 is human IL-15R-alpha-Su (65aa truncated extracellular domain).

[00285] SEQ ID NO:261 is human IL-15 isoform 2.

[00286] SEQ ID NO:262 is human IL-15 isoform 1.

[00287] SEQ ID NO:263 is human IL-15 (without signal peptide).

[00288] SEQ ID NO:264 is human IL-15R-alpha (85 aa truncated extracellular domain).

[00289] SEQ ID NO:265 is human IL-15R-alpha (182aa truncated extracellular domain).

[00290] SEQ ID NO:266 is human IL-15R-alpha.

[00291] SEQ ID NO:267 is human IL-12 p35 subunit.

[00292] SEQ ID NO:268 is human IL-12 p40 subunit.

[00293] SEQ ID NO:269 is human IL-18.

[00294] SEQ ID NO:270is a human IL-18 variant.

[00295] SEQ ID NO:271 is human IL-21.

[00296] SEQ ID NO: 272 is human IL-2.

[00297] SEQ ID NO:273 is human CD40L.

[00298] SEQ ID NO:274 is agonistic anti-human CD40 VH (Sotigalimab).

[00299] SEQ ID NO:275 is agonistic anti-human CD40 VL (Sotigalimab).

[00300] SEQ ID NO:276 is agonistic anti-human CD40 scFv (Sotigalimab).

[00301] SEQ ID NO:277 is agonistic anti-human CD40 VH (Dacetuzumab).

[00302] SEQ ID NO:278 is agonistic anti-human CD40 VL (Dacetuzumab).

[00303] SEQ ID NO:279 is agonistic anti-human CD40 scFv (Dacetuzumab).

[00304] SEQ ID NO:280 is agonistic anti-human CD40 VH (Lucatutuzumab).

[00305] SEQ ID NO:281 is agonistic anti-human CD40 VL (Lucatutuzumab).

[00306] SEQ ID NO:282 is agonistic anti-human CD40 scFv (Lucatutuzumab).

[00307] SEQ ID NO:283 is agonistic anti-human CD40 VH (Selicrelumab).

[00308] SEQ ID NO:284 is agonistic anti-human CD40 VL (Selicrelumab).

[00309] SEQ ID NO:285 is agonistic anti-human CD40 scFv (Selicrelumab).

[00310] SEQ ID NO:286 is a target PD-1 sequence.

[00311] SEQ ID NO:287 is a target PD-1 sequence.

[00312] SEQ ID NO:288 is a repeat PD-1 left repeat sequence.

[00313] SEQ ID NO:289 is a repeat PD-1 right repeat sequence.

[00314] SEQ ID NO:290 is a repeat PD-1 left repeat sequence.

[00315] SEQ ID NO:291 is a repeat PD-1 right repeat sequence.

[00316] SEQ ID NO:292 is a PD-1 left TALEN nuclease sequence.

[00317] SEQ ID NO:293 is a PD-1 right TALEN nuclease sequence.

[00318] SEQ ID NO:294 is a PD-1 left TALEN nuclease sequence.

[00319] SEQ ID NO:295 is a PD-1 right TALEN nuclease sequence.

[00320] SEQ ID NO:296 is an exemplary piggyBac (PB) transposase enzyme amino acid sequence.

[00321] SEQ ID NO:297 is an exemplary Sleeping Beauty transposase enzyme amino acid sequence.

[00322] SEQ ID NO:298 is an exemplary hyperactive Sleeping Beauty (SB100X) transposase amino acid sequence.

[00323] SEQ ID NO:299 is an exemplary Clo05 1 nuclease domain amino acid sequence.

[00324] SEQ ID NO:300 is an exemplary the Myc polypeptide sequence.

[00325] SEQ ID NO:301 is an exemplary MYC fusion protein amino acid sequence.

[00326] SEQ ID NO:302 is HHHHHH.

[00327] SEQ ID NO:303 is an exemplary V5 tag amino acid sequence: GKPIPNPLLGLDST.

[00328] SEQ ID NO:304 is an exemplary V5 tag amino acid sequence: IPNPLLGLD.

I. Definitions

[00329] 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.

[00330] 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.

[00331] The term "in vivo" refers to an event that takes place in a subject's body.

[00332] 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.

[00333] 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.

[00334] 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.

[00335] 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.

[00336] 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.

[00337] 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.

[00338] 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.

[00339] 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.

[00340] 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.

[00341] The term "central memory T cell" refers to a subset of T cells that in the human are CD45R0+ and constitutively express CCR7 (CCR7hi) and CD62L (CD62hi). 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.

[00342] 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 (CCR7lo) and are heterogeneous or low for CD62L expression (CD62Llo). 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.

[00343] 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.

[00344] 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.

[00345] 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.

[00346] 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+.

[00347] 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.

[00348] 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 60 NQKFKDKATL TTDKSSSTAY MQLSSLTSED SAVYYCARYY DDHYCLDYWG QGTTLTVSSA 120 KTTAPSVYPL APVCGGTTGS SVTLGCLVKG YFPEPVTLTW NSGSLSSGVH TFPAVLQSDL 180 YTLSSSVTVT SSTWPSQSIT CNVAHPASST KVDKKIEPRP KSCDKTHTCP PCPAPELLGG 240 PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300 STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE 360 LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW 420 QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
SEQ ID NO:2 muromonab light chain	QIVLTQSPAI MSASPGEKVT MTCSASSSVS YMNWYQQKSG TSPKRWIYDT SKLASGVPAH 60 FRGSGSGTSY SLTISGMEAE DAATYYCQQW SSNPFTFGSG TKLEINRADT APTVSIFPPS 120 SEQLTSGGAS VVCFLNNFYP KDINVKWKID GSERQNGVLN SWTDQDSKDS TYSMSSTLTL 180 TKDEYERHNS YTCEATHKTS TSPIVKSFNR NEC 213

[00349] 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 N6 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 are described in U.S. Patent Application Publication No. US 2014/0328791 A1 and International Patent Application Publication No. WO 2012/065086 A1, 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.

[00350] 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.

[00351] 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 (Cys125>Ser51), fused via peptidyl linker (60GG61) to human interleukin 2 fragment (62-132), fused via peptidyl linker (133GSGGGS138) 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 [Cys125(51)>Ser]-mutant (1-59), fused via a G2 peptide linker (60-61) to human interleukin 2 (IL-2) (4-74)-peptide (62-132) and via a GSG3S 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	60 120 180

	YMLCTGNSSH SSWDNQCQCT SSATRNTTKQ VTPQPEEQKE RKTTEMQSPM QPVDQASLPG	240
	ECREPPPWEN EATERIYHFV VGQMVYYQCV QGYRALHRGP AESVCKMTHG KTRWTQPQLI	300
	CTG	303
SEQ ID NO:7 IL-2 form	MDAMKRGLCC VLLLCGAVFV SARRPSGRKS SKMQAFRIWD VNQKTFYLRN NQLVAGYLQG	60
	PNVNLEEKID VVPIEPHALF LGIHGGKMCL SCVKSGDETR LQLEAVNITD LSENRKQDKR	120
	FAFIRSDSGP TTSFESAACP GWFLCTAMEA DQPVSLTNMP DEGVMVTKFY FQEDESGSGG	180
	ASSESSASSD GPHPVITESR ASSESSASSD GPHPVITESR EPKSSDKTHT CPPCPAPELL	240
	GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ	300
	YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR	360
	EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS	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	60
	EKDTRCLGAT AQQFHRHKQL IRFLKRLDRN LWGLAGLNSC PVKEANQSTL ENFLERLKTI	120
	MREKYSKCSS	130
SEQ ID NO:10 recombinant human IL-7 (rhIL-7)	MDCDIEGKDG KQYESVLMVS IDQLLDSMKE IGSNCLNNEF NFFKRHICDA NKEGMFLFRA	60
	ARKLRQFLKM NSTGDFDLHL LKVSEGTTIL LNCTGQVKGR KPAALGEAQP TKSLEENKSL	120
	KEQKKLNDLC FLKRLLQEIK TCWNKILMGT KEH	153
SEQ ID NO:11 recombinant human IL-15 (rhIL-15)	MNWVNVISDL KKIEDLIQSM HIDATLYTES DVHPSCKVTA MKCFLLELQV ISLESGDASI	60
	HDTVENLIIL ANNSLSSNGN VTESGCKECE ELEEKNIKEF LQSFVHIVQM FINTS	115
SEQ ID NO:12 recombinant human IL-21 (rhIL-21)	MQDRHMIRMR QLIDIVDQLK NYVNDLVPEF LPAPEDVETN CEWSAFSCFQ KAQLKSANTG	60
	NNERIINVSI KKLKRKPPST NAGRRQKHRL TCPSCDSYEK KPPKEFLERF KSLLQKMIHQ	120
	HLSSRTHGSE DS	132

[00352] 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 (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 VH or the VL, 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 (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 VH or the VL, 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 VH or the VL, 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.

[00353] In some embodiments, an IL-2 molecule or a fragment thereof is engrafted into HCDR1 of the VH, 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 VH, 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 VH, 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 VL, 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 VL, 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.

[00354] 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.

[00355] 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.

[00356] 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.

[00357] 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 VH 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 VL 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 VH region comprising the amino acid sequence of SEQ ID NO:28 and a VL 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 than 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 60 TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE 120 TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 153
SEQ ID NO:14 IL-2 mutein	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE 60 EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120 WITFCQSIIS TLT 133
SEQ ID NO:15 IL-2 mutein	APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE 60 EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120 WITFCQSIIS TLT 133
SEQ ID NO:16 HCDR1_IL-2	GFSLAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TAMLTFKFYM PKKATELKHL 60 QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE 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 60 EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120 WITFCQSIIS TLTSTSGMSV G 141
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 60 QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE 120 FLNRWITFCQ SIISTLTSTS GM 142

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	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	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR	60

V_L	FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIK 106
SEQ ID NO:37 Light chain	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR 60 FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIKRTVA APSVFIFPPS 120 DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180 SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC 213
SEQ ID NO:38 Light chain	QVTLRESGPA LVKPTQTLTL TCTFSGFSLA PTSSSTKKTQ LQLEHLLLDL QMILNGINNY 60 KNPKLTRMLT AKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 120 IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LTSTSGMSVG WIRQPPGKAL 180 EWLADIWWDD KKDYNPSLKS RLTISKDTSK NQVVLKVTNM DPADTATYYC ARSMITNWYF 240 DVWGAGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV TVSWNSGALT 300 SGVETFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH KPSNTKVDKR VEPKSCDKTH 360 TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV AVSHEDPEVK FNWYVDGVEV 420 HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALAAPIEK TISKAKGQPR 480 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 540 FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK 583
SEQ ID NO:39 Light chain	DIQMTQSPST LSASVGDRVT ITCKAQLSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR 60 FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFGGG TKLEIKRTVA APSVFIFPPS 120 DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180 SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC 213

[00358] 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 IgG1 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).

[00359] 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).

[00360] 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).

[00361] The term "IL-18" (also referred to herein as "interleukin 18," "IL18," "IGIF," "IL-1g," "interferon-gamma inducing factor," or "IL1F4,") refers 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.

[00362] 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 in Table 21.

[00363] 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.

[00364] 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).

[00365] 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 104 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 (including, in some cases, genetically engineered TILs) 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.

[00366] 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.

[00367] 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.

[00368] 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.

[00369] 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 $mg/m^2/d$ 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 invention, the patient receives an intravenous infusion of IL-2 intravenously at 720,000 IU/kg every 8 hours to physiologic tolerance.

[00370] 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.

[00371] 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.

[00372] 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.

[00373] 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).

[00374] 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.

[00375] 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.

[00376] 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, including TILs referred to as reREP TILs).

[00377] 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.

[00378] 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.

[00379] 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.

[00380] 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.

[00381] 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.

[00382] 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."

[00383] 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 VH) 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 VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The VH and VL 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 VH and VL 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.

[00384] 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.

[00385] 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.

[00386] 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 VL, VH, CL 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 VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH 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 VH or a VL domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, 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 VL and VH 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 VH portion and a VL portion. A scFv molecule is denoted as either VL-L-VH if the VL domain is the N-terminal part of the scFv molecule, or as VH-L-VL if the VH 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.

[00387] 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.

[00388] 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.

[00389] 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 VH and VL regions of the recombinant antibodies are sequences that, while derived from and related to human germline VH and VL sequences, may not naturally exist within the human antibody germline repertoire in vivo.

[00390] As used herein, "isotype" refers to the antibody class (e.g., IgM or IgG1) that is encoded by the heavy chain constant region genes.

[00391] 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."

[00392] 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.

[00393] 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.

[00394] 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.

[00395] A "diabody" is a small antibody fragment with two antigen-binding sites. The fragments comprises a heavy chain variable domain (VH) connected to a light chain variable domain (VL) in the same polypeptide chain (VH-VL or VL-VH). 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.

[00396] 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.

[00397] "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 (C1-C10)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.

[00398] 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.

II. Gen 2 TIL Manufacturing Processes

[00399] 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.

[00400] 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.

[00401] 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.

[00402] In some embodiments, the first expansion (including processes referred to as the pre-REP 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.

[00403] 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

[00404] 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.

[00405] 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 endometrial cancer. The solid tumor may be of skin tissue. In some embodiments, useful TILs are obtained from a melanoma.

[00406] 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% 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.

[00407] 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.

[00408] 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.

[00409] 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 289.2 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.

[00410] 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.

[00411] 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.

[00412] 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.

[00413] 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.

[00414] 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.

[00415] In some embodiments, the tumors are digested in an enzyme mixture comprising collagenase, DNase, and neutral protease. In some embodiments, the tumors are digested in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours. In some embodiments, the tumors are digested in an enzyme mixture comprising collagenase, DNase, and neutral protease for 1-2 hours at 37°C, 5% CO_2. In some embodiments, the tumors are digested in an enzyme mixture comprising collagenase, DNase, and neutral protease 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.

[00416] In some embodiments, the tumor is reconstituted with the lyophilized enzymes in a sterile buffer. In some embodiments, the buffer is sterile HBSS.

[00417] 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.

[00418] In some embodiments, the enzyme mixture comprises DNAse. In some embodiments, the working stock for the DNAse is a 10,000 IU/mL 10X working stock.

[00419] 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.

[00420] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 1000 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[00421] In some embodiments, the enzyme mixture comprises 10 mg/mL collagenase, 500 IU/mL DNAse, and 1 mg/mL hyaluronidase.

[00422] In general, the harvested cell suspension is called a "primary cell population" or a "freshly harvested" cell population.

[00423] 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.

[00424] 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.

[00425] 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.

[00426] 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.

[00427] 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.

[00428] 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.

[00429] 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.

1. Pleural effusion T-cells, ascites fluid T-cells, and TILs

[00430] 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.

[00431] In some embodiments, the sample is an ascites fluid sample. In some embodiments, the source of the T-cells or TILs for expansion according to the processes described herein is an ascites fluid sample. In some embodiments, the sample is an ascites derived sample. In any of the foregoing embodiments, the ascites fluid sample or ascites derived sample is obtained from an endometrial cancer patient. In some embodiments, ascites fluid from the abdomen of an endometrial cancer patient may be used to obtain TILs for expansion according to the processes described herein and for treatment of the endometrial cancer patient using TILs and optional co-therapies described herein.

[00432] 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.

[00433] In some embodiments, the pleural or ascites fluid is in unprocessed form, directly as removed from the patient. In some embodiments, the unprocessed pleural or ascites 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 or ascites fluid is placed in a standard CellSave® tube (Veridex) prior to 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 or ascites 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.

[00434] In some embodiments, the pleural or ascites fluid sample from the chosen subject may be diluted. In some embodiments, the dilution is 1:10 pleural or ascites fluid to diluent. In other embodiments, the dilution is 1:9 pleural or ascites fluid to diluent. In other embodiments, the dilution is 1:8 pleural or ascites fluid to diluent. In other embodiments, the dilution is 1:5 pleural or ascites fluid to diluent. In other embodiments, the dilution is 1:2 pleural or ascites fluid to diluent. In other embodiments, the dilution is 1:1 pleural or ascites 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 or ascites 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 or ascites 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.

[00435] In still other embodiments, pleural or ascites fluid samples are concentrated by conventional means prior to further processing steps. In some embodiments, this pre-treatment of the pleural or ascites fluid is preferable in circumstances in which the pleural or ascites 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 or ascites fluid sample is prepared by centrifuging the pleural or ascites fluid sample after its withdrawal from the subject and resuspending the centrifugate or pellet in buffer. In some embodiments, the pleural or ascites fluid sample is subjected to multiple centrifugations and resuspensions, before it is cryopreserved for transport or later analysis and/or processing.

[00436] In some embodiments, pleural or ascites fluid samples are concentrated prior to further processing steps by using a filtration method. In some embodiments, the pleural or ascites fluid sample used in 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 or ascites 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 other 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.

[00437] In some embodiments, the pleural or ascites fluid sample (including, for example, the untreated pleural or ascites fluid), the diluted pleural or ascites 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 or ascites 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 or ascites 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.

[00438] In some embodiments, the pleural or ascites 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.

B. STEP B: First Expansion

[00439] 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 in 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.

[00440] 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 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).

[00441] 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.

[00442] 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.

[00443] In some 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.

[00444] 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 some 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.

[00445] 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.

[00446] 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.

[00447] 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+, Al3+, Ba2+, Cd2+, CO_2+, Cr3+, Ge4+, Se4+, Br, T, Mn2+, P, Si4+, V5+, Mo6+, Ni2+, Rb+, Sn2+ and Zr4+. In some embodiments, the defined medium further comprises L-glutamine, sodium bicarbonate and/or 2-mercaptoethanol.

[00448] 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.

[00449] 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.

[00450] 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.

[00451] 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.

[00452] 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.

[00453] 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.

[00454] 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+, Al3+, Ba2+, Cd2+, CO_2+, Cr3+, Ge4+, Se4+, Br, T, Mn2+, P, Si4+, V5+, Mo6+, Ni2+, Rb+, Sn2+ and Zr4+. 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.

[00455] 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.

[00456] 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 below. 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

[00457] 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).

[00458] 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.

[00459] 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).

[00460] 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.

[00461] 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.

[00462] 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.

[00463] 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.

[00464] 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.

[00465] 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.

[00466] 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 some 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.

[00467] 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.

[00468] 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.

[00469] 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.

[00470] 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. 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

[00471] 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.

[00472] 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.

[00473] 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

[00474] 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.

[00475] 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.

[00476] 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.

[00477] 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.

[00478] 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 bioreactor. In some embodiments, the closed system bioreactor is a single bioreactor.

D. STEP D: Second Expansion

[00479] 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.

[00480] 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.

[00481] 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.

[00482] 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.

[00483] 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.

[00484] 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.

[00485] 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.

[00486] 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.

[00487] 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).

[00488] 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.

[00489] 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.

[00490] 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.

[00491] 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.

[00492] 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.

[00493] 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 x 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 x 10^6 cells/mL.

[00494] 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.

[00495] 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.

[00496] 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.

[00497] 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.

[00498] 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.

[00499] 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 (491 g) 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 some 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.

[00500] 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).

[00501] In some embodiments, the second expansion culture medium (*e.g.*, sometimes referred to as CM^2 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.

[00502] 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.

[00503] 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.

[00504] 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.

[00505] 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.

[00506] 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.

[00507] 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.

[00508] 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.

[00509] 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.

[00510] 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.

[00511] 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.

[00512] 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.

[00513] 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.

[00514] 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).

[00515] 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.

[00516] 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).

[00517] 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.

[00518] 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.

[00519] 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.

[00520] In some embodiments, the first small scale TIL culture is apportioned into a plurality of about 2 to 5 subpopulations of TILs.

[00521] 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.

[00522] 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.

[00523] 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.

[00524] 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.

[00525] 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.

[00526] 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.

[00527] 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.

[00528] 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.

[00529] 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.

[00530] 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.

[00531] 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.

[00532] 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.

[00533] In some embodiments, the splitting of the rapid expansion occurs in a closed system.

[00534] 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

[00535] 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.

[00536] In general, the allogeneic 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.

[00537] 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).

[00538] 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.

[00539] 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.

[00540] 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.

[00541] 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 other embodiments, the second expansion procedures described herein require a ratio of about $2.5x10^9$ feeder cells to about $50x10^6$ TIL. In yet other embodiments, the second expansion procedures described herein require about $2.5x10^9$ feeder cells to about $25x10^6$ TIL.

[00542] 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.

[00543] In general, the allogeneic 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.

[00544] In some embodiments, artificial antigen presenting cells are used in the second expansion as a replacement for, or in combination with, PBMCs.

2. Cytokines and Other Additives

[00545] 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.

[00546] 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, 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.

[00547] 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

[00548] 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.

[00549] 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.

[00550] 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.

[00551] 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.

[00552] 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.

[00553] 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

[00554] 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.

[00555] 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.

III. Further Gen 2 and Other TIL Manufacturing Process Embodiments

A. PBMC Feeder Cell Ratios

[00556] In some embodiments, the culture media used in expansion methods described herein 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.

[00557] In some embodiments, the number of PBMC feeder layers is calculated as follows:

[00558] A. Volume of a T-cell (10 μm diameter): $V = (4/3)\pi r^3 = 523.6\ \mu m^3$

[00559] B. Column of G-REX-100 (M) with a 40 μm (4 cells) height: $V = (4/3)\pi r^3 = 4\times10^{12}\ \mu m^3$

[00560] C. Number of cells required to fill column B: $4\times10^{12}\ \mu m^3 / 523.6\ \mu m^3 = 7.6\times10^{8}\ \mu m^3 * 0.64 = 4.86\times10^{8}$

[00561] D. Number cells that can be optimally activated in 4D space: $4.86\times10^{8} / 24 = 20.25\times10^{6}$

[00562] E. Number of feeders and TIL extrapolated to G-REX-500: TIL: 100×10^{6} and Feeder: 2.5×10^{9}

[00563] 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.

[00564] In some 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.

[00565] 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.

[00566] 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.

[00567] 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.

[00568] 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.

[00569] 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.

[00570] 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.

[00571] 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.

[00572] 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.

[00573] 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.

[00574] 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.

[00575] 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.

[00576] 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.

[00577] 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.

[00578] 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.

[00579] 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.

[00580] 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.

[00581] 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.

[00582] 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.

[00583] 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.

[00584] 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.

[00585] 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.

[00586] 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.

[00587] 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.

[00588] 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.

[00589] 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.

[00590] 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.

[00591] 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.

[00592] 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.

[00593] 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.

[00594] 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.

[00595] 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.

[00596] 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.

[00597] 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.

[00598] 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.

[00599] 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.

[00600] 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.

[00601] 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.

[00602] 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.

[00603] 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.

[00604] In some 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).

[00605] 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.

[00606] 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.

[00607] 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.

[00608] 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.

[00609] 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.

[00610] 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.

[00611] 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.

[00612] 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.

[00613] 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.

[00614] 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.

[00615] 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, 3.4×10^6, 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.

[00616] 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.

[00617] 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.

[00618] 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.

[00619] 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.

[00620] 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.

[00621] 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.

[00622] 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.

[00623] 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.

[00624] 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.

[00625] 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.

[00626] 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.

[00627] 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.

[00628] 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.

[00629] 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.

[00630] 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.

[00631] 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.

[00632] 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.

[00633] 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.

[00634] 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.

[00635] 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.

[00636] 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.

[00637] 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.

[00638] 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.

[00639] 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.

[00640] 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.

[00641] 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.

[00642] 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.

[00643] 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.

[00644] 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.

[00645] 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.

[00646] 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.

[00647] 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.

[00648] 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.

[00649] 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.

[00650] 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.

[00651] 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.

[00652] 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.

[00653] 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.

[00654] 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.

[00655] 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).

[00656] 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).

[00657] 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).

[00658] 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).

[00659] 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)

[00660] In some 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.

[00661] 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.

[00662] 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.

[00663] 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.

[00664] 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.

[00665] 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.

[00666] 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, 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.

[00667] 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.

[00668] 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.

[00669] 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.

[00670] 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.

[00671] 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.

[00672] 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.

[00673] 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.

[00674] 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.

[00675] 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.

[00676] 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.

[00677] 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.

[00678] 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.

[00679] 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.

[00680] 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.

[00681] 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.

[00682] 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.

[00683] 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.

[00684] 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.

[00685] 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.

[00686] 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.

[00687] 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.

[00688] 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.

[00689] 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.

[00690] 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.

[00691] 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

[00692] In some embodiments, the culture media used in expansion methods described herein (see for example, Figure 1) 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.

[00693] 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). See, Table 1.

[00694] 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

[00695] 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.

[00696] 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.

[00697] 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.

[00698] In some embodiments, the 4-1BB agonists are characterized by binding to human 4-1BB (SEQ ID NO:40) 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

[00699] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds human or murine 4-1BB with a KD of about 100 pM or lower, binds human or murine 4-1BB with a KD of about 90 pM or lower, binds human or murine 4-1BB with a KD of about 80 pM or lower, binds human or murine 4-1BB with a KD of about 70 pM or lower, binds human or

murine 4-1BB with a KD of about 60 pM or lower, binds human or murine 4-1BB with a KD of about 50 pM or lower, binds human or murine 4-1BB with a KD of about 40 pM or lower, or binds human or murine 4-1BB with a KD of about 30 pM or lower.

[00700] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with a kassoc of about 7.5 $\times 10^5$ 1/M·s or faster, binds to human or murine 4-1BB with a kassoc of about 7.5 $\times 10^5$ 1/M·s or faster, binds to human or murine 4-1BB with a kassoc of about 8 $\times 10^5$ l/M·s or faster, binds to human or murine 4-1BB with a kassoc of about 8.5 $\times 10^5$ 1/M·s or faster, binds to human or murine 4-1BB with a kassoc of about 9 $\times 10^5$ 1/M·s or faster, binds to human or murine 4-1BB with a kassoc of about 9.5 $\times 10^5$ 1/M·s or faster, or binds to human or murine 4-1BB with a kassoc of about 1 $\times$ 10^6 1/M·s or faster.

[00701] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with a kdissoc of about 2 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.1 $\times$ 10^{-5} 1/s or slower , binds to human or murine 4-1BB with a kdissoc of about 2.2 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.3 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.4 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.5 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.6 $\times$ 10^{-5} 1/s or slower or binds to human or murine 4-1BB with a kdissoc of about 2.7 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.8 $\times$ 10^{-5} 1/s or slower, binds to human or murine 4-1BB with a kdissoc of about 2.9 $\times$ 10^{-5} 1/s or slower, or binds to human or murine 4-1BB with a kdissoc of about 3 $\times$ 10^{-5} 1/s or slower.

[00702] In some embodiments, the compositions, processes and methods described include a 4-1BB agonist that binds to human or murine 4-1BB with an IC50 of about 10 nM or lower, binds to human or murine 4-1BB with an IC50 of about 9 nM or lower, binds to human or murine 4-1BB with an IC50 of about 8 nM or lower, binds to human or murine 4-1BB with an IC50 of about 7 nM or lower, binds to human or murine 4-1BB with an IC50 of about 6 nM or lower, binds to human or murine 4-1BB with an IC50 of about 5 nM or lower, binds to human or murine 4-1BB with an IC50 of about 4 nM or lower, binds to human or murine 4-1BB with an IC50 of about 3 nM or lower, binds to human or murine 4-1BB with an IC50 of about 2 nM or lower, or binds to human or murine 4-1BB with an IC50 of about 1 nM or lower.

[00703] 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 (VH-VL), 143-199 (CH1-CL), 256-316 (CH2) and 362-420 (CH3); light chain intrachain disulfide bridges at positions 22'-87' (VH-VL) and 136'-195' (CH1-CL); 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.

[00704] 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.

[00705] 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 (VH) comprises the sequence shown in SEQ ID NO:44, and the 4-1BB agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:45, and conservative amino acid substitutions thereof. In some embodiments, a 4-1BB agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 99% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45.

[00706] 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.

[00707] 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	60
	YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCARG YGIFDYWGQ GTLVTVSS	118
SEQ ID NO:45 light chain variable region for utomilumab	SYELTQPPSV SVSPGQTASI TCSGDNIGDQ YAHWYQQKPG QSPVLVIYQD KNRPSGIPER	60
	FSGSNSGNTA TLTISGTQAM DEADYYCATY TGFGSLAVFG GGTKLTVL	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

[00708] 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 (VH-VL), 148-204 (CH1-CL), 262-322 (CH2) and 368-426 (CH3) (and at positions 22"-95", 148"-204", 262"-322", and 368"-426"); light chain intrachain disulfide bridges at positions 23'-88' (VH-VL) and 136'-196' (CH1-CL) (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.

[00709] 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.

[00710] 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 (VH) comprises the sequence shown in SEQ ID NO:54, and the 4-1BB agonist light chain

variable region (VL) comprises the sequence shown in SEQ ID NO:55, and conservative amino acid substitutions thereof. In some embodiments, a 4-1BB agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 99% identical to the sequences shown in SEQ ID NO:54 and SEQ ID NO:55.

[00711] 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.

[00712] 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	60
	GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ	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

[00713] 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.

[00714] 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.

[00715] 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 7). 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 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. 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.

[00716] Amino acid sequences for the other polypeptide domains of structure I-A given in Figure 7 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

[00717] Amino acid sequences for the other polypeptide domains of structure I-B given in Figure 7 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	METDTLLLWV LLLWVPAGNG DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT	60
Fc domain	CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK	120
	CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE	180
	WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS	240
	LSLSPG	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

[00718] 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 10, any combination of a variable heavy chain and variable light chain of the foregoing, and fragments, derivatives, conjugates, variants, and biosimilars thereof.

[00719] 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.

[00720] 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:44 and SEQ ID NO:45, respectively, wherein the VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the VH and VL sequences given in Table 10, wherein the VH and VL 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 SPGSAASPRL REGPELSPDD PAGLLDLRQG MFAQLVAQNV LLIDGPLSWY SDPGLAGVSL TGGLSYKEDT KELVVAKAGV YYVFFQLELR RVVAGEGSGS VSLALHLQPL RSAAGAAALA LTVDLPPASS EARNSAFGFQ GRLLHLSAGQ RLGVHLHTEA RARHAWQLTQ GATVLGLFRV TPEIPAGLPS PRSE	60 120 180 240 254
SEQ ID NO:78 4-1BBL soluble domain	LRQGMFAQLV AQNVLLIDGP LSWYSDPGLA GVSLTGGLSY KEDTKELVVA KAGVYYVFFQ LELRRVVAGE GSGSVSLALH LQPLRSAAGA AALALTVDLP PASSEARNSA FGFQGRLLHL SAGQRLGVHL HTEARARHAW QLTQGATVLG LFRVTPEIPA GLPSPRSE	60 120 168
SEQ ID NO:79 variable heavy chain for 434-1-1 version 1	QVQLQQPGAE LVKPGASVKL SCKASGYTFS SYWMHWVKQR PGQVLEWIGE INPGNGHTNY NEKFKSKATL TVDKSSSTAY MQLSSLTSED SAVYYCARSF TTARGFAYWG QGTLVTVS	60 118
SEQ ID NO:80 variable light chain for 434-1-1 version 1	DIVMTQSPAT QSVTPGDRVS LSCRASQTIS DYLHWYQQKS HESPRLLIKY ASQSISGIPS RFSGSGSGSD FTLSINSVEP EDVGVYYCQD GHSFPPTFGG GTKLEIK	60 107
SEQ ID NO:81 variable heavy chain for 434-1-1 version 2	QVQLQQPGAE LVKPGASVKL SCKASGYTFS SYWMHWVKQR PGQVLEWIGE INPGNGHTNY NEKFKSKATL TVDKSSSTAY MQLSSLTSED SAVYYCARSF TTARGFAYWG QGTLVTVSA	60 119
SEQ ID NO:82 variable light chain for 434-1-1 version 2	DIVMTQSPAT QSVTPGDRVS LSCRASQTIS DYLHWYQQKS HESPRLLIKY ASQSISGIPS RFSGSGSGSD FTLSINSVEP EDVGVYYCQD GHSFPPTFGG GTKLEIKR	60 10^{8}
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	MEAPAQLLFL LLLWLPDTTG DIVMTQSPDS LAVSLGERAT INCKSSQSLL SSGNQKNYL	60

chain for H39E3-2	WYQQKPGQPP KLLIYYASTR QSGVPDRFSG SGSGTDFTLT ISSLQAEDVA	110

[00721] 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 trimerization 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.

[00722] 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.

[00723] In some embodiments, the 4-1BB agonist is a 4-1BB agonistic scFv antibody comprising any of the foregoing VH domains linked to any of the foregoing VL domains.

[00724] 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

[00725] 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).

[00726] 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.

[00727] 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.

[00728] 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

[00729] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds human or murine OX40 with a KD of about 100 pM or lower, binds human or murine OX40 with a KD of about 90 pM or lower, binds human or murine OX40 with a KD of about 80 pM or lower, binds human or murine OX40 with a KD of about 70 pM or lower, binds human or murine OX40 with a KD of about 60 pM or lower, binds human or murine OX40 with a KD of about 50 pM or lower, binds human or murine OX40 with a KD of about 40 pM or lower, or binds human or murine OX40 with a KD of about 30 pM or lower.

[00730] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds to human or murine OX40 with a kassoc of about 7.5×10^5 1/M·s or faster, binds to human or murine OX40 with a kassoc of about 7.5×10^5 1/M·s or faster, binds to human or murine OX40 with a kassoc of about 8×10^5 1/M·s or faster, binds to human or murine OX40 with a kassoc of about 8.5×10^5 1/M·s or faster, binds to human or murine OX40 with a kassoc of about 9×10^5 1/M·s or faster, binds to human or murine OX40 with a kassoc of about 9.5×10^5 1/M·s or faster, or binds to human or murine OX40 with a kassoc of about 1×10^6 1/M·s or faster.

[00731] In some embodiments, the compositions, processes and methods described include a OX40 agonist that binds to human or murine OX40 with a kdissoc of about 2×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.1×10^{-5} 1/s or slower , binds to human or murine OX40 with a kdissoc of about 2.2×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.3×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.4×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.5×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.6×10^{-5} 1/s or slower or binds to human or murine OX40 with a kdissoc of about 2.7×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.8×10^{-5} 1/s or slower, binds to human or murine OX40 with a kdissoc of about 2.9×10^{-5} 1/s or slower, or binds to human or murine OX40 with a kdissoc of about 3×10^{-5} 1/s or slower.

[00732] In some embodiments, the compositions, processes and methods described include OX40 agonist that binds to human or murine OX40 with an IC50 of about 10 nM or lower, binds to human or murine OX40 with an IC50 of about 9 nM or lower, binds to human or murine OX40 with an IC50 of about 8 nM or lower, binds to human or murine OX40 with an IC50 of about 7 nM or lower, binds to human or murine OX40 with an IC50 of about 6 nM or lower, binds to human or murine OX40 with an IC50 of about 5 nM or lower, binds to human or murine OX40 with an IC50 of about 4 nM or lower, binds to human or murine OX40 with an IC50 of about 3 nM or lower, binds to human or murine OX40 with an IC50 of about 2 nM or lower, or binds to human or murine OX40 with an IC50 of about 1 nM or lower.

[00733] 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 (VH-VL), 148-204 (CH1-CL), 265-325 (CH2) and 371-429 (CH3) (and at positions 22''-95'', 148''-204'', 265''-325'', and 371''-429''); light chain intrachain disulfide bridges at positions 23'-88' (VH-VL) and 134'-194' (CH1-CL) (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.

[00734] 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.

[00735] 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 (VH) comprises the sequence shown in SEQ ID NO:89, and the OX40 agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:90, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 99% identical to the sequences shown in SEQ ID NO:89 and SEQ ID NO:90.

[00736] 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.

[00737] In some embodiments, the OX40 agonist is a OX40 agonist biosimilar monoclonal antibody approved by drug regulatory authorities with reference to tavolixizumab. 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 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	60
	PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY DYDGGHAMDY WGQGTLVTVS	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 PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY DYDGGHAMDY WGQGTLVT	60 118
SEQ ID NO:90 light chain variable region for tavolixizumab	DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY TSKLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GSALPWTFGQ GTKVEIKR	60 10^{8}
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

[00738] 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.

[00739] 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.

[00740] 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 (VH) comprises the sequence shown in SEQ ID NO:99, and the OX40 agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:100, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:99 and SEQ ID NO:100, respectively.

[00741] 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:10[6], respectively, and conservative amino acid substitutions thereof.

[00742] 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

[00743] 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.

[00744] 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.

[00745] 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 (VH) comprises the sequence shown in SEQ ID NO:109, and the OX40 agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:110, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 96% identical to

the sequences shown in SEQ ID NO:10[9] and SEQ ID NO:110, respectively. In some embodiments, a OX40 agonist comprises VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:10[9] and SEQ ID NO:110, respectively.

[00746] 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.

[00747] 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

[00748] 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.

[00749] 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 (VH) comprises the sequence shown in SEQ ID NO:117, and the OX40 agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:118, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:117 and SEQ ID NO:118, respectively.

[00750] 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.

[00751] 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

[00752] 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.

[00753] 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 (VH) comprises the sequence shown in SEQ ID NO:125, and the OX40 agonist light chain variable region (VL) comprises the sequence shown in SEQ ID NO:126, and conservative amino acid substitutions thereof. In some embodiments, a OX40 agonist comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:125 and SEQ ID NO:126, respectively.

[00754] 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.

[00755] 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	60
	RFSGSGSGTD FTFTISSLQP EDIATYYCQQ HYSTPRTFGQ GTKLEIK	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

[00756] 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.

[00757] 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.

[00758] 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.

[00759] 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 7 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 7 are found in Table 10. 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.

[00760] 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.

[00761] 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.

[00762] 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:10[9] and SEQ ID NO:110, respectively, wherein the VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the VH and VL sequences given in Table 17, wherein the VH and VL 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	60
	SIKVQFTEYK KEKGFILTSQ KEDEIMKVQN NSVIINCDGF YLISLKGYFS QEVNISLHYQ	120
	KDEEPLFQLK KVRSVNSLMV ASLTYKDKVY LNVTTDNTSL DDFHVNGGEL ILIHQNPGEF	180
	CVL	183
SEQ ID NO:134 OX40L soluble domain	SHRYPRIQSI KVQFTEYKKE KGFILTSQKE DEIMKVQNNS VIINCDGFYL ISLKGYFSQE	60
	VNISLHYQKD EEPLFQLKKV RSVNSLMVAS LTYKDKVYLN VTTDNTSLDD FHVNGGELIL	120
	IHQNPGEFCV L	131
SEQ ID NO:135 OX40L soluble domain (alternative)	YPRIQSIKVQ FTEYKKEKGF ILTSQKEDEI MKVQNNSVII NCDGFYLISL KGYFSQEVNI	60
	SLHYQKDEEP LFQLKKVRSV NSLMVASLTY KDKVYLNVTT DNTSLDDFHV NGGELILIHQ	120
	NPGEFCVL	128
SEQ ID NO:136 variable heavy chain for 008	EVQLVESGGG LVQPGGSLRL SCAASGFTFS NYTMNWVRQA PGKGLEWVSA ISGSGGSTYY	60
	ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR YSQVHYALDY WGQGTLVTVS	120
SEQ ID NO:137 variable light chain for 008	DIVMTQSPDS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKAGQSPQ LLIYLGSNRA	60
	SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYYNHP TTFGQGTK	108
SEQ ID NO:138 variable heavy chain for 011	EVQLVESGGG VVQPGRSLRL SCAASGFTFS DYTMNWVRQA PGKGLEWVSS ISGGSTYYAD	60
	SRKGRFTISR DNSKNTLYLQ MNNLRAEDTA VYYCARDRYF RQQNAFDYWG QGTLVTVSSA	120
SEQ ID NO:139 variable light chain for 011	DIVMTQSPDS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKAGQSPQ LLIYLGSNRA	60
	SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYYNHP TTFGQGTK	108
SEQ ID NO:140 variable heavy chain for 021	EVQLVESGGG LVQPRGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVAV ISYDGSNKYY	60
	ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR YITLPNALDY WGQGTLVTVS	120
SEQ ID NO:141 variable light chain for 021	DIQMTQSPVS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ LLIYLGSNRA	60
	SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCQQYKSNP PTFGQGTK	108
SEQ ID NO:142 variable heavy chain for 023	EVQLVESGGG LVHPGGSLRL SCAGSGFTFS SYAMHWVRQA PGKGLEWVSA IGTGGGTYYA	60
	DSVMGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARYDN VMGLYWFDYW GQGTLVTVSS	120
SEQ ID NO:143 variable light chain for 023	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA	60
	RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPAFGG GTKVEIKR	108
SEQ ID NO:144 heavy chain variable region	EVQLQQSGPE LVKPGASVKM SCKASGYTFT SYVMHWVKQK PGQGLEWIGY INPYNDGTKY	60
	NEKFKGKATL TSDKSSSTAY MELSSLTSED SAVYYCANYY GSSLSMDYWG QGTSVTVSS	119
SEQ ID NO:145 light chain variable region	DIQMTQTTSS LSASLGDRVT ISCRASQDIS NYLNWYQQKP DGTVKLLIYY TSRLHSGVPS	60
	RFSGSGSGTD YSLTISNLEQ EDIATYFCQQ GNTLPWTFGG GTKLEIKR	108
SEQ ID NO:146 heavy chain variable region	EVQLQQSGPE LVKPGASVKI SCKTSGYTFK DYTMHWVKQS HGKSLEWIGG IYPNNGGSTY	60
	NQNFKDKATL TVDKSSSTAY MEFRSLTSED SAVYYCARMG YHGPHLDFDV WGAGTTVTVS	120
	P	121

SEQ ID NO:147 light chain variable region	DIVMTQSEKF 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	DIVMTQSEKF MSTSVRDRVS ITCKASQDVS TAVAWYQQKP GQSPKLLIYS ASYLYTGVPD RFTGSGSGTD FTFTISSVQA EDLAVYYCQQ HYSTPRTFGG GTKLEIK	60 107
SEQ ID NO:151 light chain variable region of humanized antibody	DIVMTQSEKF 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 of humanized antibody	DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYMHWY QQKPGQPPKL LIYLASNLES GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSRELPL TFGAGTKLEL K	60 111
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

[00763] 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.

