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(12) **United States Patent**
Ostertag et al.(10) **Patent No.:** US 12,385,061 B2
(45) **Date of Patent:** Aug. 12, 2025(54) **COMPOSITIONS AND METHODS FOR CHIMERIC LIGAND RECEPTOR (CLR)-MEDIATED CONDITIONAL GENE EXPRESSION**(71) Applicant: **Poseida Therapeutics, Inc.**, San Diego, CA (US)(72) Inventors: **Eric M. Ostertag**, San Diego, CA (US); **Devon Shedlock**, San Diego, CA (US)(73) Assignee: **Poseida Therapeutics, Inc.**, San Diego, CA (US)

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<i>A61K 40/42</i>	(2025.01)
<i>A61P 7/04</i>	(2006.01)
<i>C07K 14/725</i>	(2006.01)
<i>C07K 16/28</i>	(2006.01)
<i>CI2N 9/06</i>	(2006.01)
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CPC	<i>CI2N 15/85</i> (2013.01); <i>A61K 40/11</i> (2025.01); <i>A61K 40/31</i> (2025.01); <i>A61K 40/40</i> (2025.01); <i>A61K 40/4215</i> (2025.01); <i>A61P 7/04</i> (2018.01); <i>C07K 14/7051</i> (2013.01); <i>C07K 16/2878</i> (2013.01); <i>CI2N 9/003</i> (2013.01); <i>CI2N 9/644</i> (2013.01); <i>CI2Y 105/01003</i> (2013.01); <i>CI2Y 304/21022</i> (2013.01); <i>C07K 2319/02</i> (2013.01); <i>C07K 2319/03</i> (2013.01); <i>CI2N 2830/002</i> (2013.01)
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(58) **Field of Classification Search**

None

See application file for complete search history.

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Primary Examiner — Christian L Fronda(74) *Attorney, Agent, or Firm* — Haley Giuliano LLP;
Brian M. Gummow(57) **ABSTRACT**

Disclosed are composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a receptor construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous receptor, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic sequence of a cell, the exogenous reporter is expressed, and wherein the exogenous reporter, upon binding a ligand, transduces an intracellular signal that targets the inducible promoter of (a) to modify gene expression. Methods for introducing compositions into cells and the use of the resultant cells in adoptive cell therapies are also provided.

