What is claimed is:

1. Use of VEGF-C in the manufacture of a medicament for inducing lymphangiogenesis in a subject, wherein the VEGF-C comprises a minor-mature form of VEGF-C.

2. The use of claim 1, wherein the VEGF-C comprises a dimer.

3. The use of claim 2, wherein the dimer comprises the minor mature form of VEGF-C in each monomer.

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

(i) the VEGF-C comprises a mutated variant of the minor mature form of VEGF-C; and/or

(ii) the VEGF-C comprises the amino acid substitution of C137A, numbered according to SEQ ID NO: 725.

5. The use of any one of claims 1-4, wherein the VEGF-C comprises the amino acid sequence of SEQ ID NO: 740, or an amino acid sequence having at least 85% sequence identity thereto.

6. The use of any one of claims 1-5, wherein the VEGF-C comprises the amino acid sequence of SEQ ID NO: 736, or an amino acid sequence with at least 95% or 99% sequence identity thereto.

7. The use of any one of claims 1-6, wherein the VEGF-C comprises:

(i) a linker; and/or

(ii) a his tag.

8. The use of claim 7, wherein the linker is:

(a) a glycine-serine linker; and/or

(b) present C-terminal of SEQ ID NO: 736, or a sequence with at least 95% or 99% sequence identity thereto.

9. The use of any one of claims 1-8, wherein the VEGF-C comprises the amino acid sequence of SEQ ID NO: 735, or an amino acid sequence with at least 95% or 99% sequence identity thereto.

10. The use of any one of claims 1-9, wherein induction of lymphangiogenesis:

(i) comprises an increase in the level of lymphatic endothelial cells (LECs) compared to a reference level prior to administration of the VEGF-C, optionally wherein the level of LECs is increased by at least 10%, 20%, 30%, 40%, 50%, 60, 70%, 75%, 80%, 85%, 90%, 95%, 100%, or 200% as compared to the reference level; and/or

(ii) results in at least 50 LECs per milligram of tissue.

11. The use of any one of claims 1-10, which recruits T cells, optionally wherein the T cells comprise naïve T cells.

12. The use of claim 11, wherein recruitment of T cells comprises an increase in the level of T cells, optionally wherein the level of T cells is increased by at least 10%, 20%, 30%, 40%, 50%, 60, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 200%, or 300% as compared to a reference level prior to administration of the VEGF-C.

13. The use of any one of claims 1-12, wherein the subject has or has been diagnosed with having a disease, disorder, or condition.

14. A plurality of compositions, comprising:

a first composition comprising:

a biomaterial and a minor mature form of VEGF-C peptide; and

a second composition comprising:

a viral vector.

15. A composition, comprising:

a biomaterial; and

a minor mature form of VEGF-C peptide comprising the amino acid sequence of SEQ ID NO: 741, or an amino acid sequence with at least 80%, 85%, 90%, 95%, or 99% sequence identity thereto, provided that the amino acid at position 26 of SEQ ID NO: 741 is Alanine (A).

16. Use of the composition of claim 15 in the manufacture of a medicament for transducing cells of a subject, comprising:

use of the composition, and

use of a viral vector or a nucleic acid comprising a transgene to the subject.

17. Use of a composition comprising a viral vector or a nucleic acid comprising a transgene in the manufacture of a medicament for treating a disease, disorder or condition in a subject, wherein the use comprises:

use of the composition of claim 15; and

use of the viral vector or a nucleic acid comprising a transgene.

18. Use of a composition comprising a viral vector or a nucleic acid comprising a transgene in the manufacture of a medicament for transducing cells or treating a disease, disorder or condition in a subject, wherein the subject has previously received the composition of claim 15, in an amount sufficient to induce lymphangiogenesis and/or recruitment of T cells to a site in the subject.