[00764] 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.

[00765] 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.

[00766] In some embodiments, the OX40 agonist is an OX40 agonistic scFv antibody comprising any of the foregoing VH domains linked to any of the foregoing VL domains.

[00767] In some embodiments, the OX40 agonist is Creative Biolabs OX40 agonist monoclonal antibody MOM-18455, commercially available from Creative Biolabs, Inc., Shirley, NY, USA.

[00768] In some embodiments, the OX40 agonist is OX40 agonistic antibody clone Ber-ACT35 commercially available from BioLegend, Inc., San Diego, CA, USA.

4. Myc Fusion Proteins

[00769] In some embodiments, the cell culture medium of the first expansion and/or the second expansion comprises a Myc fusion protein. Myc fusion proteins are described in US Patent No. 11,369,678, the content of which is incorporated by reference in its entirety.

[00770] Disclosed herein, in certain embodiments, is a MYC fusion protein comprising (a) a transporter peptide sequence; and (b) a MYC sequence. In some embodiments, the MYC fusion protein is a peptide of Formula (I):

transporter peptide sequence —MYC sequence.

[00771] In some embodiments, a MYC fusion protein disclosed herein comprises (a) a transporter peptide sequence; (b) a MYC sequence; and (c) one or more molecules that link the transporter

peptide sequence and the MYC sequence. In some embodiments, the MYC fusion protein is a peptide of Formula (II):

transporter peptide sequence—X—MYC sequence,

wherein —X— is molecule that links the transporter peptide sequence and the MYC sequence. In some embodiments, —X— is an amino acid. In some embodiments, —X— is at least one amino acid.

[00772] As used herein, a "transporter peptide" means a peptide sequence that promotes peptide penetration into cells and tissues. In some embodiments, a transporter peptide is the N-terminal 9-amino-acid sequence of the TAT protein transduction domain of HIV-1 (RKKRRQRRR) (SEQ ID NO: 306). In some embodiments, a transporter peptide is $TAT_{[48-57]}$. In some embodiments, a transporter peptide is $TAT_{[57-48]}$.

[00773] As used herein, a "MYC sequence" is a MYC amino acid peptide sequence. In some embodiments, the Myc polypeptide is a complete Myc polypeptide sequence. In some embodiments, the Myc polypeptide is a partial Myc polypeptide sequence. In some embodiments, the MYC is c-MYC. In some embodiments, the Myc polypeptide sequence comprises SEQ ID NO:300:

MDFFRVVENQQPPATMPLNVSFTNRNYDLDYDSVQPYFYCDEEE

NFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRRSGLCSPSYVA

VTPFSLRGDNDGGGGSFSTADQLEMVTELLGGDMVNQSFICDPDD

ETFIKNIIIQDCMWSGFSAAAKLVSEKLASYQAARKDSGSPNPARG

HSVCSTSSLYLQDLSAAASECIDPSVVFPYPLNDSSSPKSCASQDSS

AFSPSSDSLLSSTESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEEID

VVSVEKRQAPGKRSESGSPSAGGHSKPPHSPLVLKRCHVSTHQHN

YAAPPSTRKDYPAAKRVKLDSVRVLRQISNNRKCTSPRSSDTEEN

VKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVILKK

ATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLRKGELNSKLE.

[00774] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, and (b) c-MYC.

[00775] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, (b) a linker amino acid, and (c) c-MYC.

[00776] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one amino acid sequence that facilitates purification of the fusion protein. In some embodiments, a MYC fusion protein disclosed herein comprises a protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag and an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a 6-histidine tag and a V5 epitope tag.

[00777] In some embodiments, the histidine tag is a 6-histidine tag. In some embodiments, the histidine tag comprises the sequence HHHHHH (SEQ ID NO:302). In some embodiments, a histidine tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a TAT-Myc polypeptide sequence is cloned into an expression vector encoding a polyHis-tag. In some embodiments, a polyhistidine tag is added by PCR (i.e., the PCR primers comprise a polyhistidine sequence).

[00778] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein further comprises a V5 epitope tag. In some embodiments, the V5 tag comprises the amino acids: GKPIPNPLLGLDST (SEQ ID NO:303). In some embodiments, the V5 tag comprises the amino acids: IPNPLLGLD (SEQ ID NO:304). In some embodiments, a V5 tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a MYC fusion protein sequence is cloned into an expression vector encoding a V5 tag. In some embodiments, a V5 tag is added by PCR (i.e., the PCR primers comprise a V5 sequence).

[00779] In some embodiments, the amino acids are in the D formation. In some embodiments, the amino acids are in the L formation. In some embodiments, a first plurality of amino acids is in the D formation and a second plurality is in the L formation.

[00780] In some embodiments, a MYC fusion protein comprises SEQ ID NO:301:

MRKKRRQRRRMDFFRVVENQQPPATMPLNVSFTNRNYDLDYDSV

QPYFYCDEEENFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRR

SGLCSPSYVAVTPFSLRGDNDGGGGSFSTADQLEMVTELLGGDMV

NQSFICDPDDETFIKNIIIQDCMWSGFSAAAKLVSEKLASYQAARK

DSGSPNPARGHSVCSTSSLYLQDLSAAASECIDPSVVFPYPLNDSSS

PKSCASQDSSAFSPSSDSLLSSTESSPQGSPEPLVLHEETPPTTSSDSE

EEQEDEEEIDVVSVEKRQAPGKRSESGSPSAGGHSKPPHSPLVLKR

CHVSTHQHNYAAPPSTRKDYPAAKRVKLDSVRVLRQISNNRKCTS

PRSSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKA

PKVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLRK

GELNSKLEGKPIPNPLLGLDSTRTGHHHHHH.

C. Optional Cell Viability Analyses

[00781] 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

[00782] 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 FACSCantoTM 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.

[00783] 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

[00784] In some embodiments, a method for expanding TILs, including those discussed above as well as exemplified in Figure 1, 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.

[00785] 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).

[00786] 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.

[00787] 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.

[00788] 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.

[00789] 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.

[00790] 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 5×105 cells/cm^2 to between 10×10^6 and 30×10^6 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. Closed Systems for TIL Manufacturing

[00791] 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.

[00792] 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.

[00793] 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 the examples is employed. In some embodiments, the TILs are formulated into a final product formulation container according to the methods described herein in the examples.

[00794] 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.

[00795] 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%.

[00796] The closed system allows for TIL growth in the absence and/or with a significant reduction in microbial contamination.

[00797] 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.

[00798] 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.

[00799] 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.

E. Methods of Altered Protein Expression in TILs

[00800] 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 some embodiments, the altered protein expression is due to gene editing. In some embodiments, the expanded TILs of the present invention are transduced with vectors and/or other molecules capable of 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.

[00801] 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.

[00802] 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. 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. 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, the TIL population obtained from for example, Step B and included in Step C. 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. 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. 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.

[00803] 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.

[00804] 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 (Gattinoni et al. Nat Med 2009, 2011; Gattinoni, Nature Rev. Cancer, 2012; Cieri et al. Blood 2013). 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 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 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.

[00805] 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.

[00806] 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.

[00807] 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 CD279), TGFBR2, CCR4/5, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-7, IL-10, IL-12, IL-15, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, 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, 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, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-7, IL-10, IL-12, IL-15, IL-18, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, 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, 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 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-7. In some embodiments, the transient alteration of protein expression targets IL-10. 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-18. 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.

[00808] In some embodiments, the transient alteration of protein expression targets the NOTCH signaling pathway, such as through the NOTCH 1/2 ICD and/or through other NOTCH ligand, such as mDLL1 (see, for example Kondo, T. et al., NOTCH-mediated conversion of activated T cells into stem cell memory-like T cells for adoptive immunotherapy, Nature Communications, Vol. 8, Article number: 15338 (2017), which is incorporated by reference herein in its entirety).

[00809] 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 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 cAMP protein kinase A (PKA).

[00810] 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. 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 IL-2, IL-7, IL-10, IL-15, IL-18, and IL-21, and also NOTCH 1/2 intracellular domain (ICD). In some

embodiments, the transient alteration of protein expression targets the NOTCH signaling pathway, such as through the NOTCH 1/2 ICD and/or through other NOTCH ligand, such as mDLL1 (see, for example Kondo, T. et al., NOTCH-mediated conversion of activated T cells into stem cell memory-like T cells for adoptive immunotherapy, Nature Communications, Vol. 8, Article number: 15338 (2017), which is incorporated by reference herein in its entirety).

[00811] In some embodiments, the transient alteration of protein expression results in increased and/or overexpression of one or more binding partners that allow binding of exogenously administered cytokine carriers to the TILs via the one or more binding partners.

[00812] In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of PD-1, CTLA-4, TIM-3, LAG-3, TIGIT, 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 CBLB (CBL-B). In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of CISH.

[00813] 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.

[00814] 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, IL-18, and/or IL-21.

[00815] In some embodiments, the transient alteration of protein expression targets the NOTCH signaling pathway, such as through the NOTCH 1/2 ICD and/or through other NOTCH ligand, such as mDLL1 (see, for example Kondo, T. et al., NOTCH-mediated conversion of activated T cells into stem cell memory-like T cells for adoptive immunotherapy, Nature Communications, Vol. 8, Article number: 15338 (2017), which is incorporated by reference herein in its entirety). 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 a NOTCH ligand, such as mDLL1. 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,

[00816] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of cAMP protein kinase A (PKA).

[00817] 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, 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, 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, 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, LAG-3, CISH, CTLA-4, TIGIT, CBLB, TIM3, 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 LAG3, CISH, CTLA-4, TIGIT, CBLB, TIM3, 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 TIGIT. 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 CTLA-4 and TIGIT. In 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 TIGIT and LAG3. In some embodiments, the transient alteration of protein expression

results in decreased and/or reduced expression of TIGIT and CISH. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIGIT and CBLB. In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of TIGIT and TIM3. 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 CISH and CBLB. 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.

[00818] 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).

[00819] 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, 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, TIGIT, LAG3, TIM3, CISH, CBLB, and combinations thereof, and increased and/or enhanced expression of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof.

[00820] 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%.

[00821] 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%.

[00822] 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 (Sharei et al. PNAS 2013, as well as Sharei et al. PLOS ONE 2015 and Greisbeck et al. J. Immunology vol. 195, 2015) have been described, including rapid methods for deforming cells using a microfluidic constriction such that a TF or other molecule enters the cells: see, for example, 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. 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 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 the 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.

[00823] 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.

[00824] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising:

[00825] (i) obtaining a first population of TILs from a tumor resected from a patient by processing a sample from the resected tumor into multiple tumor fragments;

[00826] (ii) performing a first expansion by culturing the first population of TILs in a cell culture medium comprising IL-2, and optionally OKT-3, to produce a second population of TILs;

[00827] (iii) 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 third population of TILs is a therapeutic population of TILs; and

[00828] (iv) exposing the second and/or third population of TILs to transcription factors (TFs) and/or other molecules capable of transiently altering protein expression, wherein the TFs and/or other molecules 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 the therapeutic population of TILs.

[00829] In some embodiments, the tumor antigens are selected from, but are not limited to, IL-15, IL-21, IL-12 and IL-18. In particular, in some embodiments, the TFs alter expression of one or more of IL-15, IL-21, IL-12 and IL-18 so as to increase the expression thereof.

[00830] In some embodiments, the exposure to the TFs and/or the molecules capable of altering protein expression is mediated by sterile electroporation or a SQZ microfluidic membrane disruption.

[00831] In some embodiments, the TFs and/or the molecules capable of altering protein expression include, but are not limited to at least one short interfering RNA or one messenger RNA. In some embodiments, the short interfering RNA for inhibiting the expression of a molecule selected from the group consisting of PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, an adhesion molecule selected from the group consisting of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof is inserted into the first population of TILs, second population of TILs, or harvested population of TILs in addition to the TFs and/or the molecules capable of altering protein expression. The adhesion molecule may be inserted by, for example, a retroviral (e.g., a gammaretroviral), or a lentiviral method.

[00832] 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 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.

[00833] In some embodiments, transient alteration of protein expression is a reduction in expression induced by self-delivering RNA interference (sd-RNA), 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. Methods of using sd-RNA 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, in press, the disclosures of which are incorporated by reference herein. In some embodiments, delivery of sd-RNA 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 sd-RNA at a concentration of 1 μM/10,000 TILs in medium. In some embodiments, delivery of sd-RNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to sd-RNA at a concentration of 10 μM/10,000 TILs in medium. In some embodiments, delivery of sd-RNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to sd-RNA at a concentration of 50 μM/10,000 TILs in medium. In some embodiments, delivery of sd-RNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to sd-RNA at a concentration of between 0.1 μM/10,000 TILs and 50 μM/10,000 TILs in medium. In some embodiments, delivery of sd-RNA to a TIL population is accomplished using a 1 to 3 day period in which a TIL population is exposed to sd-RNA at a concentration of between 0.1 μM/10,000 TILs and 50 μM/10,000 TILs in medium, wherein the exposure to sd-RNA is performed two, three, four, or five times by addition of fresh sd-RNA 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.

[00834] In some embodiments, the sd-RNA encodes RNA that interferes with NOTCH 1/2 ICD, NOTCH ligand mDLL1, 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%.

1. sd-RNA Methods

[00835] 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 sd-RNAs 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 and US Patent Publication No. 20160304873) allow sd-RNAs to penetrate cultured mammalian cells without additional formulations and methods by simple addition to the culture media, capitalizing on the nuclease stability of sd-RNAs. This stability allows the support of constant levels of RNAi-mediated reduction of target gene activity simply by maintaining the active concentration of sd-RNA in the media. While not being bound by theory, the backbone stabilization of sd-RNA provides for extended reduction in gene expression effects which can last for months in non-dividing cells.

[00836] In some embodiments, over 95% transfection efficiency of TILs and a reduction in expression of the target by various specific sd-RNA occurs. In some embodiments, sd-RNAs 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 sd-RNA 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 sd-RNA results in an increase TIL proliferation.

a. sd-RNA Selection and Features

i. sd-RNA Oligonucleotide Structure

[00837] 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.

[00838] 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.

[00839] sd-RNA (self-deliverable RNA) are a new class of covalently modified RNAi compounds that do not require a delivery vehicle to enter cells and have improved pharmacology compared to traditional siRNAs. "Self-deliverable RNA" or "sd-RNA" is a hydrophobically modified RNA interfering-antisense hybrid, demonstrated to be highly efficacious in vitro in primary cells and in vivo upon local administration. Robust uptake and/or silencing without toxicity has been demonstrated. sd-RNAs are generally asymmetric chemically modified nucleic acid molecules with minimal double stranded regions. sd-RNA molecules typically contain single stranded regions and double stranded regions, and can contain a variety of chemical modifications within both the single stranded and double stranded regions of the molecule. Additionally, the sd-RNA molecules can be attached to a hydrophobic conjugate such as a conventional and advanced sterol-type molecule, as described herein. sd-RNAs (and/or RNAs capable of being employed in similar manners to sd-RNAs) and associated methods for making such sd-RNAs have also been described extensively in, for example, U.S. Patent Publication No. US 2016/0304873, International Patent Application Publication No. WO2010/033246, International Patent Application Publication No. WO2017/070151, International Patent Application Publication No. WO2009/102427, International Patent Application Publication No. WO201/1119887, International Patent Application Publication No. WO2010/033247, International Patent Application Publication No. WO2009045457, International Patent Application Publication No. WO2011/119852, International Patent Application Publication No. WO2011/119871, US Patent Publication No. US 2011/0263680, International Patent Application Publication No. WO2010/033248, International Patent Application Publication No. WO2010/078536, International Patent Application Publication No. WO2010/090762, U.S. Patent Publication No. US 20110039914,

International Publication No. WO2011/109698, International Patent Application Publication No. WO2010/090762, U.S. Patent No. US 8,815,818, International Patent Application Publication No. WO2016/094845, International Patent Application Publication No. WO2017/193053, U.S. Patent Publication No. US 2006/0276635, International Patent Application Publication No. WO2001/009312, U.S. Patent Publication No. US 2017/0043024, U.S. Patent Publication No. US 2017/0312367, U.S. Patent Publication No. US 2016/0319278, U.S. Patent Publication No. US 2017/0369882, U.S. Patent No. US 8,501,706, U.S. Patent Publication No. US 2004/0224405, U.S. Patent No. US 8,252,755, U.S. Patent Publication No. US 2007/0031844, U.S. Patent Publication No. US 2007/0039072, U.S. Patent Publication No. US 2007/0207974, U.S. Patent Publication No. US 2007/0213520, U.S. Patent Publication No. US 2007/0213521, U.S. Patent Publication No. US 2007/0219362, U.S. Patent Publication No. US 2007/0238868, U.S. Patent Publication No. US 2014/0148362, U.S. Patent Publication No. US 2016/0193242, U.S. Patent Publication No. US 2016/01946461, U.S. Patent Publication No. US 2016/0201058, U.S. Patent Publication No. US 2016/0201065, U.S. Patent Publication No. US 2017/0349904, U.S. Patent Publication No. US 2018/0119144, U.S. Patent No. US 7,834,170, U.S. Patent No. US 8,090,542, and U.S. Patent Publication No. US 2012/0052487, all of which are incorporated by reference herein in their entireties for all purposes; also sd-RNAs are commercially available from Advirna LLC, Worcester, MA, USA. To optimize sd-RNA structure, chemistry, targeting position, sequence preferences, and the like, a proprietary algorithm has been developed and utilized for sd-RNA potency prediction (see, for example, US 20160304873). Based on these analyses, functional sd-RNA sequences have been generally defined as having over 70% reduction in expression at 1 μM concentration, with a probability over 40%.

ii. sd-RNA Oligonucleotide Structure

[00840] In some embodiments, one or more sd-RNAs for use in the present invention can be generated from a linear double-stranded DNA template. In some embodiments, the linear double-stranded DNA template for generating the one or more sd-RNAs is one as described in U.S. Patent No. US 8,859,229, as well as described below.

[00841] In some embodiments, a linear double-stranded DNA template obtained by polymerase chain reaction (PCR) and suitable for in vitro transcription of an mRNA comprises from 5' to 3': an RNA polymerase promoter on the coding strand of the double-stranded DNA, a 5' untranslated region less than 3,000 nucleotides in length and effective for translation of the mRNA into a detectable polypeptide after transfection into a eukaryotic cell, an open reading frame that encodes the polypeptide, wherein the polypeptide is heterologous to the cell to be transfected and wherein the polypeptide is selected from the group consisting of a ligand or a receptor of an immune cell, a polypeptide that stimulates or inhibits a function of the immune system, and a polypeptide that

inhibits the function of an oncogenic polypeptide, 3' untranslated region effective for translation of the mRNA into a detectable polypeptide after transfection into a eukaryotic cell, and a poly(A) stretch of 50-5,000 nucleotides on the coding strand of the double-stranded DNA, wherein the promoter is heterologous to the open reading frame, and wherein the DNA template is not contained within a DNA vector and terminates with the 3' end of the poly(A) stretch. In some embodiments, the RNA polymerase promoter comprises a consensus binding sequence for an RNA polymerase selected from the group consisting of T7, T3 or SP6 RNA polymerase. In some embodiments, the open reading frame encodes a fusion polypeptide. In some embodiments, the open reading frame encodes a polypeptide selected from the group consisting of PD-1, TGFBR2, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-12, IL-15, IL-18, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, 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, cAMP protein kinase A (PKA) , and combinations thereof. In some embodiments, the open reading frame encodes a polypeptide selected from the group consisting of PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the linear double-stranded further comprises an internal ribosome entry site. In some embodiments, the poly(A) stretch is 300-400 nucleotides in length.

[00842] In some embodiments, the linear double-stranded DNA template of claim 1, wherein from 5' to 3' the template consists of an RNA polymerase promoter on the coding strand of the double-stranded DNA, a 5' untranslated region less than 3,000 nucleotides in length and effective for translation of the mRNA into a detectable polypeptide after transfection into a eukaryotic cell, an open reading frame that encodes the polypeptide, wherein the polypeptide is heterologous to the cell to be transfected and wherein the polypeptide is selected from the group consisting of a ligand or a receptor of an immune cell, a polypeptide that stimulates or inhibits a function of the immune system, and a polypeptide that inhibits the function of an oncogenic polypeptide, a 3' untranslated region effective for translation of the mRNA into a detectable polypeptide after transfection into a eukaryotic cell, and a poly(A) stretch of 50-5,000 nucleotides on the coding strand of the double-stranded DNA, wherein the promoter is heterologous to the open reading frame, and wherein the DNA template is not contained within a DNA vector and terminates with the 3' end of the poly(A) stretch. In some embodiments, the 3' untranslated region is at least 100 nucleotides in length.

[00843] In some embodiments, the present invention provides a method of generating the linear double-stranded DNA template described above, wherein the method comprises generating forward and reverse primers, wherein the forward primer comprises a plurality of nucleotides that are substantially complementary to the non-coding strand of a target double-stranded DNA of interest, and a plurality of nucleotides that function as a binding site for an RNA polymerase, wherein the

reverse primer comprises a plurality of nucleotides that are substantially complementary to the coding strand of a target double-stranded DNA of interest, and a plurality of deoxythymidine nucleotides, and performing polymerase chain reaction amplification of the target DNA using the forward and reverse primers to form the linear double-stranded DNA template. In some embodiments, the present invention provides a method of generating the linear double-stranded DNA template described above, wherein the method comprises generating forward and reverse primers, wherein the forward primer comprises a plurality of nucleotides that are substantially complementary to a region of nucleotides directly upstream of a target double-stranded DNA of interest, wherein the reverse primer comprises a plurality of nucleotides that are substantially complementary to a region of nucleotides directly downstream of a target double-stranded DNA of interest, and performing polymerase chain reaction amplification of the target DNA using the forward and reverse primers to form the linear double-stranded DNA template. In some embodiments, the primers comprise nucleotide sequences that are substantially complementary to stretches of nucleotides in the 5' and 3' untranslated regions of a double-stranded DNA of interest. In some embodiments, the primers comprise nucleotide sequences that are substantially complementary to stretches of nucleotides within the open reading frame of a double-stranded DNA of interest. In some embodiments, the primers comprise nucleotide sequences that are substantially complementary to stretches of nucleotides within the open reading frame of a double-stranded DNA of interest, wherein the primers further comprise stretches of nucleotides that comprise 5' and 3' untranslated regions, wherein the stretch of nucleotides in the forward primer that comprise the 5' untranslated region is between the nucleotides that comprise the RNA polymerase promoter and the nucleotides that are substantially complementary to the non-coding strand of a target double-stranded DNA of interest, and wherein the stretch of nucleotides in the reverse primer that comprise the 3' untranslated region is between the plurality of deoxythymidine nucleotides and the nucleotides that are substantially complementary to the coding strand of a target double-stranded DNA of interest. In some embodiments, the forward primer and open reading frame comprise a consensus Kozak sequence.

[00844] In some embodiments, the invention provides a method of generating one or more RNAs for transfection of cells comprising performing in vitro transcription from the linear double-stranded DNA template. In some embodiments, the method further comprises using a poly(A) polymerase to extend the poly(A) tail of the RNA with one or more adenine nucleotides or analogs thereof. In some embodiments, the method further comprises adding nucleotides during transcription that function as a 5' cap for the transcribed RNA. In some embodiments, the RNA targets a polypeptide selected from the group consisting of PD-1, TGFBR2, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-12, IL-15, IL-18, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, 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, cAMP protein kinase A (PKA), and combinations thereof. In some embodiments, the RNA targets a polypeptide selected from the group consisting of PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof.

[00845] In some embodiments, the invention employs the use of one or more isolated RNAs comprising one or more open reading frames, produced from the linear double-stranded DNA template. In some embodiments, the invention provides a method for expressing one or more RNAs in a cell comprising contacting cells with one or more RNAs produced from the linear double-stranded DNA template. In some embodiments, the RNAs are present in unequal molar amounts to provide separate expression levels of the RNAs in the cells. In some embodiments, the one or more RNAs target a polypeptide selected from the group consisting of PD-1, TGFBR2, CBLB (CBL-B), CISH, CCRs (chimeric co-stimulatory receptors), IL-2, IL-12, IL-15, IL-18, IL-21, NOTCH 1/2 ICD, TIM3, LAG3, TIGIT, 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, cAMP protein kinase A (PKA), and combinations thereof. In some embodiments, the one or more RNAs target a polypeptide selected from the group consisting of PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof.

Untranslated Regions

[00846] Chemical structures with the ability to promote stability and/or translation efficiency may also be used. The RNA preferably has 5' and 3' UTRs. The examples below demonstrate that inclusion of 44 base pairs of 5' UTR into the PCR template enabled greater translation efficiency of transcribed CFP RNA when compared to PCR templates containing only 6 base pairs of 5' UTR. The examples also demonstrate that the addition of 113 base pairs of 3, UTR enables greater translation efficiency of transcribed GFP RNA when compared to PCR templates containing only 11 base pairs of 3, UTR. In general, the length of the 3' UTR exceeds 100 nucleotides, and therefore 3' UTR longer than 100 nucleotides is preferred. In some embodiments the 3' UTR sequence is between 100 and 5000 nucleotides. The length of the 5' UTR is not as critical as the length of the 3' UTR and can be shorter. In some embodiments, the 5' UTR is between zero and 3000 nucleotides in length. The length of 5' and 3' UTR sequences to be added to the coding region can be altered by different methods, including, but not limited to, designing primers for PCR that anneal to different regions of the UTRs. Using this approach, one of ordinary skill in the art can modify the 5' and 3' UTR lengths required to achieve optimal translation efficiency following transfection of the transcribed RNA.

[00847] The 5' and 3' UTRs can be the naturally occurring, endogenous 5' and 3' UTRs for the gene of interest. Alternatively, UTR sequences that are not endogenous to the gene of interest can be added by incorporating the UTR sequences into the forward and reverse primers or by any other modifications of the template. The use of UTR sequences that are not endogenous to the gene of interest can be useful for modifying the stability and/or translation efficiency of the RNA. For example, it is known that AU-rich elements in 3' UTR sequences can decrease the stability of mRNA. Therefore, 3' UTRs can be selected or designed to increase the stability of the transcribed RNA based on properties of UTRs that are well known in the art.

[00848] In some embodiments, the 5' UTR can contain the Kozak sequence of the endogenous gene. Alternatively, when a 5' UTR that is not endogenous to the gene of interest is being added by PCR as described above, a consensus Kozak sequence can be redesigned by adding the 5' UTR sequence. Kozak sequences can increase the efficiency of translation of some RNA transcripts, but does not appear to be required for all RNAs to enable efficient translation. The requirement for Kozak sequences for many mRNAs is known in the art. In other embodiments the 5' UTR can be derived from an RNA virus whose RNA genome is stable in cells. In other embodiments various nucleotide analogues can be used in the 3' or 5' UTR to impede exonuclease degradation of the mRNA.

RNA Polymerase Promoter

[00849] To enable synthesis of RNA from a DNA template without the need for gene cloning, a promoter of transcription should be attached to the DNA template upstream of the sequence to be transcribed. Bacteriophage RNA polymerase promoter sequences can be attached to the St UTR by different genetic engineering methods, such as DNA ligation, or can be added to the forward primer (5') of the sequence that is substantially complementary to the target DNA. When a sequence that functions as a promoter for an RNA polymerase is added to 5' end of the forward primer, the RNA polymerase promoter becomes incorporated into the PCR product upstream of the open reading frame that is to be transcribed. In one preferred embodiment, the promoter is a T7 polymerase promoter, as described above. Other useful promoters include, but are not limited to, T3 and SP6 RNA polymerase promoters. Consensus nucleotide sequences for T7, T3 and SP6 promoters are known in the art.

Poly(A) Tail and 5' Cap

[00850] In a preferred embodiment, the mRNA has both a cap on the 5' end and a 3' poly(A) tail which determine ribosome binding, initiation of translation and stability mRNA in the cell. On a circular DNA template, for instance, plasmid DNA, RNA polymerase produces a long concatameric product which is not suitable for expression in eukaryotic cells. The transcription of plasmid DNA linearized at the end of the 3' UTR results in normal sized mRNA which is not effective in eukaryotic transfection even if it is polyadenylated after transcription.

[00851] On a linear DNA template, phage T7 RNA polymerase can extend the 3' end of the transcript beyond the last base of the template (Schenborn and Mierendorf, Nuc. Acids Res., 13:6223-36 (1985); Nacheva and Berzal-Herranz, Eur. J. Biochem., 270:1485-65 (2003). This could lead to runoff transcript bending followed by template exchange with the second DNA strand or transcription of RNA itself (Triana-Alonso et al., J. Biol. Chem., 270:6298-307 (1995); Dunn and Studier, J. Mol. Biol., 166:477-535 (1983); Arnaud-Barbe et al., Nuc. Acids Res., 26:3550-54 (1998); Macdonald et al., 1993), and then to the aberrant transcription in a reverse direction and accumulation of double stranded RNA, which can inhibit gene expression. DNA linearization itself is not sufficient for correct transcription (Triana-Alonso et al., J. Biol. Chem., 270:6298-307 (1995); Dunn and Studier, J. Mol. Biol., 166:477-535 (1983); Arnaud-Barbe et al., 1998 Nuc. Acids Res., 26:3550-54 (1998); Macdonald et al., J. Mol. Biol., 232:1030-47 (1993); Nakano et al., Biotechnol. Bioeng., 64:194-99 (1999), plasmid DNA linearized downstream of a poly(A/T) stretch of 64-100 nucleotides results in good templates (Saeboe-Larssen et al., J. Immunol. Meth., 259:191-203 (2002); Boczkowski et al., Cancer Res., 60:1028-34 (2000); Elango et al., Biochem Riophys Res Commun., 330:958-966 2005). An endogenous termination signal for T7 RNA polymerase encodes an RNA that can fold into a stem-loop structure followed by a track of uridine residues (Dunn and Studier, J. Mol. Biol., 166:477-535 (1983); Arnaud-Barbe et al., 1998 Nuc. Acids Res., 26:3550-54 (1998)). Even without a hairpin, a track of synthesized uridines can attenuate transcription (Kiyama and Oishi, Nuc. Acids Res., 24:4577-4583 (1996). It was hypothesized that the linearization of plasmid DNA downstream of the poly(A/T) stretch probably formed a type of "dynamic" terminator preventing potential aberrant transcription: a 3' extension of the RNA transcript over a poly(A/T) stretch and transcription in the reverse direction will create a growing termination-like signal--an extended poly(U) stretch and a poly(A/U) hairpin. Accordingly, reversed PCR primers were designed with a 3' anchoring sequence downstream of the GFP gene and a 5' 100 base stretch of poly(T).

[00852] The conventional method of integration of polyA/T stretches into a DNA template is molecular cloning. However, polyA/T sequence integrated into plasmid DNA can cause plasmid instability, which is why plasmid DNA templates obtained from bacterial cells are often highly contaminated with deletions and other aberrations. This makes cloning procedures not only laborious and time consuming but often not reliable. That is why a method which allows construction of DNA templates with polyA/T 3' stretch without cloning highly desirable.

[00853] The polyA/T segment of the transcriptional DNA template can be produced during PCR by using a reverse primer containing a polyT tail, such as 100T tail (size can be 50-5000 T), or after PCR by any other method, including, but not limited to, DNA ligation or in vitro recombination. Poly(A) tails also provide stability to RNAs and reduce their degradation. Generally, the length of a poly(A) tail positively correlates with the stability of the transcribed RNA. In some embodiments, the poly(A)

tail is between 100 and 5000 adenosines. The examples below demonstrate that a 100 base pair stretch of poly(A) is sufficient to enable efficient translation of an RNA transcript.

[00854] Poly(A) tails of RNAs can be further extended following in vitro transcription with the use of a poly(A) polymerase, such as E. coli polyA polymerase (E-PAP). The examples below demonstrate that increasing the length of a poly(A) tail from 100 nucleotides to between 300 and 400 nucleotides results in about a two-fold increase in the translation efficiency of the RNA. Additionally, the attachment of different chemical groups to the 3' end can increase mRNA stability. Such attachment can contain modified/artificial nucleotides, aptamers and other compounds. For example, ATP analogs can be incorporated into the poly(A) tail using poly(A) polymerase. ATP analogs can further increase the stability of the RNA. Suitable ATP analogs include, but are not limited to, cordiocipin and 8-azaadenosine.

[00855] 5' caps can also provide stability to RNA molecules. In a preferred embodiment, RNAs produced by the methods disclosed herein include a 5' cap. The 5' cap may, for example, be m7G(5')ppp(5')G, m7G(5')ppp(5')A, G(5')ppp(5')G or G(5')ppp(5')A cap analogs, which are all commercially available. The 5' cap can also be an anti-reverse-cap-analog (ARCA) (see, Stepinski, et al., RNA, 7:1468-95 (2001)) or any other suitable analog. The 5' cap is provided using techniques known in the art and described herein (Cougot, et al., Trends in Biochem. Sci., 29:436-444 (2001); Stepinski, et al., RNA, 7:1468-95 (2001); Elango, et al., Biochim. Biophys. Res. Commun., 330:958-966 (2005)).

[00856] The RNAs produced by the methods disclosed herein can also contain an internal ribosome entry site (IRES) sequence. The IRES sequence may be any viral, chromosomal or artificially designed sequence which initiates cap-independent ribosome binding to mRNA and facilitates the initiation of translation. Any solutes suitable for cell electroporation, which can contain factors facilitating cellular permeability and viability such as sugars, peptides, lipids, proteins, antioxidants, and surfactants can be included.

[00857] In some embodiments, the sd-RNA sequences used in the invention exhibit a 70% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit a 75% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit an 80% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit an 85% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit a 90% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit a 95% reduction in expression of the target gene. In some embodiments, the sd-RNA sequences used in the invention exhibit a 99% reduction in expression of the target gene. In some

embodiments, the sd-RNA 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 10 μM, in some embodiments, about 0.25 μM to about 4 μM. In some embodiments, the sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA 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 sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 4.0 μM. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 5.0 μM. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 6.0 μM. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 7.0 μM. In some embodiments, the sd-RNA sequences used in

the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 8.0 μM. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 9.0 μM. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 10.0 μM. In some embodiments, the sd-RNA 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 10 μM/10,000 TILs, or about 0.25 μM to about 4 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.25 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.5 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.75 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.25 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.5 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.75 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.25 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.5 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.75 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.25 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.5 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.75 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a

reduction in expression of the target gene when delivered at a concentration of about 4.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 5.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 6.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 7.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 8.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 9.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 10.0 μM/10,000 TILs. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.25 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.5 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 0.75 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.0 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.25 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.5 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 1.75 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.0 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.25 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.5 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 2.75 μM/10,000 TILs/100 μL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.0 μM/10,000

TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.25 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.5 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 3.75 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 4.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 5.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 6.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 7.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 8.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 9.0 µM/10,000 TILs/100 µL media. In some embodiments, the sd-RNA sequences used in the invention exhibit a reduction in expression of the target gene when delivered at a concentration of about 10.0 µM/10,000 TILs/100 µL media.

sd-RNA Modifications

[00858] In some embodiments, the 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, a 2'-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 an additional particular embodiment, 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 (-OCH2CH=CH2), 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 (Augustyns, K., et al., Nucl. Acids. Res., 18:4711 (1992)).

[00859] In some embodiments, the double-stranded 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 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.

[00860] In some embodiments, a double-stranded 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 some embodiments, a double-stranded 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 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 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.

[00861] In some embodiments, the oligonucleotide can be substantially protected from nucleases e.g., by modifying the 3' or 5' linkages (e.g., U.S. Pat. No. 5,849,902 and WO 98/13526). 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 (CH2-CH2-CH3), glycol (-0-CH2-CH2-O-) phosphate (PO32"), 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.

[00862] In some embodiments, at least a portion of the contiguous polynucleotides within the sd-RNA are linked by a substitute linkage, e.g., a phosphorothioate linkage.

[00863] 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, 500 enhancements in cellular uptake. 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.

[00864] In some embodiments, the sd-RNA or sd-rxRNAs exhibit enhanced endosomal release of sd-rxRNA molecules 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 sd-RNA 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 sd-RNA 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 sd-RNA compounds of the invention also include a unique chemical modification pattern, which provides stability and is compatible with RISC entry.

[00865] 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.

[00866] In some embodiments, at least 30% of the nucleotides in the sd-RNA or sd-rxRNA are 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 sd-RNA or sd-rxRNA are modified. In some embodiments, 100% of the nucleotides in the sd-RNA or sd-rxRNA are modified.

[00867] In some embodiments, the sd-RNA 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.

[00868] In some embodiments, the sd-RNA molecules have increased stability. In some instances, a chemically modified sd-RNA or sd-rxRNA 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 sd-rxRNA has a half-life in media that is longer than 12 hours.

[00869] In some embodiments, the sd-RNA 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 sd-RNA has no 2'F modification and yet are characterized by equal efficacy in cellular uptake and tissue penetration.

[00870] 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 contains 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.

Delivery of sd-RNA

[00871] The self-deliverable RNAi technology provides a method of directly transfecting cells with the RNAi agent, 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 sd-RNA 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 sd-RNAi methods allows direct delivery of chemically synthesized compounds to a wide range of primary cells and tissues, both ex-vivo and in vivo. The sd-RNAs described In some embodiments, of the invention herein are commercially available from Advirna LLC, Worcester, MA, USA.

[00872] sd-RNA are formed as hydrophobically-modified siRNA-antisense oligonucleotide hybrid structures, and are disclosed, for example in Byrne et al., December 2013, J. Ocular Pharmacology and Therapeutics, 29(10): 855-864, incorporated by reference herein in its entirety.

[00873] In some embodiments, the sd-RNA oligonucleotides can be delivered to the TILs described herein using sterile electroporation.

[00874] 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.

[00875] In some embodiments, the oligonucleotides, such as RNAs or sd-RNAs described herein, can be introduced into target cells using different methods, for instance, commercially available methods which include, but are not limited to, electroporation (Amaxa Nucleofector-II (Amaxa Biosystems, Cologne, Germany)), (ECM 830 (BTX) (Harvard Instruments, Boston, MA), NeonTM Transfection System (commercially available from ThermoFisher Scientific, Waltham, MA), and/or the Gene Pulser II (BioRad, Denver, CO), Multiporator (Eppendort, Hamburg Germany), cationic

liposome mediated transfection using lipofection, polymer encapsulation, peptide mediated transfection, or biolistic particle delivery systems such as "gene guns" (see, for example, Nishikawa, et al. Hum Gene Ther., 12(8):861-70 (2001), incorporated by reference herein in its entirety. See, also, U.S. Patent No. 8,859,229, U.S. Patent Application No. 2016/0230188, as well as the Amaxa Nucleofector ® II Manual (available on the World Wide Web at http://icob.sinica.edu.tw/pubweb/biochem/Core%20Facilities/Data/R401-core/Nucleofector_Manual_II_Apr06.pdf).

[00876] In some embodiments, electroporation can be performed using an Amaxa NUCLEOFECTOR.TM.-II in accordance with manufacturer recommendations. In some embodiments, TILs can be transfected using NUCLEOFECTOR.TM.-II solution V and the set of recommended regimes for electroporation. In some embodiments, TILs can be transfected using solutions V, T and R and different regimes of electroporation. In some embodiments, TILs can be transfected using T cell NUCLEOFECTOR.TM.-II solution and different regimes of electroporation. Alternative methods of nucleic acids delivery can also be employed to transfect the oligonucleotides described herein used: cationic liposome mediated transfection was performed using LIPOFECTIN or LIPOFECTAMIN (Invitrogen). Electroporation was also performed with the ECM 830 (BTX) (Harvard Instruments, Boston, MA), the Gene Pulser II (BioRad, Denver, CO), Multiporator (Eppendorf, Hamburg Germany), and/or the NeonTM Transfection System (commercially available from ThermoFisher Scientific, Waltham, MA). In some embodiments, a pmaxGFP plasmid DNA (Amaxa Biosystems) can be employed as the DNA control. In some embodiments, the efficiency of transfection (ET) can be determined approximately 3, 6, 9, 12, 15, and/or 18 hours after transfection by fluorescence activated cell sorting (FACS). In some experiments transfectants can be further analyzed every 12 hours to 24 hours until GFP could no longer be detected for GFP controls. In some embodiments, cell viability can be determined by trypan blue dye exclusion.

[00877] 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 sd-RNA 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. Moreover, sd-RNA can be added after thawing from any cryopreservation step in Step F. In some embodiments, one or more sd-RNAs targeting genes as described herein, including PD-1, LAG-3, TIM-3, CISH, 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 sd-RNAs targeting

genes as described herein, including PD-1, LAG-3, TIM-3, CISH, CTLA-4, TIGIT, 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 sd-RNA/10,000 TILs/100 μL media, 0.5 μM sd-RNA/10,000 TILs /100 μL media, 0.75 μM sd-RNA/10,000 TILs /100 μL media, 1 μM sd-RNA/10,000 TILs /100 μL media, 1.25 μM sd-RNA/10,000 TILs /100 μL media, 1.5 μM sd-RNA/10,000 TILs /100 μL media, 2 μM sd-RNA/10,000 TILs /100 μL media, 5 μM sd-RNA/10,000 TILs /100 μL media, or 10 μM sd-RNA/10,000 TILs /100 μL media. In some embodiments, one or more sd-RNAs targeting genes as described herein, including PD-1, CTLA-4, TIGIT, LAG-3, TIM-3, CISH, 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. In some embodiments, one or more sd-RNAs targeting genes as described herein, including PD-1, CTLA-4, TIGIT, LAG-3, TIM-3, CISH, 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 sd-RNA/10,000 TILs, 0.5 μM sd-RNA/10,000 TILs, 0.75 μM sd-RNA/10,000 TILs, 1 μM sd-RNA/10,000 TILs, 1.25 μM sd-RNA/10,000 TILs, 1.5 μM sd-RNA/10,000 TILs, 2 μM sd-RNA/10,000 TILs, 5 μM sd-RNA/10,000 TILs, or 10 μM sd-RNA/10,000 TILs. In some embodiments, one or more sd-RNAs targeting genes as described herein, including PD-1, CTLA-4, TIGIT, LAG-3, TIM-3, CISH, and CBLB, may be added to TIL cultures during the first, second, and or additional expansion 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.