14 Claims, 20 Drawing Sheets**Specification includes a Sequence Listing.**

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FIGURE 1A

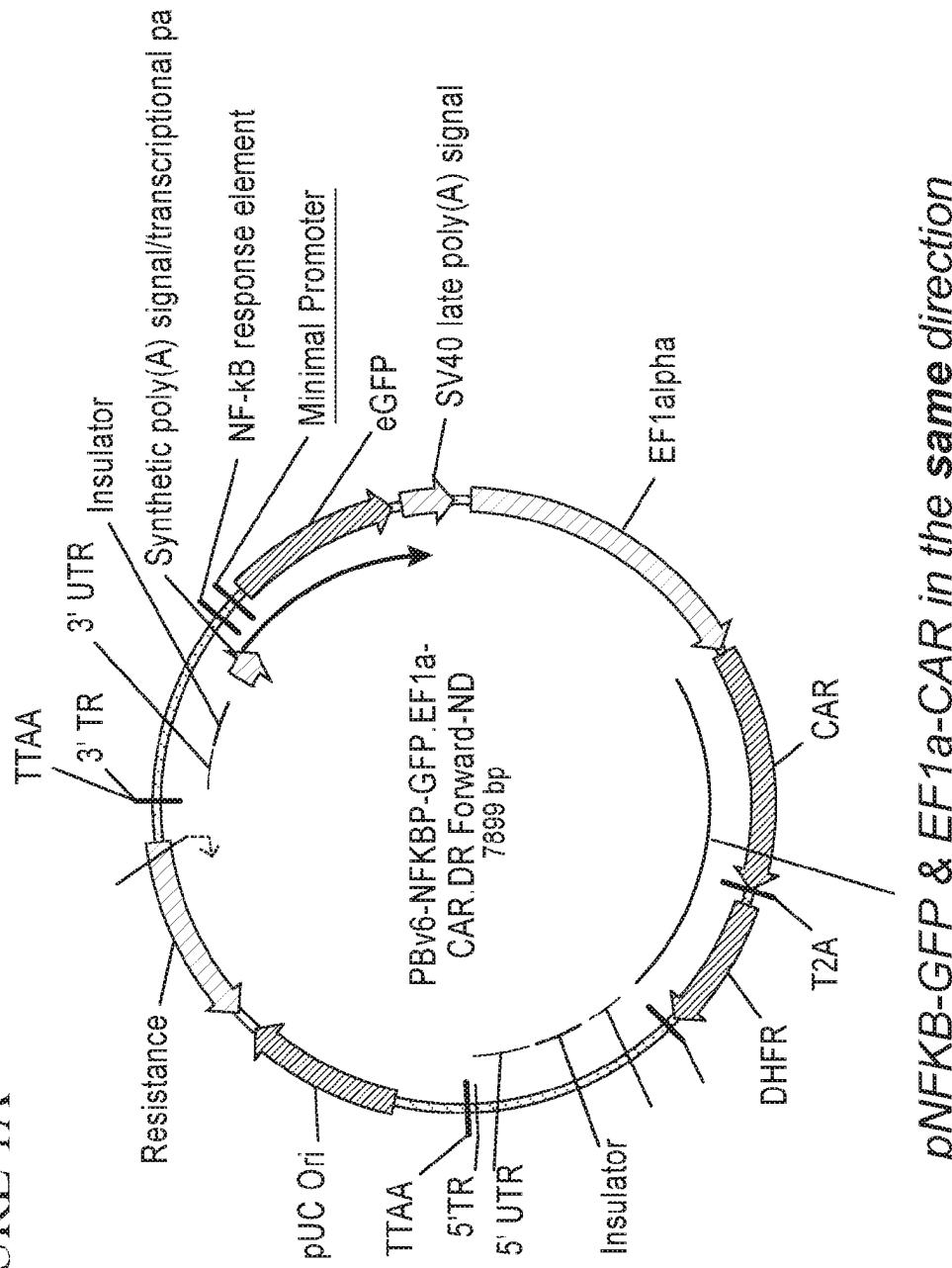


FIGURE 1B

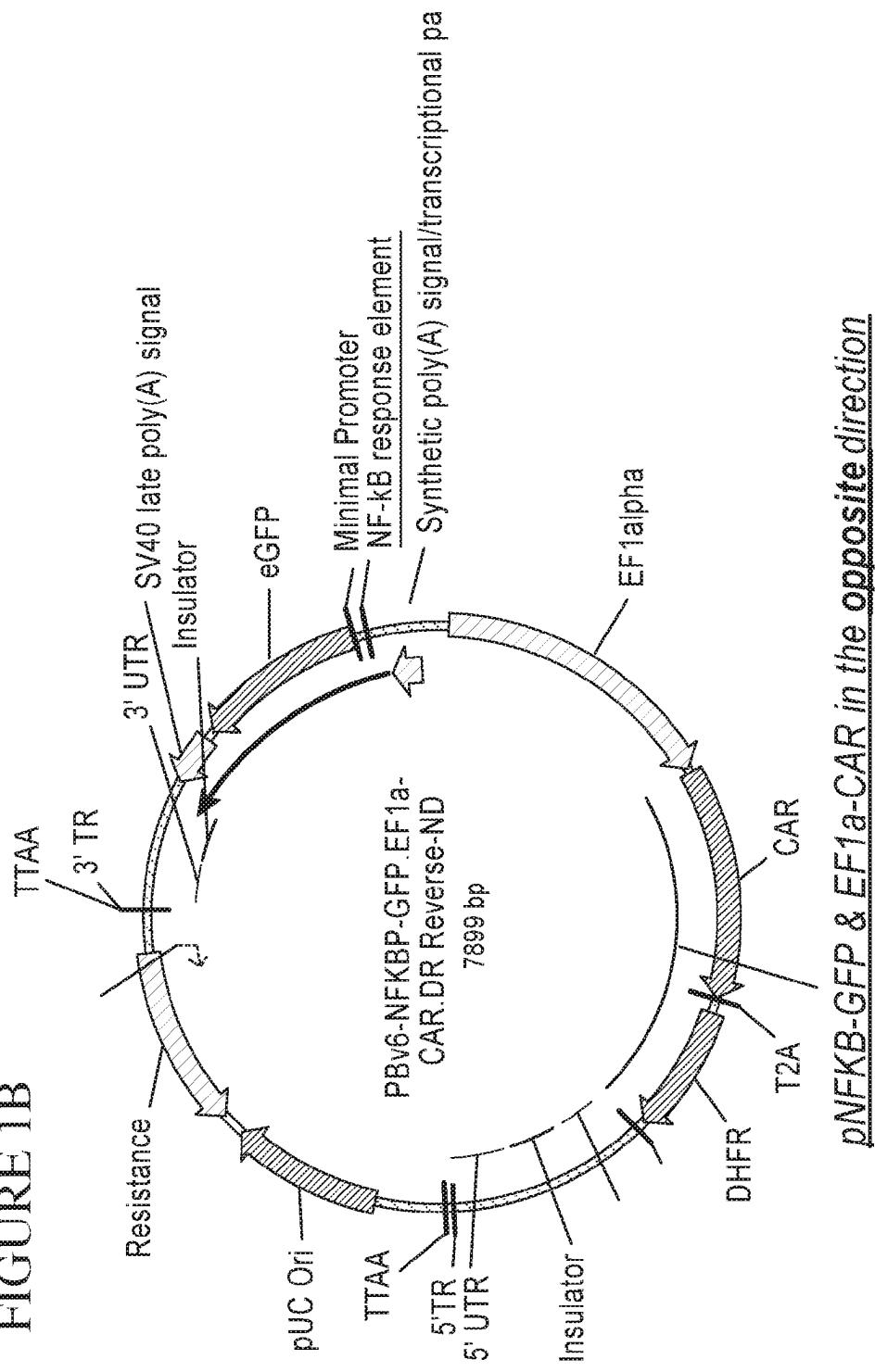
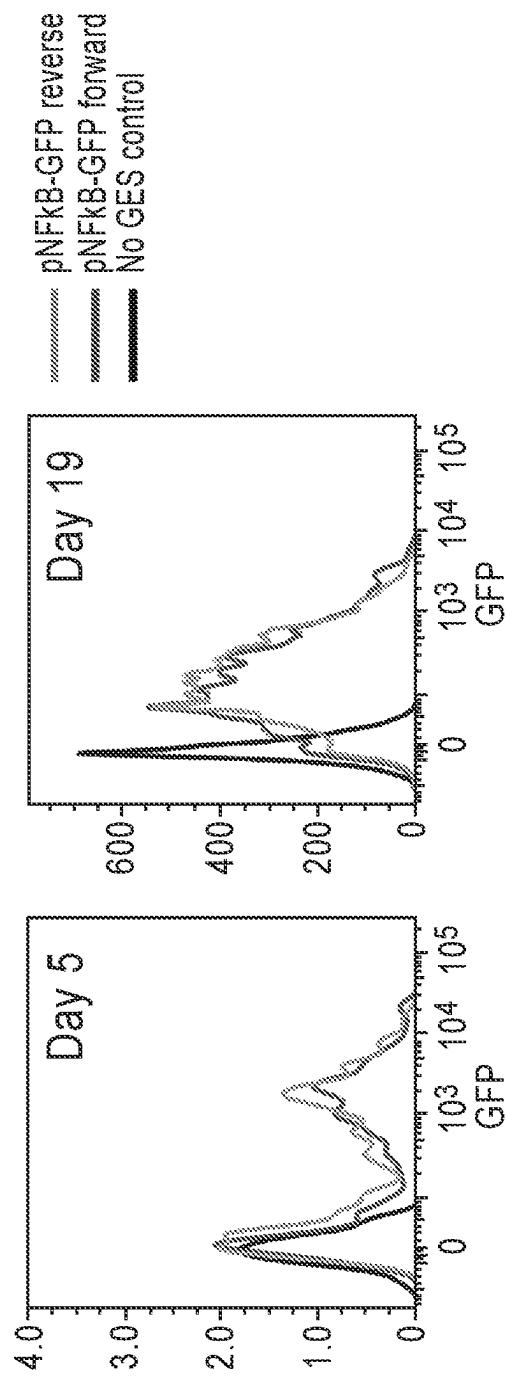


FIGURE 2



- At Day 5 post T cell activation (Day 5), T cells are proliferating and are highly stimulated; GFP expression is strong since NFkB activity is high
- By Day 19, T cells are almost fully resting, GFP expression is significantly lower than Day 5 (~1/8 MFI), since NFkB activity is low
- GFP expression is still observed at Day 19, which may due to the long half life of GFP protein (~30hr), or, basal level of NFkB activity through TCR, CAR, cytokine, growth factor, etc...