19. The plurality of compositions of claim 14, or the use of any one of claims 16-18, wherein:

(i) the viral vector or nucleic acid is comprised in a second composition;

(ii) the viral vector comprises a lentivirus, retrovirus, adenovirus, adeno-associated virus, or herpes virus;

(iii) the viral vector comprises an expression vector comprising a nucleotide sequence encoding: a chimeric antigen receptor (CAR), an engineered TCR, a cytokine, a chemokine, an shRNA, or a polypeptide engineered to target a tumor antigen;

(iv) the viral vector encodes a CAR that comprises an antigen binding domain, a transmembrane domain, a costimulatory signaling region, and a signaling domain, wherein:

(a) the antigen binding domain binds an antigen selected from the group consisting of CD19, CD123, CD22, CD20, EGFRvIII, BCMA, Mesothelin, CD33, CLL-1, and any combination thereof;

(b) the transmembrane domain comprises a CD8 hinge;

(c) the costimulatory signaling region is selected from a 4-1BB or CD28 costimulatory signaling domain; and/or

(d) the signaling domain comprises a CD3 zeta signaling domain.

20. The plurality of composition of 14 or 19, the use of any one of claims 16-18 or 19, which further comprises a cell activation agent.

21. An antibody molecule that binds CD28, comprising a heavy chain variable region (VH) comprising a heavy chain complementarity determining region 1 (HCDR1), a HCDR2, and a HCDR3, and a light chain variable region (VL) comprising a light chain complementarity determining region 1 (LCDR1), a LCDR2, and a LCDR3, wherein:

(i) the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprise the amino acid sequences of SEQ ID NOs: 538, 539, 540, 530, 531, and 532, respectively;

(ii) the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprise the amino acid sequences of SEQ ID NOs: 541, 539, 540, 530, 531, and 532, respectively;

(iii) the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprise the amino acid sequences of SEQ ID NOs: 542, 543, 540, 533, 534, and 535, respectively; or

(iv) the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprise the amino acid sequences of SEQ ID NOs: 544, 545, 546, 536, 534, and 532, respectively.

22. The antibody molecule of claim 21, comprising:

(i) a VH comprising the amino acid sequence of SEQ ID NO: 547 or 548, or a sequence with at least 95% sequence identity to SEQ ID NO: 547 or 548;

(ii) a VL comprising the amino acid sequence of SEQ ID NO: 537, or a sequence with at least 95% sequence identity thereto;

(iii) a VH comprising the amino acid sequence of SEQ ID NO: 547 or a sequence with at least 95% sequence identity thereto, and a VL comprising the amino acid sequence of SEQ ID NO: 537, or a sequence with at least 95% sequence identity thereto; or

(iv) a VH comprising the amino acid sequence of SEQ ID NO: 548 or a sequence with at least 95% sequence identity thereto, and a VL comprising the amino acid sequence of SEQ ID NO: 537, or a sequence with at least 95% sequence identity thereto.

23. A multispecific binding molecule comprising:

(i) an anti-CD3 binding domain, and

(ii) a costimulatory molecule binding domain, wherein the costimulatory binding domain comprises an anti-CD28 binding domain comprising the antibody molecule of claim 21 or 22.

24. The plurality of compositions of claim 23, the use of claim 23, wherein the cell activation agent:

(a) comprises an agent that stimulates CD3/TCR complex and/or an agent that stimulates a costimulatory molecule and/or growth factor receptor;

(b) is a multispecific binding molecule comprising: (i) an anti-CD3 binding domain, and (ii) a costimulatory molecule binding domain (e.g., an anti-CD2 binding domain or an anti-CD28 binding domain); and/or

(c) the amino acid sequence of any heavy chain provided in Table 20, or an amino acid sequence with at least 95% sequence identity thereto; and/or the amino acid sequence of any light chain provided in Table 20, or an amino acid sequence with at least 95% sequence identity thereto.

25. The plurality of compositions of claim 24, the use of claim 24, or the multispecific binding molecule of claim 23, wherein the multispecific binding molecule comprises:

(i) a first polypeptide comprising from N-terminal to C-terminal: VH of the costimulatory molecule binding domain, CH1, CH2, CH3, VH of the anti-CD3 binding domain, and VL of the anti-CD3 binding domain; and a second polypeptide comprising from N-terminal to C-terminal: VL of the costimulatory molecule binding domain and CL;

(ii) a first polypeptide comprising from N-terminal to C-terminal: VH of the anti-CD3 binding domain, VL of the anti-CD3 binding domain, VH of the costimulatory molecule binding domain, CH1, CH2, and CH3; and a second polypeptide comprising from N-terminal to C-terminal: VL of the costimulatory molecule binding domain and CL; or

(iii) a first polypeptide comprising from N-terminal to C-terminal: VH of the costimulatory molecule binding domain, CH1, VH of the anti-CD3 binding domain, VL of the anti-CD3 binding domain, CH2, and CH3; and a second polypeptide comprising from N-terminal to C-terminal: VL of the costimulatory molecule binding domain and CL.