[00878] Oligonucleotide compositions of the invention, including sd-RNA, can be contacted with TILs as described herein during the expansion process, for example by dissolving sd-RNA at high concentrations in cell culture media and allowing sufficient time for passive uptake to occur. In some embodiments, the high concentrations include 0.1 μM sd-RNA/10,000 TILs, 0.5 μM sd-RNA/10,000 TILs, 0.75 μM sd-RNA/10,000 TILs, 1 μM sd-RNA/10,000 TILs, 1.25 μM sd-RNA/10,000 TILs, 1.5 μM sd-RNA/10,000 TILs, 2 μM sd-RNA/10,000 TILs, 5 μM sd-RNA/10,000 TILs, or 10 μM sd-RNA/10,000 TILs. In some embodiments, the high concentrations include 2 μM sd-RNA/10,000 TILs, 5 μM sd-RNA/10,000 TILs, or 10 μM sd-RNA/10,000 TILs. In some embodiments, the high concentrations include 5 μM sd-RNA/10,000 TILs or up to 10 μM sd-RNA/10,000 TILs.

[00879] 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 (see, e.g., WO 90/14074; WO 91/16024; WO 91/17424; U.S. Pat. No. 4,897,355; Bergan et a 1993. Nucleic Acids Research. 21 :3567).

sd-RNA Combinations

[00880] In some embodiments, more than one sd-RNA is used to reduce expression of a target gene. In some embodiments, one or more of PD-1, CTLA-4, TIGIT, TIM-3, CBLB, LAG3 and/or CISH targeting sd-RNAs are used together. In some embodiments, a PD-1 sd-RNA is used with one or more of CTLA-4, TIGIT, TIM-3, CBLB, LAG3 and/or CISH in order to reduce expression of more than one gene target. In some embodiments, a LAG3 sd-RNA is used in combination with a CISH targeting sd-RNA to reduce gene expression of both targets. In some embodiments, the sd-RNAs targeting one or more of PD-1, CTLA-4, TIGIT, TIM-3, CBLB, LAG3 and/or CISH herein are commercially available from Advirna LLC, Worcester, MA, USA.

[00881] In some embodiments, the sd-RNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the sd-RNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, one sd-RNA targets PD-1 and another sd-RNA targets a gene selected from the group consisting of LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the sd-RNA targets a gene selected from PD-1, LAG-3, CISH, CBLB, TIM3, and combinations thereof. In some embodiments, the sd-RNA targets a gene selected from PD-1 and one of CTLA-4, TIGIT, LAG3, CISH, CBLB, TIM3, and combinations thereof. In some embodiments, one sd-RNA targets PD-1 and one sd-RNA targets CTLA-4. In some embodiments, one sd-RNA targets PD-1 and one sd-RNA targets TIGIT. In some embodiments, one sd-RNA targets PD-1 and one sd-RNA targets LAG3. In some embodiments, one sd-RNA targets PD-1 and one sd-RNA targets CISH. In some embodiments, one sd-RNA targets PD-1 and one sd-RNA targets CBLB. In some embodiments, one sd-RNA targets CTLA-4 and one sd-RNA targets TIGIT. In some embodiments, one sd-RNA targets CTLA-4 and one sd-RNA targets LAG3. In some embodiments, one sd-RNA targets CTLA-4 and one sd-RNA targets CISH. In some embodiments, one sd-RNA targets CTLA-4 and one sd-RNA targets CBLB. In some embodiments, one sd-RNA targets CTLA-4 and one sd-RNA targets TIM3. In some embodiments, one sd-RNA targets TIGIT and one sd-RNA targets LAG3. In some embodiments, one sd-RNA targets TIGIT and one sd-RNA targets CISH. In some embodiments, one sd-RNA targets TIGIT and one sd-RNA targets CBLB. In some embodiments, one sd-RNA targets TIGIT and one sd-RNA targets TIM3. In some embodiments, one sd-RNA targets LAG3 and one sd-RNA targets CISH. In some embodiments, one sd-RNA targets LAG3 and one sd-RNA targets CBLB. In some embodiments, one sd-RNA targets LAG3 and one sd-RNA targets CTLA-4. In some embodiments, one sd-RNA targets LAG3 and one sd-RNA targets TIGIT. In some embodiments, one sd-RNA targets CISH and one sd-RNA targets CBLB. In some embodiments, one sd-RNA targets TIM3 and one sd-RNA targets PD-1. In some embodiments, one sd-RNA targets TIM3 and one sd-RNA targets LAG3. In some embodiments, one

sd-RNA targets TIM3 and one sd-RNA targets CISH. In some embodiments, one sd-RNA targets TIM3 and one sd-RNA targets CBLB.

Overexpression of Co-Stimulatory Receptors or Adhesion Molecules

[00882] According to additional embodiments, altering the protein expression of TILs during the TIL expansion method can also allow for expression of one or more immune checkpoint genes to be enhanced in at least a portion of the therapeutic population of TILs. For example, altering the protein expression may cause the expression of a stimulatory receptor to be enhanced, which means that it is overexpressed as compared to the expression of a stimulatory receptor that has not been genetically modified. Non-limiting examples of immune checkpoint genes that may exhibit enhanced expression by transiently altering the protein expression in 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-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

CCRs & CCLs

[00883] 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.

[00884] According to particular embodiments, altering the protein expression 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/or CX3CR1. Over-expression of CCRs may help promote effector function and proliferation of TILs following adoptive transfer. In some embodiments, altering the protein expression methods of the present invention may be used to increase the expression of CCL2 (MCP-1), CCL3 (MIP-1α), CCL4 (MIP1-β), CCL5 (RANTES), CXCL1, CXCL8, CCL22, and/or CCL17 in the TILs.

[00885] According to particular embodiments, expression of one or more of CCR2, CCR4, CCR5, CXCR2, CXCR3 and/or 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), wherein the method comprises gene-editing at least a portion of the TILs by enhancing the expression of one or more of CCR2, CCR4, CCR5, CXCR2, CXCR3 and/or CX3CR1. 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.

[00886] 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.

Interleukins & Others

[00887] 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, and also the NOTCH 1/2 intracellular domain (ICD). Certain interleukins have been demonstrated to augment effector functions of T cells and mediate tumor control.

Gene-Editing Processes

Overview: TIL Expansion + Gene-Editing

[00888] Embodiments of the present invention are directed to methods for expanding TIL populations, the methods comprising 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.

[00889] 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 PCT/US2017/058610, PCT/US2018/012605, or PCT/US2018/012633, which are incorporated by reference herein in their entireties, wherein the method further comprises gene-editing at least a portion of the TILs. Thus, an embodiment 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. Specific embodiments of the process of gene-editing are described in detail herein as well as in PCT/2019/029286, and PCT/US2019/012729, each of which is incorporated herein by reference in its entirety.

Timing of Gene-Editing During TIL Expansion

[00890] According to 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 patient by processing a sample from the resected tumor 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, gene-editing at least a portion of the TILs.

[00891] In some embodiments, the gene-editing results in a genetic modification of the TILs that causes expression of one or more cytokines, under control of an NFAT promoter, that modulate tumor microenvironment to promote expansion of administered population of TILs. For example, in some

embodiments, the gene-editing comprises transduction of TILs with an NFAT-IL-18 expression cassette. In some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to overexpress IL-18.

[00892] In some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to express ortho-IL2 receptor.

[00893] In some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to express a drug responsive domain (DRD)-cytokine construct that modulate tumor microenvironment to promote expansion of administered population of TILs, wherein the expressed DRD-cytokine is activated by an exogenously administered ligand that binds to the DRD of the DRD-cytokine to activate the cytokine. In some embodiments, the cytokine may be IL-2.

[00894] Thus, in some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to express IL2-fusion protein, wherein the IL-2 fusion protein releases IL-2 in response to a subsequent administration of a drug to the subject. In some embodiments, the fusion protein may be an IL-2-DRD, wherein the DRD is selected to separate from IL-2 in response to an administered drug.

[00895] In some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to express IL2-fusion protein, wherein the IL-2 fusion protein suppresses IL-2 activity in response to a subsequent administration of a drug to the subject. In some embodiments, the DRD is selected to mask active domains of IL-2 in response to the administered drug.

[00896] In some embodiments, the gene-editing results in a genetic modification that causes the administered TILs to express a dual IL-15-IL-21 protein.

[00897] In some embodiments, the gene-editing results in a genetic modification that causes TILs to express one or more binding partners that allow binding of exogenously administered cytokine carriers to the TILs via the one or more binding partners. In some embodiments, the binding partners may extend extracellularly from hydrophobic tails anchored in the cell membranes for the TILs.

[00898] In some embodiments, the binding partners include proteins or peptides having (i) a segment of hydrophobic amino acids at or close to the C-terminus such that the segment is anchored in the cell membrane of the TILs; and (ii) an antigen or epitope binding domain extending extracellularly from the segment.

[00899] For example, in some embodiments, the binding partner includes an antigen-binding fragment of an antibody and the cytokine carrier may include at least a portion of the antigen recognized by the antibody such that the binding partner recognizes the antigen and binds to the

cytokine carrier. In some embodiments, the binding partner can be a variable fragment of an scFv. In such embodiments, the cytokine carriers may include an epitope (e.g., a peptide epitope) extending therefrom such that the binding partner recognizes and binds the epitope.

[00900] In some embodiments, the binding partner includes an antigen recognized by an antigen-binding fragment of an antibody, and the cytokine carrier may include at least the antigen-binding fragment of the antibody such that the antigen-binding fragment recognizes the antigen and binds the cytokine carrier to the binding partner of the TIL cell surface. In some embodiments, the antigen-binding fragment can be a variable fragment of an scFv. In some embodiments, the TIL cells may include an epitope (e.g., a peptide epitope) extending therefrom such that the variable fragment of the scFv recognizes and binds the epitope.

[00901] In some embodiments, the binding partner may include a glycosyl-phosphatidylinositol (GPI) anchor enabling the binding partner to be anchored extracellularly in the cell membrane of the TILs. In such embodiments, the binding partner may include an antigen displayed on the TIL that can be recognized by an antibody provided on the cytokine carriers enabling the binding partner to bind with the cytokine carriers. *Brown and Waneck* (3(4) J. Am. Soc. Nephr. 1992, 895-906) provide a deailed review of GPI-anchored proteins.

[00902] Any of the gene-editing techniques described herein may be used for inducing the genetic modification in TILs to cause the TILs to express one or more binding partners described herein.

[00903] In some embodiments, the gene-editing results in a genetic modification that reduces expression of one or more of the following immune checkpoint genes selected from the group comprising PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[00904] In some embodiments, the gene-editing causes a genetic modification that causes the administered TILs to express cytokine carriers on surface of the genetically modified TILs that modulate tumor microenvironment to promote expansion of administered population of TILs, wherein the carriers link to binding partners extending extracellularly from hydrophobic tails anchored in cell membranes of the modified TILs, and release contents thereof by, one or both of: (i) gradual shedding with click chemistry, and (ii) redox reaction or enzymatic cleavage in the tumor microenvironment. In

some embodiments, the cytokine may be selected from the group of: IL-2, IL-4, IL-7, IL-12, IL-15, IL-18, IL-21, and combinations thereof.

[00905] As stated in step (g) of the embodiment described above, the gene-editing process may 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) outlined in the method above, or before or after any of steps (a)-(f) 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.

[00906] 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.

[00907] 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 another embodiment, 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.

[00908] According to another embodiment, 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.

[00909] According to another embodiment, 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.

[00910] 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)).

[00911] 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 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 another embodiment, the cell culture medium comprises OKT-3 during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the OKT-3 is introduced into the cell culture medium.

[00912] 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 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 another embodiment, the cell culture medium comprises a 4-1BB agonist during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the 4-1BB agonist is introduced into the cell culture medium.

[00913] 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 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 another embodiment, the cell culture

medium comprises IL-2 during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the IL-2 is introduced into the cell culture medium.

[00914] 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 an example, 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 another example, 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.

[00915] According to 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 at least a portion of a tumor resected from a patient by processing a sample from the resected tumor 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 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 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, and 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.

[00916] According to some embodiments, the foregoing method may be used to provide an autologous harvested TIL population for the treatment of a human subject with cancer.

[00917] In some embodiments, 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%.

[00918] 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.

[00919] In some emodiments, the 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 an additional particular embodiment, 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 (-OCH2CH=CH2), 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 (Augustyns, K., et al., Nucl. Acids. Res. 18:4711 (1992)).

[00920] In some embodiments, the double-stranded 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 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.

[00921] In some embodiments, a double-stranded 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 some embodiments, a double-stranded 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 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 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.

[00922] In some embodiments, the oligonucleotide can be substantially protected from nucleases e.g., by modifying the 3' or 5' linkages (e.g., U.S. Pat. No. 5,849,902 and WO 98/13526). 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 (CH2-CH2-CH3), glycol (-0-CH2-CH2-O-) phosphate (PO32"), 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.

[00923] In some embodiments, at least a portion of the contiguous polynucleotides within the sdRNA are linked by a substitute linkage, e.g., a phosphorothioate linkage.

[00924] 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, 500 enhancements in cellular uptake. 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.

[00925] In some embodiments, the sdRNA or sd-rxRNAs exhibit enhanced endosomal release of sd-rxRNA molecules 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 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 sdRNA comprises 2-12 phosphorothioate intemucleotide linkages (referred to as phosphorothioate modifications). In some embodiments, 6-8 phosphorothioate intemucleotide linkages are employed. In some embodiments, the sdRNA compounds of the invention also include a unique chemical modification pattern, which provides stability and is compatible with RISC entry.

[00926] 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.

[00927] In some embodiments, at least 30% of the nucleotides in the sdRNA or sd-rxRNA are 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 sdRNA or sd-rxRNA are modified. In some embodiments, 100% of the nucleotides in the sdRNA or sd-rxRNA are modified.

[00928] In some embodiments, the 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.

[00929] In some embodiments, the sdRNA molecules have increased stability. In some instances, a chemically modified sdRNA or sd-rxRNA 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 sd-rxRNA has a half-life in media that is longer than 12 hours.

[00930] In some embodiments, the 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 sdRNA has no 2'F modification and yet are characterized by equal efficacy in cellular uptake and tissue penetration.

[00931] 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 l9 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.

[00932] The self-deliverable RNAi technology provides a method of directly transfecting cells with the RNAi agent, 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 sdRNAi methods 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.

[00933] The sdRNA are formed as hydrophobically-modified siRNA-antisense oligonucleotide hybrid structures, and are disclosed, for example in Byrne et al., December 2013, J. Ocular Pharmacology and Therapeutics, 29(10): 855-864, incorporated by reference herein in its entirety.

[00934] In some embodiments, the 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 sdRNA oligonucleotides.

[00935] In some embodiments, the oligonucleotides can be delivered to the cells in combination with a transmembrane delivery system. In some embodimets, 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 sdRNA oligonucleotides to a population of TILs.

[00936] 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. Mroeover, 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, 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, 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, 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.

[00937] Oligonucleotide compositions of the invention, including 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.

[00938] 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 (see, e.g., WO 90/14074; WO 91/16024; WO 91/17424; U.S. Pat. No. 4,897,355; Bergan et al 1993. Nucleic Acids Research. 21 :3567).

[00939] In some embodiments, more than one sdRNA is used to reduce expression of a target gene. In some embodiments, one or more of PD-1, TIM-3, CBLB, LAG3 and/or CISH targeting sdRNAs are used together. In some embodiments, a PD-1 sdRNA is used with one or more of TIM-3, CBLB, LAG3 and/or CISH in order to reduce expression of more than one gene target. In some embodiments, a LAG3 sdRNA is used in combination with a CISH targeting sdRNA to reduce gene expression of both targets. In some embodiments, the sdRNAs targeting one or more of PD-1, TIM-3, CBLB, LAG3 and/or CISH herein are commercially available from Advirna LLC, Worcester, MA, USA.

[00940] In some embodiments, the sdRNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the sdRNA targets a gene selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, one sdRNA targets PD-1 and another sdRNA targets a gene selected from the group consisting of LAG3, TIM3, CTLA-4, TIGIT, CISH, TGFβR2, PKA, CBLB, BAFF (BR3), and combinations thereof. In some embodiments, the sdRNA targets a gene selected from PD-1, LAG-3, CISH, CBLB, TIM3, and combinations thereof. In some embodiments, the sdRNA targets a gene selected from PD-1 and one of LAG3, CISH, CBLB, TIM3, and combinations thereof. In some embodiments, one sdRNA targets PD-1 and one sdRNA targets LAG3. In some embodiments, one sdRNA targets PD-1 and one sdRNA targets CISH. In some embodiments, one sdRNA targets PD-1 and one sdRNA targets CBLB. In some embodiments, one sdRNA targets LAG3 and one sdRNA targets CISH. In some embodiments, one sdRNA targets LAG3 and one sdRNA targets CBLB. In some embodiments, one sdRNA targets CISH and one sdRNA targets CBLB. In some embodiments, one sdRNA targets TIM3 and one sdRNA targets PD-1. In some embodiments, one sdRNA targets TIM3 and one sdRNA targets LAG3. In some embodiments, one sdRNA targets TIM3 and one sdRNA targets CISH. In some embodiments, one sdRNA targets TIM3 and one sdRNA targets CBLB.

2. Transposon/Transposase Methods

[00941] 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 piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases). According to particular embodiments, the use of a piggyBac method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface of at least a portion of the therapeutic population of TILs. In some embodiments, the use of a piggyBac method during the TIL expansion process causes expression of one or more binding partners that allow binding of exogenously administered cytokine carriers to the TILs via the one or more binding partners. Alternatively, the use of a piggyBac method during the TIL expansion process causes expression of at least one immunomodulatory composition at the cell surface of, and optionally causes expression of one or more immune checkpoint genes to be modified (e.g., suppressed or 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.

[00942] The piggyBac transposon is a mobile genetic element that efficiently transposes between the donor vector and host chromosomes. This system has almost no cargo limit, and is fully reversible, leaving no footprint in the genome after excision. The piggyBac transposon/transposase system consists of a transposase that recognizes piggyBac-specific inverted terminal repeat sequences (ITRs) located on both sides of the transposon cassette. The transposase excises the transposable element to integrate it into TT/AA chromosomal sites that are preferentially located in euchromatic regions of mammalian genomes (Ding et al. 2005; Cadinaños and Bradley 2007; Wilson et al. 2007; Wang et al. 2008; Li et al. 2011).

[00943] Exemplary piggyBac systems include those described in WO2019/046815, the contents of which are incorporated herein by reference in their entirety. In some embodiments, the piggyBac system comprises a transposon/transposase system.

[00944] In some embodiments, a piggyBac method comprises delivering to the TILs, (a) a nucleic acid or amino acid sequence comprising a sequence encoding a transposase enzyme and (b) a recombinant and non-naturally occurring DNA sequence comprising a DNA sequence encoding a transposon.

[00945] In some embodiments, the sequence encoding a transposase enzyme is an mRNA sequence. In some embodiments, the sequence encoding a transposase enzyme is a DNA sequence. In some embodiments, the DNA sequence is a cDNA sequence. In some embodiments, the sequence encoding a transposase enzyme is an amino acid sequence. A protein Super piggybac transposase (SPB) may be delivered following pre-incubation with transposon DNA.

[00946] Exemplary transposon/transposase systems that can be used to genetically modify the subject TILs described herein include, but are not limited to, Sleeping Beauty transposons and transposases, Helraiser transposons and transposases and Tol2 transposons and transposases.

[00947] The piggyBac transposase recognizes transposon-specific inverted terminal repeat sequences (ITRs) on the ends of the transposon, and moves the contents between the ITRs into TTAA chromosomal sites. The piggyBac transposon system has no payload limit for the genes of interest that can be included between the ITRs. In some embodiments, the transposon is a piggyBac transposon or a piggyBac-like transposon.

[00948] Examples of piggyBac and piggyBac-like transposases and transposons include, for example, those disclosed in WO2019/046815, the contents of which are incorporated herein by reference in their entirety. In some embodiments, the piggyBac or piggyBac-like transposase is hyperactive. A hyperactive piggyBac or piggyBac-like transposase is a transposase that is more active than the naturally occurring variant from which it is derived. In some embodiments, the hyperactive piggyBac or piggyBac-like transposase enzyme is isolated or derived from Bombyx mori. A list of hyperactive amino acid substitutions can be found in US patent No. 10,041,077, the contents of which are incorporated herein by reference in their entirety. In some embodiments, the piggyBac or piggyBac-like transposase is integration deficient. In some embodiments, an integration deficient piggyBac or piggyBac-like transposase is a transposase that can excise its corresponding transposon, but that integrates the excised transposon at a lower frequency than a corresponding wild-type transposase. A list of integration deficient amino acid substitutions can be found in US patent No. 10,041,077, the contents of which are incorporated by reference in their entirety.

[00949] In some embodiments, the piggyBac or piggyBac-like transposon is capable of insertion by a piggyBac or piggyBac-like transposase at the sequence 5'-TTAT-3 within a target nucleic acid. In some embodiments, and, in particular, embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac transposase. In some embodiments, and, in particular, embodiments

wherein the transposon is a piggyBac- like transposon, the transposase is a piggyBac-like transposase. In some embodiments, and, in particular, embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac™ or a Super piggyBac™ (SPB) transposase. In some embodiments, and, in particular, embodiments wherein the transposase is a Super piggyBac™ (SPB) transposase, the sequence encoding the transposase is an mRNA sequence.

[00950] The sleeping beauty (SB) transposon is transposed into the target genome by the Sleeping Beauty transposase that recognizes ITRs, and moves the contents between the ITRs into TA chromosomal sites. In some embodiments, the transposon is a Sleeping Beauty transposon. In some embodiments, the transposase enzyme is a Sleeping Beauty transposase enzyme (see, for example, US Patent No. 9,228,180, the contents of which are incorporated herein in their entirety). In some embodiments, the Sleeping Beauty transposase is a hyperactive Sleeping Beauty (SB100X) transposase.

[00951] The Helraiser transposon is transposed by the Helitron transposase. Unlike other transposases, the Helitron transposase does not contain an RNase-H like catalytic domain, but instead comprises a RepHel motif made up of a replication initiator domain (Rep) and a DNA helicase domain. The Rep domain is a nuclease domain of the HUH superfamily of nucleases. In some embodiments, the transposon is a Helraiser transposon. In some embodiments of the Helraiser transposon sequence, the transposase is flanked by left and right terminal sequences termed LTS and RTS. In some embodiments, these sequences terminate with a conserved 5'-TC/CTAG-3' motif. In some embodiments, a 19 bp palindromic sequence with the potential to form the hairpin termination structure is located 11 nucleotides upstream of the RTS and comprises the sequence GTGCACGAATTTCGTGCACCGGGCCACTAG. In some embodiments, and, in particular embodiments wherein the transposon is a Helraiser transposon, the transposase enzyme is a Helitron transposase enzyme.

[00952] Tol2 transposons may be isolated or derived from the genome of the medaka fish, and may be similar to transposons of the hAT family. Exemplary Tol2 transposons of the disclosure are encoded by a sequence comprising about 4.7 kilobases and contain a gene encoding the Tol2 transposase, which contains four exons. In some embodiments, the transposon is a Tol2 transposon. In certaln some embodiments of the methods of the disclosure, and, in particular those embodiments wherein the transposon is a Tol2 transposon, the transposase enzyme is a Tol2 transposase enzyme.

[00953] In some embodiments, a vector comprises the recombinant and non-naturally occurring DNA sequence encoding the transposon. In some embodiments, the vector comprises any form of DNA and wherein the vector comprises at least 100 nucleotides (nts), 500 nts, 1000 nts, 1500 nts, 2000 nts, 2500 nts, 3000 nts, 3500 nts, 4000 nts, 4500 nts, 5000 nts, 6500 nts, 7000 nts, 7500 nts,

8000 nts, 8500 nts, 9000 nts, 9500 nts, 10,000 nts or any number of nucleotides in between. In some embodiments, the vector comprises single-stranded or double-stranded DNA. In some embodiments, the vector comprises circular DNA. In some embodiments, the vector is a plasmid vector, a nanoplasmid vector, a minicircle. In some embodiments, the vector comprises linear or linearized DNA. In some embodiments, the vector is a double-stranded doggybone™ DNA sequence.

[00954] In some embodiments, the recombinant and non-naturally occurring DNA sequence encoding a transposon further comprises a sequence encoding one or more immune checkpoint genes.

[00955] In some embodiments, the nucleic acid sequence encoding the transposase enzyme is a DNA sequence, and an amount of the DNA sequence encoding the transposase enzyme and an amount of the DNA sequence encoding the transposon is equal to or less than 10.0 μg per 100 μL, less than 7.5 μg per 100 μL, less than 6.0 μg per 100 μL, less than 5.0 μg per 100 μL, less than 2.5 μg per 100 μL, or less than 1.67 μg per 100 μL, less than 0.55 μg per 100 μL, less than 0.19 μg per 100 μL, less than 0.10 μg per 100 μL of an electroporation or nucleofection reaction. In certaIn some embodiments, a concentration of the amount of the DNA sequence encoding the transposase enzyme and an amount of the DNA sequence encoding the transposon in the electroporation or nucleofection reaction is equal to or less than 100 μg/mL, equal to or less than 75 μg/mL, equal to or less than 60 μg/mL, equal to or less than 50 μg/mL, equal to or less than 25 μg/mL, equal to or less than 16.7 μg/mL, equal to or less than 5.5 μg/mL, equal to or less than 1.9 μg/mL, equal to or less than 1.0 μg/mL.

[00956] In some embodiments, the nucleic acid sequence encoding the transposase enzyme is an RNA sequence, and an amount of the RNA sequence encoding the transposase enzyme and an amount of the RNA sequence encoding the transposon is equal to or less than 10.0 μg per 100 μL, less than 7.5 μg per 100 μL, less than 6.0 μg per 100 μL, less than 5.0 μg per 100 μL, less than 2.5 μg per 100 μL, or less than 1.67 μg per 100 μL, less than 0.55 μg per 100 μL, less than 0.19 μg per 100 μL, less than 0.10 μg per 100 μL of an electroporation or nucleofection reaction. In certain embodiments, a concentration of the amount of the RNA sequence encoding the transposase enzyme and an amount of the RNA sequence encoding the transposon in the electroporation or nucleofection reaction is equal to or less than 100 μg/mL, equal to or less than 75 μg/mL, equal to or less than 60 μg/mL, equal to or less than 50 μg/mL, equal to or less than 25 μg/mL, equal to or less than 16.7 μg/mL, equal to or less than 5.5 μg/mL, equal to or less than 1.9 μg/mL, equal to or less than 1.0 μg/mL.

[00957] In some embodiments, the TILs are further modified by a second gene editing tool, including, but not limited to those described herein. In some embodiments, the second gene editing tool may include an excision-only piggyBac transposase to re-excise the inserted sequences or any

portion thereof. For example, the excision-only piggyBac transposase may be used to "re-excise" the transposon.

[00958] According to some embodiments, a piggyBac system comprises a transposon/transposase system, wherein the transposase recognizes the ITRs located on both sides of the transposon cassette comprising a cargo encoding one or more immune checkpoint genes, and excises the transposable element to integrate it into TT/AA chromosomal sites, resulting in genomic insertion of the transposon cassette and expression of the one or more immune checkpoint genes. According to some embodiments, the cargo encodes two or more immune checkpoint molecules.

[00959] Non-limiting examples of genes that may be enhanced by permanently gene-editing TILs via a piggyBac 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.

[00960] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a piggyBac method, and which may be used in accordance with embodiments of the present invention, are described in WO2019/046815, WO2015006700, WO2010085699, WO2010099301, WO2010099296, WO2006122442, WO2001081565, and WO1998040510, the contents of which are incorporated herein by reference in their entirety.

[00961] Resources for carrying out piggyBac methods, such as plasmids for expressing transposons/transposases, are commercially available from companies such as Demcetra and Hera Biolabs.

[00962] 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 comprising a piggyBac 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.

[00963] 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 at least one gene editor system comprising a piggyBac system, which at least one gene editor system effects expression of at least one immunomodulatory composition at the cell surface of 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.

[00964] In some embodiments, a method of genetically modigying a polulation of TILs includes the use of a non-viral technique such as a piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases). In some embodiments, the method comprises delivering to the TILs: (a) a nucleic acid or amino acid sequence comprising a sequence encoding a transposase enzy; and (b) a recombinant and non-naturally occurring DNA sequence comprising a DNA sequence encoding a transposon. In certain embodiments of the methods of the disclosure, the sequence encoding a transposase enzyme is an mRNA sequence. The mRNA sequence encoding a

transposase enzyme may be produced in vitro. In certain embodiments of the methods of the disclosure, the sequence encoding a transposase enzyme is a DNA sequence. The DNA sequence encoding a transposase enzyme may be produced in vitro. The DNA sequence may be a cDNA sequence. In certain embodiments of the methods of the disclosure, the sequence encoding a transposase enzyme is an amino acid sequence. The amino acid sequence encoding a transposase enzyme may be produced in vitro. A protein Super piggybac transposase (SPB) may be delivered following pre-incubation with transposon DNA. In certain embodiments, the transposon is a piggyBac transposon or a piggyBac-like transposon. In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac transposase. In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac- like transposon, the transposase is a piggyBac-like transposase. In certain embodiments, the piggyBac transposase comprises an amino acid sequence comprising SEQ ID NO: 238. In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac™ or a Super piggyBac™ (SPB) transposase. In certain embodiments, and, in particular, those embodiments wherein the transposase is a Super piggyBac™ (SPB) transposase, the sequence encoding the transposase is an mRNA sequence. In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac™ (PB) transposase enzyme. The piggyBac (PB) transposase enzyme may comprise or consist of an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

MGSSLDDEHILSALLQSDDELVGEDSDSEISDHVSEDDVQSDTEEAFIDEVHEVQPTSSGSEILDEQN
VIEQPGSSLASNRILTLPQRTIRGKNKHCWSTSKSTRRSRVSALNIVRSQRGPTRMCRNIYDPLLCFKL
FFTDEIISEIVKWTNAEISLKRRESMTGATFRDTNEDEIYAFFGILVMTAVRKDNHMSTDDLFDRSLSMV
YVSVMSRDRFDFLIRCLRMDDKSIRPTLRENDVFTPVRKIWDLFIHQCIQNYTPGAHLTIDEQLLGFRG
RCPFRMYIPNKPSKYGIKILMMCDSGTKYMINGMPYLGRGTQTNGVPLGEYYVKELSKPVHGSCRNI
TCDNWFTSIPLAKNLLQEPYKLTIVGTVRSNKREIPEVLKNSRSRPVGTSMFCFDGPLTLVSYKPKPAK
MVYLLSSCDEDASINESTGKPQMVMYYNQTKGGVDTLDQMCSVMTCSRKTNRWPMALLYGMINIAC
INSFIIYSHNVSSKGEKVQSRKKFMRNLYMSLTSSFMRKRLEAPTLKRYLRDNISNILPNEVPGTSDDS
TEEPVMKKRTYCTYCPSKIRRKANASCKKCKKVICREHNIDMCQSCF (SEQ ID NO:296; SEQ ID NO: 14487 of WO2019046815).

[00965] In certain embodiments of the methods of the disclosure, the transposon is a Sleeping Beauty transposon. In certain embodiments of the methods of the disclosure, the transposase enzyme is a Sleeping Beauty transposase enzyme (see, for example, US Patent No. 9,228,180, the contents of which are incorporated herein in their entirety). In certain embodiments, the Sleeping Beauty transposase is a hyperactive Sleeping Beauty (SB100X) transposase. In certain embodiments, the Sleeping Beauty transposase enzyme comprises an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

MGKSKEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKHHGTTQPSYRSGRRRVLSPRD
ERTLVRKVQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKKPLLQNRHKKARLRFATA
HGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSIMLWGCFAAGGT
GALHKIDGIMRKENYVDILKQHLKTSVRKLKLGRKWVFQMDNDPKHTSKVVAKWLKDNKVKVLEWPS
QSPDLNPIENLWAELKKRVRARRPTNLTQLHQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNA
TKY (SEQ ID NO: 297; SEQ ID NO: 14485 of WO2019046815).

[00966] In certain embodiments, including those wherein the Sleeping Beauty transposase is a hyperactive Sleeping Beauty (SB100X) transposase, the Sleeping Beauty transposase enzyme comprises an amino acid sequence at least at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

MGKSKEISQDLRKRIVDLHKSGSSLGAISKRLAVPRSSVQTIVRKYKHHGTTQPSYRSGRRRVLSPRD
ERTLVRKVQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGHSARKKPLLQNRHKKARLRFATA
HGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSIMLWGCFAAGGT
GALHKIDGIMDAVQYVDILKQHLKTSVRKLKLGRKWVFQHDNDPKHTSKVVAKWLKDNKVKVLEWPS
QSPDLNPIENLWAELKKRVRARRPTNLTQLHQLCQEEWAKIHPNYCGKLVEGYPKRLTQVKQFKGNA
TKY (SEQ ID NO: 298; SEQ ID NO: 14486 of WO2019046815).

F. Gene Editing Processes

[00967] Embodiments of the present invention are directed to methods for expanding TIL populations, the methods comprising 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 some embodiments, the DNA sequence exhibiting enhanced expression is an endogenous DNA sequence. In some embodiments, the DNA sequence exhibiting expression is an exogenous DNA sequence that originates from outside the edited cell. In accordance with embodiments of the present invention, gene-editing technology is used to enhance the effectiveness of a therapeutic population of TILs.

[00968] 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 PCT/US2017/058610, PCT/US2018/012605, or PCT/US2018/012633, which are incorporated by reference herein in their entireties, wherein the

method further comprises gene-editing at least a portion of the TILs. Thus, an embodiment 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. Specific embodiments of the process of gene-editing are described in detail herein as well as in PCT/2019/029286, and PCT/US2019/012729, each of which is incorporated herein by reference in its entirety.

[00969] 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.

[00970] 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.

[00971] 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.

[00972] 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. 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. 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. 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. 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 (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.

[00973] 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.

[00974] 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 (Gattinoni et al. Nat Med 2009, 2011; Gattinoni, Nature Rev. Cancer, 2012; Cieri et al. Blood 2013). 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.

[00975] 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.

[00976] 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.

[00977] In some embodiments, transient alteration of protein results in altered expression of a particular gene. In some embodiments, transient alteration of protein results in altered expression of an immune checkpoint 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, TIM3, LAG3, TIGIT, 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, 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 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 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 cAMP protein kinase A (PKA).

[00978] 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.

[00979] In some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of PD-1, CTLA-4, TIM-3, LAG-3, TIGIT, 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 CBLB (CBL-B). In

some embodiments, the transient alteration of protein expression results in a decrease and/or reduced expression of CISH.

[00980] 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.

[00981] 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.

[00982] 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,

[00983] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of cAMP protein kinase A (PKA).

[00984] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of an immune checkpoint. 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, TGIT, TET2, TGFβR2, PRA, BAFF (BR3),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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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 TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of PD-1, LAG-3, CISH, CBLB, TIM3, 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 LAG3, CISH, CBLB, TIM3, and combinations thereof. 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 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 CISH and CBLB. 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.

[00985] 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 (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) 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).

[00986] In some embodiments, the transient alteration of protein expression results in decreased and/or reduced expression of one or two molecules selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, 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 one or two molecules selected from the group consisting of PD-1, LAG3, TIM3, CTLA-4, TIGIT, CISH, CBLB, and combinations thereof, and increased and/or enhanced expression of CCR2, CCR4, CCR5, CXCR2, CXCR3, CX3CR1, and combinations thereof.

[00987] 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%.

[00988] 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%.

[00989] 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 (Sharei et al. PNAS 2013, as well as Sharei et al. PLOS ONE 2015 and Greisbeck et al. J. Immunology vol. 195, 2015) have been described; see, for example, International Patent Publications WO 2013/059343A1, WO 2017/008063A1, and WO 2017/123663A1, all of which are incorporated by reference herein in their entireties. Such methods as described in International Patent Publications WO 2013/059343A1, WO 2017/008063A1, and WO 2017/123663A1 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.

[00990] 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.

[00991] 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.

[00992] 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. 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.

[00993] In some embodiments, the method comprises a method of genetically modifying a population of TILs which include 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 (e.g., lentiviral transduction methods disclosed herein). 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. Additional suitable transposon-mediated gene transfer systems useful for genetically modifying subject TILs described herein include, but are not limited to, a piggyBac system (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty system (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser system (e.g., Helraiser ahd Helraise-like transposons and transposases), and a Tol2 system (e.g., Tol2 and Tol2-like transposons and transposases), as described herein.

[00994] In some embodiments, the method comprises a method of genetically modifying a population of TILs e.g. 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.

[00995] 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.

[00996] 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.

[00997] 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, ZFN methods, Cas-CLOVER methods and shRNA 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 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 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.

[00998] In some embodiments, of the present invention, electroporation is used for delivery of a gene editing system, such as CRISPR, TALEN,ZFN, Cas-CLOVER, and shRNA 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.

[00999] 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

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 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.

[001000] 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.

[001001] 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).

[001002] 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001003] 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.

[001004] 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.

[001005] 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.

[001006] 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 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 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.

[001007] 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.

[001008] 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 which are incorporated by reference herein.

[001009] 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001010] 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.

[001011] 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.

[001012] 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 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 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.

[001013] 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.

[001014] 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).

[001015] 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001016] 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.

[001017] 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.

[001018] 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.

[001019] In some embodiments, the TILs are optionally genetically engineered to include additional functionalities, including, but not limited to, a high-affinity T cell receptor (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 genetic engineering [methods described in International Patent Publication No. WO 2019/160829 A1, the disclosure of which is incorporated by reference herein, may be employed to genetically edit TILs, including knockout of specific target genes such as the genes that code for PD-1 and CTLA-4. In certain embodiments, the method comprises genetically engineering a population of TILs to include a high-affinity T cell receptor (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.

1. Timing of Gene-Editing During TIL Expansion

[001020] According to 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 at least a portion of a tumor resected from a patient by processing a sample from the resected tumor 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, gene-editing at least a portion of the TILs.

[001021] As stated in step (g) of the embodiment described above, the gene-editing process may 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) outlined in the method above, or before or after any of steps (a)-(f) 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.

[001022] 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.

[001023] 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 another embodiment, 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.

[001024] According to another embodiment, 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.

[001025] According to another embodiment, 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.

[001026] 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)).

[001027] 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 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 another embodiment, the cell culture medium comprises OKT-3 during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the OKT-3 is introduced into the cell culture medium.

[001028] 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 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 another embodiment, the cell culture medium comprises a 4-1BB agonist during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the 4-1BB agonist is introduced into the cell culture medium.

[001029] 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 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 another embodiment, the cell culture medium comprises IL-2 during the first expansion and/or during the second expansion, and the gene-editing 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 is carried out after the IL-2 is introduced into the cell culture medium.

[001030] 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 an example, 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 another example, 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.

[001031] According to 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 at least a portion of a tumor resected from a patient by processing a sample obtained from the resected tumor 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 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 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, and 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.

[001032] According to some embodiments, the foregoing method may be used to provide an autologous harvested TIL population for the treatment of a human subject with cancer.

[001033] 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 i) 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/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in 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. In some embodiments, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof.

[001034] 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.

[001035] 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. In some embodiments, the RNA molecule suppresses expression of PD-1.

[001036] 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.

[001037] 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: i) 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/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in 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

[001038] (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 embodimetns, the endogenous gene encodes an immune checkpoint. 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 immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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. In some embodiments, the RNA molecule suppresses expression of PD-1.

[001039] 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.

[001040] 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: i) an immunomodulatory composition comprising an immunomodulatory agent on the surface of the TIL cells (e.g., a membrane anchored immunomodulatory fusion protein described herein), and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in 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. In some embodiments, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001041] 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.

[001042] 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.

[001043] 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.

[001044] 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.

[001045] 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.

[001046] 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.

[001047] 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.

[001048] 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.

[001049] 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)).

[001050] 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)).

[001051] 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.

[001052] 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.

[001053] 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.

[001054] 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.

[001055] 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: i) 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/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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. In some embodiments, the RNA molecule suppresses expression of PD-1.

[001056] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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 combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001057] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2,

PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001058] 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: i) an immunomodulatory composition on the surface of the cells. and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001059] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF

(BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001060] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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 combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). In some embodiments, the microfluidic platform is a SQZ vector-free microfluidic platform.

[001061] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the endogenous gene

encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001062] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001063] 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: i) 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/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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.

[001064] 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001065] 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

(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 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is

selected from PD-1, LAG-3, TIM-3, CTLA-4. TIGIT, TET2. CISH, TGFβR2. PRA. CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments. the endogenous gene is selected from PD-1. TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001066] 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: i) 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/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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.

[001067] 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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^{TM} 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. In some embodiments, the RNA molecule suppresses expression of PD-1.

[001068] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2,

TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001069] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001070] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001071] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001072] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001073] 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, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2,

TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001074] 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.

[001075] 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.

[001076] 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.

[001077] 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.

[001078] 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.

[001079] 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.

[001080] 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.

[001081] 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.

[001082] 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.

[001083] 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.

[001084] 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.

[001085] 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.

[001086] 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.

[001087] 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.

[001088] 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.

[001089] 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.

[001090] 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.

[001091] 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.

[001092] 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.

[001093] 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.

[001094] 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.

[001095] 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.