FIGURE 3

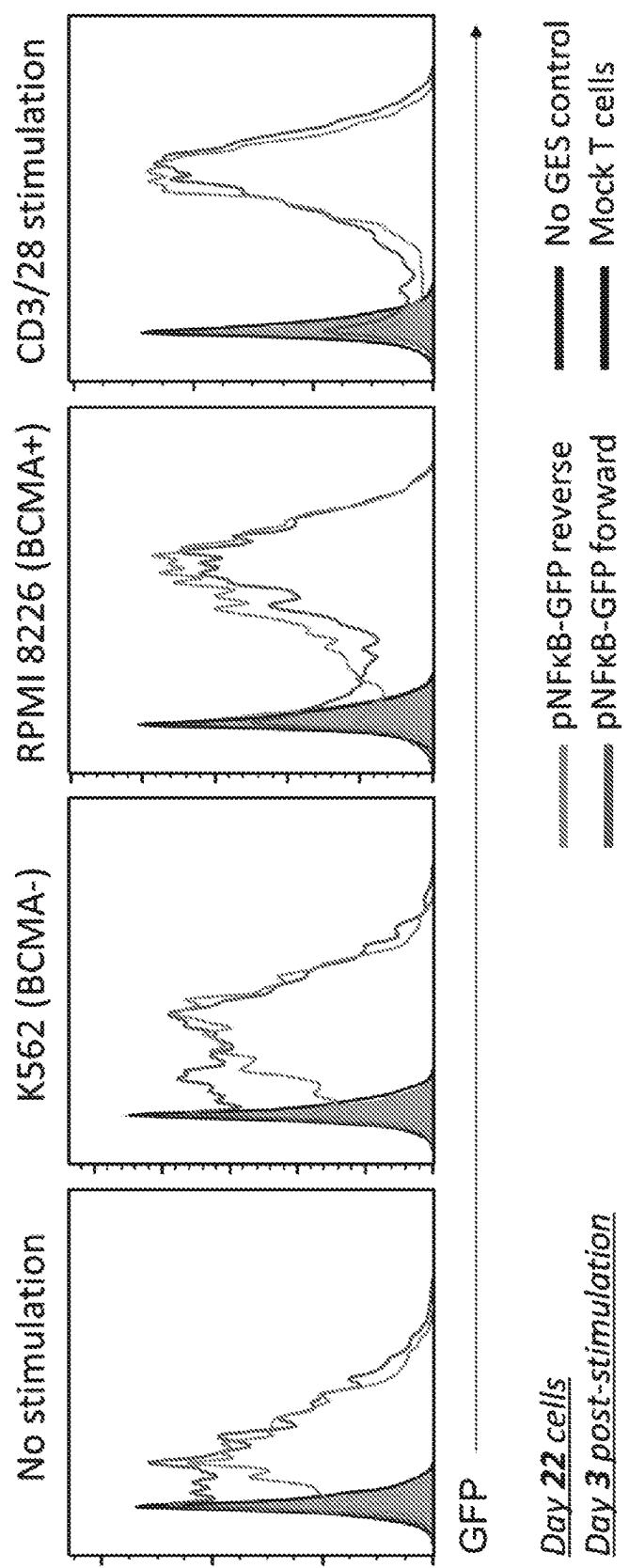


FIGURE 4

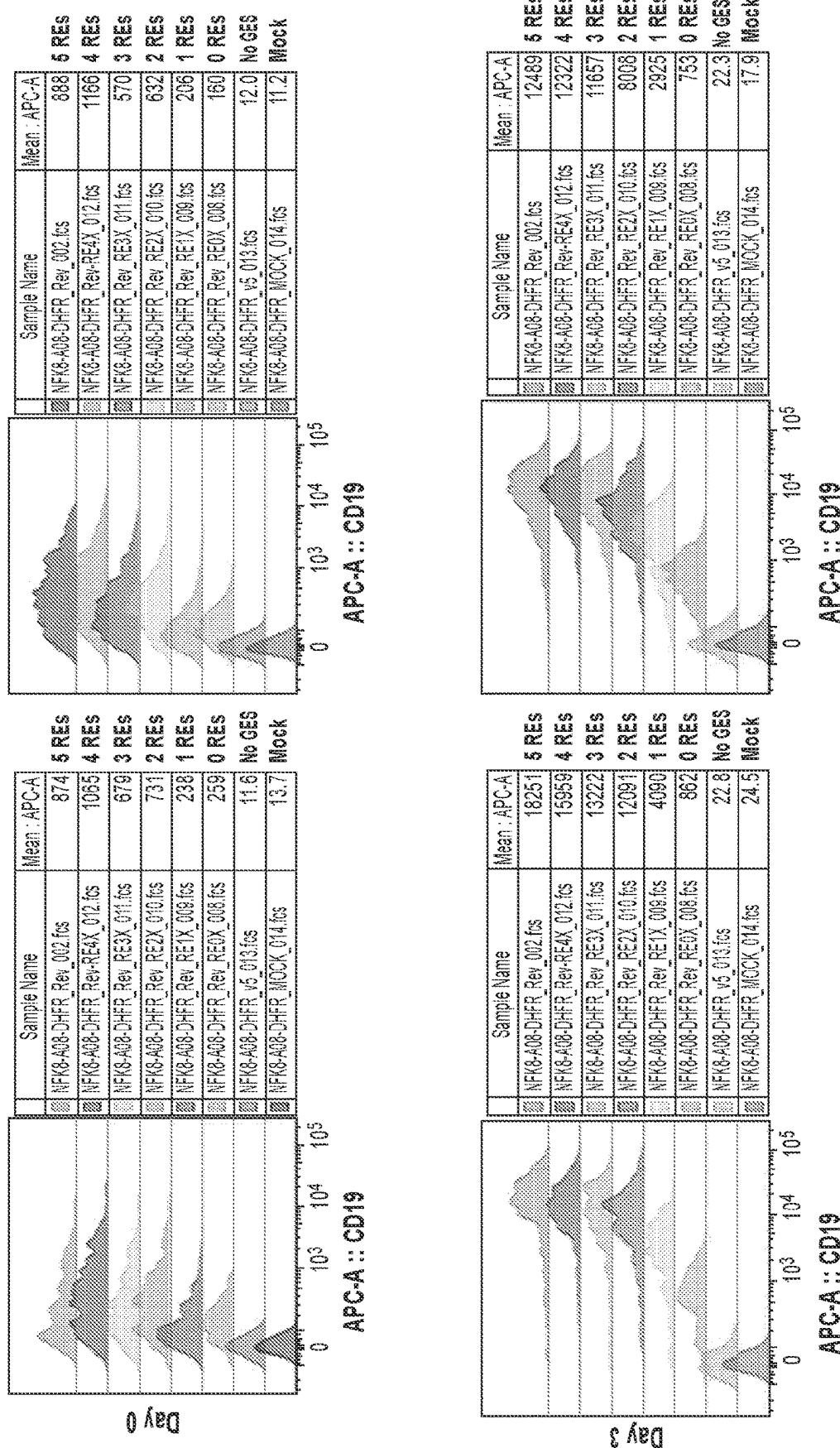


FIGURE 4 (cont.)

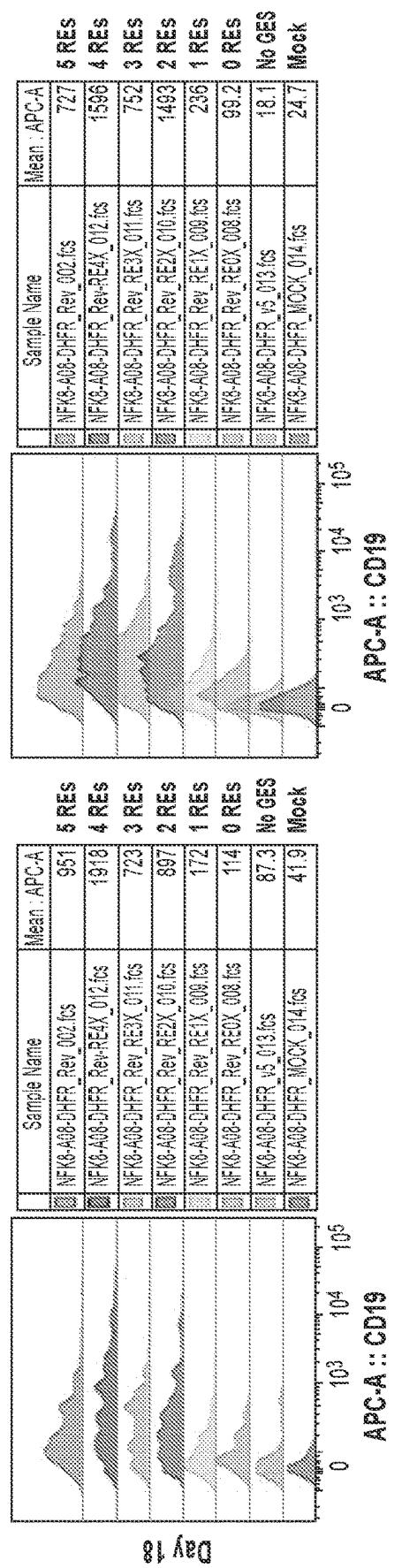


FIGURE 4 (cont.)