26. The plurality of compositions of claim 24 or 25, the use of claim 24 or 25, or the multispecific binding molecule of claim 23 or 25, wherein the anti-CD3 binding domain comprises a HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 comprising the amino acid sequences of:

(i) SEQ ID NOs: 488, 486, 487, 477, 478, and 479, respectively;

(ii) SEQ ID NOs: 489, 490, 487, 480, 481, and 482, respectively;

(iii) SEQ ID NOs: 491, 492, 493, 483, 481, and 479, respectively;

(iv) SEQ ID NOs: 485, 486, 487, 477, 478, and 479, respectively;

(v) SEQ ID NOs: 431, 429, 430, 420, 421, and 422, respectively;

(vi) SEQ ID NOs: 432, 433, 430, 423, 424, and 425, respectively;

(vii) SEQ ID NOs: 434, 435, 436, 426, 424, and 422, respectively;

(viii) SEQ ID NOs: 428, 429, 430, 420, 421, and 422, respectively;

(ix) SEQ ID NOs: 450, 448, 449, 438, 439, and 440, respectively;

(x) SEQ ID NOs: 451, 452, 449, 441, 442, and 443, respectively;

(xi) SEQ ID NOs: 453, 454, 455, 444, 442, and 440, respectively;

(xii) SEQ ID NOs: 447, 448, 449, 438, 439, and 440, respectively;

(xii) SEQ ID NOs: 471, 448, 470, 458, 459, and 460, respectively;

(xiv) SEQ ID NOs: 472, 452, 470, 461, 462, and 463, respectively;

(xv) SEQ ID NOs: 473, 454, 474, 464, 465, and 466, respectively; or

(xvi) SEQ ID NOs: 469, 448, 470, 458, 459, and 460, respectively.

27. The plurality of compositions of any one of claims 24-26, the use of any one of claims 24-26, wherein the costimulatory molecule binding domain comprises an anti-CD28 binding domain.

28. The plurality of compositions of claim 27, the use of claim 27, or the multispecific binding molecule of any one of claims 23, 25, or 26, wherein:

(i) the anti-CD3 binding domain comprises:

(a) a VH comprising the amino acid sequence of any one of SEQ ID NOs: 437, 456, 457, 475, 476, or 494, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of any one of SEQ ID NOs: 427, 445, 446, 467, 468, or 484, or an amino acid sequence at least 95% identical thereto;

(b) a VH comprising the amino acid sequence of SEQ ID NO: 494, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of SEQ ID NO: 484, or an amino acid sequence at least 95% identical thereto;

(c) a VH comprising the amino acid sequence of SEQ ID NO: 437, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of SEQ ID NO: 427, or an amino acid sequence at least 95% identical thereto;

(d) a VH comprising the amino acid sequence of SEQ ID NO: 456, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of SEQ ID NO: 445, or an amino acid sequence at least 95% identical thereto;

(e) a VH comprising the amino acid sequence of SEQ ID NO: 457, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of SEQ ID NO: 446, or an amino acid sequence at least 95% identical thereto;

(f) a VH comprising the amino acid sequence of SEQ ID NO: 475, or an amino acid sequence at least 95% identical thereto; and/or a VL comprising the amino acid sequence of SEQ ID NO: 467, or an amino acid sequence at least 95% identical thereto;

(g) a VH comprising the amino acid sequence of SEQ ID NO: 476, or an amino acid sequence at least 95% identical thereto; and/or (b) a VL comprising the amino acid sequence of SEQ ID NO: 468, or an amino acid sequence at least 95% identical thereto; and/or

(ii) the anti-CD28 binding domain comprises a VH comprising the amino acid sequence of SEQ ID NO: 547 or 548, or a sequence with at least 95% sequence identity thereto, and a VL

comprising the amino acid sequence of SEQ ID NO: 537, or a sequence with at least 95% sequence identity thereto; and the anti-CD3 binding domain comprises a VH comprising the amino acid sequence of SEQ ID NO: 494, or an amino acid sequence at least 95% identical thereto; and a VL comprising the amino acid sequence of SEQ ID NO: 484, or an amino acid sequence at least 95% identical thereto.