[001096] 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.

[001097] 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.

[001098] 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.

[001099] 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.

[001100] 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.

[001101] 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.

[001102] 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.

[001103] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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 endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF

(BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001104] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the 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., 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 endogenous gene encodes an immune checkpoint. In some embodiments, the

immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001105] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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. In some embodiments, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001106] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001107] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001108] 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: i) an

immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001109] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001110] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001111] 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.

[001112] 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.

[001113] 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.

[001114] 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.

[001115] 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.

[001116] 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.

[001117] 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.

[001118] 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.

[001119] 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.

[001120] 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.

[001121] 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.

[001122] 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.

[001123] 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.

[001124] 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.

[001125] 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.

[001126] 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.

[001127] 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.

[001128] 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.

[001129] 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.

[001130] 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.

[001131] 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.

[001132] 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.

[001133] 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.

[001134] 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.

[001135] 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.

[001136] 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.

[001137] 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.

[001138] 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.

[001139] 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.

[001140] 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.

[001141] 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.

[001142] 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.

[001143] 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.

[001144] 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.

[001145] 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.

[001146] 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.

[001147] 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.

[001148] 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.

[001149] 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.

[001150] 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.

[001151] 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.

[001152] 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.

[001153] 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.

[001154] 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.

[001155] 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.

[001156] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001157] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001158] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001159] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001160] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some

embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001161] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001162] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001163] 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: i) an immunomodulatory composition on the surface of the cells, and/or ii) an RNA molecule (e.g., an shRNA) for suppressing expression of an endogenous gene in the TIL 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, the endogenous gene encodes an immune checkpoint. In some embodiments, the immune checkpoint is selected from PD-1, LAG-3, TIM-3, CTLA-4, TIGIT, TET2, CISH, TGFβR2, PRA, CBLB, BAFF (BR3), and combinations thereof (e.g., two or more of the above immune checkpoints). In some embodiments, the endogenous gene is selected from PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.). 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.

[001164] 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.

[001165] 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.

[001166] In some embodiments, the anti-CD3 and anti-CD28 beads or antibodies comprise the OKT-3 in the first culture medium.

[001167] 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.

[001168] In some embodiments, the anti-CD3 and anti-CD28 beads or antibodies comprise the OKT-3 in the second culture medium.

[001169] 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.

[001170] 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.

[001171] 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.

[001172] 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.

[001173] 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.

[001174] 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.

[001175] 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.

[001176] 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.

[001177] 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.

[001178] 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.

[001179] 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.

[001180] 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.

[001181] 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.

[001182] 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.

[001183] 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.

[001184] 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.

[001185] 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.

[001186] 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.

[001187] 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.

[001188] 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.

[001189] 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.

[001190] 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.

[001191] 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.

[001192] 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.

[001193] 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.

[001194] 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.

[001195] 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.

[001196] 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.

[001197] 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.

[001198] 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.

[001199] 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.

[001200] 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.

[001201] 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.

[001202] 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.

[001203] 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.

[001204] 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.

[001205] 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.

[001206] 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.

[001207] 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.

[001208] 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.

[001209] 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.

[001210] 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.

[001211] 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.

[001212] 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.

[001213] 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.

[001214] 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.

[001215] 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.

[001216] 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.

[001217] 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.

[001218] 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.

[001219] 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.

[001220] 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.

[001221] 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.

[001222] 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.

[001223] 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.

[001224] 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.

[001225] 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.

[001226] 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.

[001227] 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.

[001228] 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.

[001229] 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.

[001230] 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.

[001231] 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.

[001232] 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.

[001233] 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.

[001234] 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.

[001235] 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.

[001236] 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.

[001237] 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.

[001238] 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.

[001239] 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.

[001240] 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.

[001241] 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.

G. Gene Editing Methods

[0001] 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. 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, including transient gene-editing technologies to transiently alter protein expression in a population of TILs, which are suitable for use in accordance with the present invention.

[001242] 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 or nucleic acid (e.g., an immunomodulatory fusion protein and/or an RNA (e.g., an shRNA) for modifying gene expression as described herein). 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.

[001243] Lentiviral vector for genetically modify the subject TILs can be made using any suitable technique known in the art. In some embodiments, the lentiviral vector is made using a stable lentiviral producer cell line. In some embodiments, the stable lentiviral producer cell line is made using transposon/transposase (e.g. piggyBac and Sleeping Beauty systems described herein) to integrate various genes for lentiviral vector production (e.g., VSV-g, gag, and pol genes, gene of interest, etc.) into the producer cell line genome. In some embodiments, the genes for lentiviral vector production are under the control of inducible expression systems (e.g., Tet-on and Tet-off systems) that allow for inducible production of the lentiviral vectors. Exemplary inducible stable producer cell lines for lentiviral production, include for example, the EuLV® (Eureka Bio) system, see, e.g., Xue et al., Cell & Gene Therapy Insights 8(2):199-209 (2022), WO2021218000A1, WO2021232632A1, and WO2021232633A1, which are incorporated by reference in their entireties, particularly for pertinent parts relating to the production of inducible stable producer cell line for lentiviral production.

[001244] 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.

[001245] 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. Additional suitable transposon-mediated gene transfer systems useful for genetically modifying subject TILs described herein include, but are not limited to, a piggyBac system (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty system (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser system (e.g., Helraiser ahd Helraise-like transposons and transposases), and a Tol2 system (e.g., Tol2 and Tol2-like transposons and transposases), as described herein.

[001246] 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.

[001247] 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.

[001248] 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.

[001249] 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 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., 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, an sd-RNA method, an shRNA 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.

[001250] In some embodiments, of the present invention, electroporation is used for delivery of a gene editing system, such as CRISPR, TALEN, ZFN, sd-RNA, an shRNA,. 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.

1. CRISPR Methods

[001251] 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 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.

[001252] 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.

[001253] 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).

[001254] 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 an embodiment, the expression of two or more immune checkpoint molecules is altered. According to an embodiment, 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.

[001255] 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 an embodiment, 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.

[001256] 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.

[001257] 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.

[001258] 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 an embodiment, 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).

[001259] 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 an embodiment 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.

[001260] 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 an embodiment, 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

[001261] 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).

[001262] 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.

[001263] 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.

[001264] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a CRISPR method include PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001265] 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-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[001266] 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.

[001267] 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.

[001268] According to 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 at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 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 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, and 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 Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 or CRISPR/Cpf1 system for modulating the expression of at least one protein.

[001269] According to 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 at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 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 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, and 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 Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)/Cas9 or CRISPR/Cpf1 system for inhibiting the expression of PD-1 and LAG-3.

2. TALE Methods

[001270] 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 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.

[001271] 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.

[001272] 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.

[001273] According to an embodiment 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.

[001274] According to another embodiment, 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.

[001275] 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 an embodiment, 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.

[001276] According to another embodiment, 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.

[001277] According to an embodiment 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:127 and the T3v1 TALEN does so by using target SEQ ID NO:128.

[001278] According to another embodiment, 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.

[001279] 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.

[001280] 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 comprising 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 mRNA encoding transcription activator-like effector nucleases to obtain a 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.

[001281] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising 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 mRNA encoding transcription activator-like effector nucleases in cytoporation medium to obtain a 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.

[001282] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising 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 mRNA encoding transcription activator-like effector nucleases in cytoporation medium to obtain a 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.

[001283] According to some 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.

[001284] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a TALE method include PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001285] 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)	LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETV QRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIA SHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQA HGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALE TVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAI ASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQ AHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQAL ETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVV AIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLC QAHGLTPQQVVAIASNGGGRPALE
Repeat PD-1-right (SEQ ID NO: 289)	LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETV QALLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIAS NNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQA HGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQAL ETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVV AIASNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLC QAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQ ALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQ VVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLP VLCQAHGLTPQQVVAIASNGGGRPALE
PD-1-left TALEN (SEQ ID NO:290)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATTACCCATACGATGTTCCAG ATTACGCTATCGATATCGCCGATCTACGCACGCTCGGCTACAGCCAGCAGCAACAG GAGAAGATCAAACCGAAGGTTCGTTCGACAGTGGCGCAGCACCACGAGGCACT

	GGTCGGCCACGGGTTTACACACGCGCACATCGTTGCGTTAAGCCAACACCCGGC
	AGCGTTAGGGACCGTCGCTGTCAAGTATCAGGACATGATCGCAGCGTTGCCAGA
	GGCGACACACGAAGCGATCGTTGGCGTCGGCAAACAGTGGTCCGGCGCACGCG
	CTCTGGAGGCCTTGCTCACGGTGGCGGGAGAGTTGAGAGGTCCACCGTTACAGT
	TGGACACAGGCCAACTTCTCAAGATTGCAAAACGTGGCGGCGTGACCGCAGTGG
	AGGCAGTGCATGCATGGCGCAATGCACTGACGGGTGCCCCGCTCAACTTGACCC
	CCCAGCAGGTGGTGGCCATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAG
	ACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAG
	CAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGT
	CCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGT
	GGTGGCCATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAGACGGTCCAGC
	GGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTG
	GCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCT
	GTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCAT
	CGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGC
	CGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCGCCA
	GCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG
	CTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCGCCAGCCAC
	GATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTG
	CCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCATCGCCAGCAATATTGG
	TGGCAAGCAGGCGCTGGAGACGGTGCAGGCGCTGTTGCCGGTGCTGTGCCAGG
	CCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATAATGGTGGCA
	AGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCAC
	GGCTTGACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCA
	GGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCT
	TGACCCCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCG
	CTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACC
	CCGGAGCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGA
	GACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCA
	GCAGGTGGTGGCCATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAGACG
	GTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAG
	GTGGTGGCCATCGCCAGCAATAATGGTGGCAAGCAGGCGCTGGAGACGGTCCA
	GCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGG
	TGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGG
	CTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCTCAGCAGGTGGTGGCC

	ATCGCCAGCAATGGCGGCGGCAGGCCGGCGCTGGAGAGCATTGTTGCCCAGTTA TCTCGCCCTGATCCGGCGTTGGCCGCGTTGACCAACGACCACCTCGTCGCCTTGG CCTGCCTCGGCGGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGGGAT CCTATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAATCCGAG TTGAGGCACAAGCTGAAGTACGTGCCCCACGAGTACATCGAGCTGATCGAGATC GCCCGGAACAGCACCCAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTC ATGAAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCGA CGGCGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCGTGATCGTGGACACC AAGGCCTACTCCGGCGGCTACAACCTGCCCATCGGCCAGGCCGACGAAATGCAG AGGTACGTGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCAACGAGTG GTGGAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTTCGTGTCCGGC CACTTCAAGGGCAACTACAAGGCCCAGCTGACCAGGCTGAACCACATCACCAAC TGCAACGGCGCCGTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGATC AAGGCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAACGGCG AGATCAACTTCGCGGCCGACTGATAA
PD-1-right TALEN (SEQ ID NO:291)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATAAGGAGACCGCCGCTGCC AAGTTCGAGAGACAGCACATGGACAGCATCGATATCGCCGATCTACGCACGCTCG GCTACAGCCAGCAGCAACAGGAGAAGATCAAACCGAAGGTTCGTTCGACAGTG GCGCAGCACCACGAGGCACTGGTCGGCCACGGGTTTACACACGCGCACATCGTT GCGTTAAGCCAACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGTATCAGGAC ATGATCGCAGCGTTGCCAGAGGCGACACACGAAGCGATCGTTGGCGTCGGCAAA CAGTGGTCCGGCGCACGCGCTCTGGAGGCCTTGCTCACGGTGGCGGGAGAGTT GAGAGGTCCACCGTTACAGTTGGACACAGGCCAACTTCTCAAGATTGCAAAACG TGGCGGCGTGACCGCAGTGGAGGCAGTGCATGCATGGCGCAATGCACTGACGG GTGCCCCGCTCAACTTGACCCCCCAGCAAGTCGTCGCAATCGCCAGCAATAACGG AGGGAAGCAAGCCCTCGAAACCGTGCAGCGGTTGCTTCCTGTGCTCTGCCAGGC CCACGGCCTTACCCCTGAGCAGGTGGTGGCCATCGCAAGTAACATTGGAGGAAA GCAAGCCTTGGAGACAGTGCAGGCCCTGTTGCCCGTGCTGTGCCAGGCACACG GCCTCACACCAGAGCAGGTCGTGGCCATTGCCTCCAACATCGGGGGGAAACAGG CTCTGGAGACCGTCCAGGCCCTGCTGCCCGTCCTCTGTCAAGCTCACGGCCTGAC TCCCCAACAAGTGGTCGCCATCGCCTCTAATAACGGCGGGAAGCAGGCACTGGA AACAGTGCAGAGACTGCTCCCTGTGCTTTGCCAAGCTCATGGGTTGACCCCCCAA CAGGTCGTCGCTATTGCCTCAAACAACGGGGGCAAGCAGGCCCTTGAGACTGTG

	CAGAGGCTGTTGCCAGTGCTGTGTCAGGCTCACGGGCTCACTCCACAACAGGTG GTCGCAATTGCCAGCAACGGCGGCGGAAAGCAAGCTCTTGAAACCGTGCAACG CCTCCTGCCCGTGCTCTGTCAGGCTCATGGCCTGACACCACAACAAGTCGTGGCC ATCGCCAGTAATAATGGCGGGAAACAGGCTCTTGAGACCGTCCAGAGGCTGCTC CCAGTGCTCTGCCAGGCACACGGGCTGACCCCCCAGCAGGTGGTGGCTATCGCC AGCAATAATGGGGGCAAGCAGGCCCTGGAAACAGTCCAGCGCCTGCTGCCAGT GCTTTGCCAGGCTCACGGGCTCACTCCCGAACAGGTCGTGGCAATCGCCTCCAA CGGAGGGAAGCAGGCTCTGGAGACCGTGCAGAGACTGCTGCCCGTCTTGTGCC AGGCCCACGGACTCACACCTCAGCAGGTCGTCGCCATTGCCTCTAACAACGGGG GCAAACAAGCCCTGGAGACAGTGCAGCGGCTGTTGCCTGTGTTGTGCCAAGCCC ACGGCTTGACTCCTCAACAAGTGGTCGCCATCGCCTCAAATGGCGGCGGAAAAC AAGCTCTGGAGACAGTGCAGAGGTTGCTGCCCGTCCTCTGCCAAGCCCACGGCC TGACTCCCCAACAGGTCGTCGCCATTGCCAGCAACGGCGGAGGAAAGCAGGCTC TCGAAACTGTGCAGCGGCTGCTTCCTGTGCTGTGTCAGGCTCATGGGCTGACCCC CCAGCAAGTGGTGGCTATTGCCTCTAACAATGGAGGCAAGCAAGCCCTTGAGAC AGTCCAGAGGCTGTTGCCAGTGCTGTGCCAGGCCCACGGGCTCACACCCCAGCA GGTGGTCGCCATCGCCAGTAACGGCGGGGGCAAACAGGCATTGGAAACCGTCC AGCGCCTGCTTCCAGTGCTCTGCCAGGCACACGGACTGACACCCGAACAGGTGG TGGCCATTGCATCCCATGATGGGGGCAAGCAGGCCCTGGAGACCGTGCAGAGAC TCCTGCCAGTGTTGTGCCAAGCTCACGGCCTCACCCCTCAGCAAGTCGTGGCCAT CGCCTCAAACGGGGGGGGCCGGCCTGCACTGGAGAGCATTGTTGCCCAGTTATC TCGCCCTGATCCGGCGTTGGCCGCGTTGACCAACGACCACCTCGTCGCCTTGGCC TGCCTCGGCGGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGGGATCCT ATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAATCCGAGTTG AGGCACAAGCTGAAGTACGTGCCCCACGAGTACATCGAGCTGATCGAGATCGCC CGGAACAGCACCCAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTCATG AAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCGACGG CGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCGTGATCGTGGACACCAAG GCCTACTCCGGCGGCTACAACCTGCCCATCGGCCAGGCCGACGAAATGCAGAGG TACGTGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCAACGAGTGGTG GAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTTCGTGTCCGGCCAC TTCAAGGGCAACTACAAGGCCCAGCTGACCAGGCTGAACCACATCACCAACTGC AACGGCGCCGTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGATCAAG GCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAACGGCGAGAT CAACTTCGCGGCCGACTGATAA

TALEN PD-1 No. 2 Sequences	
Target PD-1 Sequence (SEQ ID NO:287)	TACCTCTGTGGGGCCATctccctggcccccaaGGCGCAGATCAAAGAGA
Repeat PD-1-left (SEQ ID NO:292)	LTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGRPALE
Repeat PD-1-right (SEQ ID NO: 293)	LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGRPALE
PD-1-left TALEN (SEQ ID NO:294)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATTACCCATACGATGTTCCAGATTACGCTATCGATATCGCCGATCTACGCACGCTCGGCTACAGCCAGCAGCAACAGGAGAAGATCAAACCGAAGGTTCGTTCGACAGTGGCGCAGCACCACGAGGCACTGGTCGGCCACGGGTTTACACACGCGCACATCGTTGCGTTAAGCCAACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGTATCAGGACATGATCGCAGCGTTGCCAGA

	GGCGACACACGAAGCGATCGTTGGCGTCGGCAAACAGTGGTCCGGCGCACGCG
	CTCTGGAGGCCTTGCTCACGGTGGCGGGAGAGTTGAGAGGTCCACCGTTACAGT
	TGGACACAGGCCAACTTCTCAAGATTGCAAAACGTGGCGGCGTGACCGCAGTGG
	AGGCAGTGCATGCATGGCGCAATGCACTGACGGGTGCCCCGCTCAACTTGACCC
	CGGAGCAGGTGGTGGCCATCGCCAGCAATATTGGTGGCAAGCAGGCGCTGGAG
	ACGGTGCAGGCGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGA
	GCAGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGG
	TCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGG
	TGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAG
	CGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTG
	GCCATCGCCAGCAATGGCGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCT
	GTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTGGCCAT
	CGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGC
	CGGTGCTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCA
	GCAATGGCGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTG
	CTGTGCCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAAT
	AATGGTGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTG
	CCAGGCCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATGGCGG
	TGGCAAGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGG
	CCCACGGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATAATGGTGGCA
	AGCAGGCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCAC
	GGCTTGACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATAATGGTGGCAAGCAG
	GCGCTGGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTT
	GACCCCCCAGCAGGTGGTGGCCATCGCCAGCAATAATGGTGGCAAGCAGGCGCT
	GGAGACGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCC
	CCAGCAGGTGGTGGCCATCGCCAGCAATAATGGTGGCAAGCAGGCGCTGGAGA
	CGGTCCAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGC
	AGGTGGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTC
	CAGCGGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGT
	GGTGGCCATCGCCAGCCACGATGGCGGCAAGCAGGCGCTGGAGACGGTCCAGC
	GGCTGTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCGGAGCAGGTGGTG
	GCCATCGCCAGCAATATTGGTGGCAAGCAGGCGCTGGAGACGGTGCAGGCGCT
	GTTGCCGGTGCTGTGCCAGGCCCACGGCTTGACCCCTCAGCAGGTGGTGGCCAT
	CGCCAGCAATGGCGGCGGCAGGCCGGCGCTGGAGAGCATTGTTGCCCAGTTATC
	TCGCCCTGATCCGGCGTTGGCCGCGTTGACCAACGACCACCTCGTCGCCTTGGCC

	TGCCTCGGCGGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGGGATCCT ATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAATCCGAGTTG AGGCACAAGCTGAAGTACGTGCCCCACGAGTACATCGAGCTGATCGAGATCGCC CGGAACAGCACCCAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTCATG AAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCGACGG CGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCGTGATCGTGGACACCAAG GCCTACTCCGGCGGCTACAACCTGCCCATCGGCCAGGCCGACGAAATGCAGAGG TACGTGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCAACGAGTGGTG GAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTTCGTGTCCGGCCAC TTCAAGGGCAACTACAAGGCCCAGCTGACCAGGCTGAACCACATCACCAACTGC AACGGCGCCGTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGATCAAG GCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAACGGCGAGAT CAACTTCGCGGCCGACTGATAA
PD-1-right TALEN (SEQ ID NO:295)	ATGGGCGATCCTAAAAAGAAACGTAAGGTCATCGATAAGGAGACCGCCGCTGCC AAGTTCGAGAGACAGCACATGGACAGCATCGATATCGCCGATCTACGCACGCTCG GCTACAGCCAGCAGCAACAGGAGAAGATCAAACCGAAGGTTCGTTCGACAGTG GCGCAGCACCACGAGGCACTGGTCGGCCACGGGTTTACACACGCGCACATCGTT GCGTTAAGCCAACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGTATCAGGAC ATGATCGCAGCGTTGCCAGAGGCGACACACGAAGCGATCGTTGGCGTCGGCAAA CAGTGGTCCGGCGCACGCGCTCTGGAGGCCTTGCTCACGGTGGCGGGAGAGTT GAGAGGTCCACCGTTACAGTTGGACACAGGCCAACTTCTCAAGATTGCAAAACG TGGCGGCGTGACCGCAGTGGAGGCAGTGCATGCATGGCGCAATGCACTGACGG GTGCCCCGCTCAACTTGACCCCCGAGCAAGTCGTCGCAATCGCCAGCCATGATGG AGGGAAGCAAGCCCTCGAAACCGTGCAGCGGTTGCTTCCTGTGCTCTGCCAGGC CCACGGCCTTACCCCTCAGCAGGTGGTGGCCATCGCAAGTAACGGAGGAGGAAA GCAAGCCTTGGAGACAGTGCAGCGCCTGTTGCCCGTGCTGTGCCAGGCACACG GCCTCACACCAGAGCAGGTCGTGGCCATTGCCTCCCATGACGGGGGGAAACAG GCTCTGGAGACCGTCCAGAGGCTGCTGCCCGTCCTCTGTCAAGCTCACGGCCTG ACTCCCCAACAAGTGGTCGCCATCGCCTCTAATGGCGGCGGGAAGCAGGCACTG GAAACAGTGCAGAGACTGCTCCCTGTGCTTTGCCAAGCTCATGGGTTGACCCCCC AACAGGTCGTCGCTATTGCCTCAAACGGGGGGGGCAAGCAGGCCCTTGAGACT GTGCAGAGGCTGTTGCCAGTGCTGTGTCAGGCTCACGGGCTCACTCCACAACAG GTGGTCGCAATTGCCAGCAACGGCGGCGGAAAGCAAGCTCTTGAAACCGTGCA ACGCCTCCTGCCCGTGCTCTGTCAGGCTCATGGCCTGACACCACAACAAGTCGTG

	GCCATCGCCAGTAATAATGGCGGGAAACAGGCTCTTGAGACCGTCCAGAGGCTG CTCCCAGTGCTCTGCCAGGCACACGGGCTGACCCCCGAGCAGGTGGTGGCTATC GCCAGCAATATTGGGGGCAAGCAGGCCCTGGAAACAGTCCAGGCCCTGCTGCCA GTGCTTTGCCAGGCTCACGGGCTCACTCCCCAGCAGGTCGTGGCAATCGCCTCCA ACGGCGGAGGGAAGCAGGCTCTGGAGACCGTGCAGAGACTGCTGCCCGTCTTG TGCCAGGCCCACGGACTCACACCTGAACAGGTCGTCGCCATTGCCTCTCACGATG GGGGCAAACAAGCCCTGGAGACAGTGCAGCGGCTGTTGCCTGTGTTGTGCCAA GCCCACGGCTTGACTCCTCAACAAGTGGTCGCCATCGCCTCAAATGGCGGCGGA AAACAAGCTCTGGAGACAGTGCAGAGGTTGCTGCCCGTCCTCTGCCAAGCCCAC GGCCTGACTCCCCAACAGGTCGTCGCCATTGCCAGCAACAACGGAGGAAAGCA GGCTCTCGAAACTGTGCAGCGGCTGCTTCCTGTGCTGTGTCAGGCTCATGGGCTG ACCCCCGAGCAAGTGGTGGCTATTGCCTCTAATGGAGGCAAGCAAGCCCTTGAG ACAGTCCAGAGGCTGTTGCCAGTGCTGTGCCAGGCCCACGGGCTCACACCCCAG CAGGTGGTCGCCATCGCCAGTAACAACGGGGGCAAACAGGCATTGGAAACCGTC CAGCGCCTGCTTCCAGTGCTCTGCCAGGCACACGGACTGACACCCGAACAGGTG GTGGCCATTGCATCCCATGATGGGGGCAAGCAGGCCCTGGAGACCGTGCAGAG ACTCCTGCCAGTGTTGTGCCAAGCTCACGGCCTCACCCCTCAGCAAGTCGTGGCC ATCGCCTCAAACGGGGGGGGCCGGCCTGCACTGGAGAGCATTGTTGCCCAGTTA TCTCGCCCTGATCCGGCGTTGGCCGCGTTGACCAACGACCACCTCGTCGCCTTGG CCTGCCTCGGCGGGCGTCCTGCGCTGGATGCAGTGAAAAAGGGATTGGGGGAT CCTATCAGCCGTTCCCAGCTGGTGAAGTCCGAGCTGGAGGAGAAGAAATCCGAG TTGAGGCACAAGCTGAAGTACGTGCCCCACGAGTACATCGAGCTGATCGAGATC GCCCGGAACAGCACCCAGGACCGTATCCTGGAGATGAAGGTGATGGAGTTCTTC ATGAAGGTGTACGGCTACAGGGGCAAGCACCTGGGCGGCTCCAGGAAGCCCGA CGGCGCCATCTACACCGTGGGCTCCCCCATCGACTACGGCGTGATCGTGGACACC AAGGCCTACTCCGGCGGCTACAACCTGCCCATCGGCCAGGCCGACGAAATGCAG AGGTACGTGGAGGAGAACCAGACCAGGAACAAGCACATCAACCCCAACGAGTG GTGGAAGGTGTACCCCTCCAGCGTGACCGAGTTCAAGTTCCTGTTCGTGTCCGGC CACTTCAAGGGCAACTACAAGGCCCAGCTGACCAGGCTGAACCACATCACCAAC TGCAACGGCGCCGTGCTGTCCGTGGAGGAGCTCCTGATCGGCGGCGAGATGATC AAGGCCGGCACCCTGACCCTGGAGGAGGTGAGGAGGAAGTTCAACAACGGCG AGATCAACTTCGCGGCCGACTGATAA

[001286] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising 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 mRNA encoding transcription activator-like effector nucleases targeting PDCD1 in cytoporation medium to obtain a 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.

[001287] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising 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 mRNA encoding transcription activator-like effector nucleases targeting SEQ ID NO:128 in cytoporation medium to obtain a 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.

[001288] In some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprising 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 mRNA according to SEQ ID NO:135 and SEQ ID NO:136 in cytoporation medium to obtain a 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.

[001289] 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.

[001290] 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.

[001291] 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.

[001292] According to some embodiments, the invention provides a method for expanding tumor infiltrating lymphocytes (TILs) into a therapeutic population of TILs comprises:

(a) obtaining a first population of TILs from at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 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 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, and 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 for modulating the expression of at least one protein.

[001293] According to 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 at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 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 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, and 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 for suppressing the expression of PD-1 and LAG-3.

3. Zinc Finger Methods

[001294] 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 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.

[001295] 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.

[001296] 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).

[001297] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a zinc finger method include PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, SOCS1, ANKRD11, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001298] 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-21, the NOTCH 1/2 intracellular domain (ICD), and/or the NOTCH ligand mDLL1.

[001299] 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.

[001300] 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.

[001301] According to 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 at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 a 4-1BB agonist antibody for 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 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, and 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 for modulating the expression of at least one protein.

[001302] According to 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 at least a portion of a tumor resected from a subject by processing a sample from the resected tumor 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 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 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, and 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 for suppressing the expression of PD-1 and LAG-3. Optional Cryopreservation of TILs

[001303] 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. 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 Oncologics 2013, 52, 978-986.

[001304] 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.

[001305] 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.

[001306] As discussed above, and exemplified in Steps A through E as provided in Figure 1, 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 Figure 1 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.

[001307] 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.

[001308] In some cases, the Step B from Figure 1 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 Figure 1 and then cryopreserved after Step D from Figure 1. Similarly, in the case where genetically modified TILs will be used in therapy, the Step B or Step D from Figure 1 TIL populations can be subjected to genetic modifications for suitable treatments.

4. Cas-CLOVER Methods

[001309] 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 Cas-CLOVER method. According to particular embodiments, the use of a Cas-CLOVER 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 Cas-CLOVER 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.

[001310] Cas-CLOVER is a dimeric, high-fidelity site-specific nuclease (SSN) that consists of a fusion of catalytically dead SpCas9 (dCas9) with the nuclease domain from a Clostridium Clo051 type IIs restriction endonuclease (Madison, et al., "Cas-CLOVER is a novel high-fidelity nuclease for safe and robust generation of T SCM-enriched allogeneic CAR-T cells," Molecular Therapy - Nucleic Acids, 2022). This yields a nuclease whose activity is predicated upon the dimerization of the Clo051 nuclease domain, enabled by RNA-guided recognition of two adjacent 20-nt target sequences. Unlike a paired nickase approach, e.g., when using the Cas9-D10A mutant, monomeric Cas-CLOVER does not introduce a nick or a DSB. Cas-CLOVER has been shown to have low off-target nuclease activity.

[001311] Exemplary Cas-CLOVER systems include those described in WO2019/126578, the contents of which are incorporated herein by reference in their entirety. In some embodiments, the Cas-CLOVER system comprises a fusion protein comprising, consisting essentially of, or consisting of a DNA localization component and an effector molecule.

I. DNA localization components

[001312] In some embodiments, the DNA localization components are capable of binding a specific DNA sequence. In some embodiments, the DNA localization component is selected from, for example, a DNA-binding oligonucleotide, a DNA-binding protein, a DNA binding protein complex, and combinations thereof. Other suitable DNA binding components will be recognized by one of ordinary skill in the art.

[001313] In some embodiments, the DNA localization components comprise an oligonucleotide directed to a specific locus or loci in the genome. The oligonucleotide may be selected from DNA, RNA, DNA/RNA hybrids, and combinations thereof.

[001314] In some embodiments, the DNA localization components comprise a nucleotide binding protein or protein complex that binds an oligonucleotide when bound to a target DNA. The protein or protein complex may be capable of recognizing a feature selected from RNA-DNA heteroduplexes, R-loops, or combinations thereof. In some embodiments, the DNA localization component comprises a protein or protein complex capable of recognizing an R-loop selected from Cas9, Cascade complex, RecA, RNase H, RNA polymerase, DNA polymerase, or a combination thereof. In some embodiments, the DNA localization component comprises an engineered protein capable of binding to target DNA. In some embodiments, the DNA localization component comprises a protein capable of binding a DNA sequence selected from meganuclease, zinc finger array, transcription activator-like (TAL) array, and combinations thereof. In some embodiments, the DNA localization component comprises a protein that contains a naturally occurring DNA binding domain. In some embodiments, the DNA localization component comprises a bZIP domain, a Helix-loop-helix, a Helix-turn-helix, a HMG-box, a Leucine zipper, a Zinc finger, or a combination thereof. In some embodiments, the DNA localization component comprises an oligonucleotide directed to a specific locus in the genome. Exemplary oligonucleotides include, but are not limited to, DNA, RNA, DNA/RNA hybrids, and any combination thereof. In some embodiments, the DNA localization component comprises a protein or a protein complex capable of recognizing a feature selected from RNA-DNA heteroduplexes, R-loops, and any combination thereof. Exemplary proteins or protein complexes capable of recognizing an R-loop include, but are not limited to, Cas9, Cascade complex, RecA, RNase H, RNA polymerase, DNA polymerase, and any combination thereof. In some embodiments, the protein or protein complex capable of recognizing an R-loop comprises Cas9. In some embodiments, the DNA localization component comprises a protein capable of binding a DNA sequence selected from meganuclease, Zinc Finger array, TAL array, and any combination thereof. In some embodiments, the DNA localization component comprises an oligonucleotide directed to a target location in a genome and a protein capable of binding to a target DNA sequence.

[001315] In some embodiments, the DNA localization components comprise, consist essentially of, or consist of, at least one guide RNA (gRNA). In some embodiments, the DNA localization components comprise, consist essentially of, or consist of, two gRNAs, wherein a first gRNA specifically binds to a first strand of a double-stranded DNA target sequence and a second gRNA specifically binds to a second strand of the double-stranded DNA target sequence. Alternatively, in embodiments, DNA localization components comprise, consist essentially of, or consist of, a DNA binding domain of a transcription activator-like effector nuclease (TALEN, also referred to as a TAL protein). In some embodiments DNA localization components comprise, consist essentially of, or consist of, a DNA-binding domain of a TALEN, or TAL protein, derived from Xanthomonas or Ralstonia.

II. Effector molecules

[001316] In some embodiments, effector molecules are capable of a predetermined effect at a specific locus in the genome. Exemplary effector molecules, but are not limited to, a transcription factor (activator or repressor), chromatin remodeling factor, nuclease, exonuclease, endonuclease, transposase, methytransferase, demethylase, acetyltransferase, deacetylase, kinase, phosphatase, integrase, recombinase, ligase, topoisomerase, gyrase, helicase, fluorophore, or any combination thereof.

[001317] In some embodiments, effector molecules comprise a transposase. In some embodiments, effector molecules comprise a PB transposase (PBase). In some embodiments, effector molecules comprise a nuclease. Non-limiting examples of nucleases include restriction endonucleases, homing endonucleases, S1 nuclease, mung bean nuclease, pancreatic DNase I, micrococcal nuclease, yeast HO endonuclease, or any combination thereof. In certain embodiments, the effector molecule comprises a restriction endonuclease. In certain embodiments, the effector molecule comprises a Type IIS restriction endonuclease. In some embodiments, effector molecules comprise an endonuclease. Non-limiting examples of the endonuclease include AciI, Mn1I, AlwI, BbvI, BccI, BceAI, BsmAI, BsmFI, BspCNI, BsrI, BtsCI, HgaI, HphI, HpyAV, Mbo1I, My1I, PleI, SfaNI, AcuI, BciVI, BfuAI, BmgBI, BmrI, BpmI, BpuEI, BsaI, BseRI, BsgI, BsmI, BspMI, BsrBI, BsrBI, BsrDI, BtgZI, BtsI, EarI, EciI, MmeI, NmeAIII, BbvCI, Bpu10I, BspQI, SapI, BaeI, BsaXI, CspCI, BfiI, MboII, Acc36I and Clo051. In some embodiments, the effector molecule comprises BmrI, BfiI, or Clo051.

[001318] In some embodiments, effector molecules comprise, consist essentially of, or consist of, a homodimer or a heterodimer. In some embodiments, effector molecules comprise, consist essentially of, or consist of, a nuclease, optionally an endonuclease. In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a Cas9, a Cas9 nuclease domain or a fragment thereof. In some embodiments, the Cas9 is a catalytically inactive or "inactivated" Cas9 (dCas9 (SEQ ID NO: 302 and 303 of WO2019/126578)). In some embodiments, the Cas9 is a catalytically inactive or "inactivated" nuclease domain of Cas9. In some embodiments, the dCas9 is encoded by a shorter sequence that is derived from a full length, catalytically inactivated, Cas9, referred to herein as a "small" dCas9 or dSaCas9 (SEQ ID NO: 23 of WO2019/126578).

[001319] In some embodiments of the fusion protein, the effector molecule comprises, consists essentially of, or consists of a homodimer or a heterodimer of one or more Type II nucleases. In some embodiments of the fusion protein, the effector molecule comprises, consists essentially of, or consists of a homodimer or a heterodimer of a Type II nuclease. In some embodiments, the Type II nuclease comprises one or more of AciI, Mn1I, AlwI, BbvI, BccI, BceAI, BsmAI, BsmFI, BspCNI, BsrI,

BtsCI, HgaI, HphI, HpyAV, Mbo1I, My1I, PleI, SfaNI, AcuI, BciVI, BfuAI, BmgBI, BmrI, BpmI, BpuEI, BsaI, BseRI, BsgI, BsmI, BspMI, BsrBI, BsrBI, BsrDI, BtgZI, BtsI, EarI, EciI, MmeI, NmeAIII, BbvCI, Bpu10I, BspQI, SapI, BaeI, BsaXI, CspCI, BfiI, MboII, Acc36I or Clo051.

[001320] In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, Clo051, BfiI or BmrI. In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a Cas9, a Cas9 nuclease domain or a fragment thereof that forms a heterodimer with Clo051, BfiI or BmrI. In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a catalytically-inactive form of Cas9 (e.g. dCas9 or dSaCas9) or a fragment thereof that forms a heterodimer with Clo051. An exemplary Clo05 l nuclease domain may comprise, consist essentially of or consist of, the amino acid sequence of:
EGIKSNISLLKDELRGQISHISHEYLSLIDLAFDSKQNRLFEMKVLELLVNEYGFKGRH
LGGSRKPDGIVYSTTLEDNFGIIVDTKAYSEGYSLPISQADEMERYVRENSNRDEEVN
PNKWWENFSEEVKKYYFVFISGSFKGKFEEQLRRLSMTTGVNGSAVNVVNLLLGAE
KIRSGEMTIEELERAMFNNSEFILKY (SEQ ID NO:299).

[001321] In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a DNA-binding domain of a TALEN, or TAL protein, derived from Xanthomonas or Ralstonia. In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a DNA-binding domain of a TALEN, or TAL protein, derived from Xanthomonas or Ralstonia that forms a homodimer or a heterodimer with Clo051, BfiI or BmrI. In some embodiments, effector molecules, including those effector molecules comprising a homodimer or a heterodimer, comprise, consist essentially of, or consist of, a DNA-binding domain of a TALEN, or TAL protein, derived from Xanthomonas or Ralstonia that forms a homodimer or a heterodimer with Clo051.

III. Linkages

[001322] In some embodiments, the fusion protein comprises, consists essentially of, or consists of, a DNA localization component and an effector molecule. In some embodiments, the nucleic acid sequences encoding one or more components of the fusion protein can be operably linked, for example, in an expression vector. In some embodiments, the fusion proteins are chimeric proteins. In some embodiments, the fusion proteins are encoded by one or more recombinant nucleic acid sequences. In some embodiments, the fusion proteins also include a linker region to operatively-link two components of the fusion protein. For example, in embodiments, the fusion protein comprises,

consists essentially of, or consists, of a DNA localization component and an effector molecule, operatively-linked by a linker region. In some embodiments, the DNA localization component, the linker region, and the effector molecule can be encoded by one or more nucleic acid sequences inserted into an expression cassette and/or expression vector such that translation of the nucleic acid sequence results in the fusion protein. in embodiments, the fusion protein can comprise a non-covalent linkage between the DNA localization component and the effector molecule. The non-covalent linkage can comprise an antibody, an antibody fragment, an antibody mimetic, or a scaffold protein.

IV. Fusion proteins

[001323] In some embodiments, the DNA localization component comprises, consists essentially of or consists of, at least one gRNA, and the effector molecule comprises, consists essentially of, or consists of a Cas9, a Cas9 nuclease domain, or a fragment thereof. In some embodiments, the DNA localization component comprises, consists essentially of, or consists of, at least one gRNA, and the effector molecule comprises, consists essentially of, or consist of an inactivated Cas9 (dCas9) or an inactivated nuclease domain. In some embodiments, the DNA localization component comprises, consists essentially of, or consists of, at least one gRNA, and the effector molecule comprises, consists essentially of, or consist of an inactivated small Cas9 (dSaCas9). In some embodiments, the effector molecule comprises, consists essentially of, or consists of a Cas9, dCas9, dSaCas9, or nuclease domain thereof, and a second endonuclease. The second endonuclease can comprise, consist essentially of, or consist of a Type IIS endonuclease, including, but not limited to, one or more of AciI, Mn1I, AlwI, BbvI, BccI, BceAI, BsmAI, BsmFI, BspCNI, BsrI, BtsCI, HgaI, HphI, HpyAV, Mbo1I, My1I, PleI, SfaNI, AcuI, BciVI, BfuAI, BmgBI, BmrI, BpmI, BpuEI, BsaI, BseRI, BsgI, BsmI, BspMI, BsrBI, BsrBI, BsrDI, BtgZI, BtsI, EarI, EciI, MmeI, NmeAIII, BbvCI, Bpu10I, BspQI, SapI, BaeI, BsaXI, CspCI, BfiI, MboII, Acc36I, FokI or Clo051.

[001324] In some embodiments of the fusion proteins, the DNA localization component comprises, consists essentially of, or consists of, a DNA-binding domain of a transcription activator-like effector nuclease (TALEN, also referred to as a TAL protein), and the effector molecule comprises, consists essentially of, or consists of, an endonuclease. In some embodiments of the fusion proteins of the disclosure, the DNA localization component comprises, consists essentially of, or consists of, a DNA-binding domain of a TALEN, or TAL protein, derived from Xanthomonas or Ralstonia, and the effector molecule comprises, consists essentially of, or consists of, a Type IIS endonuclease, including, but not limited to, one or more of AciI, Mn1I, AlwI, BbvI, BccI, BceAI, BsmAI, BsmFI, BspCNI, BsrI, BtsCI, HgaI, HphI, HpyAV, Mbo1I, My1I, PleI, SfaNI, AcuI, BciVI, BfuAI, BmgBI,

BmrI, BpmI, BpuEI, BsaI, BseRI, BsgI, BsmI, BspMI, BsrBI, BsrBI, BsrDI, BtgZI, BtsI, EarI, EciI, MmeI, NmeAIII, BbvCI, Bpu10I, BspQI, SapI, BaeI, BsaXI, CspCI, BfiI, MboII, Acc36I or Clo051.

[001325] In certain embodiments, an exemplary dCas9-Clo051 fusion protein may comprise, consist essentially of or consist of the amino acid sequence of SEQ ID NO: 305 or 307 of WO2019/126578 or the nucleic acid sequence of SEQ ID NO: 306 or 308 of WO2019/126578.