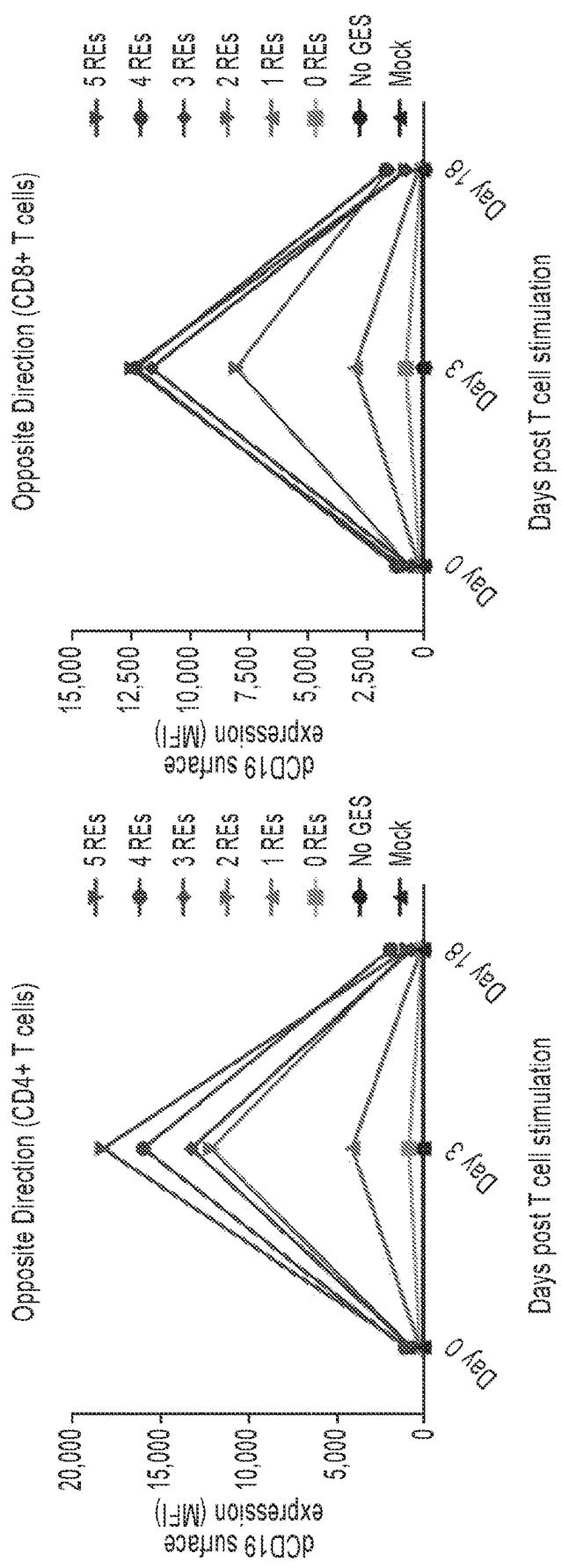


FIGURE 5

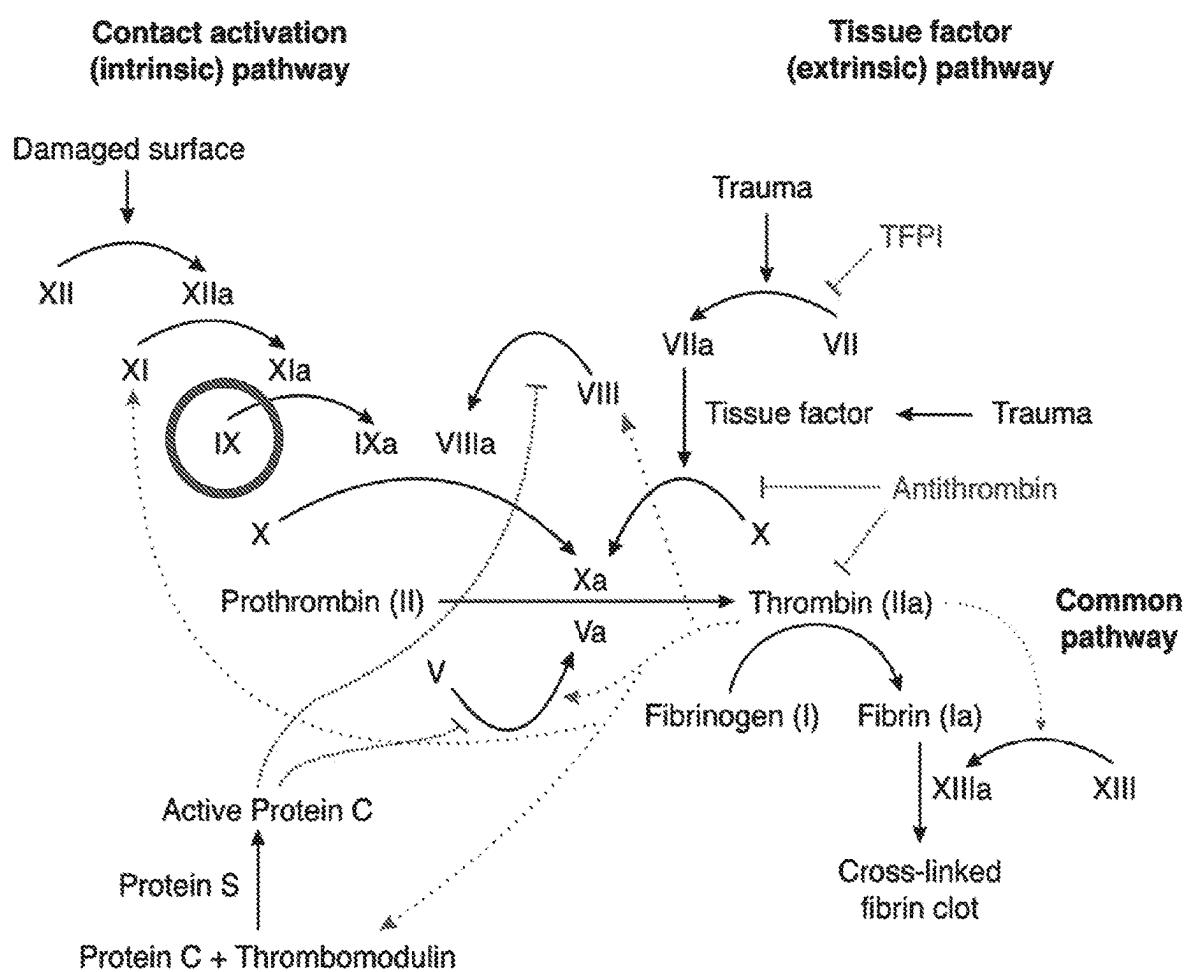


FIGURE 6

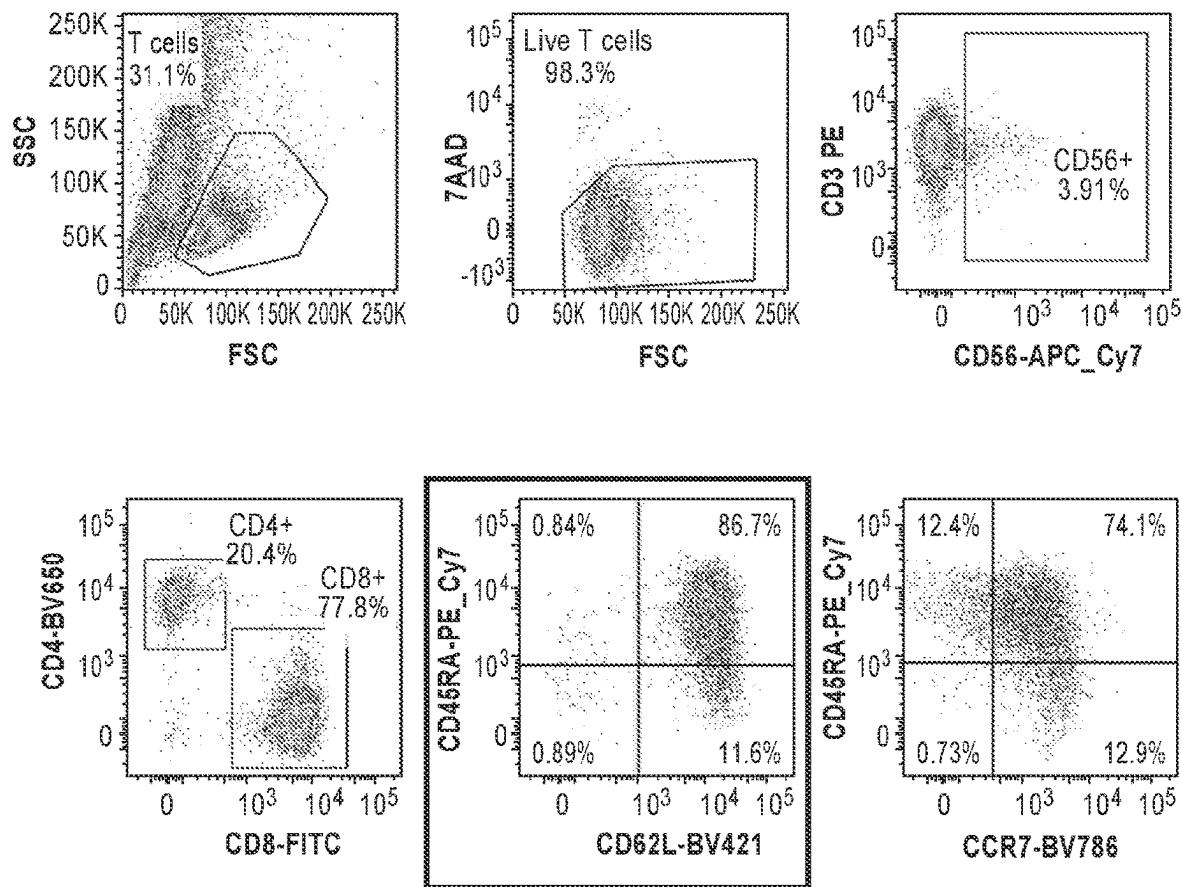


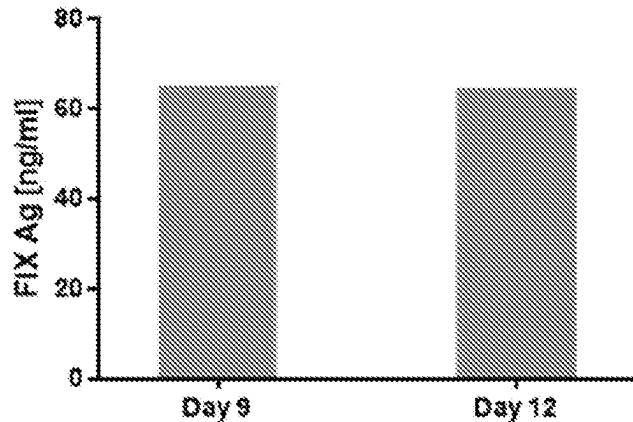
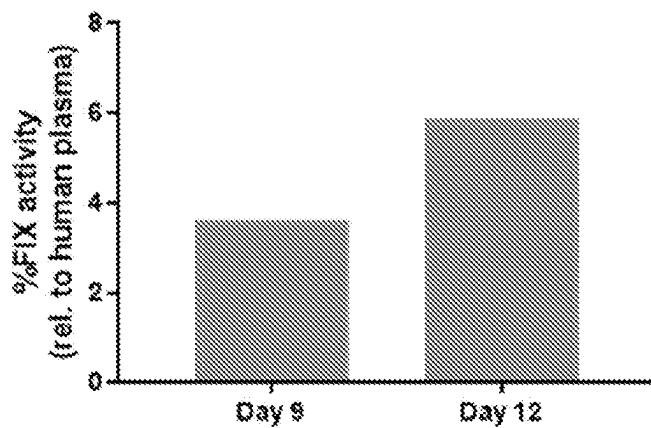
FIGURE 7A**Factor IX expression during production****FIGURE 7B****Secreted Factor IX Activity**