29. The plurality of compositions of claim 27 or 28, the use of claim 27 or 28, or the multispecific binding molecule of any one of claims 23, 25, 26, or 28, wherein:

(i) the anti-CD28 binding domain is a Fab and the anti-CD3 binding domain is an scFv or a VH linked to a VL by a linker, optionally a glycine-serine linker such as a $(G_4S)_4$ linker; and/or

(ii) the anti-CD28 binding domain is situated N-terminal to the anti-CD3 binding domain, wherein an Fc region is situated between the anti-CD28 binding domain and the anti-CD3 binding domain.

30. The plurality of compositions of any one of claims 24-29, the use of any one of claims 24-29, or the multispecific binding molecule of any one of claims 23, 25, 26, 28, or 29, wherein the multispecific binding molecule comprises an Fc region comprising:

(i) a L234A, L235A, S267K, and P329A mutation (LALASKPA), numbered according to the Eu numbering system;

(ii) a L234A, L235A, and P329G mutation (LALAPG), numbered according to the Eu numbering system;

(iii) a G237A, D265A, P329A, and S267K mutation (GADAPASK), numbered according to the Eu numbering system;

(iv) a L234A, L235A, and G237A mutation (LALAGA), numbered according to the Eu numbering system;

(v) a D265A, P329A, and S267K mutation (DAPASK), numbered according to the Eu numbering system;

(vi) a G237A, D265A, and P329A mutation (GADAPA), numbered according to the Eu numbering system;

(vii) a L234A, L235A, and P329A mutation (LALAPA), numbered according to the Eu numbering system;

(viii) an amino acid sequence of any of the Fc regions in Table 20 or an amino acid sequence having at least 95% identity thereto; or

(ix) the amino acid sequence of SEQ ID NO: 886, or amino acid sequence at least 95% identical thereto.

31. The plurality of compositions of any one of claims 24-30, the use of any one of claims 26-32, or the multispecific binding molecule of any one of claims 23, 25, 26, or 28-30, wherein the multispecific binding molecule comprises:

(i) a heavy chain comprising the amino acid sequence of any of SEQ ID NOs: 726, 893, or 895, or an amino acid sequence having at least 95% sequence identity thereto; and/or a light chain comprising the amino acid sequence of any of SEQ ID NOs: 728, 730, 892, or 894, or an amino acid sequence having at least 95% sequence identity thereto;

(ii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 726 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 728, or an amino acid sequence having at least 95% sequence identity thereto;

(iii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 726 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 730, or an amino acid sequence having at least 95% sequence identity thereto;

(iv) a heavy chain comprising the amino acid sequence of SEQ ID NO: 1416 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 728, or an amino acid sequence having at least 95% sequence identity thereto;

(v) a heavy chain comprising the amino acid sequence of SEQ ID NO: 1416 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 730, or an amino acid sequence having at least 95% sequence identity thereto;

(vi) a heavy chain comprising the amino acid sequence of SEQ ID NO: 893 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the

amino acid sequence of SEQ ID NO: 892, or an amino acid sequence having at least 95% sequence identity thereto;

(vii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 1417 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 892, or an amino acid sequence having at least 95% sequence identity thereto; or

(viii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 895 or an amino acid sequence having at least 95% sequence identity thereto, and a light chain comprising the amino acid sequence of SEQ ID NO: 894, or an amino acid sequence having at least 95% sequence identity thereto.