V. Constructs

[001326] In some embodiments, the nuclease domain comprises, consists essentially of, or consists of, a dCas9 and Clo051. In some embodiments, the nuclease domain comprises, consists essentially of, or consists of, a dSaCas9 and Clo051. In some embodiments, the nuclease domain comprises, consists essentially of, or consists of, a Xanthomonas-TALE and Clo051. In some embodiments, the nuclease domain comprises, consists essentially of, or consists of, a Ralstonia-TALE and Clo051. In some embodiments, the fusion protein comprises dCas9-Clo051, dSaCas9-Clo051, Xanthomonas-TALE-Clo051, or Ralstonia-TALE-Clo051. In some embodiments, a vector encoding the fusion protein comprises Csy4-T2A-Clo051-G4Slinker-dCas9 (Streptoccocus pyogenes) or pRT1-Clo051-dCas9 double NLS.

[001327] According to some embodiments, a Cas-CLOVER system comprises a fusion protein comprising a DNA localization component and an effector molecule, wherein the DNA localization component 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 effector molecule cleaves the DNA molecule, whereby expression of the at least one immune checkpoint molecule is altered.

[001328] According to particular embodiments, a Cas-CLOVER method comprises silencing or reducing the expression of one or more immune checkpoint genes in TILs by introducing a Cas-CLOVER system (e.g., dCas9-Clo051, dSaCas9-Clo051, Xanthomonas-TALE-Clo051, or Ralstonia-TALE-Clo051 fusion protein) specific to a target DNA sequence of the immune checkpoint gene(s). The fusion protein may be delivered as DNA, mRNA, protein. Upon contact of the genome with the Cas-CLOVER system, one or more strand of the target double-stranded DNA may be cut. If the cut is made in the presence of one or more DNA repair pathways or components thereof, the Cas-CLOVER method either interrupts gene expression or modifies the genomic sequence by insertion, deletion, or substitution of one or more base pairs. 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.

[001329] Alternatively, DSBs induced by Cas-CLOVER systems 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 Cas-CLOVER system. 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).

[001330] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via a Cas-CLOVER method include PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.).

[001331] Examples of systems, methods, and compositions for altering the expression of a target gene sequence by a Cas-CLOVER method, and which may be used in accordance with embodiments of the present invention, are described in WO2019126578, US2017/0107541, US2017/0114149, US2018/0187185, and U.S. Patent No. 10,415,024, the contents of which are incorporated herein by reference in their entirety. Resources for carrying out Cas-CLOVER methods, such as CLOVER mRNA and Cas-CLOVER mRNA constructs, are commercially available from companies such as Demeetra and Hera Biolabs.

[001332] 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 comprising a Cas-CLOVER system, which at least one gene editor system modulates expression of at least one checkpoint protein in the plurality of cells of the second population of TILs.

[001333] 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 at least one gene editor system comprising a Cas-CLOVER system, which at least one gene editor system inhibits expression of at least one checkpoint protein in the plurality of cells of the second population of TILs.

5. Short Hairpin RNA (shRNA) Methods

[001334] In some embodiments, the subject TILs described herein are modified to reduce endogenous protein expression using a short hairpin RNA (shRNA). In some embodiments, a nucleic acid is introduced into subject TIL that encodes for an RNA (e.g., an shRNA) that suppresses expression of an endogenous gene.

[001335] An "shRNA" as used herein is a short hairpin RNA, which is a sequence of RNA that makes a tight hairpin turn that can also be used to silence gene expression via RNA interference. Expression of shRNA in cells is typically accomplished by delivery of plasmids or through viral or

bacterial vectors. shRNA is an advantageous mediator of RNAi in that it has a relatively low rate of degradation and turnover.

[001336] shRNA design is typically divided into two formats, the simple stem-loop shRNA and the microRNA-adapted shRNA. Basic shRNAs are modeled on precursor microRNA (pre-miRNA), and are cloned into viral vectors where they are transcribed under the control of a promoter. Exemplary promoters include, but are not limited to RNA Polymerase II (Pol II) and Polymerase III (Pol III) promoters (e.g., U6 and H1 promoters). shRNAs are produced as single-strand molecules of about 40–70 nucleotides in length, and form stem loop structures consisting of a 19-29 base-pair region of double-strand RNA (the stem) bridged by a region of single-strand RNA (the loop) and a short 3' overhang. Once transcribed, shRNAs exit the nucleus, are cleaved at the loop by the nuclease Dicer in the cytoplasm, and enter the RNA-induced silencing complex (RISC) to direct cleavage and subsequent degradation of a target complementary mRNA. A microRNA-adapted shRNA consists of an shRNA stem structure with microRNA-like mismatches surrounded by the loop and flanking sequence of an endogenous microRNA. microRNA-adapted shRNAs are transcribed from RNA Polymerase ll (Pol ll) promoters, cleaved by the endogenous RNase III Drosha enzyme in the nucleus, and then exported to the cytoplasm where they are processed by Dicer and loaded into the RISC complex. Studies have suggested that the use of a microRNA scaffold, which is processed by both Drosha and Dicer, may promote more efficient processing and reduce toxicity for in vivo RNAi. In some embodiments, the shRNA for TIL modification is a simple stem-loop shRNA. In some embodiments, the shRNA for TIL modification is a microRNA-adapted shRNA.

[001337] In some embodiments, the shRNA for subject TIL modification disclosed herein comprises a sequence complementary to at least 13 nucleotides, at least 14 nucleotides, at least 15 nucleotides, at least 16 nucleotides, at least 17 nucleotides, at least 18 nucleotides, at least 19 nucleotides, at least 20 nucleotides, at least 21 nucleotides, at least 22 nucleotides, at least 23 nucleotides, , at least 24 nucleotides, at least 25 nucleotides, at least 26 nucleotides, , at least 27 nucleotides, at least 28 nucleotides, at least 29 nucleotides, or at least 30 nucleotides of the mRNA a target protein. In some embodiments, the shRNA for subject TIL modification disclosed herein comprises a sequence complementary to 13 nucleotides, 14 nucleotides, 15 nucleotides, 16 nucleotides, 17 nucleotides, 18 nucleotides, 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, , 24

nucleotides, 25 nucleotides, 26 nucleotides, , 27 nucleotides, 28 nucleotides, 29 nucleotides, or 30 nucleotides of the mRNA a target protein.

[001338] In some embodiments, the shRNA used for TIL modification is 40–50 nucleotides in length, 45-55 nucleotides in length, 50-60 nucleotides in length, 55-65 nucleotides in length, or 60-70 nucleotides in length.

[001339] shRNAs can be delivered to cells (e.g., the modified TILs provided herein) using any suitable method. For plasmids, typical transfection methods such as use of lipid transfection reagents or electroporation can be employed. In some embodiments, lentiviral particles are used to introduce the shRNA into the cell for modification. In some embodiments, a selectable marker is included to allow for elimination of cells in the culture that were not successfully transfected or transduced with the shRNA, thereby allowing for a pure culture of modified cells that include the shRNA.

[001340] Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via an shRNA method include one or two immune checkpoints. Non-limiting examples of genes that may be silenced or inhibited by permanently gene-editing TILs via an shRNA method include PD-1, TGIT, TET2, TGFβR2, PRA, BAFF (BR3), 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, BCOR, ss thereof (e.g., two more more of the above immune checkpoints, such as PD-1 and LAG3, PD-1 and TIM3, TIM3 and CTLA-4, etc.) .

[001341] In some embodiments, the shRNA is for reducing the expression of an immune checkpoint (e.g., any of the immune checkpoint provided herein) in a subject TIL described herein. In some embodiments, one or more shRNAs is introduced into a TIL for modifying the expression of one or more of the following immune checkpoint proteins: PD-1, CTLA-4, LAG-3, TGIT, TIM-3, Cish, TGFβ, PKA, CBLB, TOX. Exemplary shRNA sequences useful for modifying subject TILs are described in the Examples.

H. Cytokine Carriers

[001342] As discussed herein, in some embodiments, the TILs can be genetically modified to express binding partners for cytokine carriers (also referred to herein as cytokine backpacks). The cytokine carriers may be liposomes, vesicles, or nanoparticles that enclose or present cytokines.

[001343] Any suitable genetic modification method can be used to genetically modify the subject TILs to include such binding partners for cytokine carriers, including, for example, any of the gene editing methods described herein. In some embodiments, the genetic modification method is a CRISPR, TALE, zinc finger, or Cas-CLOVER method described herein. In some embodiments, such modified TILs are produced using any one of the retroviral methods (e.g., lentiviral methods) provided herein. In some embodiments, such modified are produced using any of the transposon/transposase systems described herein, e.g., a piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty method (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser method (e.g., Helraiser ahd Helraiser-like transposons and transposases), and a Tol2 method (e.g., Tol2 and Tol2-like transposons and transposases).

[001344] In some embodiments, the cytokines enclosed or presented by the cytokine carriers include, but are not limited, cytokines that modulate the tumor microenvironment to promote expansion of administered TILs. Non-limiting examples of such cytokines include, IL-2, IL-15, IL-21, IL-12 and IL-18.

[001345] The cytokine backpacks may include epitopes or antibodies that are recognized by the binding partners expressed on the surface of the genetically modified TILs such that cytokine backpacks bind to the genetically modified TILs. In addition, the cytokine backpacks are designed to release the cytokines upon binding to the genetically modified TILs and exposure to the tumor microenvironment such that the cytokines can then promote expansion of the TILs.

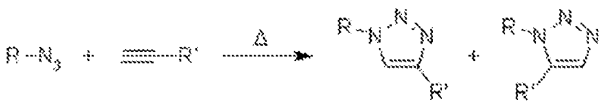
[001346] Thus, in some embodiments, the cytokine backpacks may include a molecule having a structure B1-$(L1)_n$-C1-$(L2)_m$-B2, wherein B1 is the moiety (e.g., an antibody or an epitope) that recognizes and binds the binding partner expressed on the TIL surface, C1 is a labile moiety that allows release of the cytokine backpack in the TME, L1 is a linker, L2 is a linker, n and m are independently zero or one, and B2 is the cytokine carrier (e.g., a liposome, a vesicle or a nanoparticle enclosing or presenting the cytokine). In some embodiments, C1 is or comprises a labile chemical bond. In some embodiments, C1 is or comprises a labile chemical structure.

[001347] In some embodiments, the cytokine backpacks B2 are attached to the binding moiety B1 through click chemistry, wherein C1 contains a chemical structure susceptible to one or more nucleophilic ring opening reactions.

[001348] Click chemistry refers to several types of thermodynamically-favored reactions that lead specifically to one product, such as nucleophilic ring opening reactions of epoxides and aziridines, non-aldol type carbonyl reactions, such as formation of hydrazones and heterocycles,

additions to carbon-carbon multiple bonds, such as oxidative formation of epoxides and Michael Additions, and cycloaddition reactions.

[001349] One example of a click chemistry reaction that can be used for conjugating a binding moiety B1 with an appropriate backpack moiety B2 is the azide-alkyne cycloaddition shown in Equation (I),



- Equation (I).

wherein C1 is or comprises the 1,2,3-triazole product of the cycloaddition reaction.

[001350] Many of the starting monosubstituted alkynes and organic azides are available commercially, many others can easily be synthesized with a wide range of functional groups, and their cycloaddition reaction selectively gives 1,2,3-triazoles.

[001351] In one example, C1 may be a biotin-streptavidin bond. In some embodiments, binding partner B1 is a reaction product of N-azidosialic acid, and sulfo-dibenzylcyclooctyne-biotin conjugate. The genetically modified TILs can be incubated with a cell culture medium supplemented with tetra-acylated N-azidoacetylmannosamine (Ac_4-ManNAz), which is metabolized and incorporated as N-azido-sialic acid into glycan structures of the binding partner expressed on the TIL surface. The sulfo-dibenzylcyclooctyne-biotin conjugate can then be added to obtain a biotin presenting TIL-B1. In such embodiments, L1 may be absent ($(L1)_{n=0}$) and L2 ($(L2)_{m=1}$) may be streptavidin conjugated to the liposome, vesicle or nanoparticle (B2). The $(L2)_{m=1}$-B2 construct can be added to TIL-B1 to form the streptavidin-biotin (C1) bond, linking B1 to $(L2)_{m=1}$-B2 to form TIL-B1-C1-$(L2)_{m=1}$-B2.

[001352] Upon administration, the TILs can release the cytokine backpacks when the biotin-streptavidin bond is gradually cleaved.

[001353] In some embodiments, the cytokine backpacks can be formed by conjugating the cytokine backpack with a moiety that is enzymatically cleavable. Thus, in such embodiments, the bond or enzymatic recognition site in C1 between B1 and B2 can be enzymatically cleaved to release the cytokine backpacks from the TILs. Non-limiting examples of enzymatically cleavable moeties include peptide moieties that are cleavable by hydrolytic enzymes, and β-glucuronide moieties. In some embodiments, C1 is an esterase cleavable PEG-lipid (e.g., PEG-distearoyl phosphatidylethandamine).

[001354] In some embodiments, the bond in C1 between B1 and B2 can be cleavable by a redox reaction driven by the reductive conditions of the TME. Non-limiting examples of the redox cleavable bond in C1 between B1 and B2 include vinyl ether bonds, hydrazone bonds, disulfide bonds and ester bonds. Thus, C1 can be suitably selected to enable cleavage in the reductive conditions of the TME. In some embodiments, L1 may be absent ($(L1)_{n=0}$), L2 ($(L2)_{m=1}$) is and C1 is selected from a vinyl ether lipid (e.g., glycerophospholipids). In some embodiments, L1 may be absent ($(L1)_{n=0}$), L2 ($(L2)_{m=1}$) is a PEG (e.g., PEG aldehydes) and C1 a hydrazone lipid (e.g., hydrazone cholesteryl hemisuccinate). In some embodiments, L1 may be absent ($(L1)_{n=0}$), L2 ($(L2)_{m=1}$) is a PEG-amine and C1 is an unsaturated anhydride-lipid. In some embodiments, L1 may be absent ($(L1)_{n=0}$), L2 ($(L2)_{m=1}$) is a PEG-L-cysteine and C1 is selected from a PEG-L-cysteine or a lipid-L-cysteine.

[001355] In some embodiments, the cytokine backpacks can be liposomes, vesicles, or nanogels loaded with or presenting the desired cytokines. In addition, the cytokine backpacks may include, on surfaces thereof (interchangably referred to herein as "decorated by"), one or more moieties recognized by the binding partners presented on the surface of the modified TILs described herein. Thus, B2 may be the liposome, vesicle or nanogel, or the moiety recognizable by the binding partners.

[001356] In some embodiments, the cytokine backpacks may be liposomes enclosing (e.g., containing) the desired cytokines. Liposomes are often composed of phospholipids, such as phosphatidylcholine, and further include cholesterol. Liposomes can be designed to present surface ligands in some embodiments. The particular lipids used for making the liposomes may be selected based on the charges and size of the desired cytokines being encapsulated.

[001357] Cytokine enclosing liposome may be formed using any of the known methods for forming liposomes. Typically, liposomes are formed by sonicating a dispersion of amphiphatic lipids in water. However, because sonication can damage the structure of the molecules that are being encapsulated in the liposomes, other methods of forming liposomes such as extrusion, and micromixing may be preferable. In some embodiments, the micromixing may involve convective-diffusive mixing as described by Jahn, et al, in 4(4) ACS Nano (2010), 2077-2087, or millisecond mixing of aqueous and ethanol streams at high flow rate ratios using a staggered herringbone micromixer as described by Zhigaltsev, et al, in 28(7) Langmuir (2012), 3633-3640. In some embodiments, the liposomes can be prepared using the Mofazari method described by Colas et al, in 38(8) Micron (2007), 841-847.

[001358] In some embodiments, the liposomes may be constructed with PEG studding the outside of the lipid membrane. The PEG may be conjugated with moieties that are recognizable by the binding partners, as first described by Blume et al, in 1149(1) Biomembranes (1993), 180-184.

[001359] In a non-limiting example, liposomes encapsulating desired cytokines (e.g., IL-12) can be conjugated with a (bicyclo[6.1. 0]nonyne) (BCN) group attached to one of the hydrophobic tails of the the phospholipids forming the liposomes. The TILs manufactured by any of the methods described herein can then be surface-modified with phospholipids having PEG-azide molecules tagged thereto via. The BCN group from the liposomes can then react with the azide molecules, via click chemistry, resulting in the TILs having the liposomes encapsulating the desired cytokines. FIG. 8A shows an example of structure and synthesis of lipid click molecule having a BCN group, and FIG. 8B shows an example of structure and synthesis of an anchoring molecule having a PEG-azide molecule tagged thereto. The detailed chemistry of attaching BCN group to the liposomes is described, e.g., in Hao et al., 571(12) Sci. Transl. Med. (2020).

[001360] In some embodiments, the cytokine backpacks may be vesicles containing, encapsulating and/or presenting the desired cytokines. Vesicles may be large unilamellar vesicles (LUVs) ranging in size from about 100 nm to about 1000 nm, or giant unilamellar vesicles (GUVs) ranging in size from about 1 μm to about 200 μm. Like liposomes, vesicles can be prepared by extrusion, sonication or rapid injection of a phospholipid solution into an aqueous buffer (containing the molecule to be encapsulated). Various methods of preparing vesicles are known in the art. Non-limiting examples of vesicle formation methods include those described by Walde et al., 11(7) ChemBioChem (2010) 848-865; Barenholz et al., 16(2) Biochemistry (1977) 2806-2810; Batzri and Kom, 298(4) Biomembranes (1093) 1015-1019; Litschel and Schwille, 50 Annual Review of Biophysics (2021) 525-548; and Sato and Takinoue 10(4) Micromachines (2019) 216.

[001361] In some embodiments, vesicles may be decorated with moieties that are recognizable by the binding partners presented by the modified TILs described herein. Methods of providing vesicles with surface moieties are similar to those used for providing liposomes with surface moieties.

[001362] In some embodiments, the cytokine backpacks may be nanogels. Nanogels are three-dimensional hydrogels formed by crosslinked swellable polymer networks that can hold water and hyrdophilic molecules. In some embodiments, the nanogels are spherical particles with a core-shell structure or a core-shell-corona structure. Nanogels can be composed of natural polymers, synthetic polymers or a combination thereof. Soni et al., 240 J. Control Release (2016) 109-126 provides an excellent review including various methods of synthesis of nanogels encapsulating or enclosing desired molecules. Non-limiting examples of nanogel synthesis methods include those described by O'Reilly et al., 35 Chem Soc Rev. (2006) 1068–1083 (reviewing stabilization, functionalization and decoration of core-shell nonoparticles); Oishi and Nagasaki, 5 Nanomedicine (2010) 451–468 (describing preparation and characterization of stimuli-responsive PEGylated nanogels composed of a crosslinked poly(2-[N,N-diethylamino]ethyl methacrylate) (PEAMA) core and PEG tethered chains

loaded with biomolecules); Elsabahy et al., 115 Chem Rev. (2015) 10967-110[11] (reviewing methods of synthesis of drug and peptide loaded nanoparticles and nanogels); Massi et al., 8 J. Mat. Chem. B (2020) 8894-8907 (describing formulation of peptide-crosslinked, temperature-sensitive nanogels for protein delivery were designed to respond to MMP-7); Kordalivand et. al, 315 J. Control. Release (2019) 114-125 (describing cationic dextran nanogels conjugated to long peptides containing CTL and $CD4^+$ helper epitopes); Simonson et al., 17 Nanomedicine: Nanotech., Bio., Med. (2019) 391-400 (describing design, synthesis and efficacy of proten encapsulating nanogels formed by assembling anionic hyaluronic acod polysaccharides with poly-L-lysine).

[001363] In a non-limiting example, TILs manufactured using any of the methods disclosed herein can be genetically modified to express binding partners (e.g., CD45) for IL-15 nanogels that are surface modified to be decorated with anti-(binding partner) antibodies (e.g., murine anti-CD45 antibodies) via PEG-b-PLL linkage as described in Tang et al., 36(8) Nat Biotechnol, (2018) 707.

[001364] In some embodiments, the nanogels can be loaded with desired cytokines. In some embodiments, the nanogels can additionally be decorated with moieties that are recognizable by binding partners presented by the modified TILs described herein.

I. Immunomodulatory Fusion Proteins

[001365] 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.

[001366] Any suitable genetic modification method can be used to genetically modify the subject TILs to include such immunomodulatory fusion proteins, including, for example, any of the gene editing methods described herein. In some embodiments, the genetic modification method is a CRISPR, TALE, zinc finger, or Cas-CLOVER method described herein. In some embodiments, such modified TILs are produced using any one of the retroviral methods (e.g., lentiviral methods) provided herein. In some embodiments, such modified TILs are produced using any of the transposon/transposase systems described herein, e.g., a piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty method (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser method (e.g., Helraiser ahd Helraiser-like transposons and transposases), and a Tol2 method (e.g., Tol2 and Tol2-like transposons and transposases).

[001367] Aspects of these fusion proteins are further discussed in detail below.

1. Membrane Anchored Immunomodulatory Fusion Proteins

[001368] 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.

[001369] 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.

[001370] 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.

[001371] 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).

[001372] 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. 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).

[001373] 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)).

[001374] 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.

[001375] 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 NIKGSPWKGSLLLLVSNLLLCQSVAP (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).

[001376] In some embodiments, the membrane anchored immunomodulatory fusion protein is according to the formula, from N- to C-terminus:

[001377] S-IA-L-C,

[001378] wherein S is a signal peptide, IA is an immunomodulatory agent, L is a linker and C is a cell membrane anchor moiety.

[001379] In some embodiments, the signal peptide S is any one of SEQ ID NOs:252-254. In some embodiments, 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 embodiments, C is a B7-1 transmembrane-intracellular domain (e.g., SEQ ID NO:239).

[001380] 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.

[001381] 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:

[001382] S1-IA1-L1-C1-L2-S2-IA2-L3-C2,

[001383] 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.

[001384] 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, any of the gene editing methods described herein. In some embodiments, the gene editing method is a CRISPR, TALE, zinc finger, and Cas-CLOVER method described herein. In some embodiments, such modified TILs are produced using any one of the retroviral (e.g., lentiviral) or non-retroviral methods provided herein. In some embodiments, such modified TILs are produced using any of the transposon/transposase systems described herein, e.g., a piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty method (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser method (e.g., Helraiser ahd Helraise-like transposons and transposases), and a Tol2 method (e.g., Tol2 and Tol2-like transposons and transposases).

[001385] 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, TILs produced from the second step in the Process 2A 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.

[001386] 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, TILs produced from the first expansion step in the Process 2A 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 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.

[001387] 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. Vectors for expression of the subject membrane anchored immunomodulatory fusion proteins include, but are not limited to adenoviral vectors, retroviral vectors, lentiviral vectors, and adeno-associated vectors (AAV). In some embodiments, a piggyBac transposon is used for expression of the subject membrane anchored immunomodulatory fusion proteins.

[001388] 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, m7GpppN (cap 0), m7GpppNm (cap 1), and m7GpppNmpNm (cap 2) caps. In some embodiments, the 5' cap is according ot the formula: m7Gppp[N2'Ome]n[N]m wherein m7G 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.

[001389] 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.

[001390] 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.

[001391] 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 18 – NFAT Promoter Related Sequences.

Description	Amino Acid Sequence
6X NFAT IL-2 minimal promoter	TCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTA GGAGGAAAAACTGTTTCATACAGAAGGCGTCAATTA GGAGGAAAAACTGTTTCATACAGAAGGCGTCAATTA GGAGGAAAAACTGTTTCATACAGAAGGCGTCAATTG GTCCCATCGAATTAGGAGGAAAAACTGTTTCATACAG AAGGCGTCAATTAGGAGGAAAAACTGTTTCATACAG AAGGCGTCAATTAGGAGGAAAAACTGTTTCATACAG AAGGCGTCAATTGGTCCCGGGACATTTTGACACCCCC ATAATATTTTTCCAGAATTAACAGTATAAATTGCATCTC TTGTTCAAGAGTTCCCTATCACTCTCTTTAATCACTACT CACAGTAACCTCAACTCCTGGCCACC (SEQ ID NO: 255)

NFAT responsive element	GGAGGAAAAACTGTTTCATACAGAAGGCGT (SEQ ID NO: 256)
Human IL-2 Promoter	CATTTTGACACCCCCATAATATTTTTCCAGAATTAACA GTATAAATTGCATCTCTTGTTCAAGAGTTCCCTATCACT CTCTTTAATCACTACTCACAGTAACCTCAACTCCTG (SEQ ID NO:257)

[001392] 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. 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.

[001393] 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.

[001394] 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:

[001395] S1-IA1-L1-C1-L2-S2-IA2-L3-C2,

[001396] 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.

[001397] 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.

[001398] 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) 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.

[001399] 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).

[001400] 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.

[001401] 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).

[001402] 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).

[001403] 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).

[001404] 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).

[001405] 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.

[001406] 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.

[001407] 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.

[001408] 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.

[001409] 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).

[001410] 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.

[001411] 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.

[001412] 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.

[001413] 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).

[001414] 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.

[001415] 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.

[001416] 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).

[001417] 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.

[001418] 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).

[001419] 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).

[001420] 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.

[001421] Exemplary membrane anchored immunomodulatory fusion proteins to be included in the modified TILs provided herein are depicted in Tables 58 and 59.

[001422] 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.

J. Immunomodulatory Agents

[001423] 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

[001424] 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).

[001425] 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.

[001426] 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)).

[001427] 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.

[001428] 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 19 – IL-15 Related Sequences.

Description	Amino Acid Sequence

Human IL-15 (N72D mutant)	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTA MKCFLLELQVISLESGDASIHDTVENLIILANDSLSSNGN VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 258)
Human IL-15R-alpha-Su/Fc domain	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIREPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 259)
Human IL-15R-alpha-Su (65aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIR (SEQ ID NO: 260)
Human IL-15 isoform 2	MVLGTIDLCSCFSAGLPKTEANWVNVISDLKKIEDLIQS MHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDA SIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIK EFLQSFVHIVQMFINTS (SEQ ID NO: 261)
Human IL-15 isoform 1	MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSA GLPKTEANWVNVISDLKKIEDLIQSMHIDATLYTESDVH PSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANN SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFI NTS (SEQ ID NO: 262)
Human IL-15 (without signal peptide)	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTA MKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 263)
Human IL-15R-alpha (85 aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS TVTTAGV (SEQ ID NO: 264)

Human IL-15R-alpha (182aa truncated extracellular domain)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGT SSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS TVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIV PGSQLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWEL TASASHQPPGVYPQGHSDTTVAISTST (SEQ ID NO: 265)
Human IL-15R-alpha	MAPRRARGCRTLGLPALLLLLLLRPPATRGITCPPPMSV EHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLN KATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVT PQPESLSPSGKEPAASSPSSNNTAATTAAIVPGSQLMPS KSPSTGTTEISSHESSHGTPSQTTAKNWELTA SASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLAC YLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL (SEQ ID NO: 266)

[001429] 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.

[001430] 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.

[001431] 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.

[001432] 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.

[001433] 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.

[001434] 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).

[001435] 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.

[001436] 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).

[001437] 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).

[001438] 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).

[001439] 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).

[001440] 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.

[001441] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-15 or a bioactive variant thereof.

[001442] 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 an NFAT promoter, an EF-1a promoter, an MND promoter, or an SSFV promoter, as described herein.

2. IL-12

[001443] 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).

[001444] 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.

[001445] 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.

[001446] 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 20 – IL-12 Related Sequences.

Description	Amino Acid Sequence
Human IL-12 p35 subunit	RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT LEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNS RETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEF KTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNS ETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSY LNAS (SEQ ID NO:267)
Human IL-12 p40 subunit	IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGIT WTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVL SHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNY SGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAAT LSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMV DAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQV EVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRV FTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPC S (SEQ ID NO:268)

[001447] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-12 or a bioactive variant thereof.

[001448] 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 an NFAT promoter, an EF-1a promoter, an MND promoter, or an SSFV 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 Table 58.

3. IL-18

[001449] 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).

[001450] 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.

[001451] 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, 10, 11, 12, 13, 14, 15, 16, 17,. 18, 19, or 20 mutations as compared to a wild-type IL-18 (SEQ ID NO:269). In some embodiments, the bioactive variant is a decoy resistant IL-18 variant ("DR-IL18," or "DR-IL-18") that provides IL-18 signaling activity even in the presence of an inhibitory molecule such as IL-18 binding protein (IL-18BP). Exemplary IL-18 variants that can be included in the subject modified TILs described herein are shown below in Table 21. Additional IL-18 variants that can be included in the subject modified TILs are described in WO 2022/094473, which is incorporated by reference in its entirety and particular with respect to disclosures relating to variant DR-IL-18.

[001452] In some embodiments, the variant IL-18 includes a stability mutation pair selection fromL C38S/C68S, C38S/C68G, C38S/C68A, C38S/C68D, and C38S/C68N [relative to the human wild-type IL-18 - SEQ ID NO: 269]. In some embodiments, the variant IL-18 includes mutations at amino acid positions M51 (e.g., M51E, M51R, M51K, M51T, M51D, or M51N), K53 (e.g., K53G, K53S, K53T, or K53R), Q56 (e g., Q56G, Q56R, Q56L, Q56E, Q56A, Q56V, or Q56K), D110 (e.g., D110S, DI 10N, D110G, D110K, D110H, D110Q, or D110E) and N111 (e.g., N111G, N111R, Ni l IS, Ni l ID, N111H, or N111Y) in addition to a stabilizing mutation pair selected from: C38S/C68S, C38S/C68G, C38S/C68A, C38S/C68D, and C38S/C68N [relative to the human wild type IL-18 - SEQ ID NO: 269], In some such cases the stabilized IL-18 variant polypeptide additionally includes a mutation at amino acid position S105 (e.g., S105D, SI 05 A, S105N, S105R, S105D, or S105K); and in some cases, further includes mutations at amino acid positions P57 (e.g., P57A, P57L, P57G, or P57K) and M60 (e.g., M60L, M60R, M60K, or M60Q).

TABLE 21 – IL-18 Related Sequences.

Description	Amino Acid Sequence
Human IL-18	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISMYKDSQPRGMAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFQRSVPGHDNKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE D (SEQ ID NO: 269)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARVPGHGRKTQFESSSYE GYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 270)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKSEKISTLSCENKII SFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 331)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDS DSRDNAPRTIFIISKYSDSLARGLAVTISVKGEKISTLSC ENKIISFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKM QFESSSYEGYFLACEKERDLFKLILKKEDELGDRSIMF TVQNED (SEQ ID NO: 332)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKAEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 333)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKVEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS

Description	Amino Acid Sequence
	YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 334)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKDEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 335)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKEEKISTLSCENKII SFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 336)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDS RDNAPRTIFIISKYSDSLARGLAVTISVKNEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDEL (SEQ ID NO: 337)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 338)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDKQPRAKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS

Description	Amino Acid Sequence
	SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQNED (SEQ ID NO: 339)
Human IL-18 variant	RFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 340)
Human IL-18 variant	RFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRNVPGHKYKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 341)
Human IL-18 variant	YFGKLESQLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDKQPRTKAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRRVPGHHNKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 342)
Human IL-18 variant	YFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYKDKQPRAQAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQNED (SEQ ID NO: 343)
Human IL-18 variant	YFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISDYKDKQPRAXAAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFES

Description	Amino Acid Sequence
	SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQNED (SEQ ID NO: 344) X= any naturally occuring amino acid
Human IL-18 variant	YFGKHESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHNNKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTTQNED (SEQ ID NO: 345)
Human IL-18 variant	YFGKIESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYKDKQPRAQAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRKVPGHQHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 346
Human IL-18 variant	YFGKIESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDRQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERDVPGHHHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQNED (SEQ ID NO: 347)
Human IL-18 variant	YFGKIESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDKQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTTQHED (SEQ ID NO: 348)
Human IL-18 variant	YFGKIESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDKQPRAKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRRVPGHHHKMQFESS

Description	Amino Acid Sequence
	SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQKED (SEQ ID NO: 349)
Human IL-18 variant	YFGKIESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDKQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHDYKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQKED (SEQ ID NO: 350)
Human IL-18 variant	YFGKYESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHEHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 351)
Human IL-18 variant	HFGKYESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHHNKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 352)
Human IL-18 variant	RFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRAKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHQHKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTAQKED (SEQ ID NO: 353)
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISDYRDSQPRGRAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFKRNVPGHKYKMQFESS

Description	Amino Acid Sequence
	SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQHED (SEQ ID NO: 354)
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISNYRDSQPRGQAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFKRRVPGHNHKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 355)
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 356)
Human IL-18 variant	RFGKHESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERNVPGHKYKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 357)
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRAKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERDVPGHQHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQXED (SEQ ID NO: 358) X= any naturally occuring amino acid
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRTKAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRNVPGHHDKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQHED (SEQ ID NO: 359)

Description	Amino Acid Sequence
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDSQPRAKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERDVPGHQHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTIQKED (SEQ ID NO: 360)
Human IL-18 variant	RFGKHESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRGKAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERNVPGHKYKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 361)
Human IL-18 variant	RFGKYESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYKDSQPRTKAVTISVKCEKISTLSCDNK IISFKEMNPPDNIKDTKSDIIFFQRDVPGHKHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 362)
Human IL-18 variant	RFGKLESRLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISTYRDSQPRTKAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRKVPGHNHKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKED (SEQ ID NO: 363)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISEYKDSELRGRAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFPRAVPGHNRKVQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 364)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYKDSAGRGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFERDVPGHSNKVQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 365)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSAARGLAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFQRSVPGHKRKMQFESS

Description	Amino Acid Sequence
	SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 366)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSRGRGLAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERDVPGHNSKRQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 367)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSVPRGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARAVPGHSRKTQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 368)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSGARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARAVPGHGRKTQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 369)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSKARGMAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFARDVPGHSSKRQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 370)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSLARGLAVTISVKCEKISTLSCENKII SFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 371)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRNVPGHGRKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 372

Description	Amino Acid Sequence
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARSVPGHGRKTQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 373)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARDVPGHSGKRQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 374)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYTDSRPRGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFERDVPGHSSKKQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 375)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYTDSRARGMAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFERDVPGHNDKRQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE D (SEQ ID NO: 376)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISRYKDSGKRGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFRRSVPGHSRKVQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 377)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSGARGLAVTISVKCEKISTLSCENK IISFKEMNPPDNIKDTKSDIIFFERDVPGHSGKVQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 378)

Description	Amino Acid Sequence
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSRPRGMAVTISVKCEKISTLSCEN KIISFKEMNPPDNIKDTKSDIIFFQRAVPGHNRKMQFES SSYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE D (SEQ ID NO: 379
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSLARGLAVTISVKCEKISTLSCENKII SFKEMNPPDNIKDTKSDIIFFQRDVPGHSRKMQFESSS YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 380)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARSVPGHGRKTQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE (SEQ ID NO: 381)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFQRNVPGHGRKMQFESS SYEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 382)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYGDSVPRGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARAVPGHSRKTQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 383)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARSVPGHGRKTQFESSSY EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 384)
Human IL-18 variant	YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDC RDNAPRTIFIISKYSDSRARGLAVTISVKCEKISTLSCENKI ISFKEMNPPDNIKDTKSDIIFFARDVPGHSGKRQFESSS

Description	Amino Acid Sequence
	YEGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNED (SEQ ID NO: 385)

[001453] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-18 or a bioactive variant thereof (e.g., any one of the IL-18 variants included in Table 21).

[001454] 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 an NFAT promoter, an EF-1a promoter, an MND promoter, or an SSFV promoter, as described herein.

4. IL-21

[001455] 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).

[001456] 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.

[001457] 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 22 – IL-21 Related Sequences.

Description	Amino Acid Sequence

Human IL-21	QGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPED VETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLK RKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSL LQKMIHQHLSSRTHGSEDS (SEQ ID NO:271)

[001458] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-21 or a bioactive variant thereof. .

[001459] 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 an NFAT promoter, an EF-1a promoter, an MND promoter, or an SSFV promoter, as described herein.

5. IL-2

[001460] 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).

[001461] 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.

[001462] 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 23 – IL-2 Related Sequences.

Description	Amino Acid Sequence
Human IL-2	MYRMQLLSCIALSLALVTNSAPTSSSTKKTQLQLEHLLL DLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK GSETTFMCEYADETATIVEFLNRWITFCQSIISTLT (SEQ ID NO:272)

[001463] In some embodiments, the TIL compositions include an immunomodulatory fusion protein or nanoparticle composition that includes a IL-2 or a bioactive variant thereof.

[001464] 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 an NFAT promoter, an EF-1a promoter, an MND promoter, or an SSFV promoter, as described herein.

6. CD40 Agonists

[001465] 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).

[001466] 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.

[001467] 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.

[001468] 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 24 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 24. 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 24. 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 24. 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 24.

[001469] In some embodiments, the anti-CD40 binding domain is a variant of an anti-CD40 scFv in Table 24 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 24.

[001470] 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.

[001471] 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.

[001472] 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.

[001473] 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 24 – CD40 Agonist Related Sequences.

Description	Amino Acid Sequence
Human CD40L	MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITQMIGS ALFAVYLHRRLDKIEDERNLHEDFVFMKTIQRCNTGER SLSLLNCEEIKSQFEGFVKDIMLNKEETKKENSFEMQKG DQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLV TLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIAS LCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFEL QPGASVFVNVTDPSQVSHGTGFTSFGLLKL (SEQ ID NO: 273)
Anti-human CD40 VH (Sotigalimab)	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSTYVCWV RQAPGKGLEWIACIYTGDGTNYSASWAKGRFTISKDSS KNTVYLQMNSLRAEDTAVYFCARPDITYGFAINFWGP GTLVTVSS (SEQ ID NO: 274)
Anti-human CD40 VL (Sotigalimab)	DIQMTQSPSSLSASVGDRVTIKCQASQSISSRLAWYQQ KPGKPPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCQCTGYGISWPIGGGTKVEIK (SEQ ID NO: 275)
Anti-human CD40 scFv (Sotigalimab)	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSTYVCWV RQAPGKGLEWIACIYTGDGTNYSASWAKGRFTISKDSS KNTVYLQMNSLRAEDTAVYFCARPDITYGFAINFWGP GTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQS PSSLSASVGDRVTIKCQASQSISSRLAWYQQKPGKPPKL LIYRASTLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYY CQCTGYGISWPIGGGTKVEIK (SEQ ID NO: 276)
Anti-human CD40 VH (Dacetuzumab)	QLVESGGGLVQPGGSLRLSCAASGYSFTGYYIHWVRQ APGKGLEWVARVIPNAGGTSYNQKFKGRFTLSVDNSK NTAYLQMNSLRAEDTAVYYCAREGIYWWGQGTLVTVS S (SEQ ID NO: 277)

Anti-human CD40 VL (Dacetuzumab)	DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTFL HWYQQKPGKAPKLLIYTVSNRFSGVPSRFSGSGSGTDF TLTISSLQPEDFATYFCSQTTHVPWTFGQGTKVEIK (SEQ ID NO: 278)
Anti-human CD40 scFv (Dacetuzumab)	QLVESGGGLVQPGGSLRLSCAASGYSFTGYYIHWVRQ APGKGLEWVARVIPNAGGTSYNQKFKGRFTLSVDNSK NTAYLQMNSLRAEDTAVYYCAREGIYWWGQGTLVTVS SGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASV GDRVTITCRSSQSLVHSNGNTFLHWYQQKPGKAPKLLI YTVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFC SQTTHVPWTFGQGTKVEIK (SEQ ID NO: 279)
Anti-CD40 VH (Lucatutuzumab)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVISYEESNRYHADSVKGRFTISRDN SKITLYLQMNSLRTEDTAVYYCARDGGIAAPGPDYWG QGTLVTVSS (SEQ ID NO: 280)
Anti-CD40 VL (Lucatutuzumab)	DIVMTQSPLSLTVTPGEPASISCRSSQSLLYSNGYNYLD WYLQKPGQSPQVLISLGSNRASGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCMQARQTPFTFGPGTKVDIR (SEQ ID NO: 281)
Anti-CD40 scFv (Lucatutuzumab)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHW VRQAPGKGLEWVAVISYEESNRYHADSVKGRFTISRDN SKITLYLQMNSLRTEDTAVYYCARDGGIAAPGPDYWG QGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIVMTQ SPLSLTVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKP GQSPQVLISLGSNRASGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQARQTPFTFGPGTKVDIR (SEQ ID NO: 282)
Anti-CD40 VH (Selicrelumab)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHW VRQAPGQGLEWMGWINPDSGGTNYAQKFQGRVTM TRDTSISTAYMELNRLRSDDTAVYYCARDQPLGYCTNG VCSYFDYWGQGTLVTVSS (SEQ ID NO: 283)
Anti-CD40 VL (Selicrelumab)	DIQMTQSPSSVSASVGDRVTITCRASQGIYSWLAWYQ QKPGKAPNLLIYTASTLQSGVPSRFSGSGSGTDFTLTISS

	LQPEDFATYYCQQANIFPLTFGGGTKVEIK (SEQ ID NO: 284)
Anti-CD40 scFv (Selicrelumab)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHW VRQAPGQGLEWMGWINPDSGGTNYAQKFQGRVTM TRDTSISTAYMELNRLRSDDTAVYYCARDQPLGYCTNG VCSYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGG GGSDIQMTQSPSSVSASVGDRVTITCRASQGIYSWLA WYQQKPGKAPNLLIYTASTLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQANIFPLTFGGGTKVEIK (SEQ ID NO: 285)

K. Myc Fusion Proteins

[001474] In some embodiments, the modified TILs provided herein include a Myc fusion protein. Myc fusion proteins are described in US Patent No. 11,369,678, the content of which is incorporated by reference in its entirety.