FIGURE 8

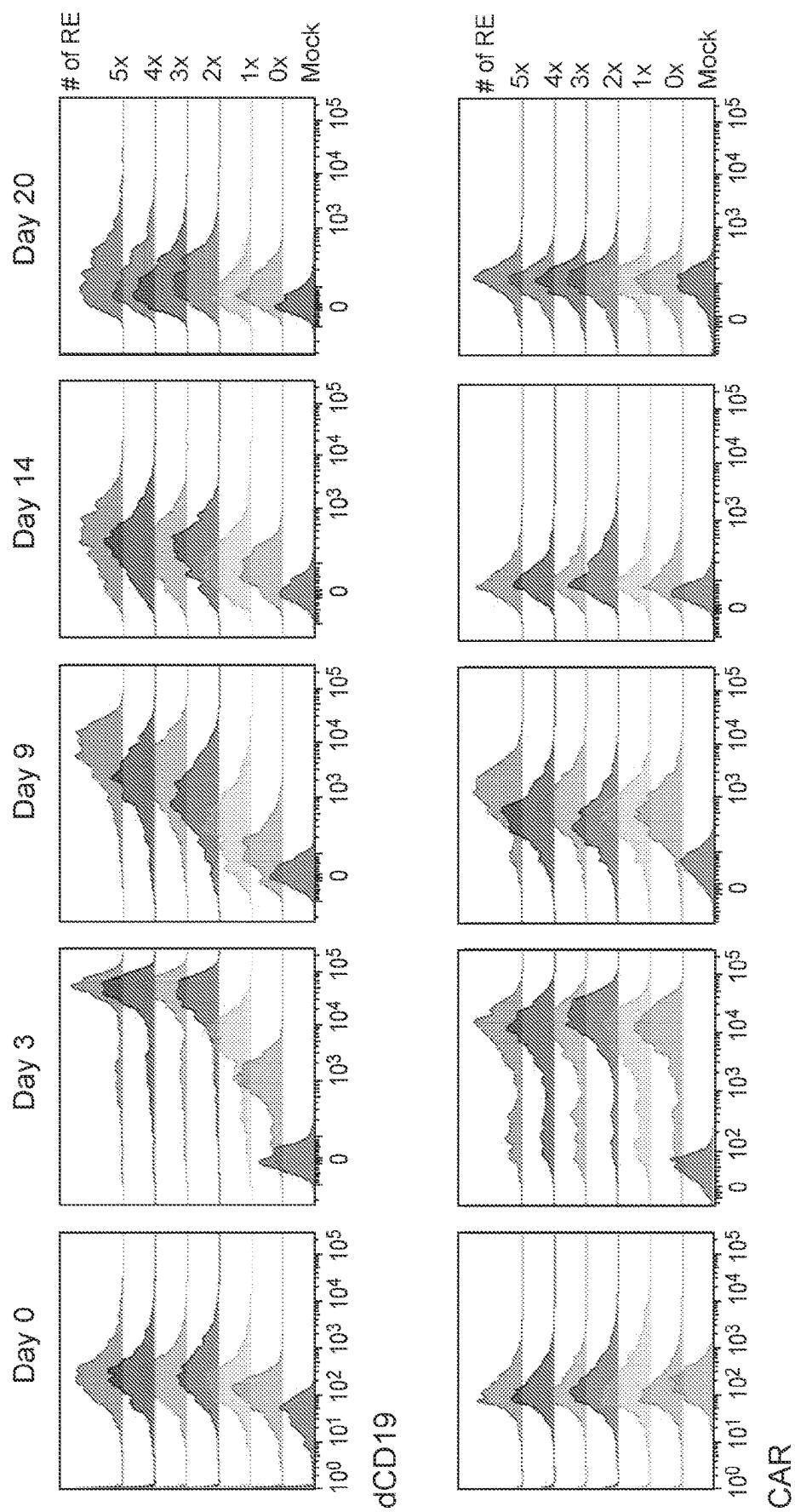


FIGURE 9
CD8+ Cells

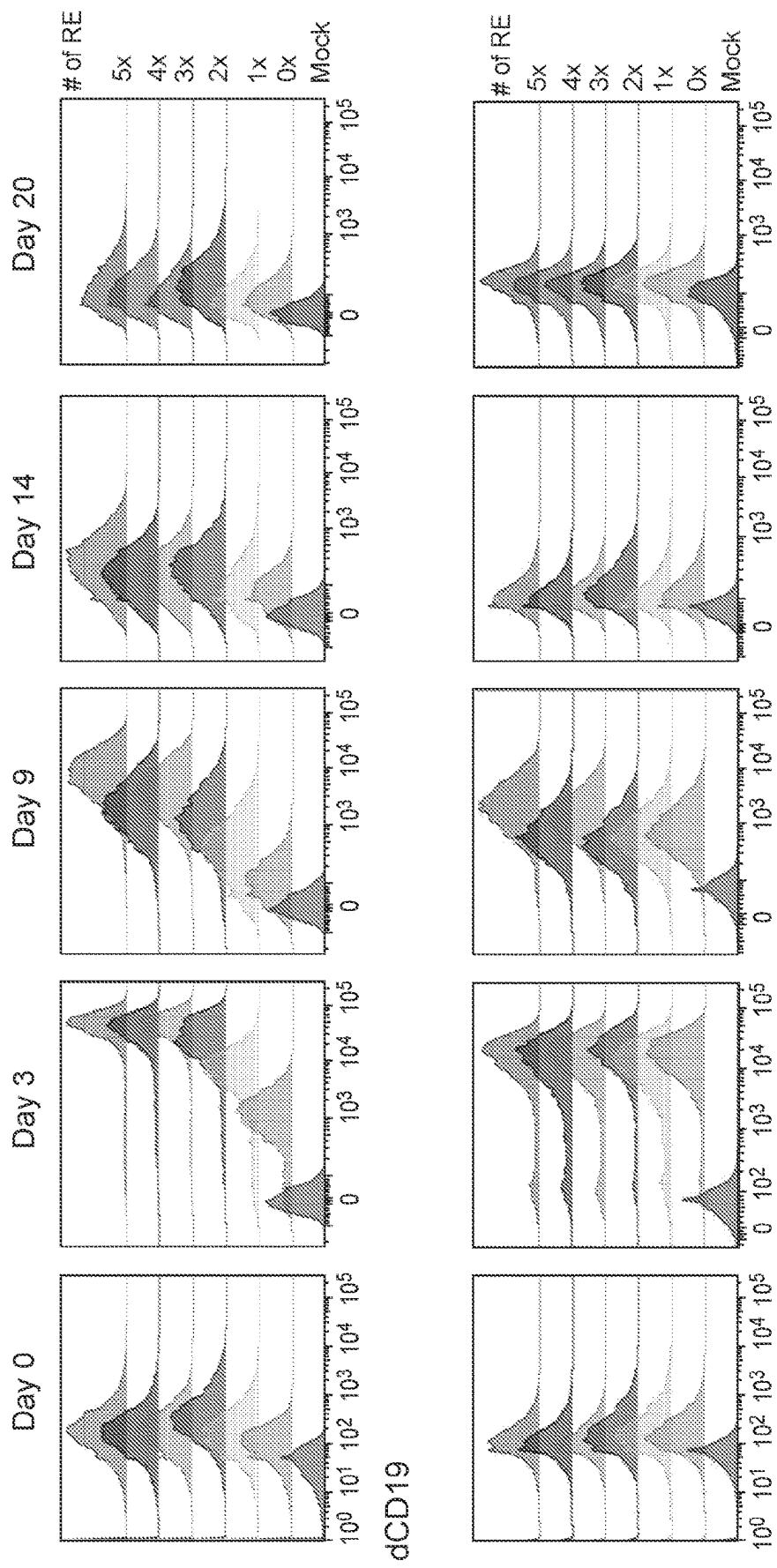


FIGURE 10

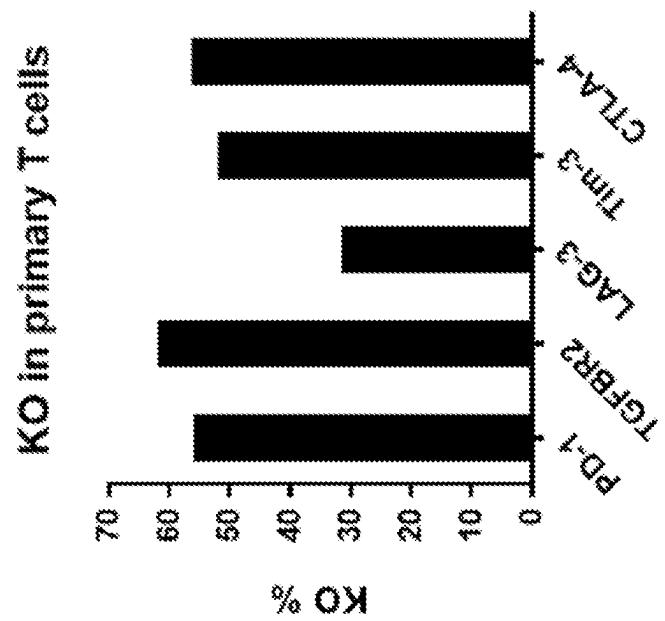


FIGURE 11

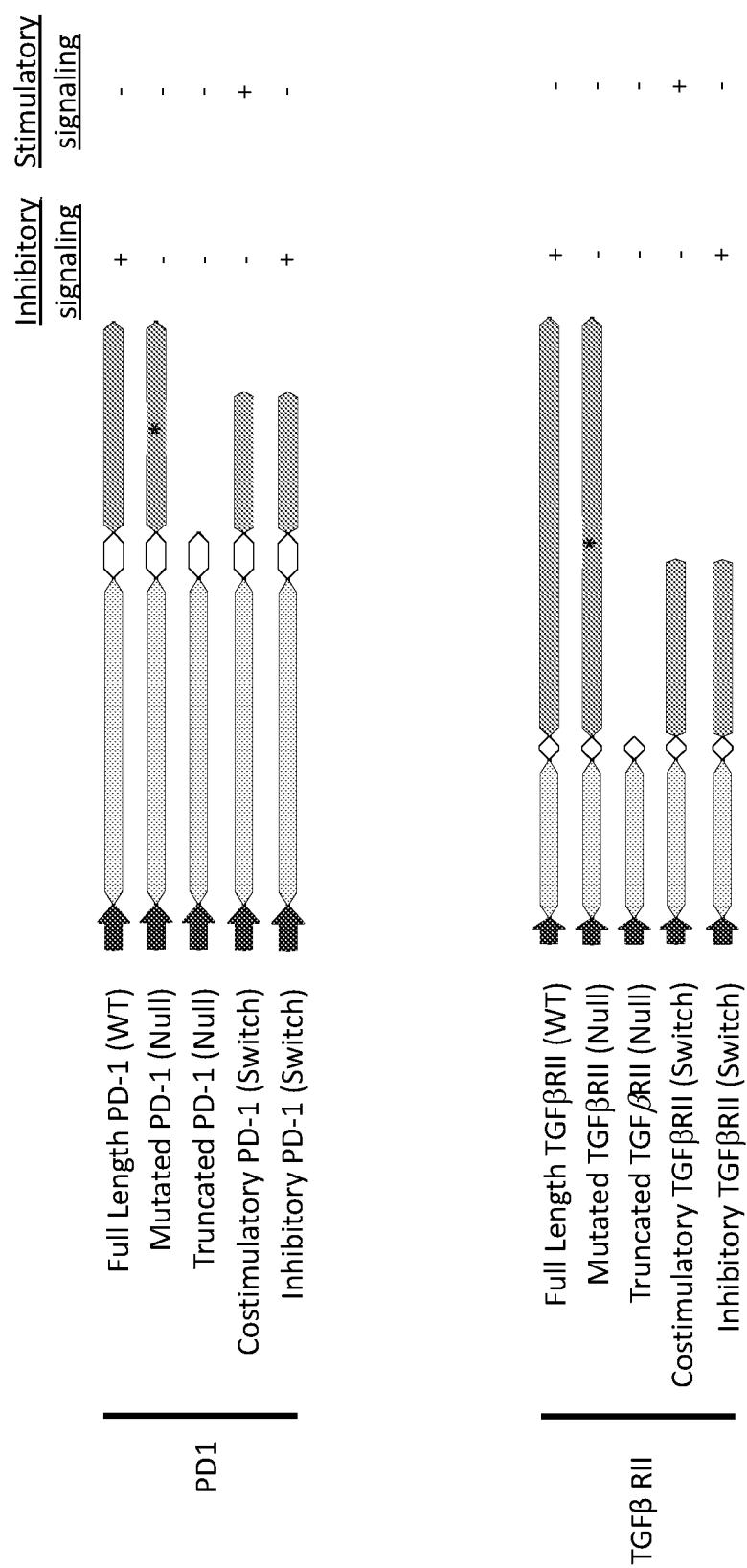


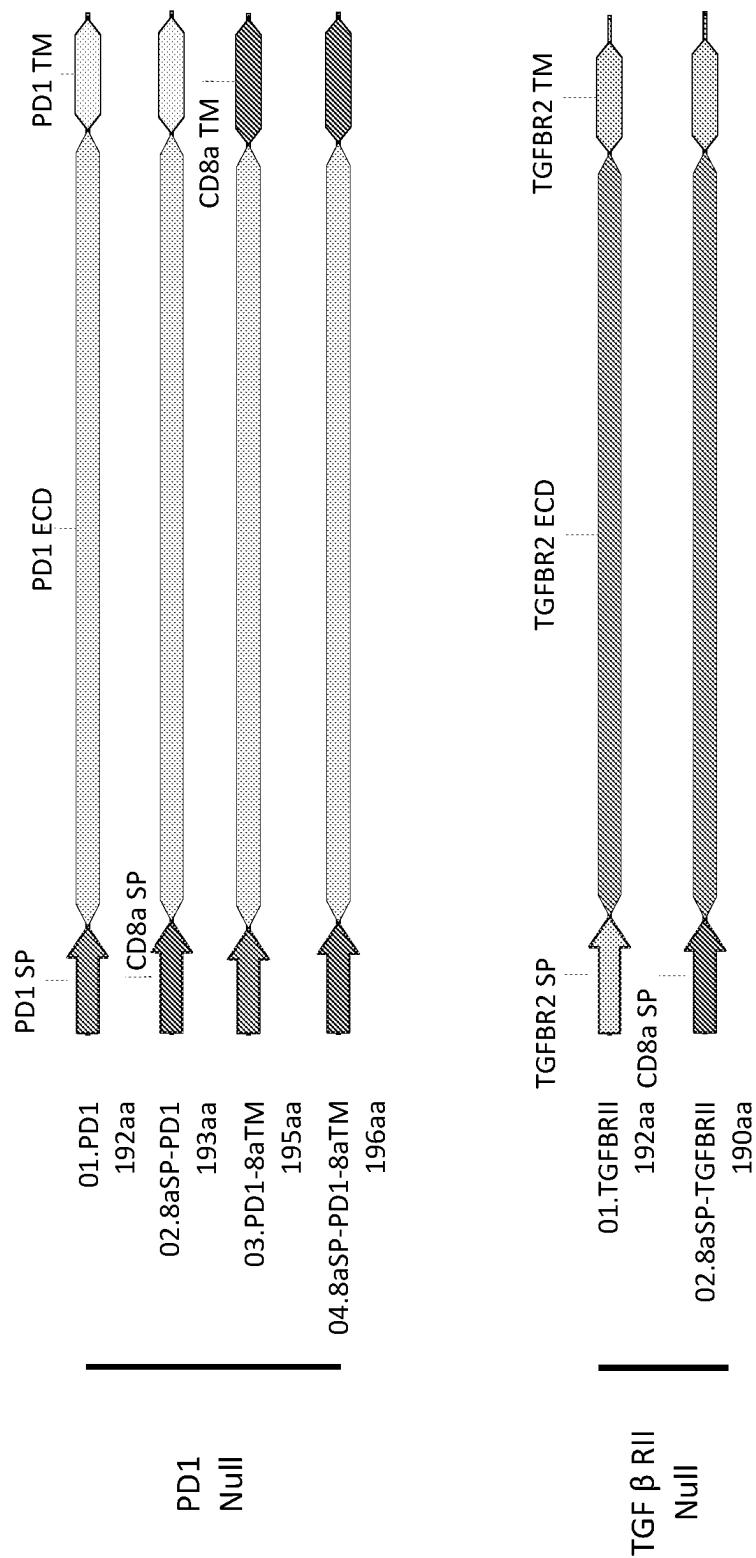
FIGURE 12

FIGURE 13

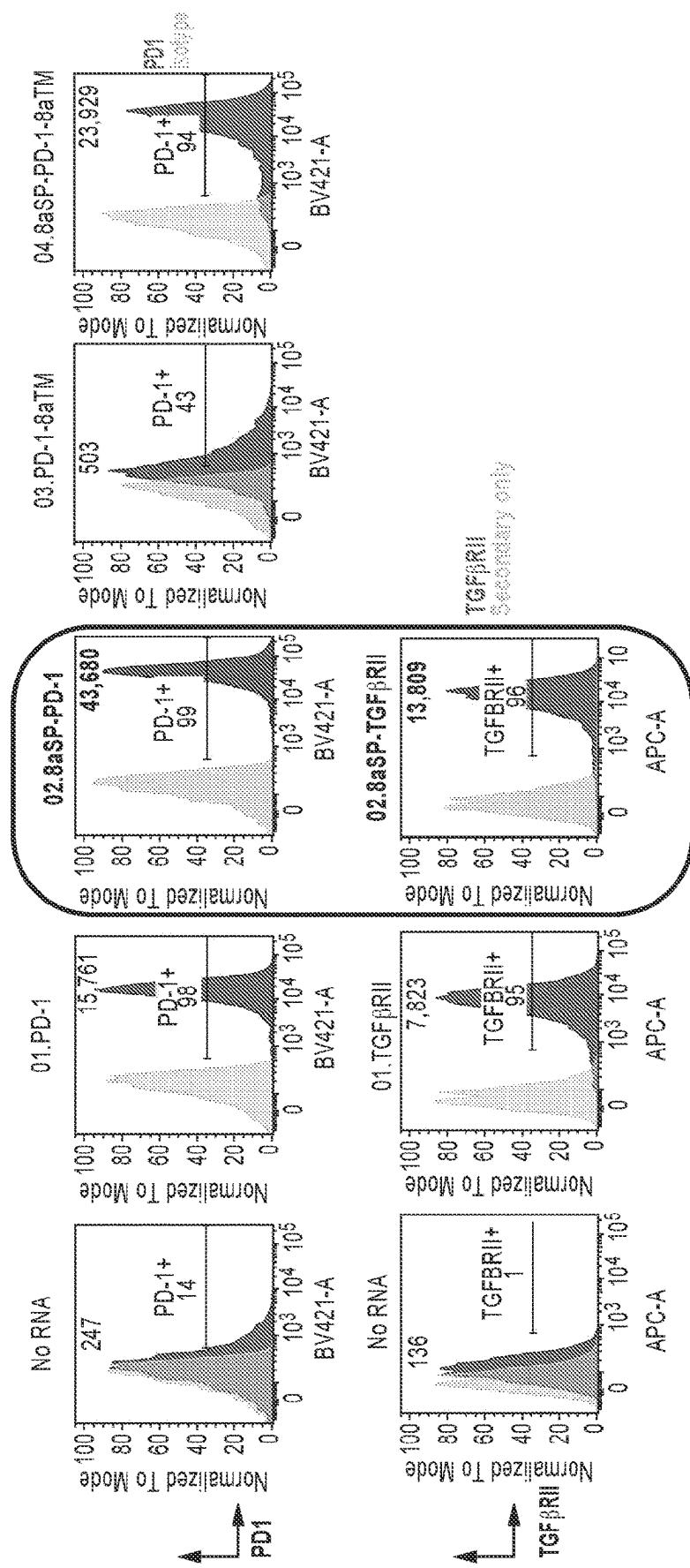


FIGURE 14

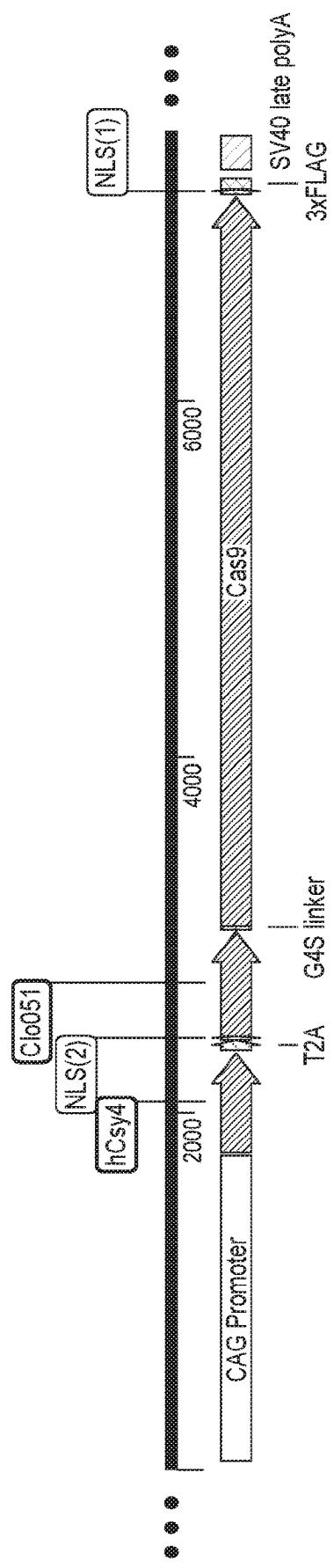


FIGURE 15

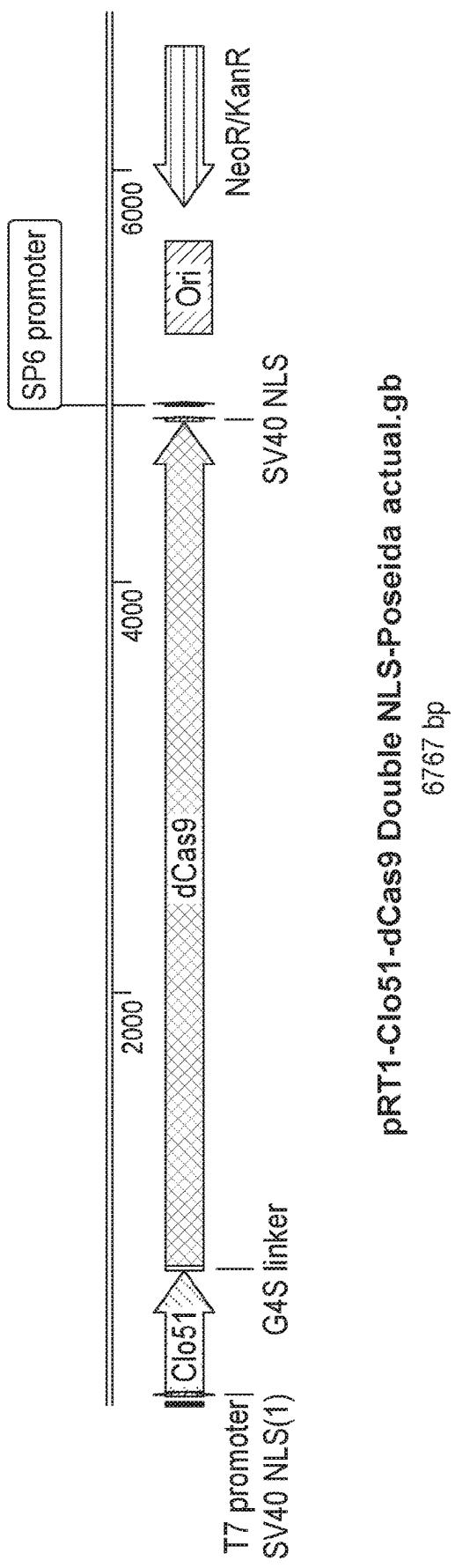


FIGURE 16

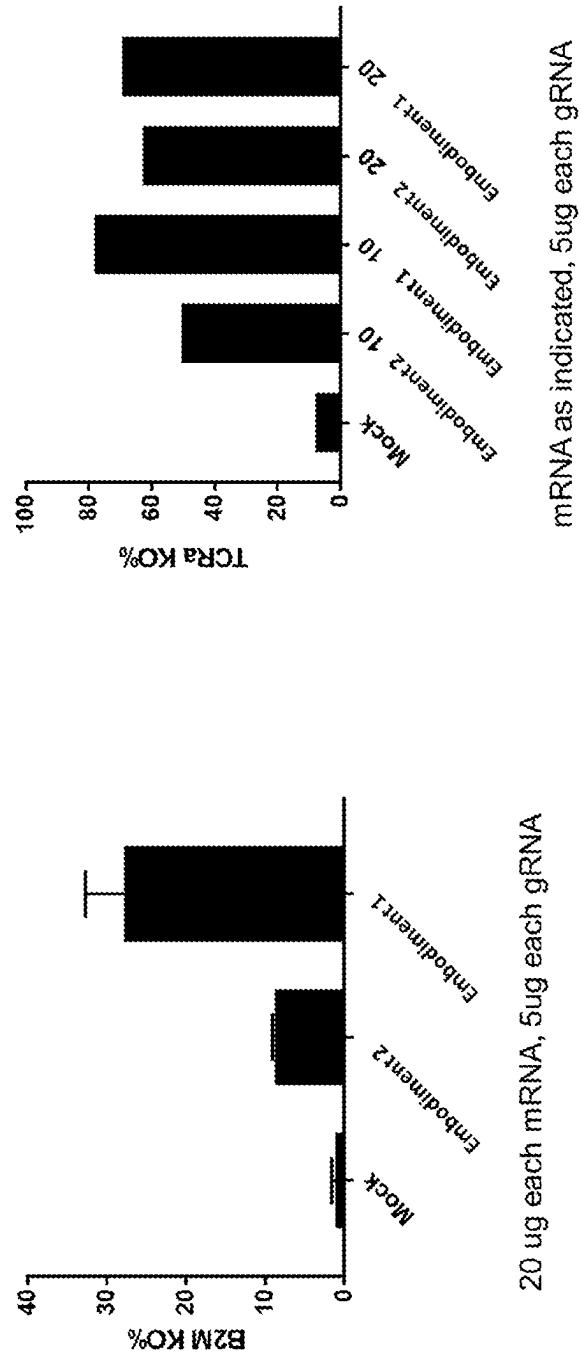
Cas-Clover mRNA Comparison
Embodiment 1 vs Embodiment 2

Pan T cells

B2M KO

Jurkat cells

TCRa KO%

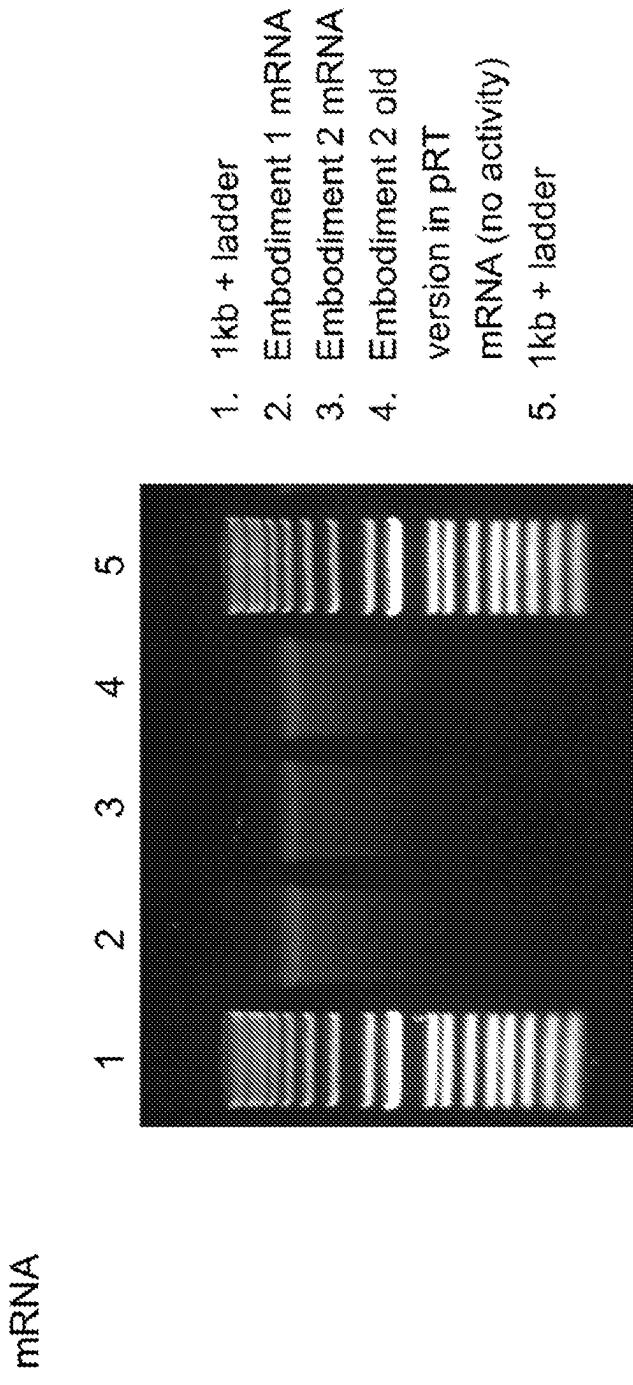


20 ug each mRNA, 5ug each gRNA

mRNA as indicated, 5ug each gRNA

FIGURE 17

Cas-Clover mRNA Comparison Embodiment 1 v. Embodiment 2