32. The use of any one of claims 17-20 or 24-31, which further comprises use of:

(i) a Tet2 inhibitor, optionally wherein the Tet2 inhibitor comprises: (1) a gene editing system targeted to one or more sites within the gene encoding Tet2, or its corresponding regulatory elements; (2) a nucleic acid (e.g., an siRNA or shRNA) that inhibits expression of Tet2; (3) a protein (e.g., a dominant negative, e.g., catalytically inactive) Tet2, or a binding partner of Tet2 (e.g., a dominant negative binding partner of Tet2); (4) a small molecule that inhibits expression and/or function of Tet2; (5) a nucleic acid encoding any of (1)-(3); or (6) any combination of (1) –(5); and/or

(ii) a ZBTB32 inhibitor, optionally wherein the ZBTB32 inhibitor comprises: (1) a gene editing system targeting the ZBTB32 gene or one or more components thereof; (2) a nucleic acid encoding one or more components of the gene editing system; or (3) a combination of (1) and (2).

33. The use of any one of claims 13, 18-20, or 24-32, wherein the disease, disorder, or condition comprises:

(i) a cancer;

(ii) a hematological cancer;

(iii) a hematological cancer, wherein the hematological cancer comprises a leukemia or lymphoma;

(iv) a hematological cancer chosen from chronic lymphocytic leukemia (CLL), mantle cell lymphoma (MCL), multiple myeloma, acute lymphoid leukemia (ALL), Hodgkin lymphoma, B-cell acute lymphoid leukemia (BALL), T-cell acute lymphoid leukemia (TALL), small lymphocytic leukemia (SLL), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma (DLBCL), DLBCL associated with chronic inflammation, chronic myeloid leukemia, myeloproliferative neoplasms, follicular lymphoma, pediatric follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma (extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue), Marginal zone lymphoma, myelodysplasia, myelodysplastic syndrome, non-Hodgkin lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, splenic marginal zone lymphoma, splenic lymphoma/leukemia, splenic diffuse red pulp small B-cell lymphoma, hairy cell leukemia-variant, lymphoplasmacytic lymphoma, a heavy chain disease, plasma cell myeloma, solitary plasmocytoma of bone, extraosseous plasmocytoma, nodal marginal zone lymphoma, pediatric nodal marginal zone lymphoma, primary cutaneous follicle center lymphoma, lymphomatoid granulomatosis, primary mediastinal (thymic) large B-cell lymphoma, intravascular large B-cell lymphoma, ALK+ large B-cell lymphoma, large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease, primary effusion lymphoma, B-cell lymphoma, acute myeloid leukemia (AML), or unclassifiable lymphoma;

(v) a solid cancer;

(vi) a solid cancer chosen from: one or more of mesothelioma, malignant pleural mesothelioma, non-small cell lung cancer, small cell lung cancer, squamous cell lung cancer, large cell lung cancer, pancreatic cancer, pancreatic ductal adenocarcinoma, esophageal adenocarcinoma , breast cancer, glioblastoma, ovarian cancer, colorectal cancer, prostate cancer, cervical cancer, skin cancer, melanoma, renal cancer, liver cancer, brain cancer, thymoma, sarcoma, carcinoma, uterine cancer, kidney cancer, gastrointestinal cancer, urothelial cancer, pharynx cancer, head and neck cancer, rectal cancer, esophagus cancer, or bladder cancer, or a metastasis thereof; or

(vii) an autoimmune disease.

34. The plurality of compositions of claim 14, or the use of any one of claims 17-20 or 24-33, wherein the viral vector or the nucleic acid encodes:

(i) a first CAR that binds to a B cell antigen and a second CAR that binds to (a) a solid tumor antigen, (b) a myeloid tumor antigen, or (c) an antigen of a hematological tumor not of B-cell lineage; or

(2) a CAR that comprises a first binding domain that binds to a B cell antigen and a second binding domain that binds to (a) a solid tumor antigen, (b) a myeloid tumor antigen, or (c) an antigen of a hematological tumor not of B-cell lineage.

35. The use of any one of claims 18-20, or 26-34, wherein the disease, disorder or condition is an autoimmune disease, and wherein the viral vector or nucleic acid encodes a CAR that binds to a B cell antigen, e.g., CD 19, CD20, CD22, CD123, FcRn5, FcRn2, BCMA, CS-1 and CD138.