[001475] Any suitable genetic modification method can be used to genetically modify the subject TILs to include such Myc fusion proteins, including, for example, any of the gene editing methods described herein. In some embodiments, the genetic modification method is a CRISPR, TALE, zinc finger, or Cas-CLOVER method described herein. In some embodiments, such modified TILs are produced using any one of the retroviral methods (e.g., lentiviral methods) provided herein. In some embodiments, such modified TILs are produced using any of the transposon/transposase systems described herein, e.g., a piggyBac method (e.g., piggyBac transposons and transposases or piggyBac-like transposons and transposases), a Sleeping Beauty method (e.g., Sleeping Beauty or Sleeping Beauty-like transposons and transposases), a Helraiser method (e.g., Helraiser ahd Helraiser-like transposons and transposases), and a Tol2 method (e.g., Tol2 and Tol2-like transposons and transposases).

[001476] Disclosed herein, in certain embodiments, is a MYC fusion protein comprising (a) a transporter peptide sequence; and (b) a MYC sequence. In some embodiments, the MYC fusion protein is a peptide of Formula (I):

transporter peptide sequence —MYC sequence.

[001477] In some embodiments, a MYC fusion protein disclosed herein comprises (a) a transporter peptide sequence; (b) a MYC sequence; and (c) one or more molecules that link the

transporter peptide sequence and the MYC sequence. In some embodiments, the fusi MYC fusion protein is a peptide of Formula (II):

transporter peptide sequence—X—MYC sequence,

wherein —X— is molecule that links the transporter peptide sequence and the MYC sequence. In some embodiments, —X— is an amino acid. In some embodiments, —X— is at least one amino acid.

[001478] As used herein, a "transporter peptide" means a peptide sequence that promotes peptide penetration into cells and tissues. In some embodiments, a transporter peptide is the N-terminal 9-amino-acid sequence of the TAT protein transduction domain of HIV-1 (RKKRRQRRR) (SEQ ID NO: 306). In some embodiments, a transporter peptide is $TAT_{[48-57]}$. In some embodiments, a transporter peptide is $TAT_{[57-48]}$.

[001479] As used herein, a "MYC sequence" is a MYC amino acid peptide sequence. In some embodiments, the Myc polypeptide is a complete Myc polypeptide sequence. In some embodiments, the Myc polypeptide is a partial Myc polypeptide sequence. In some embodiments, the MYC is c-MYC. In some embodiments, the Myc polypeptide sequence comprises SEQ ID NO:300.

[001480] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, and (b) c-MYC.

[001481] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, (b) a linker amino acid, and (c) c-MYC.

[001482] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one amino acid sequence that facilitates purification of the fusion protein. In some embodiments, a MYC fusion protein disclosed herein comprises a protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag and an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a 6-histidine tag and a V5 epitope tag.

[001483] In some embodiments, the histidine tag is a 6-histidine tag. In some embodiments, the histidine tag comprises the sequence HHHHHH (SEQ ID NO:302). In some embodiments, a histidine

tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a TAT-Myc polypeptide sequence is cloned into an expression vector encoding a polyHis-tag. In some embodiments, a polyhistidine tag is added by PCR (i.e., the PCR primers comprise a polyhistidine sequence).

[001484] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein further comprises a V5 epitope tag. In some embodiments, the V5 tag comprises the amino acids: GKPIPNPLLGLDST (SEQ ID NO:303). In some embodiments, the V5 tag comprises the amino acids: IPNPLLGLD (SEQ ID NO:304). In some embodiments, a V5 tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a MYC fusion protein sequence is cloned into an expression vector encoding a V5 tag. In some embodiments, a V5 tag is added by PCR (i.e., the PCR primers comprise a V5 sequence).

[001485] In some embodiments, the amino acids are in the D formation. In some embodiments, the amino acids are in the L formation. In some embodiments, a first plurality of amino acids is in the D formation and a second plurality is in the L formation.

[001486] In some embodiments, a MYC fusion protein comprises SEQ ID NO:301.

L. Immune Checkpoints

[001487] 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 modify expression of one or more immune checkpoints in the TIL population. In some embodiments, one or more immune checkpoint genes is genetically modified in the TIL population. In some embodiments, 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. In some embodiments, an RNA molecule is used to suppress expression of one or more immune checkpoints. In exemplary embodiments, a nucleic acid encoding a short hairpin RNA (shRNA) is introduced into the TIL population to suppress expression of one or more immune checkpoints in the modified TIL population.

[001488] 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.

[001489] 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. In some embodiments, an endogenous immune checkpoint is modified by the gene-editing process to cause expression of the immune checkpoint gene to be silenced or reduced. In some embodiments, an exogenous RNA interference element (e.g., a nucleotide encoding an shRNA) is introduced into the TIL process during the gene-editing process. In such embodiments, the RNAi element causes expression of the immune checkpoint gene to be silenced or reduced.

[001490] 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.

[001491] Non-limiting examples of immune checkpoint genes that may be silenced or inhibited by 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints). 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 any combinations thereof (e.g., two or more of the above immune checkpoints).

[001492] 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) introducing into the second population of TILs a nucleotide, wherein the nucleotide encodes:

(i) at least one immunomodulatory composition that comprises an immunomodulatory agent fused to a membrane anchor (e.g., a membrane anchored immunomodulatory fusion protein described herein); and/or

ii) an RNA interference element (e.g., an shRNA) that suppresses expression of an immune checkpoint selected from the group consisting of 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints), in the plurality 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, 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. The nucleotide can be introduced into the second population of TILs using any suitable method. In some embodiments, the

[001493] 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 sffects expression of at least one immunomodulatory composition at the cell surface of and, wherein the inhibits expression of a molecule selected from the group consisting of: 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, BCOR, and any combinations thereof (e.g., two more more of the above immune checkpoints), 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

[001494] 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.

[001495] 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or reduce the expression of PD1 in the TILs.

2. CTLA-4

[001496] 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.

[001497] According to particular embodiments, expression of CTLA-4 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), 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, an RNA interference method (e.g., shRNA), 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).

3. LAG-3

[001498] 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.

[001499] According to particular embodiments, expression of LAG-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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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. TIGIT

[001500] TIGIT (T cell immunoreceptor with Ig and ITIM domains) is an immune receptor present on some T cells and natural killer (NK) cells. TIGIT and PD-1 have been shown to be over-expressed on tumor antigen-specific CD8+ T cells and CD8+ TILs from individuals with melanoma. Blockage of TIGIT and PD-1 has lead to increased cell proliferation, cytokine production, and degranulation of TA-specific CD8+ T cells and TIL CD8+ T cells.

[001501] According to particular embodiments, expression of TIGIT 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), 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 TGIT 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. According to particular embodiments, a CRISPR method, a TALE method, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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).

5. TIM-3

[001502] 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.

[001503] 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), 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, an RNA interference method (e.g., shRNA), 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).

6. Cish

[001504] 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).

[001505] According to particular embodiments, expression of Cish 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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).

7. TGFβ

[001506] 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).

[001507] According to particular embodiments, expression of TGFβ 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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).

[001508] 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.

8. PKA

[001509] 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.

[001510] According to particular embodiments, expression of PKA 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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).

9. CBLB

[001511] 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.

[001512] According to particular embodiments, expression of CBLB 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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). 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.

1. TIGIT

[001513] 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.

[001514] According to particular embodiments, expression of TIGIT 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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).

10. TOX

[001515] 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.

[001516] 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.

[001517] According to particular embodiments, expression of TOX 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), 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, an RNA interference method (e.g., shRNA), or a zinc finger method may be used to silence or repress the expression of 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. Additional Process Embodiments

[001518] 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.

[001519] 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.

[001520] 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-g500MCS 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.

[001521] 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).

[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 culture medium is supplemented with additional exogenous APCs.

[001523] 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.

[001524] 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.

[001525] 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.

[001526] 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.

[001527] 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.

[001528] 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.

[001529] 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.

[001530] 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.

[001531] 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.

[001532] 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.

[001533] 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.

[001534] 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.

[001535] 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.

[001536] 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.

[001537] 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.

[001538] 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.

[001539] 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.

[001540] 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.

[001541] 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.

[001542] 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.

[001543] 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.

[001544] 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.

[001545] 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.

[001546] 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.

[001547] 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.

[001548] 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.

[001549] 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.

[001550] 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.

[001551] 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.

[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 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.

[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 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.

[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 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.

[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 number of APCs added in the rapid second expansion to the number of APCs added in step (b) is at or about 2:1.

[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 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.

[001557] 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.

[001558] 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.

[001559] 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.

[001560] 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.

[001561] 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.

[001562] 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).

[001563] 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).

[001564] 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.

[001565] 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.

[001566] 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.

[001567] 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.

[001568] 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.

[001569] 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.

[001570] 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.

[001571] 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.

[001572] 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.

[001573] 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.

[001574] 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.

[001575] 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.

[001576] 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.

[001577] 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.

[001578] 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.

[001579] 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.

[001580] 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.

[001581] 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.

[001582] 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.

[001583] 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.

[001584] 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.

[001585] 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.

[001586] 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.

[001587] 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.

[001588] 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.

[001589] 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.

[001590] 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.

[001591] 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.

[001592] 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.

[001593] 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.

[001594] 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.

[001595] 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.

[001596] 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.

[001597] 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.

[001598] 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.

[001599] 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.

[001600] 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.

[001601] 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.

[001602] 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.

[001603] 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.

[001604] 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.

[001605] 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.

[001606] 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.

[001607] 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.

[001608] 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.

[001609] 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.

[001610] 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.

[001611] 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.

[001612] 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.

[001613] 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.

[001614] 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.

[001615] 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.

[001616] 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.

[001617] 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.

[001618] 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.

[001619] 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.

[001620] 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.

[001621] 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.

[001622] 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.

[001623] 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.

[001624] 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.

[001625] 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.

[001626] 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.

[001627] 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.

[001628] 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.

[001629] 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.

[001630] 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.

[001631] 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.

[001632] 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.

[001633] 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).

[001634] 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.

[001635] 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.

[001636] 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.

[001637] 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.

[001638] 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.

[001639] 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.

[001640] 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.

[001641] 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.

[001642] 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).

[001643] 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).

[001644] 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).

[001645] 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).

[001646] 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).

[001647] 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).

[001648] 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).

[001649] 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).

[001650] 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).

[001651] 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).

[001652] 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).

[001653] 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.

[001654] 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.

[001655] 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.

[001656] 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.

[001657] 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.

[001658] 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.

[001659] 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.

[001660] 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.

[001661] 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.

[001662] 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.

[001663] 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.

[001664] 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.

[001665] 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.

[001666] 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.

[001667] 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.

[001668] 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).

[001669] 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.

[001670] 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.

[001671] 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.

[001672] 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.

[001673] 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.

[001674] 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.

[001675] 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.

[001676] 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.

[001677] 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.

[001678] 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.

[001679] 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.

[001680] 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.

[001681] 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.

[001682] 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.

[001683] 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.

[001684] 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.

[001685] 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.

[001686] 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.

[001687] 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.

[001688] 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.

[001689] 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.

[001690] 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.

[001691] 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.

[001692] 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.

[001693] 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.

[001694] 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}.

[001695] 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.

[001696] 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.

[001697] 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.

[001698] 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.

[001699] 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).

[001700] 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.

[001701] 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.

[001702] 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.

[001703] 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.

[001704] 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.

[001705] 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.

[001706] 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.

[001707] 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).

[001708] 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.

[001709] 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.

[001710] 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.

[001711] 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.

[001712] 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.

[001713] 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.

[001714] 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.

[001715] 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.

[001716] 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 some 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.

[001717] 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 some 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.

[001718] 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 some 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.

[001719] 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 some 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.

[001720] 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 some 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.

[001721] 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 some 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.

[001722] 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 some 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.

[001723] 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 some

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.

[001724] 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 some 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.

[001725] 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.

[001726] 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.

[001727] 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.

[001728] 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).

[001729] 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.

[001730] 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.

[001731] 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.

[001732] 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.

[001733] 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.

[001734] 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.

[001735] 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.

[001736] 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.

[001737] 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.

[001738] 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.

[001739] 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.

[001740] 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.

[001741] 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.

[001742] 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.

[001743] 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.

[001744] 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.

[001745] 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.

[001746] 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.

[001747] 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.

[001748] 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.

[001749] 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.

[001750] 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.

[001751] 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.

[001752] 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.

[001753] 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 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.

[001754] 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 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 CM^2 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.

[001755] In other 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 other

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 other 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 other 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 other 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.

[001756] In other 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.

[001757] In other 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.

[001758] In other 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.

[001759] In other 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.

[001760] In other 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.

[001761] In other 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.

[001762] In other 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.

[001763] In other 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.

[001764] In other 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.

[001765] In other 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.

[001766] In other 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.

[001767] In other 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.

[001768] In other 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.

[001769] In other 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.

[001770] In other 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.

[001771] In other 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.

[001772] In other 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.

[001773] In other 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.

[001774] In other 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.

[001775] In other 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.

[001776] In other 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).

[001777] In other 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).

[001778] 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 first population of T cells is cultured in a second culture medium comprising OKT-3, IL-2 and antigen-presenting cells (APCs).

[001779] In other 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).

[001780] In other 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.

[001781] In other 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.

[001782] In other 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.

[001783] In other 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.

[001784] 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 APCs in the second population of APCs to the number of APCs in the first population of APCs is about 2:1.

[001785] 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 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.

[001786] In other 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.

[001787] 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 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.

[001788] 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 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.

[001789] In other 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.

[001790] In other 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.

[001791] In other 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.

[001792] In other 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.

[001793] 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 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.

[001794] 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 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.

[001795] 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 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.

[001796] 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 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.

[001797] In other 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.

[001798] In other 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.

[001799] In other 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.

[001800] In other 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.

[001801] In other 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).

[001802] 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 exogenous to the donor of the first population of T cells.

[001803] In other 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).

[001804] In other 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).

[001805] In other 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).

[001806] 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 T cells is obtained by separation from the whole blood of the donor.

[001807] 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 T cells is obtained by separation from the apheresis product of the donor.

[001808] 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 T cells is separated from the whole blood or apheresis product of the donor by positive or negative selection of a T cell phenotype.

[001809] In other 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+.

[001810] In other 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 other 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 other 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 other 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 other 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 other 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 other 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 other 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 other 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 other embodiments, the foregoing method is utilized for the expansion of T cells in tumor tissue obtained from a patient suffering from ovarian cancer.

[001811] In other 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.

[001812] 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 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.

[001813] 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 T cells harvested in step (c) is a therapeutic population of TILs.

[001814] 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 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.

[001815] 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 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.

[001816] 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 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.

[001817] 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 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.

[001818] 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 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.

[001819] 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 T cells is obtained from one or more core biopsies of tumor tissue from the donor.

[001820] 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 T cells is obtained from 1 to 20 core biopsies of tumor tissue from the donor.

[001821] 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 T cells is obtained from 1 to 10 core biopsies of tumor tissue from the donor.

[001822] 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 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.

[001823] 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 T cells is obtained from 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 core biopsies of tumor tissue from the donor.

[001824] 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 T cells is obtained from one or more fine needle aspirates of tumor tissue from the donor.

[001825] 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 T cells is obtained from 1 to 20 fine needle aspirates of tumor tissue from the donor.

[001826] 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 T cells is obtained from 1 to 10 fine needle aspirates of tumor tissue from the donor.

[001827] 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 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.

[001828] 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 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.

[001829] 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 T cells is obtained from one or more small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001830] 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 T cells is obtained from 1 to 20 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001831] 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 T cells is obtained from 1 to 10 small biopsies (including, for example, a punch biopsy) of tumor tissue from the donor.

[001832] 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 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.

[001833] 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 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.

[001834] 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 T cells is obtained from one or more core needle biopsies of tumor tissue from the donor.

[001835] 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 T cells is obtained from 1 to 20 core needle biopsies of tumor tissue from the donor.

[001836] 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 T cells is obtained from 1 to 10 core needle biopsies of tumor tissue from the donor.

[001837] 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 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.

[001838] 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 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.

[001839] In other 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.

[001840] In other 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).

[001841] In other 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.

[001842] In other 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.

[001843] In other 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.

[001844] In other 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.

[001845] In other 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.

[001846] 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).

IV. Pharmaceutical Compositions, Dosages, and Dosing Regimens

[001847] 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.

[001848] 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, 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. n some embodiments, the therapeutically effective dosage is about 7.8×10^{10} TILs, particularly of the cancer is 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.

[001849] 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}.

[001850] 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.

[001851] 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.

[001852] 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.

[001853] 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.

[001854] 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.

[001855] 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.

[001856] 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.

[001857] 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.

[001858] 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}.

[001859] 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.

[001860] 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 about10^5mg, 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.

[001861] 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.

[001862] In other embodiments, the invention provides an infusion bag comprising the therapeutic population of TILs described in any of the preceding paragraphs above.

[001863] In other 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.

[001864] In other embodiments, the invention provides an infusion bag comprising the TIL composition described in any of the preceding paragraphs above.

[001865] In other embodiments, the invention provides a cryopreserved preparation of the therapeutic population of TILs described in any of the preceding paragraphs above.

[001866] In other 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.

[001867] In other embodiments, the invention provides the TIL composition described in any of the preceding paragraphs above modified such that the cryopreservation media contains DMSO.

[001868] In other 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.

[001869] In other embodiments, the invention provides a cryopreserved preparation of the TIL composition described in any of the preceding paragraphs above.

[001870] 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.

[001871] 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.

[001872] 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}.

[001873] 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.

[001874] 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.

[001875] 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.

[001876] 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.

[001877] 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.

[001878] 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.

[001879] 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.

[001880] 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.

[001881] 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}.

[001882] 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.

[001883] 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 about10^5mg, 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.

[001884] 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.

[001885] Methods of Treating Patients

[001886] 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.

[001887] 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) 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.

[001888] 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), 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), are selected for an additional second expansion according to Step D of Figure 1.

[001889] 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.

[001890] In some embodiments, the TILs produced by the methods provided herein, for example those exemplified in Figure 1, 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, 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. 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.

[001891] 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. In some embodiments, IFN-gamma (IFN-γ) is indicative of treatment efficacy and/or increased clinical efficacy in the treatment of cancer.

[001892] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1in 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. 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.

[001893] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1, exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 1, 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. 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.

[001894] 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.

A. Methods of Treating Cancers

[001895] The compositions and methods described herein, including the Gen 2 TIL product and methods, 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.

[001896] 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 endometrial cancer, uterine cancer, 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) and small-cell lung cancer), melanoma (including uveal melanoma, choroidal melanoma, ciliary body melanoma, or iris 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.

[001897] In some embodiments, the hyperproliferative disorder is an endometrial cancer. In some embodiments, the hyperproliferative disorder is a uterine or uterine body cancer. In some embodiments, the compositions and methods described herein are used to treat endometrial cancer.

[001898] In some embodiments, the hyperproliferative disorder is a type I (endometroid) endometrial cancer. In some embodiments, the hyperproliferative disorder is a type I (endometroid) uterine cancer. In some embodiments, the compositions and methods described herein are used to treat type I (endometroid) endometrial cancer. In some embodiments, the hyperproliferative disorder is a type II (serous) endometrial cancer. In some embodiments, the hyperproliferative disorder is a type II (serous) uterine cancer. In some embodiments, the compositions and methods described herein are used to treat type I (serous) endometrial cancer.

[001899] In some embodiments, the hyperproliferative disorder is a dMMR endometrial cancer. In some embodiments, the hyperproliferative disorder is a dMMR uterine cancer. In some embodiments, the compositions and methods described herein are used to treat dMMR endometrial cancer.

[001900] In some embodiments, the hyperproliferative disorder is an MSI-H endometrial cancer. In some embodiments, the hyperproliferative disorder is an MSI-H uterine cancer. In some embodiments, the compositions and methods described herein are used to treat MSI-H endometrial cancer.

[001901] In some embodiments, the hyperproliferative disorder is a pMMR endometrial cancer. In some embodiments, the hyperproliferative disorder is a pMMR uterine cancer. In some embodiments, the compositions and methods described herein are used to treat pMMR endometrial cancer.

[001902] In some embodiments, the hyperproliferative disorder is an MSS endometrial cancer. In some embodiments, the hyperproliferative disorder is an MSS uterine cancer. In some

embodiments, the compositions and methods described herein are used to treat MSS endometrial cancer.

[001903] In some embodiments, the hyperproliferative disorder is an p53 abnormal (p53abn) endometrial cancer. In some embodiments, the hyperproliferative disorder is an p53 abnormal (p53abn) uterine cancer. In some embodiments, the compositions and methods described herein are used to treat p53 abnormal (p53abn) endometrial cancer.

[001904] In some embodiments, the hyperproliferative disorder is an p53 mutant (p53mut, TP53 mutated) endometrial cancer. In some embodiments, the hyperproliferative disorder is an p53 mutant (p53mut, TP53 mutated) uterine cancer. In some embodiments, the compositions and methods described herein are used to treat p53 mutant (p53mut, TP53 mutated) endometrial cancer.

[001905] In some embodiments, the hyperproliferative disorder is an p53 wildtype (p53wt) endometrial cancer. In some embodiments, the hyperproliferative disorder is an p53 wildtype (p53wt) uterine cancer. In some embodiments, the compositions and methods described herein are used to treat p53 wildtype (p53wt) endometrial cancer.

[001906] In some embodiments, the hyperproliferative disorder is a POLE mutant endometrial cancer. In some embodiments, the hyperproliferative disorder is a POLE mutant uterine cancer. In some embodiments, the compositions and methods described herein are used to treat POLE mutant endometrial cancer.

[001907] In some embodiments, the hyperproliferative disorder is a POLE ultramutant endometrial cancer. In some embodiments, the hyperproliferative disorder is a POLE ultramutant uterine cancer. In some embodiments, the compositions and methods described herein are used to treat POLE ultramutant endometrial cancer.

[001908] In some embodiments, the hyperproliferative disorder is a PTEN (phosphatase and tensin homolog) mutated endometrial cancer. In some embodiments, the hyperproliferative disorder is a PTEN (phosphatase and tensin homolog) mutated uterine cancer. In some embodiments, the compositions and methods described herein are used to treat PTEN (phosphatase and tensin homolog) mutated endometrial cancer.

[001909] In some embodiments, the hyperproliferative disorder is a KRAS mutated endometrial cancer. In some embodiments, the hyperproliferative disorder is a KRAS mutated uterine cancer. In some embodiments, the compositions and methods described herein are used to treat KRAS mutated endometrial cancer.

[001910] In some embodiments, the hyperproliferative disorder is a PIK3R1 mutated endometrial cancer. In some embodiments, the hyperproliferative disorder is a PIK3R1 mutated uterine cancer. In some embodiments, the compositions and methods described herein are used to treat PIK3R1 mutated endometrial cancer.

[001911] In some embodiments, the hyperproliferative disorder is a PIK3CA mutated endometrial cancer. In some embodiments, the hyperproliferative disorder is a PIK3CA mutated uterine cancer. In some embodiments, the compositions and methods described herein are used to treat PIK3CA mutated endometrial cancer.

[001912] In some embodiments, the hyperproliferative disorder is a RAS mutated endometrial cancer. In some embodiments, the hyperproliferative disorder is a RAS mutated uterine cancer. In some embodiments, the compositions and methods described herein are used to treat RAS mutated endometrial cancer.

[001913] In some embodiments, the hyperproliferative disorder is a ARID1A altered endometrial cancer. In some embodiments, the hyperproliferative disorder is a ARID1A altered uterine cancer. In some embodiments, the compositions and methods described herein are used to treat ARID1A altered endometrial cancer.

[001914] In some embodiments, the hyperproliferative disorder is a beta-catenin (3p21) altered endometrial cancer. In some embodiments, the hyperproliferative disorder is a beta-catenin (3p21) altered uterine cancer. In some embodiments, the compositions and methods described herein are used to treat beta-catenin (3p21) altered endometrial cancer.

[001915] In some embodiments, the hyperproliferative disorder is an endometrial cancer characterized by loss of heterozygosity in chromosome 17p. In some embodiments, the hyperproliferative disorder is a uterine cancer characterized by loss of heterozygosity in chromosome 17p. In some embodiments, the compositions and methods described herein are used to treat an endometrial cancer characterized by loss of heterozygosity in chromosome 17p.

[001916] In some embodiments, the hyperproliferative disorder is a HER2/neu amplified endometrial cancer. In some embodiments, the hyperproliferative disorder is a HER2/neu amplified uterine cancer. In some embodiments, the compositions and methods described herein are used to treat HER2/neu amplified endometrial cancer.

[001917] In some embodiments, the hyperproliferative disorder is an endometrial cancer characterized by the loss of ER (estrogen receptor). In some embodiments, the hyperproliferative disorder is a uterine cancer characterized by the loss of ER (estrogen receptor). In some

embodiments, the compositions and methods described herein are used to treat endometrial cancer characterized by the loss of ER (estrogen receptor).

[001918] In some embodiments, the hyperproliferative disorder is an endometrial cancer characterized by the loss of PR (progesterone receptor). In some embodiments, the hyperproliferative disorder is a uterine cancer characterized by the loss of PR (progesterone receptor). In some embodiments, the compositions and methods described herein are used to treat endometrial cancer characterized by the loss of PR (progesterone receptor).

[001919] In some embodiments, the hyperproliferative disorder is an endometrial cancer characterized by the loss of E-cadherin. In some embodiments, the hyperproliferative disorder is a uterine cancer characterized by the loss of E-cadherin. In some embodiments, the compositions and methods described herein are used to treat endometrial cancer characterized by the loss of E-cadherin.

[001920] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the endometrial cancer is characterized by MLH-1 promoter hypermethylation. In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the endometrial cancer is characterized by high mutation rates due to mismatch repair. In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the endometrial cancer is characterized by high mutation rates due to mismatch repair resulting from a defect in the MLH-1, MSH2, MSH6, or PMS2 genes.

[001921] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the endometrial cancer is metastatic or unresectable. In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the endometrial cancer is metastatic or unresectable, and the patient receives a TIL therapy.

[001922] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer was refractory to or progressed following prior treatment with a PD-1 or PD-L1 inhibitor.

[001923] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer was refractory to or progressed following prior treatment with chemotherapy.

[001924] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer was refractory to or progressed following prior treatment with chemotherapy, wherein the chemotherapy is a platinum chemotherapy and a taxane.

[001925] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer was refractory to or progressed following prior treatment with chemotherapy, wherein the chemotherapy is a platinum chemotherapy and a taxane, wherein the platinum chemotherapy is selected from the group consisting of cisplatin, carboplatin, and oxaliplatin.

[001926] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer was refractory to or progressed following prior treatment with chemotherapy, wherein the chemotherapy is a platinum chemotherapy and a taxane, wherein the platinum chemotherapy is selected from the group consisting of cisplatin, carboplatin, and oxaliplatin, and wherein the taxane is selected from the group consisting of paclitaxel, albumin-bound paclitaxel, and docetaxel.

[001927] In some embodiments, the hyperproliferative disorder is an endometrial cancer, wherein the patient having endometrial cancer is treatment naïve at the metastatic or unresectable stage (i.e., all prior therapies were received before the patient's diagnosis as metastatic or unresectable stage disease).

[001928] 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 express one or more CCRs, 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 express one or more CCRs, wherein the cancer is a hematological malignancy.

[001929] 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.

[001930] In some embodiments, the cancer is a microsatellite instability-high (MSI-H), microsatellite instable (MSI), or a mismatch repair deficient (dMMR) cancer. In some embodiments, the cancer is a microsatellite stable (MSS) or a mismatch repair proficient (pMMR) cancer. MSI-H, MSI, 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. In some embodiments, the cancer is dMMR endometrial cancer. In some embodiments, the cancer is MSI-H or MSI endometrial cancer. In some embodiments, the cancer is pMMR endometrial cancer. In some embodiments, the cancer is MSS endometrial cancer.

[001931] In some embodiments, the present invention includes a method of treating a patient with a cancer using TILs, MILs, or PBLs modified to express one or more CCRs, 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 express one or more CCRs, 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 express one or more CCRs, wherein the patient is a companion animal.

[001932] 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.

[001933] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the cancer is a pediatric cancer.

[001934] In some embodiments, the present invention includes a method of treating a patient with a cancer wherein the cancer is uveal melanoma.

[001935] 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.

[001936] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the pediatric cancer is a neuroblastoma.

[001937] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the pediatric cancer is a sarcoma.

[001938] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the sarcoma is osteosarcoma.

[001939] In some embodiments, the present invention includes a method of treating a patient with a cancer, wherein the sarcoma is a soft tissue sarcoma.

[001940] 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).

[001941] 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.

[001942] 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.

[001943] 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.

[001944] In some embodiments, the endometrial cancer 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.

[001945] In some embodiments, the endometrial cancer 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).

[001946] In some embodiments, the endometrial cancer 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).

[001947] In some embodiments, the endometrial cancer has been treated with an anti-PD-1 antibody. In some embodiments, the endometrial cancer has been treated with an anti-PD-L1 antibody. In some embodiments, the endometrial cancer patient is treatment naïve. In some embodiments, the endometrial cancer has not been treated with an anti-PD-1 antibody. In some embodiments, the endometrial cancer has not been treated with an anti-PD-L1 antibody. In some embodiments, the endometrial cancer has been previously treated with a chemotherapeutic agent. In some embodiments, the endometrial cancer has been previously treated with a chemotherapeutic agent but is not longer being treated with the chemotherapeutic agent. In some embodiments, the endometrial cancer patient is anti-PD-1/PD-L1 naïve. In some embodiments, the endometrial cancer patient has low expression of PD-L1. In some embodiments, the endometrial cancer patient has treatment naïve endometrial cancer or is post-chemotherapeutic treatment but anti-PD-1/PD-L1 naïve. In some embodiments, the endometrial cancer 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 endometrial cancer 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 endometrial cancer patient has no detectable expression of PD-L1. In some embodiments, the endometrial cancer 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 endometrial cancer patient has treatment naïve endometrial cancer 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 endometrial cancer.

[001948] In some embodiments, PD-L1 expression is determined by the tumor proportion score. In some embodiments, the subject with a refractory endometrial cancer tumor has a $< 1\%$ tumor proportion score (TPS). In some embodiments, the subject with a refractory endometrial cancer tumor has a $\geq 1\%$ TPS. In some embodiments, subject with the refractory endometrial cancer 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 endometrial cancer 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.

[001949] In some embodiments, the TILs prepared by the methods of the present invention, including those as described for example in Figure 1, exhibit increased polyclonality as compared to TILs produced by other methods, including those not exemplified in Figure 1, 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.

[001950] 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 endometrial cancer tumor has a < 1% tumor proportion score (TPS). In some embodiments, the endometrial cancer tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the endometrial cancer 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 endometrial cancer 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 endometrial cancer tumor has a < 1% tumor proportion score (TPS). In some embodiments, the subject or patient with a refractory or resistant endometrial cancer tumor has a ≥ 1% TPS. In some embodiments, the subject or patient with the refractory or resistant endometrial cancer 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 endometrial cancer 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.

[001951] In some embodiments, the endometrial cancer is an endometrial cancer 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 endometrial cancer is

an endometrial cancer 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 endometrial cancer is an endometrial cancer 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 endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 1%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.9%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.8%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.7%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.6%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.5%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.4%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.3%. In some embodiments, the endometrial cancer is an endometrial cancer that exhibits a TPS between 0% and 0.2%. In some embodiments, the endometrial cancer is an endometrial cancer 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.

[001952] 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.

[001953] 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.

[001954] In some embodiments, elevated soluble PD-L1 as compared to a baseline or standard level correlates with worsened prognosis in endometrial cancer. *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.

[001955] In some embodiments, the invention provides a method of treating endometrial cancer 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 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 optionally 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.

[001956] In some embodiments, the invention provides a method of treating endometrial cancer 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 optionally 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.

[001957] In some embodiments, the invention provides a method of treating endometrial cancer 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) optionally 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.

[001958] In some embodiments, the invention provides a method of treating endometrial cancer 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) optionally 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.

[001959] In some embodiments, the invention provides a method of treating endometrial cancer 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) optionally 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.

[001960] 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.

[001961] 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.

[001962] 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.

[001963] 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/m^2/day for two days followed by administration of fludarabine at a dose of 25 mg/m^2/day for five days.

[001964] 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.

[001965] 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.

[001966] 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.

[001967] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is endometrial cancer, melanoma, ovarian cancer, cervical cancer, non-small-cell lung cancer (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.

[001968] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is endometrial cancer, melanoma, HNSCC, cervical cancers, NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[001969] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is melanoma.

[001970] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is HNSCC.

[001971] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is endometrial cancer.

[001972] In other embodiments, the invention provides the method for treating a subject with cancer described herein modified such that the cancer is NSCLC.

[001973] 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).

[001974] In other embodiments, the invention provides a method for treating a subject with cancer described herein modified such that the cancer is gastrointestinal cancer.

[001975] 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.

[001976] 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.

[001977] In other embodiments, the invention provides a therapeutic TIL population described herein for use in a method for treating a subject with endometrial cancer comprising administering to the subject a therapeutically effective dosage of the therapeutic TIL population.

[001978] In other embodiments, the invention provides a TIL composition described herein for use in a method for treating a subject with endometrial cancer comprising administering to the subject a therapeutically effective dosage of the TIL composition.

[001979] 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.

[001980] 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.

[001981] 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.

[001982] 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.

[001983] 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.

[001984] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma, ovarian cancer, endometrial cancer, non-small-cell lung cancer (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.

[001985] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma, HNSCC, cervical cancers, NSCLC, glioblastoma (including GBM), and gastrointestinal cancer.

[001986] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is melanoma.

[001987] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is HNSCC.

[001988] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is endometrial cancer.

[001989] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is NSCLC.

[001990] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is glioblastoma.

[001991] In other embodiments, the invention provides a therapeutic TIL population or a TIL composition described herein modified such that the cancer is gastrointestinal cancer.

[001992] 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.

[001993] 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.

[001994] 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.

[001995] 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.

[001996] 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.

[001997] In some embodiments, the invention provides use of a therapeutic TIL population described herein or a TIL composition described herein in addition to dostarlimab/pembrolizumab as a maintenance therapy for a patient with endometrial cancer after completion of chemotherapy. See Mirza et al., *N Engl J Med* **2023**; 388:2145-2158, the content of which is incorporated by reference in its entirety. In some embodiments, the patient is treated with 6 cycles of dostarlimab/pembrolizumab at a dosage of 500 mg with a platinum chemotherapy (e.g., carboplatin, cisplatin, oxaliplatin, etc.) at a dosage of 5 mg per milliliter per minute and a taxane (e.g., paclitaxel, nab-paclitaxel, docetaxel, etc.) at a dosage of 175 mg per square meter of body-surface area every 3 weeks, followed by TIL infusion and ongoing dostarlimab/pembrolizumab at a dosage of 1,000 mg every 6 weeks until disease progression or unacceptable toxicity, or up to 3 years. In some embodiments, the TIL infusion is proceded with NMA-LD and followed with 1, 2, 3, 4, 5, or 6 doses of an IL-2 regimen as disclosed herein. In some embodiments, the NMA-LD is a reduced dose NMA-LD such as those in Tables 35 or 39.

1. Combinations with PD-1 and PD-L1 Inhibitors

[001998] In some embodiments, the TIL therapy provided to patients with cancer, including endometrial cancer, may include treatment with therapeutic populations of TILs alone or may include a combination treatment including TILs and one or more PD-1 and/or PD-L1 inhibitors. In some embodiments, the TIL therapy is administered as a one-time therapy in combination with repeat administration of a PD-1 or PD-L1 inhibitor, such as pembrolizumab, nivolumab, dostarlimab, durvalumab, atezolizumab, avelumab, or other commercially available PD-1 or PD-L1 inhbitors.

[001999] 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.

[002000] In some embodiments, TILs and a PD-1 inhibitor are administered as a combination therapy or co-therapy for the treatment of endometrial cancer.

[002001] In some embodiments, the endometrial cancer 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.

[002002] 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.

[002003] 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.

[002004] In some embodiments, the PD-1 inhibitor is one that binds human PD-1 with a KD of about 100 pM or lower, binds human PD-1 with a KD of about 90 pM or lower, binds human PD-1 with a KD of about 80 pM or lower, binds human PD-1 with a KD of about 70 pM or lower, binds human PD-1 with a KD of about 60 pM or lower, binds human PD-1 with a KD of about 50 pM or lower, binds human PD-1 with a KD of about 40 pM or lower, binds human PD-1 with a KD of about 30 pM or lower, binds human PD-1 with a KD of about 20 pM or lower, binds human PD-1 with a KD of about 10 pM or lower, or binds human PD-1 with a KD of about 1 pM or lower.

[002005] In some embodiments, the PD-1 inhibitor is one that binds to human PD-1 with a kassoc of about 7.5 $\times 10^5$ l/M·s or faster, binds to human PD-1 with a kassoc of about 7.5 $\times 10^5$ 1/M·s or faster, binds to human PD-1 with a kassoc of about 8 $\times 10^5$ 1/M·s or faster, binds to human PD-1 with a kassoc of about 8.5 $\times 10^5$ 1/M·s or faster, binds to human PD-1 with a kassoc of about 9 $\times 10^5$ 1/M·s or faster, binds to human PD-1 with a kassoc of about 9.5 $\times 10^5$ l/M·s or faster, or binds to human PD-1 with a kassoc of about 1 $\times$ 10^6 1/M·s or faster.

[002006] In some embodiments, the PD-1 inhibitor is one that binds to human PD-1 with a kdissoc of about 2 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.1 $\times$ 10^{-5} 1/s or slower , binds to human PD-1 with a kdissoc of about 2.2 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.3 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.4 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.5 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.6 $\times$ 10^{-5} 1/s or slower or binds to human PD-1 with a kdissoc of about 2.7 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.8 $\times$ 10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.9 $\times$ 10^{-5} 1/s or slower, or binds to human PD-1 with a kdissoc of about 3 $\times$ 10^{-5} 1/s or slower.

[002007] 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 IC50 of about 10 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 9 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 8 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 7 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 6 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 5 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 4 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 3 nM or lower, blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 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 IC50 of about 1 nM or lower.

[002008] 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 25. 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 CH2 84.4) at 290, 290".

[002009] 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.

[002010] 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 (VH) comprises the sequence shown in SEQ ID NO:160, and the PD-1 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:161, or conservative amino acid substitutions thereof. In some embodiments, a PD-1 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:160 and SEQ ID NO:161, respectively.

[002011] 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.

[002012] 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 25. 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	60
	ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSSASTKGPS	120
	VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS	180
	VVTVPSSSLG TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP	240
	KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT	300
	VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE MTKNQVSLTC	360
	LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV	420
	MHEALHNHYT QKSLSLSLGK	440
SEQ ID NO:159 nivolumab light chain	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA	60
	RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIKRTV AAPSVFIFPP	120
	SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT	180
	LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	214
SEQ ID NO:160 nivolumab variable heavy chain	QVQLVESGGG VVQPGRSLRL DCKASGITFS NSGMHWVRQA PGKGLEWVAV IWYDGSKRYY	60
	ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSS	113
SEQ ID NO:161 nivolumab variable light chain	EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA	60
	RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIK	107

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:162 nivolumab heavy chain CDR1	NSGMH	5
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

[002013] 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).

[002014] 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).

[002015] 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).

[002016] In some embodiments, the nivolumab is administered to treat unresectable or metastatic melanoma. In some embodiments, the nivolumab is administered to treat unresectable or metastatic melanoma and is administered at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat unresectable or metastatic melanoma and is administered at about 480 mg every 4 weeks. In some embodiments, the nivolumab is administered to treat unresectable or metastatic melanoma and is administered at about 1 mg/kg followed by ipilimumab 3 mg/kg on the same day every 3 weeks for 4 doses, then 240 mg every 2 weeks or 480 mg every 4 weeks.

[002017] In some embodiments, the nivolumab is administered for the adjuvant treatment of melanoma. In some embodiments, the nivolumab is administered for the adjuvant treatment of melanoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered for the adjuvant treatment of melanoma at about 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).

[002018] 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).

[002019] In some embodiments, the nivolumab is administered to treat small cell lung cancer. In some embodiments, the nivolumab is administered to treat small cell lung cancer at about 240 mg every 2 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).

[002020] In some embodiments, the nivolumab is administered to treat malignant pleural mesothelioma at about 360 mg every 3 weeks with ipilimumab 1 mg/kg 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).

[002021] In some embodiments, the nivolumab is administered to treat advanced renal cell carcinoma. In some embodiments, the nivolumab is administered to treat advanced renal cell carcinoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat advanced renal cell carcinoma at about 480 mg every 4 weeks. In some embodiments, the nivolumab is administered to treat advanced renal cell carcinoma at about 3 mg/kg followed by ipilimumab at about 1 mg/kg on the same day every 3 weeks for 4 doses, then 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat advanced renal cell carcinoma at about 3 mg/kg followed by ipilimumab at about 1 mg/kg on the same day every 3 weeks for 4 doses, then

240 mg every 2 weeks 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).

[002022] In some embodiments, the nivolumab is administered to treat classical Hodgkin lymphoma. In some embodiments, the nivolumab is administered to treat classical Hodgkin lymphoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat classical Hodgkin lymphoma at about 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).

[002023] In some embodiments, the nivolumab is administered to treat Recurrent or metastatic squamous cell carcinoma of the head and neck. In some embodiments, the nivolumab is administered to treat recurrent or metastatic squamous cell carcinoma of the head and neck at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat recurrent or metastatic squamous cell carcinoma of the head and neck at about 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).

[002024] In some embodiments, the nivolumab is administered to treat locally advanced or metastatic urothelial carcinoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat locally advanced or metastatic urothelial carcinoma at about 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).

[002025] In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer. In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in adult and pediatric patients. In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in adult and pediatric patients ≥40 kg at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in adult and pediatric patients ≥40 kg at about 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).

[002026] In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in pediatric patients <40 kg at about 3 mg/kg every 2 weeks. In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in adult and pediatric patients ≥40 kg at about 3 mg/kg followed by ipilimumab 1 mg/kg on the same day every 3 weeks for 4 doses, then 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer in adult and pediatric patients ≥40 kg at about 3 mg/kg followed by ipilimumab 1 mg/kg on the same day every 3 weeks for 4 doses, then 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).

[002027] In some embodiments, the nivolumab is administered to treat hepatocellular carcinoma. In some embodiments, the nivolumab is administered to treat hepatocellular carcinoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat

hepatocellular carcinoma at about 480 mg every 4 weeks. In some embodiments, the nivolumab is administered to treat hepatocellular carcinoma at about 1 mg/kg followed by ipilimumab 3 mg/kg on the same day every 3 weeks for 4 doses, then 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat hepatocellular carcinoma at about 1 mg/kg followed by ipilimumab 3 mg/kg on the same day every 3 weeks for 4 doses, then 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).

[002028] In some embodiments, the nivolumab is administered to treat esophageal squamous cell carcinoma. In some embodiments, the nivolumab is administered to treat esophageal squamous cell carcinoma at about 240 mg every 2 weeks. In some embodiments, the nivolumab is administered to treat esophageal squamous cell carcinoma at about 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).

[002029] In other 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 26. 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).

[002030] 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.

[002031] 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 (VH) comprises the sequence shown in SEQ ID NO:170, and the PD-1 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:171, or conservative amino acid substitutions thereof. In some embodiments, a PD-1 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:170 and SEQ ID NO:171, respectively.

[002032] 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.

[002033] 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.

[002034] TABLE 26. 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	60
	NEKFKNRVTL TTDSSTTTAY MELKSLQFDD TAVYYCARRD YRFDMGFDYW GQGTTVTVSS	120
	ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS	180
	GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV	240
	FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY	300
	RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK	360
	NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG	420
	NVFSCSVMHE ALHNHYTQKS LSLSLGK	447
SEQ ID NO:169 pembrolizumab light chain	EIVLTQSPAT LSLSPGERAT LSCRASKGVS TSGYSYLHWY QQKPGQAPRL LIYLASYLES	60
	GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRDLPL TFGGGTKVEI KRTVAAPSVF	120
	IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS	180
	STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC	218
SEQ ID NO:170 pembrolizumab variable heavy chain	QVQLVQSGVE VKKPGASVKV SCKASGYTFT NYYMYWVRQA PGQGLEWMGG INPSNGGTNF	60
	NEKFKNRVTL TTDSSTTTAY MELKSLQFDD TAVYYCARRD YRFDMGFDYW GQGTTVTVSS	120
SEQ ID NO:171 pembrolizumab variable light chain	EIVLTQSPAT LSLSPGERAT LSCRASKGVS TSGYSYLHWY QQKPGQAPRL LIYLASYLES	60
	GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRDLPL TFGGGTKVEI K	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	QHSRDLPLT	9

Identifier	Sequence (One-Letter Amino Acid Symbols)
pembrolizumab light chain CDR3	

[002035] 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).

[002036] 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).

[002037] 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).

[002038] In some embodiments, the pembrolizumab is administered to treat melanoma. In some embodiments, the pembrolizumab is administered to treat melanoma at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat melanoma 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).

[002039] In some embodiments, the pembrolizumab is administered to treat endometrial cancer. In some embodiments, the pembrolizumab is administered to treat endometrial cancer at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat endometrial cancer 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).

[002040] 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).

[002041] In some embodiments, the pembrolizumab is administered to treat head and neck squamous cell cancer (HNSCC). In some embodiments, the pembrolizumab is administered to treat HNSCC at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat HNSCCat 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).

[002042] In some embodiments, the pembrolizumab is administered to treat classical Hodgkin lymphoma (cHL) or primary mediastinal large B-cell lymphoma (PMBCL) at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat classical Hodgkin lymphoma (cHL) or primary mediastinal large B-cell lymphoma (PMBCL) at about 400 mg every 6 weeks for adults. In some embodiments, the pembrolizumab is administered to treat classical Hodgkin lymphoma (cHL) or primary mediastinal large B-cell lymphoma (PMBCL) at about 2 mg/kg (up to 200 mg) every 3 weeks for pediatrics. 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).

[002043] In some embodiments, the pembrolizumab is administered to treat urothelial carcinoma at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat urothelial carcinoma 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).

[002044] In some embodiments, the pembrolizumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) cancer at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat MSI-H or dMMR cancer at about 400 mg every 6 weeks for adults. In some embodiments, the pembrolizumab is administered to treat MSI-H or dMMR cancer at about 2 mg/kg (up to 200 mg) every 3 weeks for pediatrics. 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). 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).

[002045] In some embodiments, the pembrolizumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient colorectal cancer (dMMR CRC at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat MSI-H or dMMR CRC 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).

[002046] In some embodiments, the pembrolizumab is administered to treat gastric cancer at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat gastric cancer 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).

[002047] In some embodiments, the pembrolizumab is administered to treat Esophageal Cancer at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat Esophageal Cancer 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).

[002048] In some embodiments, the pembrolizumab is administered to treat cervical cancer at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat cervical cancer 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).

[002049] In some embodiments, the pembrolizumab is administered to treat hepatocellular carcinoma (HCC) at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat HCC 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).

[002050] In some embodiments, the pembrolizumab is administered to treat Merkel cell carcinoma (MCC) at about 200 mg every 3 weeks for adults. In some embodiments, the pembrolizumab is administered to treat MCC at about 400 mg every 6 weeks for adults. In some embodiments, the pembrolizumab is administered to treat MCC at about 2 mg/kg (up to 200 mg) every 3 weeks for pediatrics. 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). 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).

[002051] In some embodiments, the pembrolizumab is administered to treat renal cell carcinoma (RCC) at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat RCC at about 400 mg every 6 weeks with axitinib 5 mg orally twice daily. 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).

[002052] In some embodiments, the pembrolizumab is administered to treat endometrial carcinoma at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat endometrial carcinoma at about 400 mg every 6 weeks with lenvatinib 20 mg orally once daily for tumors that are not MSI-H or dMMR. 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).

[002053] In some embodiments, the pembrolizumab is administered to treat tumor mutational burden-high (TMB-H) Cancer at about 200 mg every 3 weeks for adults. In some embodiments, the pembrolizumab is administered to treat TMB-H Cancer at about 400 mg every 6 weeks for adults. In some embodiments, the pembrolizumab is administered to treat TMB-H Cancer at about 2 mg/kg (up to 200 mg) every 3 weeks for pediatrics. 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).

[002054] In some embodiments, the pembrolizumab is administered to treat cutaneous squamous cell carcinoma (cSCC) at about 200 mg every 3 weeks. In some embodiments, the

pembrolizumab is administered to treat cSCC 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).

[002055] In some embodiments, the pembrolizumab is administered to treat triple-negative breast cancer (TNBC) at about 200 mg every 3 weeks. In some embodiments, the pembrolizumab is administered to treat TNBC 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).

[002056] 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).

[002057] 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.

[002058] 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 other 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.

[002059] 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. In some embodiments, the PD-1 inhibitor is cemiplimab, which is commercially available from Regeneron, Inc.

[002060] 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 endometrial cancer.

[002061] In some embodiments, the endometrial cancer 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.

[002062] 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.

[002063] 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.

[002064] 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.

[002065] 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.

[002066] 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 other 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.

[002067] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that binds human PD-L1 and/or PD-L2 with a KD of about 100 pM or lower, binds human PD-L1 and/or PD-L2 with a

KD of about 90 pM or lower, binds human PD-L1 and/or PD-L2 with a KD of about 80 pM or lower, binds human PD-L1 and/or PD-L2 with a KD of about 70 pM or lower, binds human PD-L1 and/or PD-L2 with a KD of about 60 pM or lower, a KD of about 50 pM or lower, binds human PD-L1 and/or PD-L2 with a KD of about 40 pM or lower, or binds human PD-L1 and/or PD-L2 with a KD of about 30 pM or lower,

[002068] 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 kassoc of about 7.5×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a kassoc of about 8×10^5 1/M·s or faster, binds to human PD-L1 and/ or PD-L2 with a kassoc of about 8.5×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a kassoc of about 9×10^5 1/M·s or faster, binds to human PD-L1 and/or PD-L2 with a kassoc of about 9.5×10^5 1/M·s and/or faster, or binds to human PD-L1 and/or PD-L2 with a kassoc of about 1×10^6 1/M·s or faster.

[002069] In some embodiments, the PD-L1 and/or PD-L2 inhibitor is one that binds to human PD-L1 or PD-L2 with a kdissoc of about 2×10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.1×10^{-5} 1/s or slower , binds to human PD-1 with a kdissoc of about 2.2×10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.3×10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.4×10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.5×10^{-5} 1/s or slower, binds to human PD-1 with a kdissoc of about 2.6×10^{-5} 1/s or slower, binds to human PD-L1 or PD-L2 with a kdissoc of about 2.7×10^{-5} 1/s or slower, or binds to human PD-L1 or PD-L2 with a kdissoc of about 3×10^{-5} 1/s or slower.

[002070] 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 IC50 of about 10 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 9 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 8 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 7 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 6 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 5 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 4 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 of about 3 nM or lower; blocks or inhibits binding of human PD-L1 or human PD-L2 to human PD-1 with an IC50 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 IC50 of about 1 nM or lower.

[002071] 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. 8,779,10[8] 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. 8,779,10[8], the disclosure of which is incorporated by reference herein. The amino acid sequences of durvalumab are set forth in Table 27. 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".

[002072] 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.

[002073] 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 (VH) comprises the sequence shown in SEQ ID NO:180, and the PD-L1 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:181, or conservative amino acid substitutions thereof. In some embodiments, a PD-L1 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:180 and SEQ ID NO:181, respectively.

[002074] 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.

[002075] 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 27. 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 variable light chain	EIVLTQSPGT LSLSPGERAT LSCRASQRVS SSYLAWYQQK PGQAPRLLIY DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSLPWTFG QGTKVEIK	60 10^{8}
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	DASSRAT	7

Identifier	Sequence (One-Letter Amino Acid Symbols)	
durvalumab light chain CDR2		
SEQ ID NO:187 durvalumab light chain CDR3	QQYGSLPWT	9

[002076] 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 28. 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 CH2 N84.4) at 300, 300"; fucosylated complex bi-antennary CHO-type glycans; and H CHS K2 C-terminal lysine clipping at 450 and 450'.

[002077] 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.

[002078] 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:190 and SEQ ID NO:191, respectively.

[002079] 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.

[002080] 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 28. 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	60
	ADTVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARIK LGTVTTVDYW GQGTLVTVSS	120
	ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS	180
	GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG	240
	PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN	300
	STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE	360
	LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW	420
	QQGNVFSCSV MHEALHNHYT QKSLSLSPGK	450
SEQ ID NO:189 avelumab light chain	QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI YDVSNRPSGV	60
	SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTRV FGTGTKVTVL GQPKANPTVT	120
	LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADGSPVK AGVETTKPSK QSNNKYAASS	180
	YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS	216
SEQ ID NO:190 avelumab variable heavy chain	EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYIMMWVRQA PGKGLEWVSS IYPSGGITFY	60
	ADTVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARIK LGTVTTVDYW GQGTLVTVSS	120
SEQ ID NO:191 avelumab variable light chain	QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI YDVSNRPSGV	60
	SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTRV FGTGTKVTVL	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	IKLGTVTTVD Y	11

Identifier	Sequence (One-Letter Amino Acid Symbols)	
heavy chain CDR3		
SEQ ID NO:195 avelumab light chain CDR1	TGTSSDVGGY NYVS	14
SEQ ID NO:196 avelumab light chain CDR2	DVSNRPS	7
SEQ ID NO:197 avelumab light chain CDR3	SSYTSSSTRV	10

[002081] 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 29. 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 CH2 N84.4>A) at 298 and 298'.

[002082] 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.

[002083] 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 (VH) comprises the sequence shown in SEQ ID NO:200, and the PD-L1 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:201, or conservative amino acid substitutions thereof. In some embodiments, a PD-L1 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:200 and SEQ ID NO:201, respectively.

[002084] 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.

[002085] 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 29. Amino acid sequences for PD-L1 inhibitors related to atezolizumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:198	EVQLVESGGG LVQPGGSLRL SCAASGFTFS DSWIHWVRQA PGKGLEWVAW ISPYGGSTYY	60
atezolizumab	ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARRH WPGGFDYWGQ GTLVTVSSAS	120
heavy chain	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL	180
	YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS	240
	VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST	300
	YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSREEMT	360
	KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ	420
	GNVFSCSVMH EALHNHYTQK SLSLSPGK	448
SEQ ID NO:199	DIQMTQSPSS LSASVGDRVT ITCRASQDVS TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS	60
atezolizumab	RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLYHPATFGQ GTKVEIKRTV AAPSVFIFPP	120
light chain	SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT	180
	LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	214
SEQ ID NO:200	EVQLVESGGG LVQPGGSLRL SCAASGFTFS DSWIHWVRQA PGKGLEWVAW ISPYGGSTYY	60
atezolizumab	ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARRH WPGGFDYWGQ GTLVTVSA	118
variable heavy chain		
SEQ ID NO:201	DIQMTQSPSS LSASVGDRVT ITCRASQDVS TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS	60
atezolizumab	RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLYHPATFGQ GTKVEIKR	10^8

Identifier	Sequence (One-Letter Amino Acid Symbols)	
variable light chain		
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

[002086] 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 other 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.

[002087] 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.

[002088] 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.

[002089] In some embodiments, the PD-1 inhibitor is dostarlimab, or a biosimilar or variant thereof. Dostarlimab is commercially available as JEMPERLI (GlaxoSmithKline).

2. Combinations with CTLA-4 Inhibitors

[002090] In some embodiments, the TIL therapy provided to patients with cancer, including endometrial cancer, may include treatment with therapeutic populations of TILs alone or may include a combination treatment including TILs and one or more CTLA-4 inhibitors.

[002091] 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). 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 not limited to, ipilimumab (MDX-010) and tremelimumab (CP-675,206).

[002092] 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.

[002093] 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.

[002094] 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.

[002095] In some embodiments a CTLA-4 inhibitor binds to CTLA-4 with a Kd of about 10−6 M or less, 10−7M 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.

[002096] 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.

[002097] 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:211 and having a heavy chain variable region comprising SEQ ID NO:210). A pharmaceutical composition of ipilimumab includes all pharmaceutically acceptable compositions containing ipilimumab and one or more diluents, vehicles, or excipients. An example of a pharmaceutical composition containing ipilimumab is described in International Patent Application Publication No. WO 2007/67959. Ipilimumab can be administered intravenously (IV).

[002098] 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.

[002099] 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 (VH) comprises the sequence shown in SEQ ID NO:210, and the CTLA-4 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:211, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:210 and SEQ ID NO:211, respectively.

[002100] 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: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.

[002101] 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 30. 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 30. Amino acid sequences for ipilimumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)
SEQ ID NO:208 ipilimumab heavy chain	QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVTF ISYDGNNKYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG WLGPFDYWGQ GTLVTVSSAS 120 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL 180 YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTH 225
SEQ ID NO:209 ipilimumab light chain	EIVLTQSPGT LSLSPGERAT LSCRASQSVG SSYLAWYQQK PGQAPRLLIY GAFSRATGIP 60 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG QGTKVEIKRT VAAPSVFIFP 120 PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 180 TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC 215
SEQ ID NO:210 ipilimumab variable heavy chain	QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVTF ISYDGNNKYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG WLGPFDYWGQ GTLVTVSS 118
SEQ ID NO:211 ipilimumab variable light chain	EIVLTQSPGT LSLSPGERAT LSCRASQSVG SSYLAWYQQK PGQAPRLLIY GAFSRATGIP 60 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG QGTKVEIK 10^{8}
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

[002102] 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).

[002103] 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).

[002104] 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).

[002105] In some embodiments, the ipilimumab is administered to treat unresectable or metastatic melanoma. In some embodiments, the ipilimumab is administered to treat Unresectable or Metastatic Melanoma at about mg/kg every 3 weeks for a maximum of 4 doses. 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).

[002106] In some embodiments, the ipilimumab is administered for the adjuvant treatment of melanoma. In some embodiments, the ipilimumab is administered to for the adjuvant treatment of melanoma at about 10 mg/kg every 3 weeks for 4 doses, followed by 10 mg/kg every 12 weeks for up to 3 years. 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).

[002107] In some embodiments, the ipilimumab is administered to treat advanced renal cell carcinoma. In some embodiments, the ipilimumab is administered to treat advanced renal cell carcinoma at about 1 mg/kg immediately following nivolumab 3 mg/kg on the same day, every 3 weeks for 4 doses. In some embodiments, after completing 4 doses of the combination, nivolumab can be administered as a single agent according to standard dosing regimens for advanced renal cell carcinoma and/or renal cell carcinoma. 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).

[002108] In some embodiments, the ipilimumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer. In some embodiments, the ipilimumab is administered to treat microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer at about 1 mg/kg intravenously over 30 minutes immediately following nivolumab 3 mg/kg intravenously over 30 minutes on the same day, every 3 weeks for 4 doses. In some embodiments, after completing 4 doses of the combination, administer nivolumab as a single agent as recommended according to standard dosing regimens for microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) metastatic colorectal cancer. 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).

[002109] In some embodiments, the ipilimumab is administered to treat hepatocellular carcinoma. In some embodiments, the ipilimumab is administered to treat hepatocellular carcinoma at about 3 mg/kg intravenously over 30 minutes immediately following nivolumab 1 mg/kg intravenously over 30 minutes on the same day, every 3 weeks for 4 doses. In some embodiments, after completion 4 doses of the combination, administer nivolumab as a single agent according to standard dosing regimens for hepatocellular carcinoma. 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).

[002110] 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).

[002111] In some embodiments, the ipilimumab is administered to treat malignant pleural mesothelioma. In some embodiments, the ipilimumab is administered to treat malignant pleural mesothelioma at about 1 mg/kg every 6 weeks with nivolumab 360 mg every 3 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).

[002112] 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 SEQ ID NOs:218 and 219, 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.

[002113] 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.

[002114] 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 (VH) comprises the sequence shown in SEQ ID NO:220, and the CTLA-4 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:221, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:220 and SEQ ID NO:221, respectively.

[002115] 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.

[002116] 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 31. 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 31. Amino acid sequences for tremelimumab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:218 tremelimumab heavy chain	QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV IWYDGSNKYY	60
	ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDP RGATLYYYYY GMDVWGQGTT	120
	VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA	180
	VLQSSGLYSL SSVVTVPSSN FGTQTYTCNV DHKPSNTKVD KTVERKCCVE CPPCPAPPVA	240
	GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVQFN WYVDGVEVHN AKTKPREEQF	300
	NSTFRVVSVL TVVHQDWLNG KEYKCKVSNK GLPAPIEKTI SKTKGQPREP QVYTLPPSRE	360
	EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP MLDSDGSFFL YSKLTVDKSR	420
	WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K	451
SEQ ID NO:219	DIQMTQSPSS LSASVGDRVT ITCRASQSIN SYLDWYQQKP GKAPKLLIYA ASSLQSGVPS	60
	RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSTPFTFGP GTKVEIKRTV AAPSVFIFPP	120

Identifier	Sequence (One-Letter Amino Acid Symbols)	
tremelimumab light chain	SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT	180
	LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	214
SEQ ID NO:220	GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY YADSVKGRFT	60
tremelimumab variable heavy chain	ISRDNSKNTL YLQMNSLRAE DTAVYYCARD PRGATLYYYY YGMDVWGQGT TVTVSSASTK	120
	GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVH	167
SEQ ID NO:221	PSSLSASVGD RVTITCRASQ SINSYLDWYQ QKPGKAPKLL IYAASSLQSG VPSRFSGSGS	60
tremelimumab variable light chain	GTDFTLTISS LQPEDFATYY CQQYYSTPFT FGPGTKVEIK RTVAAPSVFI FPPSDEQLKS	120
	GTASVVCLLN NFYPREAKV	139
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 tremelimumab light chain CDR3	QQYYSTPFT	9

[002117] 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. 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).

[002118] 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. 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).

[002119] 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. 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).

[002120] 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.

[002121] 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.

[002122] 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 (VH) comprises the sequence shown in SEQ ID NO:230, and the CTLA-4 inhibitor light chain variable region (VL) comprises the sequence shown in SEQ ID NO:231, or conservative amino acid substitutions thereof. In some embodiments, a CTLA-4 inhibitor comprises VH and VL 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 VH and VL 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 VH and VL 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 VH and VL 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 VH and VL regions that are each at least 95% identical to the sequences shown in SEQ ID NO:230 and SEQ ID NO:231, respectively.

[002123] 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.

[002124] 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 32. 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 32. Amino acid sequences for zalifrelimab.

Identifier	Sequence (One-Letter Amino Acid Symbols)	
SEQ ID NO:228 zalifrelimab heavy chain	EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS ISSSSSYIYY	60
	ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG LMGPFDIWGQ GTMVTVSSAS	120
	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL	180
	YSLSSVVTVP SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS	240
	VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST	300
	YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSREEMT	360
	KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ	420
	GNVFSCSVMH EALHNHYTQK SLSLSPGK	448
SEQ ID NO:229 zalifrelimab light chain	EIVLTQSPGT LSLSPGERAT LSCRASQSVS RYLGWYQQKP GQAPRLLIYG ASTRATGIPD	60
	RFSGSGSGTD FTLTITRLEP EDFAVYYCQQ YGSSPWTFGQ GTKVEIKRTV AAPSVFIFPP	120
	SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT	180
	LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC	214
SEQ ID NO:230 zalifrelimab variable heavy chain	EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS ISSSSSYIYY	60
	ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG LMGPFDIWGQ GTMVTVSS	118
SEQ ID NO:231	EIVLTQSPGT LSLSPGERAT LSCRASQSVS RYLGWYQQKP GQAPRLLIYG ASTRATGIPD	60
	RFSGSGSGTD FTLTITRLEP EDFAVYYCQQ YGSSPWTFGQ GTKVEIK	107

Identifier	Sequence (One-Letter Amino Acid Symbols)	
zalifrelimab variable light chain		
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

[002125] 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.

[002126] In some embodiments, the anti-CTLA-4 antibody is an anti-CTLA-4 antibody disclosed in any of the following patent publications: US 2019/0048096 A1; US 2020/0223907; US 2019/0201334; US 2019/0201334; US 2005/0201994; EP 1212422 B1; WO 2018/204760; WO 2018/204760; WO 2001/014424; WO 2004/035607; WO 2003/086459; WO 2012/120125; WO 2000/037504; WO 2009/100140; WO 2006/09649; WO2005092380; WO 2007/123737; WO 2006/029219; WO 2010/0979597; WO 2006/12168; and WO1997020574, each of which is 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; and/or U.S. Patent Nos. 5.977,318, 6,682,736, 7,109,003, and 7.132,281, each of which is incorporated herein by reference. In some embodiments, the anti-CTLA-4 antibody is, 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, 1998, 95, 10067-10071 (1998); Camacho, et al., J. Clin. Oncol., 2004, 22, 145 (Abstract No. 2505 (2004) (antibody CP-675206); or Mokyr, et al., Cancer Res., 1998, 58, 5301-5304 (1998), each of which is incorporated herein by reference.

[002127] In some embodiments, the CTLA-4 inhibitor is a CTLA-4 ligand as disclosed in WO 1996/040915 (incorporated herein by reference).

[002128] 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 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 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 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 International Patent Application Publication No. WO 2004/081021 (incorporated herein by reference).

[002129] In other embodiments, the anti-CTLA-4 RNAi molecules of the present invention are RNA molecules described 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).

[002130] In some embodiments, the anti-CTLA-4 inhibitor is gotistobart or a biosimilar or variant thereof.

3. Combinations with a Myc Fusion Protein

[002131] In some embodiments, the TIL therapy provided to patients with cancer may include treatment with therapeutic populations of TILs alone or may include a combination treatment including TILs and a Myc fusion protein as disclosed herein. Myc fusion proteins are described in US Patent No. 11,369,678, the content of which is incorporated by reference in its entirety.

[002132] Disclosed herein, in certain embodiments, is a MYC fusion protein comprising (a) a transporter peptide sequence; and (b) a MYC sequence. In some embodiments, the MYC fusion protein is a peptide of Formula (I):

transporter peptide sequence —MYC sequence.

[002133] In some embodiments, a MYC fusion protein disclosed herein comprises (a) a transporter peptide sequence; (b) a MYC sequence; and (c) one or more molecules that link the transporter peptide sequence and the MYC sequence. In some embodiments, the fusi MYC fusion protein is a peptide of Formula (II):

transporter peptide sequence—X—MYC sequence,

wherein —X— is molecule that links the transporter peptide sequence and the MYC sequence. In some embodiments, —X— is an amino acid. In some embodiments, —X— is at least one amino acid.

[002134] As used herein, a "transporter peptide" means a peptide sequence that promotes peptide penetration into cells and tissues. In some embodiments, a transporter peptide is the N-terminal 9-amino-acid sequence of the TAT protein transduction domain of HIV-1 (RKKRRQRRR) (SEQ ID NO: 306). In some embodiments, a transporter peptide is $TAT_{[48-57]}$. In some embodiments, a transporter peptide is $TAT_{[57-48]}$.

[002135] As used herein, a "MYC sequence" is a MYC amino acid peptide sequence. In some embodiments, the Myc polypeptide is a complete Myc polypeptide sequence. In some embodiments, the Myc polypeptide is a partial Myc polypeptide sequence. In some embodiments, the MYC is c-MYC. In some embodiments, the Myc polypeptide sequence comprises SEQ ID NO:300.

[002136] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, and (b) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, and (b) c-MYC.

[002137] In some embodiments, a MYC fusion protein disclosed herein comprises (a) TAT, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[48-57]}$, (b) a linker amino acid, and (c) c-MYC. In some embodiments, a MYC fusion protein disclosed herein comprises (a) $TAT_{[57-48]}$, (b) a linker amino acid, and (c) c-MYC.

[002138] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one amino acid sequence that facilitates purification of the fusion protein. In some embodiments, a MYC fusion protein disclosed herein comprises a protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a polyhistidine tag and an epitope tag. In some embodiments, a MYC fusion protein disclosed herein comprises a 6-histidine tag and a V5 epitope tag.

[002139] In some embodiments, the histidine tag is a 6-histidine tag. In some embodiments, the histidine tag comprises the sequence HHHHHH (SEQ ID NO:302). In some embodiments, a histidine tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a TAT-Myc polypeptide sequence is cloned into an expression vector encoding a polyHis-tag. In some embodiments, a polyhistidine tag is added by PCR (i.e., the PCR primers comprise a polyhistidine sequence).

[002140] In some embodiments, a MYC fusion protein disclosed herein further comprises at least one protein tag. In some embodiments, a MYC fusion protein disclosed herein comprises an epitope tag. In some embodiments, a MYC fusion protein disclosed herein further comprises a V5 epitope tag. In some embodiments, the V5 tag comprises the amino acids: GKPIPNPLLGLDST (SEQ ID NO:303). In some embodiments, the V5 tag comprises the amino acids: IPNPLLGLD (SEQ ID NO:304). In some embodiments, a V5 tag is added to a MYC fusion protein disclosed herein by any suitable method. In some embodiments, a MYC fusion protein sequence is cloned into an expression vector encoding a V5 tag. In some embodiments, a V5 tag is added by PCR (i.e., the PCR primers comprise a V5 sequence).

[002141] In some embodiments, the amino acids are in the D formation. In some embodiments, the amino acids are in the L formation. In some embodiments, a first plurality of amino acids is in the D formation and a second plurality is in the L formation.

[002142] In some embodiments, a MYC fusion protein comprises SEQ ID NO:301.

[002143] In some embodiments, the Myc fusion protein is administered at a dose of about 0.5 mg/kg to about 10 mg/kg. In some embodiments, the Myc fusion protein 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, a MYC fusion protein comprises SEQ ID NO:301.

[002144] In some embodiments, the Myc fusion protein is administered at a dose of about 200 mg to about 500 mg. In some embodiments, the Myc fusion protein 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 Myc fusion protein administration is begun 1, 2, 3, 4, or 5 days post IL-2 administration. In some embodiments, the Myc fusion protein administration is begun 1, 2, or 3 days post IL-2 administration. In some embodiments, the Myc fusion protein 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 Myc fusion protein can also be administered 1, 2, or 3 weeks pre-resection (i.e., before obtaining a tumor sample from the subject or patient). In some embodiments, a MYC fusion protein comprises SEQ ID NO:301.

[002145] In some embodiments, the Myc fusion protein is administered every 2 weeks, every 3 weeks, every 4 weeks, every 5 weeks, or every 6 weeks. In some embodiments, a MYC fusion protein comprises SEQ ID NO:301.

4. Lymphodepletion Preconditioning of Patients

[002146] 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.

[002147] 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.

[002148] 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.

[002149] 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.

[002150] 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.

[002151] 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.

[002152] 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.

[002153] 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.

[002154] 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.

[002155] 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.

[002156] 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.

[002157] 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.

[002158] 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.

[002159] 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.

[002160] 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.

[002161] 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.

[002162] 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).

[002163] 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.

[002164] 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.

[002165] 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

[002166] 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.

[002167] 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.

[002168] 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.

[002169] 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.

[002170] 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 60 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 25 mg/m^2/day	X	X	X	X	X					
TIL infusion						X				

[002171] 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 60 mg/kg	X	X							
Mesna (as needed)	X	X							
Fludarabine 25 mg/m^2/day	X	X	X	X					
TIL infusion					X				

[002172] 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 60 mg/kg	X	X						
Mesna (as needed)	X	X						
Fludarabine 25 mg/m^2/day	X	X	X					
TIL infusion				X				

[002173] 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 60 mg/kg	X	X								
Mesna (as needed)	X	X								
Fludarabine 25 mg/m^2/day			X	X	X					
TIL infusion						X				

[002174] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 37.

TABLE 37. 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					
TIL infusion						X				

[002175] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 38.

TABLE 38. 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				

[002176] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 39.

TABLE 39. 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				

[002177] In some embodiments, the non-myeloablative lymphodepletion regimen is administered according to Table 40.

TABLE 40. 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				

[002178] 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.

5. IL-2 Regimens

[002179] 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.

[002180] 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.

[002181] 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 additional 5 days of intravenous aldesleukin or a biosimilar or variant thereof, as a continuous infusion of 18 x 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.

[002182] 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.

[002183] 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.

[002184] 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.

[002185] 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.

[002186] 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 (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 VH or the VL, 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 (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 VH or the VL, 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.

[002187] In some embodiments, the antibody cytokine engrafted protein described herein has a longer serum half-life than a wild-type IL-2 molecule such as, but not limited to, aldesleukin (Proleukin®) or a comparable molecule.

[002188] 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.

VII. EXAMPLES

[002189] 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

[002190] 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 solid tumors. This media can be used for preparation of any of the TILs described in the present application and other examples.

[002191] Preparation of CM1. Removed the following reagents from cold storage and warm them in a 37°C water bath: (RPMI1640, Human AB serum, 200 mM L-glutamine). Prepared CM1 medium according to Table 41 below by adding each of the ingredients into the top section of a 0.2 µm filter unit appropriate to the volume to be filtered. Store at 4°C.

TABLE 41. 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

[002192] On the day of use, prewarmed required amount of CM1 in 37°C water bath and add 6000 IU/mL IL-2.

[002193] Additional supplementation may be performed as needed according to Table 42.

TABLE 42. Additional supplementation of CM1, as needed.

Supplement	**Stock concentration**	**Dilution**	**Final concentration**
GlutaMAX™	200 mM	1:100	2 mM
Penicillin/streptomycin	10,000 U/mL penicillin 10,000 µg/mL streptomycin	1:100	100 U/mL penicillin 100 µg/mL streptomycin
Amphotericin B	250 µg/mL	1:100	2.5 µg/mL

Preparation of CM^2

[002194] Removed prepared CM1 from refrigerator or prepare fresh CM1. Removed AIM-V® from refrigerator and prepared the amount of CM^2 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 CM^2 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

[002195] 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

[002196] CM4 was the same as CM3, with the additional supplement of 2mM GlutaMAXTM (final concentration). For every 1L of CM3, add 10 mL of 200 mM GlutaMAXTM. Prepare an amount of CM4 sufficient to experimental needs by adding IL-2 stock solution and GlutaMAXTM stock solution directly to the bottle or bag of AIM-V. Mixed well by gentle shaking. Labeled bottle with "3000 IL/mL 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 more than 7-days storage at 4°C.

EXAMPLE 2: USE OF IL-2, IL-15, AND IL-21 CYTOKINE COCKTAIL

[002197] 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 any of the examples herein.

[002198] Using the processes described herein, TILs can be grown from 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 Santegoets, et al., J. Transl. Med., 2013, 11, 37.

[002199] 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

[002200] 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.

[002201] 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.

[002202] 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.

[002203] 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.

[002204] Feeder lots were evaluated on two criteria: (1) their ability to expand TILs in co-culture >100-fold and (2) their replication incompetency.

[002205] 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.

[002206] 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.

[002207] 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

[002208] 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.

[002209] 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.

[002210] 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.

[002211] 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.

[002212] 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).

[002213] 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.

[002214] 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.

[002215] 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.

[002216] 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 CM^2 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.

[002217] 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, 37°C incubator, with the cap loosened to allow gas exchange. Recorded the counts.

[002218] 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 CM^2 supplemented with 3000 IU/mL IL-2. Returned the 50 mL conical tube to the incubator with a loosened cap.

[002219] The steps above were repeated for the second TIL line.

[002220] Just prior to plating the TIL into the T25 flasks for the experiment, TIL were diluted 1:10 for a final concentration of 1.3×10^5cells/mL as per below.

[002221] 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.

[002222] 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.

[002223] 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.)

[002224] 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.

[002225] Further information is provided in Table 43.

TABLE 43. Solution information.

Component	**Volume in co-culture flasks**	**Volume in control (feeder only) flasks**
CM^2 + 3000 IU/mL IL-2	18 mL	19 mL
MNC: 1.3×10^7/mL in CM^2 + 3000 IU IL-2 (final concentration 1.3×10^7/flask)	1 mL	1 mL
OKT3: 10 µL/mL in CM^2 = 3000 IU IL-2	60 µL	60 µL
TIL: 1.3×10^5/mL in CM^2 with 3000 IU of IL-2 (final concentration 1.3×10^5/flask)	1 mL	0

[002226] 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 N2 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.

[002227] 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.

[002228] Using a transfer pipet, the contents of feeder vials were immediately transferred into 30 mL of warm CM^2 in a 50 mL conical tube. The vial was washed with a small volume of CM^2 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 CM^2 plus 3000 IU/mL IL-2. Removed 200 µL for cell counting using the automated cell counter. Recorded the counts.

[002229] Resuspended cells at 1.3×10^7 cells/mL in warm CM^2 plus 3000 IU/mL IL-2. Diluted TIL cells from 1.3×10^6 cells/mL to 1.3×10^5cells/mL.

[002230] Setup Co-Culture. Diluted TIL cells from 1.3×10^6 cells/mL to 1.3×10^5cells/mL. Added 4.5 mL of CM^2 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.

[002231] 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.

[002232] 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.

[002233] 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.

[002234] 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.

[002235] 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.

[002236] Feeder control flasks were evaluated for replication incompetence and flasks containing TIL were evaluated for fold expansion from day 0.

[002237] 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 CM^2 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.

[002238] 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.

[002239] 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

[002240] 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.

[002241] 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 44 below.

TABLE 44. 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)

[002242] 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.

[002243] 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.

[002244] 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.

[002245] 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.

[002246] 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.

[002247] 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

[002248] 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.

[002249] Procedure. Prepared 0.2% Acetic Acid solution (HAc). Transferred 29 mL sterile water to a 50 mL conical tube. Added 1 mL 1N acetic acid to the 50 mL conical tube. Mixed well by inverting tube 2-3 times. Sterilized the HAc solution by filtration using a Steriflip filter.

[002250] Prepare 1% HSA in PBS. Added 4 mL of 25% HSA stock solution to 96 mL PBS in a 150 mL sterile filter unit. Filtered solution. Stored at 4°C. For each vial of rhIL-2 prepared, fill out forms.

[002251] 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).

[002252] Calculated the volume of 1% HSA required for rhIL-2 lot by using the equation below:

$$\left(\frac{Vial\ Mass\ (mg)\ x\ Biological\ Activity\ (\frac{IU}{mg})}{6x10^6\ \frac{IU}{mL}}\right) - HAc\ vol\ (mL) = 1\%\ HSA\ vol\ (mL)$$

[002253] For example, according to the COA of rhIL-2 lot 10200121 (Cellgenix), the specific activity for the l mg vial is 25 × 10^6 IU/mg. It recommends reconstituting the rhIL-2 in 2 mL 0.2% HAc.

$$\left(\frac{1mg\ x\ 25x10^6\ \frac{IU}{mg}}{6x10^6\ \frac{IU}{mL}}\right) - 2mL = 2.167mL\ HSA$$

[002254] Wiped rubber stopper of IL-2 vial with alcohol wipe. Using a 16G needle attached to a 3 mL 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.

[002255] 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

[002256] This example describes a cryopreservation process method for TILs prepared with the procedures described herein using the CryoMed Controlled Rate Freezer, Model 7454 (Thermo Scientific).

[002257] 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).

[002258] 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

[002259] The processes disclosed above may be performed substituting the CM1 and CM^2 media with a defined medium according (e.g., CTS™ OpTmizer™ T-Cell Expansion SFM, ThermoFisher, including for example DM1 and DM2).

EXAMPLE 7: EXEMPLARY GEN 2 PRODUCTION OF A CRYOPRESERVED TIL CELL THERAPY

[002260] This examples 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 45. 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	$5 – 200 \times 10^6$ viable cells per G-REX-500MCS	G-REX-500MCS 1 flasks	≤5000
16	REP Split	1×10^9 viable cells per G-REX-500MCS	G-REX-500MCS ≤5 flasks	≤25000
22	Harvest	Total available cells	3-4 CS-750 bags	≤530

TABLE 46. 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 ($6x10^6$ 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 ºC; 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 ºC; CO_2 Percentage: 5.0±1.5 %CO_2.

[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 ($6x10^6$ 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 CM^2 Day 11 Media" bag prepared. Prepared feeder cell transfer pack. Incubated Complete CM^2 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 CM^2 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, CO_2 Percentage: 5.0±1.5 %CO_2.

[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 + 10^8 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 ºC, 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 ($6x10^6$ 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, CO_2 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 × 104 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 6x104" 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 47. 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 assays as described herein are also employed to analyze TIL products.

EXAMPLE 8: PRODUCTION OF A CRYOPRESERVED TIL CELL THERAPY FOR ENDOMETRIAL CANCER USING THE GEN 2 PROCESS

[002334] A study was conducted using 9 endometrial cancer tumors obtained from commercial vendors with a mass of at least approximately 500 mg. The tumors were expanded using a small scale Gen 2 22-day process, wherein a GREX-6 flask with 4-6 tumor fragments was used for pre-REP with 40 mL CM1 and 6000 IU/ml IL-2, with all other parameters as described above. For the day 11 REP

stage, a GREX-6M flask was used with 4×10^5 cells, 1×10^8 PBMC feeder cells, 30 ng/mL OKT-3, 100 mL CM2 and 3000 IU/mL IL-2, with a day 16 scale up using 100 mL CM4 and 3000 IU/mL IL-2. Results are summarized in Table 48. The Gen 2 process showed reliable expansion of TILs from endometrial cancer tumors of at least approximately 500 mg mass.

TABLE 48. Results for endometrial Gen 2 expansions using tumors with masses of at least approximately 500 mg.

Tumor ID	Tumor size (mg)	Total # fragments	Pathology	MMR status	Pre-REP Total Viable Cell #	Pre-REP % viability	REP Total Viable cell #	REP % viability	Fold Expansion	Extrapolation
END22040	523	24	Endometrioid carcinoma	unknown	3.83E+06	19.15%	5.95E+08	81.40%	1947	7.46E+09
END22049	490	26	Endometrioid carcinoma	unknown	3.19E+06	28.48%	2.90E+08	77.41%	724	3.75E+09
END22053	581	30	Endometrioid carcinoma	pMMR	1.08E+06	22.68%	2.51E+08	78.41%	626	2.02E+09
END22055	500	36	Serous carcinoma	unknown	3.47E+06	66.60%	2.10E+08	68.63%	525	5.47E+09
END22056	550	24	Endometrioid carcinoma	unknown	199E+06	91.45%	3.48E+08	83.63%	869	5.19E+11
END22059	770	36	Endometrioid carcinoma	pMMR	1.35E+06	14.36%	1.31E+08	68.32%	326	1.32E+09
END22060	880	45	Endometrioid carcinoma	dMMR	1.12E+06	25.60%	2.50E+08	82.64%	932	7.80E+09
END22061	1083	63	Endometrial adenocarcinoma	pMMR	1.51E+06	39.39%	2.70E+08	87.78%	2853	2.71E+10
END22062	1100	48	Endometrium cancer	dMMR	2.90E+06	22.09%	2.84E+08	78.02%	710	1.24E+10

[002335] Another study was conducted using 11 endometrial cancer tumors. Table 49 summarizes the baseline characteristics of the tumors.

TABLE 49: Baseline characteristics of endometrial tumors.

Age	Race/ Ethnicity	Pathology	FIGO grade	TNM classification	MMR	MLH1 promoter methylation
61	White	Endometroid adenocarcinoma	FIGO grade II	pT3a, pN0	pMMR	
68	White	Endometroid adenocarcinoma	FIGO grade II	pT1b, pN0	dMMR	81%
67	White	Endometrial adenocarcinoma	FIGO grade II	pT1b, pN0	dMMR	97%
83	White	Endometroid carcinoma	FIGO grade II	pT1a, pN0	pMMR	
63	White	Endometrioid carcinoma	FIGO grade II	pT1b, pN0	pMMR	

66	White	Endometroid adenocarcinoma	FIGO grade I	pT1b,pN0	pMMR	
81	White	Serous carcinoma	High grade (grade >III)	pT3a, pN0	pMMR	
45	White	Endometroid carcinoma	FIGO grade II	pT3b, pNx	dMMR	Positive
67	Hispanic	Endometrioid carcinoma	FIGO grade II	pT1a, pN0	dMMR	Positive
69	White	Endometrioid carcinoma	FIGO grade II	pT1a, pN0	dMMR	N/A (MLH1 intact)
84	White	Serous carcinoma	FIGO grade III	pT1a, pNx	pMMR	

FIGO, Federation of Gynecology and Obstetrics; MMR, mismatch repair; pNx, no lymph node was collected.

[002336] The tumors were expanded using the small-scale Gen 2 22-day process as described above. Of the 11 EC tumor samples (5 dMMR and 6 pMMR) processed (Table 49), 10 (92%) produced an extrapolated total viable cell yield of $>1\times10^9$ TIL cells with a median yield of 1.1×10^{10} cells and a viability rate of 83% (Table 50).

TABLE 50. Summary of expanded TIL product attributes.

Tumor ID	**Tumor size (mg)**	**Total # of fragments**	**Tumor site**	**TVC (extrapolated)**	**Viability (NC200)**	**CD45+ CD3+%**	**CD4+ CD3+%**	**CD8+ CD3+%**
END22061	1083	63	Uterus	2.7E+10	90.1	96.6	75.0	23.0
END22062	1100	48	Uterus	1.2E+10	82.7	98.1	86.2	12.9
END22063	1032	52	Uterus	N/A	N/A	N/A	N/A	N/A
END22091	1013	50	Uterus	6.6E+09	72.4	98.3	76.2	22.9
END22093	1010	30	Uterus	8.6E+09	77.1	97.3	91.7	6.4
END22094	1050	53	Uterus	1.9E+10	87.9	90.2	67	31.7
END22095	1131	48	Uterus	8.1E+09	82.8	97.8	81.6	17.1
END22096	1400	59	Uterus	9.8E+09	84.9	93	78.8	19.9
END22098	1400	80	Uterus	3.5E+10	86.6	97.3	34.4	63.1
END22100	1327	50	Uterus	3.8E+09	69.3	95.6	49.4	48.5

END22102	1150	29	Uterus	1.2E+10	72.3	94.6	51.3	46.5
			Median	1.1E+10	82.7	97.0	75.6	23.0

[002337] Method

Small-Scale Gen 2 Process

1. Tumor Processing (Day 0)
    a. Tumors were washed with HBSS+Gentamicin.
    b. Tumors were fragmented into approximately 3x3x3 mm pieces.
2. Initiating Pre-REPs (Day 0)
    a. Prepare G-Rex 6 flask with 40mL of warm CM1 media supplemented with 6000IU of IL-2 into each well.
    b. Equally place 4-6 tumor fragments into each well.
    c. Transfer G-Rex 6 flask containing tumor fragments into incubator at 37°C and 5% CO_2 for 11 days.
3. Initiating REPs (Day 11)
    a. Harvest pre-REPs by resuspending cells in the G-Rex 6 flask and transferring entire content over a 70um cell strainer into 50mL conical tubes.
    b. Centrifuge conical tubes containing pre-REP cells at 500xg for 5min.
    c. Aspirate supernatant and resuspend cell pellet in 1-10mL of warm CM2.
    d. Count pre-REP cells using the Cellaca.
    e. Thaw 3 lots of iPBMC vials in 37°C water bath.
    f. Transfer iPBMC into a 50mL conical tube containing 30mL of warm CM2.
    g. Centrifuge conical tubes containing iPBMC at 500xg for 5min.
    h. Aspirate supernatant and resuspend cell pellet in 40-50mL of warm CM2.
    i. Count iPBMC using the Cellaca.
    j. In a G-Rex 6M, add 80mL of warm CM2, 50ul IL-2, 3ul MACS GMP OKT3 (anti CD3), 1e8 iPBMC, and 4e5 pre-REP cells. QS volume to 100mL with warm CM2 for final concentrations of 3000IU of IL-2 and 30 ng/mL of OKT3.
    k. Transfer G-Rex 6M into incubator at 37°C and 5% CO_2 for 5 days.
4. Scale-Out (Day 16)
    a. Carefully remove 80mL of media from the top of the G-Rex 6M without disturbing the cells.
    b. Resuspend cells in remaining media and count using the Cellaca.
    c. Transfer 2e7 cells into a new well of a G-Rex 6M.

d. QS volume to 100mL with warm CM4 supplemented with 3000 IU of IL-2.
e. Transfer G-Rex 6M into incubator at 37°C and 5% CO_2 until day 22.

5. TIL Harvest (Day 22)
   a. Carefully remove 50-60mL of media from the top of the G-Rex 6M without disturbing the cells.
   b. Resuspend cells in remaining media and transfer to a 50mL conical tube.
   c. Count cells using the Cellaca.
   d. Centrifuge the conical tube containing TIL at 500xg for 5min.
   e. Resuspend the cell pellet in CS10 to a concentration of 3e7-5e7 cells/mL.
   f. Aliquot 1mL of CS10 containing TIL into cryovials.
   g. Transfer cryovials to a Coolcell and freeze in a -80°C freezer.
   h. After 24 hours, transfer cryovials to LN2 freezer.

EXAMPLE 9: PHENOTYPIC ANALYSIS OF TIL PRODUCTS GENERATED FROM ENDOMETRIAL TUMORS

[002338] Cellular phenotypic analysis of surface marker expression related to exhaustion, activation, memory, and function in both CD4+ T and CD8+ T subsets of five TIL products generated from endometrial tumors was performed using flow staining. Results from the cellular phenotypic analysis show that TILs generated from endometrial tumor display comparable phenotype as TILs generated from other tumor types (FIG. 9).

[002339] Single cell RNA sequencing was performed on TILs generated from endometrial tumors. 10A shows twenty-six cell clusters of integrated single-cell data consisting of 6 endometrial tumor samples. FIG. 10B shows expression level of Lowery's NeoTCR8 gene set scores for all clusters. Based on the diagram, cell cluster 7 is identified as the NeoTCR8 cluster.

[002340] TCR clonotypes from the NeoTCR8 cluster were identified and tracked from tumor digest to TIL drug product using bulk TCR sequencing. Clonotype proportion (left) and number (right) of unique clonotypes for each sample are summarized (FIG. 10C). Based om the data, a majority of the putative neoantigen-specific T-cells identified by NeoTCR8 score in the tumor digest remained in the final TIL product.

[002341] Methods

Flow Staining without Stimulation

1. Prepare TIL

a. Thaw TIL in 50mL conical tube containing 10mL of warm CM4 supplemented with 300IU of IL-2.
b. Centrifuge the conical tube containing TIL at 500xg for 5min.
c. Resuspend the cell pellet in CM4 with 300IU of IL-2 and count using the Cellaca.
d. Transfer 300,000 cells to 96-well U-bottom plate.

2. Surface Staining
   a. Wash cells twice with 1X DPBS buffer.
   b. Centrifuge cells at 500xg for 3 min.
   c. Remove the supernatant by carefully flicking plate.
   d. Add 25ul of L/D master mix (containing FcX). Resuspend cells and incubate at RT for 8 min.
   e. Directly add 50ul of surface staining master mix and FMO to samples. Incubate for 25 min at 4°C.
   f. After incubation add 150ul of FACS buffer and spin down the cells. Wash a second time with 200ul of FACS buffer.
   g. For surface stain only wells, resuspend cells in 120ul of FACS buffer and transfer into filter plate placed over a new 96-well U-bottom plate. For intracellular staining wells, continue to step 3.
   h. Quick spin the plates containing cells for 8-10 seconds. Samples are now ready for running on the Ze5. Keep in fridge until use but resuspend samples prior to use if plate is not used immediately (within 10 min).
3. Intracellular staining
   a. Add 100ul of FIX buffer (from eBioscience Foxp3 staining kit) and incubate at RT in the dark for 30 min.
   b. Add 150ul of PERM buffer (from eBioscience Foxp3 staining kit) and spin down at 500xg for 3 min. Add another 200ul of PERM buffer and spin a second time.
   c. Add 50ul of intracellular staining master mix (made in PERM buffer) and incubate at RT in the dark for 40 min.
   d. Wash the cells with 150ul of PERM buffer and repeat the wash step a second time by adding 200ul of PERM buffer.
   e. After the last wash, resuspend cells in 120ul of FACS buffer and transfer into filter plate placed over a new 96-well U-bottom plate.
   f. Quick spin the plates containing cells for 8-10 seconds. Samples are now ready for running on the Ze5. Keep in fridge until use but resuspend samples prior to use if plate is not used immediately (within 10 min).

Flow Staining with Stimulation

1. Coat plate
    a. The day before staining, coat a 96 well flat bottom plate with OKT3 at 1 ug/mL.
2. Prepare TIL
    a. Thaw TIL in 50mL conical tube containing 10mL of warm CM4 supplemented with 300IU of IL-2.
    b. Centrifuge the conical tube containing TIL at 500xg for 5min.
    c. Resuspend the cell pellet in CM4 with 300IU of IL-2 and count using the Cellaca.
    d. Resuspend cells to a concentration of 3e6 cells/mL.
    e. Transfer 300,000 cells to the OKT3 coated plate.
3. Stim cells with Golgi Blocker
    a. Make golgi blocker media by adding Brefeldin A, Monensin, and CD107a to CM4 supplemented with 300IU of IL-2
    b. Add 100ul of golgi blocker media to cells in the OKT3 coated plate.
    c. Transfer plate into incubator at 37°C and 5% CO_2 for 4 hours.
4. Surface Staining
    a. Transfer cells from OKT3 coated plate to a new 96 well U bottom plate.
    b. Wash cells twice with 1X DPBS buffer.
    c. Centrifuge cells at 500xg for 3 min.
    d. Remove the supernatant by carefully flicking plate.
    e. Add 25ul of L/D master mix (containing FcX). Resuspend cells and incubate at RT for 8 min.
    f. Directly add 50ul of surface staining master mix and FMO to samples. Incubate for 25 min at 4°C.
    g. After incubation add 150ul of FACS buffer and spin down the cells. Wash a second time with 200ul of FACS buffer.
5. Intracellular Staining
    a. Add 75 uL of fixation buffer (from Biolegend fix and perm kit) to each well. Incubate cells in the dark for 12 minutes.
    b. Wash with 125ul of FACS buffer. Resuspend cells in 200ul of FACS buffer and leave at 4°C overnight.
    c. Centrifuge cells at 500xg for 3 min.
    d. Remove the supernatant by carefully flicking plate.
    e. Add 150uL of perm buffer (from Biolegend fix and perm kit) and wash. Wash again with 200uL of perm buffer.

f. Add 50ul intracellular antibody master mix made in perm buffer and stain for 1.5 hours at 4°C.
g. Wash the cells with 150ul of perm buffer and repeat the wash step a second time by adding 200ul of perm buffer.
h. After the last wash, resuspend cells in 120ul of FACS buffer and transfer into filter plate placed over a new 96-well U-bottom plate.
i. Quick spin the plates containing cells for 8-10 seconds. Samples are now ready for running on the Ze5. Keep in fridge until use but resuspend samples prior to use if plate is not used immediately (within 10 min).

Single Cell RNA Sequencing

[002342] Endometrial tumor digest samples (n=5) were obtained from cryopreservation, thawed, and washed twice with PBS + 0.04% BSA. Cell Viability was assessed using a Nexcelom Cellaca automated cell counter using AOPI. Dead cell removal was performed on any sample containing fewer than 75% viable cells, using the Miltenyi Dead Cell Removal kit, according to manufacturer guidelines. Single cell Gel-bead emulsions were prepared using 10x Chromium X controller. Sequencing libraries were prepared using 10x 5' Immune profiling v2 reagents, following manufacturers guidelines; and sequenced on Illumina NextSeq2000 instrument with an insert read length of 90 base pairs. Primary and secondary data analysis were performed using Cell Ranger v7 (10X Genomics) with default parameters. The R package Seurat[1] was used for tertiary analysis and data visualization. Genes detected in less than 3 cells were discarded and *TCRA* and *TCRB* family genes removed to avoid clonotype clustering bias. Dead cells, doublets, or low-quality cells were discarded based on the following empirically determined filter: percent mitochondria reads less than 8% and number of genes detected greater than 500 but less than 6000. Single cell TCR-seq data was added to the single cell objects meta data using scRepertoire[2]. Cells where a TCR was detected, and gene expression was consistent with a T cell (e.g. *CD3E*) were kept for downstream analysis. Individual samples were normalized using sctransform[3] and integrated using Harmony[4] with default parameters. Clustering with resolution=2 and UMAP visualization was then performed. For gene set analysis, the R packages Escape[5] and UCell[6] were used to quantify the gene set scores for the NeoTCR8 gene signature from Lowrey et al.[7]. TCRb clonotypes expressed by the NeoTCR8 cluster were identified and exported for further analysis (below).

Bulk TCR Sequencing

[002343] Matching endometrial TIL drug product samples (n=5) were obtained from cryopreservation, thawed, and washed twice with PBS + 0.04% BSA. Total RNA was extracted from approximately 1 million cells using NEB Monarch Total RNA Miniprep Kit. 500ng of purified Total

RNA was used as template for preparing TCR beta-chain libraries using Takara SMARTer Human TCR a/b Profiling Kit v2, according to manufacturer's guidelines. Equimolar quantities of each library were pooled together and sequenced on a NextSeq2000 with paired end 150bp reads. High base level sequencing quality of reads was confirmed using FASTQC. Primary analysis of fastq files to identify and quantify productive rearrangements (clones) was performed using RTCR[8] with default parameters. Clones with a less than perfect average base quality score in the CDR3 region were filtered out. Tertiary analysis was performed using the R package immunarch[9]. Clonotypes from the NeoTCR8 cluster were identified in the TIL Bulk TCR-Seq and their number and proportion of total TCR repertoire exported for visualization in GraphPad Prism.

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EXAMPLE 10: FUNCTIONAL ANALYSIS OF TIL PRODUCTS GENERATED FROM ENDOMETRIAL TUMORS

[002344] Endometrial TIL products derived from two patients (END22061 & END22062) were co-cultured with a matched tumor digest. Twenty-four hours after stimulation, 4-1BB activation in CD8 T cells and OX40 expression in CD4 T cells were assayed by flow cytometry. HLA-I/II antibodies were used as a T-cell activation block. TransACT was used as a positive T-cell activation control. Cell supernatants from co-culture assay was harvested. IFN-γ and TNF-α expressions were quantified by the BioPlex assay. EC TIL product displayed functional reactivity with upregulated 4-1BB in CD8+ T cells and upregulated OX40 in CD4+ T cells (FIG. 11) and increased production of interferon-γ and tumor necrosis factor-α when stimulated with autologous tumor digests (FIG. 12).

EXAMPLE 11: TIL PRODUCTS GENERATED FROM ENDOMETRIAL TUMORS SHOW ANTI-TUMOR ACTIVITY

[002345] Anti-tumor activity of TILs generated from endometrial tumors was measured using a MicroOrganoSphere™ (MOS) (Xilis, Durham, NC) co-culture assay. TIL and MOS were co-cultured at a ratio of 5:1 and evaluated on the Incucyte® S3 Live-Cell Imager. MOS was labeled with NIR680 before co-culture. MOS killing was assessed for 144 hours in a time series and quantified using the average (Mean ± SEM) integrated NIR Intensity (NIRCU x μm^2). MOS killing was assessed for 72 hours and rechallenged with MOS and evaluated for another 72 hours. Data were log transformed and evaluated using a two-way ANOVA using repeated measures.

[002346] The anti-tumor activity of TIL was confirmed in vitro via a tumor killing assay with autologous tumor micro-organospheres (MOS) (FIG. 13). Successful ex vivo expansion of TIL from both dMMR and pMMR EC tumors was accomplished with demonstrated anti-tumor efficacy. These data support clinical investigation of TIL cell therapy in patients with EC.

EXAMPLE 12: PRODUCTION OF A TIL CELL THERAPY FROM ENDOMETRIAL CANCER USING THE FULL-SCALE GEN 2 PROCESS

[002347] Successful full-scale manufacture of endometrial TIL products using the Gen 2 process described in Example 7 was achieved with 4 out of 4 EC tumor samples (Table 51).

TABLE 51. Successful full-scale manufacture of endometrial TIL products.

Final product attributes	**Run 1**	**Run 2**	**Run 3**	**Run 4**	**Expected results**
	END22111	END22133	END22134	END22135	

Purity (cell viability, %)	88.5	95.5	89.1	89.5	≥70%
Dose (TVC)	5.9×10^9	77.1×10^9	2.7×10^9	68.3×10^9	$1 \times 10^9 - 150 \times 10^9$ cells
Identity (% CD45+/CD3+)	96.2	99.4	96.1	99.2	≥90%
Identity (% TROP2+ or Epcam+ tumor cells)	0.06	0.04	0.06	0.08	N/A
Potency (Dynabead-based IFN-γ release)	9410	3940	12,620	6475	N/A

IFN-g, interferon-gamma; TIL, tumor-infiltrating lymphocyte; TVC, total viable cells.

EXAMPLE 13: A PHASE 2, MULTICENTER, OPEN-LABEL STUDY OF LIFILEUCEL (TUMOR-INFILTRATING LYMPHOCYTES [TIL]) IN PARTICIPANTS WITH PREVIOUSLY TREATED ADVANCED ENDOMETRIAL CANCER

[002348] There are currently limited treatment options for advanced endometrial cancer (EC) that has progressed during or after frontline platinum-based chemotherapy and anti-programmed cell death protein-1/programmed death ligand-1 (anti– PD-(L)1 or anti-PDL1 or anti-PD-L1) therapy in a recurrent or advanced setting. Lifileucel, a tumor-infiltrating lymphocyte (TIL) therapy, has demonstrated clinical responses across anti–PD-(L)1 responsive solid tumor types such as melanoma, non-small cell lung, cervical, and head and neck cancers, including in patients who have progressed on or after prior therapy with anti–PD-(L)1 agents. Anti–PD-(L)1 agents are standard of care therapy for patients with EC with both deficient mismatch repair (dMMR) and proficient mismatch repair (pMMR) tumors. This clinical study will evaluate the efficacy and safety of lifileucel in patients with previously treated advanced EC, and will enroll patients with dMMR or pMMR tumors to explore the role of MMR status in response to treatment with lifileucel.

[002349] Disclosed herein is a Phase 2, open-label, single-arm, multicenter study in patients with advanced EC who previously received chemotherapy and an anti–PD-(L)1 agent sequentially or in combination. Key eligibility criteria include histologically confirmed EC including carcinosarcoma, but not uterine sarcoma, that is not amenable to curative treatment with surgery and/or radiation therapy; progression on or after platinum-based chemotherapy and anti–PD(L)-1 therapy or nonresponse or intolerance to those therapies; ≤3 lines of systemic therapy for recurrent, metastatic, or primary unresectable disease with ≤1 line of chemotherapy; documented radiographic disease

progression during or after the last line of therapy; ≥1 measurable lesion(s) in addition to resectable lesion(s) to generate lifileucel; Eastern Cooperative Oncology Group performance status of 0–1; and adequate organ function including adequate cardiopulmonary function. Key exclusion criteria are symptomatic untreated brain metastases, prior organ allograft or cell therapy, and current systemic steroid therapy >10 mg/day of prednisone or another steroid equivalent dose. The lifileucel regimen consists of nonmyeloablative lymphodepletion (cyclophosphamide and fludarabine) followed by a single lifileucel infusion, then by interleukin-2. The primary endpoint is objective response rate (RECIST v1.1). Secondary endpoints include complete response rate, duration of response, disease control rate, progression-free survival, overall survival, and safety. Exploratory endpoints include lifileucel manufacturing feasibility, in vivo T-cell persistence, and correlative biomarkers. The study will be conducted in the United States with planned enrollment of dMMR and pMMR EC patients, with approximately 30 patients for each subtype.

[002350] Overall Design:

[002351] This is a Phase 2, open-label, single-arm, multicenter study of the lifileucel regimen in participants with advanced endometrial cancer who previously received treatment with platinum-based chemotherapy and an anti-PD-1/PD-L1 agent, either sequentially or in combination.

[002352] For each of 2 tumor subtypes (dMMR and pMMR) based on the central laboratory assessment of MMR status, the planned maximum sample size is approximately 30 participants. The Bayesian Posterior Probability will be used to monitor ORR for each tumor subtype while the study is ongoing. Enrollment of either tumor subtype might be stopped early if the Bayesian Posterior Probability crosses the prespecified futility boundary.

[002353] An Independent Data Monitoring Committee (IDMC) will provide oversight of safety considerations during the study for the protection of study participants.

[002354] Brief Summary:

[002355] The purpose of this study is to investigate the efficacy and safety of the lifileucel regimen in participants with previously treated endometrial cancer.

[002356] The length of the study for each participant may be up to 5 years after receiving lifileucel. After Screening, each participant will have surgery to remove a piece of the tumor that will be used to make the lifileucel, followed by a Baseline Visit. Participants will then receive the lifileucel treatment regimen. This includes 2 drugs (cyclophosphamide and fludarabine) for 5 days to decrease lymphocytes in the body, lifileucel infusion (1 day), and up to 4 days of interleukin-2 (IL-2) to boost the activity of the lifileucel (see FIG. 14). Participants will be hospitalized for administration of the

lifileucel infusion and IL-2. Study visits will be every 6 weeks for 6 months, then every 3 months until 5 years after the lifileucel infusion.

[002357] Number of Participants:

[002358] A maximum total sample size of up to approximately 60 participants (30 participants with dMMR tumors and 30 participants with pMMR tumors) will be enrolled and treated. The sample size calculation is based on the null hypothesis of ORR ≤ 10% versus the alternative hypothesis of ORR ≥ 30% for each tumor subtype. Using Bayesian Efficacy Monitoring via Posterior Probability, the operation characteristics show 91% power under the alternative hypothesis and a 6.9% type I error rate (one-sided) under the null hypothesis.

[002359] Intervention Groups and Duration:

[002360] Enrollment in the study for each participant begins with the surgical tumor resection for generation of lifileucel. The autologous lifileucel treatment regimen consists of the following:

	Day									
	-5	**-4**	**-3**	**-2**	**-1**	**0**	**1**	**2**	**3**	**4**
NMA-LD[1]										
Cyclophosphamide (IV, 60 mg/kg/day)[1,2]	X	X								
Mesna (dosing regimen per institutional standard or the package insert)	X	X								
Fludarabine (IV, 25 mg/m^2/day)[1,3]	X	X	X	X	X					
Lifileucel infusion[1,4]						X				
IL-2 (IV, 600,000 IU/kg every 8-12 hours for up to 6 doses)							X[1,5]			

[002361] Abbreviations: CrCl = creatinine clearance; IL-2 = interleukin-2; IV = intravenous; NMA-LD = nonmyeloablative lymphodepletion

Participants may receive bridging therapy between tumor resection and NMA-LD.

[1]Dosing of cyclophosphamide, fludarabine, lifileucel, or IL-2 must not be initiated if the participant requires supplemental oxygen.

[2]Dose reduction is allowed after consultation with the medical monitor.

[3]The fludarabine dose will be adjusted according to CrCl.

[4]If the participant is stable, lifileucel may be infused approximately 24 hours after the last fludarabine dose. If needed, up to 4 additional days of rest are allowed.

[5]IL-2 dosing is initiated approximately 18 to 24 hours after completion of the lifileucel infusion on Day 0 and continues approximately every 8 to 12 hours (but no more than 2 doses per day) for up to a maximum of 6 total doses. Dosing is allowed for up to 4 days following the lifileucel infusion to allow for proper management of IL-2 toxicity, if necessary. Participants meeting any of the criteria to stop IL-2 treatment should not receive any IL-2. If a dose is held because of safety reasons, IL-2 dosing should not be resumed.

[002362] Inclusion Criteria

Participants are eligible to be included in the study only if all of the following criteria apply:

Age

1. Participant must be ≥ 18 years of age at the time of signing the informed consent. Enrollment of participants > 70 years of age may be allowed after discussion with the medical monitor and with consideration of factors including but not limited to performance status, life expectancy, and frailty of the participant.

Type of Participant and Disease Characteristics

2. Participant has a histologically confirmed diagnosis of endometrial carcinoma. All histologies, including carcinosarcoma, will be allowed. Uterine sarcoma will not be allowed.
3. Participant has documented MMR or MSI status as determined by a validated IHC test (http://www.fda.gov/CompanionDiagnostics or consult with the sponsor), PCR, or next-generation sequencing.
4. Participants have advanced endometrial cancer that is not amenable to curative treatment with surgery and/or radiation therapy and received the following previous therapy:
    - Participants must have progressed on or after platinum-based chemotherapy and anti-PD-1/PD-L1 therapy or were nonresponsive or intolerant to platinum-based chemotherapy and anti-PD-1/PD-L1 therapy.

      Participants must have received either 1 prior platinum-based chemotherapy regimen for recurrent, metastatic, or primary unresectable disease or progressed < 1 year after completion of prior adjuvant or neoadjuvant platinum-based chemotherapy. No additional chemotherapy treatments (excluding antibody-drug conjugates [ADCs]) are permitted in the recurrent, metastatic, or primary unresectable disease setting.

Participants must have received 1 prior anti-PD-1/PD-L1 therapy either as monotherapy or in combination.

- Up to 3 lines of systemic therapy for recurrent, metastatic, or primary unresectable disease with no more than 1 line of chemotherapy for recurrent, metastatic, or primary unresectable disease are allowed.

  Targeted therapy other than anti-PD-1/PD-L1 therapy (eg, small molecules, monoclonal antibodies) and/or ADC is permitted either as monotherapy or in combination. Targeted therapy and ADC is counted as a systemic therapy but not counted as 1 line of chemotherapy.

  Hormonal therapy is not considered a line of therapy.

  If an agent was switched to another agent in the same class because of toxicity (eg, cisplatin to carboplatin, paclitaxel to docetaxel), it is not considered 2 lines.

- Participants must have documented radiographic disease progression during or after the last line of therapy.

5. The participant has an ECOG performance status of 0 or 1 and an estimated life expectancy of > 6 months.

6. Participant is assessed as having at least one resectable lesion (or aggregate lesions) with an estimated minimum diameter of 1.5 cm for lifileucel generation.

   It is preferred that the tumor targeted for resection has not been previously irradiated. If it has, the irradiation must have occurred at least 3 months prior to tumor resection and the irradiated lesion(s) must have unequivocal radiographically demonstrated progression after radiation therapy.

7. Following tumor resection for lifileucel generation, the participant will have at least one measurable lesion, as defined by RECIST v1.1, with the following considerations:

   - Lesions in previously irradiated areas (or areas treated with local therapy) should not be selected as target lesions unless subsequent progression has been demonstrated in those lesions and the irradiation/local therapy was completed at least 3 months prior to the tumor resection for lifileucel generation.

   - Lesions that are partially resected for lifileucel generation and are still measurable per RECIST v1.1 may be selected as nontarget lesions but cannot serve as a target lesion for the tumor response assessment.

8. Participant is expected to achieve washout from investigational or anticancer therapy(ies).
9. If the participant has preplanned surgical procedure(s), the procedure will take place at least 14 days (for major operative procedures) prior to the tumor resection. Wound healing will have occurred, and all complications will have resolved at the time of tumor resection.
10. Participant has recovered from all prior anticancer treatment-related AEs to Grade ≤ 1 (per NCI-CTCAE), except for peripheral neuropathy, alopecia, vitiligo, or medically controlled endocrine dysfunction (eg, thyroid or insulin replacement or replacement therapy for adrenocortical insufficiency at ≤ 10 mg/day of prednisone).

    Participants with stable Grade 2 toxicity from prior anticancer therapy must have been discussed with the medical monitor. Participants with immunotherapy-related endocrinopathies stable for at least 6 weeks (eg, hypothyroidism) and controlled with hormonal replacement are allowed.

    Participants with documented Grade ≥ 2 diarrhea or colitis as a result of previous treatment with anti-PD-1/PD-L1 therapy must have been asymptomatic for at least 6 months or had a normal colonoscopy after checkpoint inhibitor treatment, by visual assessment, prior to tumor resection.

[002363] Exclusion Criteria

Participants are excluded from the study if any of the following criteria apply:

Medical Conditions

1. Participant has symptomatic untreated brain metastases. Participants with brain metastases may be considered for study participation with the following considerations:
    - Participants with asymptomatic brain metastases who do not clinically require treatment may be considered for study participation.
    - A participant with historically treated brain metastases (ie, treatment was completed > 28 days prior to consenting for study participation) will be considered for study participation if the participant is clinically stable for ≥ 2 weeks, there are no new or worsening brain lesions via screening MRI, and the participant does not require ongoing corticosteroid treatment (> 10 mg/day prednisone or equivalent).
    - If there are progressive or new brain metastases on the screening MRI, the participant should first receive treatment for them prior to restarting or continuing screening. A participant with recently treated brain metastases (ie, treatment of brain metastases was

completed ≤ 28 days prior to consenting for study participation) may be considered for study participation if the participant is asymptomatic, clinically stable for ≥ 2 weeks, and does not require corticosteroids (> 10 mg/day prednisone or equivalent) by the end of the screening period. Repeat brain imaging is not required after treatment.

2. Participant has an active medical illness(es) that, in the opinion of the investigator, would pose increased risks for study participation, such as systemic infections; coagulation disorders; or other active major medical illnesses of the cardiovascular, respiratory, or immune systems. Participant has evidence of any active viral, bacterial, or fungal infection requiring ongoing systemic treatment or identified during screening.
    - Participants with corrected (ie, percutaneous nephrostomy tubes) urinary tract obstruction must have negative surveillance cultures from externalized tubes within 7 days prior to the start of the NMA-LD preparative regimen. Asymptomatic participants with chronic colonization of indwelling urinary diversion tubes may be eligible after active urinary infection is ruled out and discussion with the medical monitor.
3. Participant has any form of primary immunodeficiency (eg, severe combined immunodeficiency disease [SCID] or AIDS).
4. Participant has a history of hypersensitivity to any component of the study intervention, including, but not limited to, any of the following:
    - NMA-LD (cyclophosphamide, mesna, and fludarabine)
    - Proleukin®, aldesleukin, IL-2
    - Antibiotics used in lifileucel manufacturing and potentially present in the formulated product. *These participants may be eligible if current hypersensitivity has been excluded.*
    - Any component of the lifileucel product formulation, including dimethyl sulfoxide (DMSO), human serum albumin (HSA), IL-2, or dextran 40
5. Participant had another primary malignancy within the previous 3 years (except for those that do not require treatment or have been curatively treated > 1 year ago, and in the judgment of the investigator does not pose a significant risk of recurrence including, but not limited to, non-melanoma skin cancer, ductal carcinoma in situ (DCIS), lobular carcinoma in situ (LCIS), or superficial bladder cancer).

    Radiation-related secondary primary endometrial cancer following radiotherapy for cervical cancer must be excluded.

Prior/Concomitant Therapy

6. Participant has a history of allogeneic organ transplant or any form of cell therapy involving prior conditioning chemotherapy within the past 20 years.

   Participants being retreated with lifileucel are not excluded due to prior NMA-LD on this study.

7. Participant requires systemic steroid therapy > 10 mg/day of prednisone or another steroid equivalent dose.

   Participants receiving steroids as replacement therapy for adrenocortical insufficiency at ≤ 10 mg/day of prednisone or another steroid equivalent dose may be eligible.

8. Participant received or will receive a live or attenuated vaccination within 28 days prior to the start of the NMA-LD preparative regimen.

[002364] 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.

[002365] 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.

[002366] 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.

[002367] 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.

CLAIMS

What is claimed is:

1. A method of treating a subject with endometrial cancer, the method comprising administering expanded tumor infiltrating lymphocytes (TILs) comprising:
   (a) adding a tumor digest or tumor fragments from an endometrial cancer into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from the subject;
   (b) 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 (b) to step (c) occurs without opening the system;
   (c) performing a second expansion by supplementing additional cell culture medium comprising 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 (b) to step (c) occurs without opening the system;
   (d) harvesting the third population of TILs obtained from step (c), wherein the transition from step (c) to step (d) occurs without opening the system;
   (e) transferring the harvested third TIL population from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system;
   (f) cryopreserving the infusion bag comprising the harvested TIL population from step (e) using a cryopreservation process; and
   (g) administering a therapeutically effective dosage of the third population of TILs from the infusion bag in step (f) to the subject.
2. The method of claim 1, wherein the endometrial cancer is metastatic or unresectable.
3. The method of claim 1 or 2, wherein the subject was refractory to or progressed following prior treatment with a PD-1 or PD-L1 inhibitor.
4. The method according to any one of claims 1-3, wherein the subject was refractory to or progressed following prior treatment with chemotherapy.
5. The method of claim 4, wherein the chemotherapy is a platinum chemotherapy and a taxane.
6. The method of claim 5, wherein the platinum chemotherapy is selected from the group consisting of cisplatin, carboplatin, and oxaliplatin.

7. The method of claim 5, wherein the taxane is selected from the group consisting of paclitaxel, albumin-bound paclitaxel, and docetaxel.
8. The method according to any one of claims 1-7, wherein the endometrial cancer is microsatellite instability high (MSI-H).
9. The method according to any one of claims 1-7, wherein the endometrial cancer is mismatch repair deficient (dMMR).
10. The method according to any one of claims 1-7, wherein the endometrial cancer is microsatellite stable (MSS).
11. The method according to any one of claims 1-7, wherein the endometrial cancer is mismatch repair proficient (pMMR).
12. The method according to any one of claims 1-11, wherein the subject is treatment naïve.
13. The method according to according to any one of claims 1-12, comprising the additional step of administering a therapeutically effective dosage of a PD-1 or PD-L1 inhibitor.
14. The method of any one of claims 3-13, wherein the anti-PD-1 or anti-PD-L1 antibody is selected from the group consisting of dostarlimab, nivolumab, pembrolizumab, JS001, TSR-042, pidilizumab, BGB-A317, SHR-1210, REGN2810, MDX-1106, PDR001, anti-PD-l from clone: RMP1-14, an anti-PD-l antibodies disclosed in U.S. Patent No. 8,008,449, durvalumab, atezolizumab, avelumab, and fragments, derivatives, variants, as well as biosimilars thereof.
15. The method according to any one of claims 1-14, further comprising the step of treating the subject with a non-myeloablative lymphodepletion regimen prior to administering the therapeutic population of TILs to the subject.
16. The method of claim 15, 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.
17. The method according to any one of claims 1-16, further comprising the step of treating the subject with an IL-2 regimen starting on the day after administration of the therapeutic population of TILs to the subject.
18. The method of claim 17, 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.
19. The method according to any one of claims 1-18, wherein the first expansion is performed over a period of 12 days or less.
20. The method according to any one of claims 1-19, wherein the second expansion is performed over a period of 12 days or less.
21. The method according to any one of claims 1-20, wherein steps (a) through (d) are performed in about 10 days to about 22 days.

22. The method according to any one of claims 1-20, wherein steps (a) through (d) are performed in about 15 days to about 22 days.
23. The method according to any one of claims 1-20, wherein steps (a) through (d) are performed in about 20 days to about 22 days.
24. The method according to any one of claims 1-23, 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.
25. The method of any one of claims 1-24, 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 cell culture medium.
26. The method according to any one of claims 1-25, wherein the first expansion is performed using a gas permeable container.
27. The method according to any one of claims 1-26, wherein the second expansion is performed using a gas permeable container.
28. A method of expanding tumor infiltrating lymphocytes (TILs) comprising:
    (g) adding a tumor digest or tumor fragments from an endometrial cancer into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from a subject;
    (h) 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 (b) to step (c) occurs without opening the system;
    (i) performing a second expansion by supplementing additional cell culture medium comprising 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 (b) to step (c) occurs without opening the system;
    (j) harvesting the third population of TILs obtained from step (c), wherein the transition from step (c) to step (d) occurs without opening the system;
    (k) transferring the harvested third TIL population from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system; and
    (l) cryopreserving the infusion bag comprising the harvested TIL population from step (e) using a cryopreservation process.
29. The method of claim 28, wherein the tumor digest in step (a) was prepared by incubating a sample of the tumor that was resected from the subject in an enzymatic media.

30. The method of claim 28 or 29, further comprising disrupting the tumor sample mechanically so as to dissociate the tumor sample.
31. The method of claim 30, further comprising purifying the disassociated tumor sample using a density gradient separation.
32. The method according to any one of claims 29-31, wherein the enzymatic media comprises DNase.
33. The method of claim 32, wherein the enzymatic media comprises 30 units/mL of DNase.
34. The method according to any one of claims 29-31, wherein the enzymatic media comprises collagenase.
35. The method of claim 34, wherein the enzymatic media comprises 1.0 mg/mL of collagenase.
36. The method of any one of claims 28-35, wherein the medium in the first expansion and/or the second expansion is free of human serum.
37. The method according to any one of claims 28-36, wherein the first expansion is performed over a period of 12 days or less.
38. The method according to any one of claims 28-37, wherein the second expansion is performed over a period of 12 days or less.
39. The method according to any one of claims 28-38, wherein steps (a) through (d) are performed in about 10 days to about 22 days.
40. The method according to any one of claims 28-38, wherein steps (a) through (d) are performed in about 15 days to about 22 days.
41. The method according to any one of claims 28-38, wherein steps (a) through (d) are performed in about 20 days to about 22 days.
42. The method according to any one of claims 28-41, 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.
43. The method according to any one of claims 28-42, 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 cell culture medium.
44. The method according to any one of claims 28-43, wherein the first expansion is performed using a gas permeable container.
45. The method according to any one of claims 28-44, wherein the second expansion is performed using a gas permeable container.
46. The method according to any one of claims 28-45, wherein the APCs are peripheral blood mononuclear cells (PBMCs).
47. The method of claim 46, wherein the PBMCs are supplemented at a ratio of about 1:25 TIL:PBMCs.

48. A cryopreserved therapeutic population of tumor infiltrating lymphocytes (TILs) produced by a method comprising:

(a) adding a tumor digest or tumor fragments into a closed system, wherein the tumor digest or tumor fragments comprise a first population of TILs and are obtained from a tumor that was resected from a subject having endometrial cancer;

(b) 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 a first period of about 3 to 11 days to obtain the second population of TILs, and wherein the transition from step (a) to step (b) occurs without opening the system;

(c) performing a second expansion by supplementing the cell culture medium 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 a second period of about 7 to 11 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 (b) to step (c) occurs without opening the system;

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

(e) transferring the harvested therapeutic population of TILs from step (d) to an infusion bag, wherein the transfer from step (d) to (e) occurs without opening the system; and

(f) cryopreserving the infusion bag comprising the harvested therapeutic population of TILs from step (e) using a cryopreservation process.

49. The cryopreserved therapeutic population of TILs according to claim 48, wherein the tumor digest in step (a) was prepared by incubating a sample of the tumor that was resected from the subject in an enzymatic media.
50. The cryopreserved therapeutic population of TILs according to claim 48 or 49, further comprising disrupting the tumor sample mechanically so as to dissociate the tumor sample.
51. The cryopreserved therapeutic population of TILs according to claim 50, further comprising purifying the disassociated tumor sample using a density gradient separation.
52. The cryopreserved therapeutic population of TILs according to any one of claims 49-51, wherein the enzymatic media comprises DNase.
53. The cryopreserved therapeutic population of TILs according to claim 52, wherein the enzymatic media comprises 30 units/mL of DNase.

54. The cryopreserved therapeutic population of TILs according to any one of claims 49-51, wherein the enzymatic media comprises collagenase.
55. The cryopreserved therapeutic population of TILs according to claim 54, wherein the enzymatic media comprises 1.0 mg/mL of collagenase.
56. The cryopreserved therapeutic population of TILs according to any one of claims 48-55, wherein the medium in the first expansion and/or the second expansion is free of human serum.
57. The cryopreserved therapeutic population of TILs according to any one of claims 48-56, wherein the therapeutic population of TILs harvested in step (d) comprises sufficient TILs for use in administering a therapeutically effective dosage to a subject.
58. The cryopreserved therapeutic population of TILs according to claim 57, wherein the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^9 to about 5×10^9.
59. The cryopreserved therapeutic population of TILs according to claim 57, wherein the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^9 to about 9×10^{10}.
60. The cryopreserved therapeutic population of TILs according to claim 57, wherein the number of TILs sufficient for administering a therapeutically effective dosage is from about 5×10^9 to about 1×10^{10}.
61. The cryopreserved therapeutic population of TILs according to claim 57, wherein the number of TILs sufficient for administering a therapeutically effective dosage is from about 1×10^{10} to about 5×10^{10}.
62. The cryopreserved therapeutic population of TILs according to any one of claims 48-61, wherein the APCs are peripheral blood mononuclear cells (PBMCs).
63. The cryopreserved therapeutic population of TILs according to claim 62, wherein the PBMCs are supplemented at a ratio of about 1:25 TIL:PBMCs.
64. The cryopreserved therapeutic population of TILs according to any one of claims 48-63, wherein the therapeutic population of TILs harvested in step (d) exhibits an increased subpopulation of CD8+ cells relative to the first and/or second population of TILs.
65. The cryopreserved therapeutic population of TILs according to any one of claims 48-64, wherein the first expansion in step (b) and the second expansion in step (c) are each individually performed within a period of 11 days.
66. The cryopreserved therapeutic population of TILs according to any one of claims 48-65, wherein steps (a) through (e) are performed in about 10 days to about 22 days.
67. The cryopreserved therapeutic population of TILs according to any one of claims 48-65, wherein steps (a) through (e) are performed in about 15 days to about 22 days.

68. The cryopreserved therapeutic population of TILs according to any one of claims 48-65, wherein steps (a) through (e) are performed in about 20 days to about 22 days.
69. The cryopreserved therapeutic population of TILs according to any one of claims 48-68, wherein the tumor digest is a cryopreserved tumor digest.