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**COMPOSITIONS AND METHODS FOR
CHIMERIC LIGAND RECEPTOR
(CLR)-MEDIATED CONDITIONAL GENE
EXPRESSION**

**CROSS-REFERENCE TO RELATED
APPLICATIONS**

This application is a U.S. National Phase Application, filed under 35 U.S.C. § 371 of International Patent Application No. PCT/2018/050288, filed Sep. 10, 2018, which claims the benefit of provisional application U.S. Ser. No. 62/556,310, filed Sep. 8, 2017. The contents of each of these applications are herein incorporated by reference in their entirety.

INCORPORATION OF SEQUENCE LISTING

The contents of the text file named “POTH-027-N01US_SequenceListing_R.txt” which was created on Jan. 11, 2021 and is 55,448 KB in size, are hereby incorporated by reference in their entirety.

FIELD OF THE DISCLOSURE

The disclosure is directed to molecular biology, and more specifically, to compositions and methods for use in a conditional gene expression system responsive to a chimeric ligand receptor (CLR)-mediated signal.

BACKGROUND

There has been a long-felt but unmet need in the art for a method of controlling gene expression in genetically modified cells for the long-term delivery of therapeutic agents. The disclosure provides a solution by genetically modified cells that conditionally express genes upon activation of a cell-surface receptor.

SUMMARY

The disclosure provides a composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a receptor construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous receptor, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic sequence of a cell, the exogenous reporter is expressed, and wherein the exogenous reporter, upon binding a ligand, transduces an intracellular signal that targets the inducible promoter of (a) to modify gene expression. In certain embodiments, the composition modifies gene expression by increasing gene expression. In certain embodiments, the composition modifies gene expression by decreasing gene expression. In certain embodiments, the composition modifies gene expression by transiently modifying gene expression (e.g. for the duration of binding of the ligand to the exogenous receptor). In certain embodiments, the composition modifies gene expression acutely (e.g. the ligand reversibly binds to the exogenous receptor). In certain embodiments, the composition modifies gene expression chronically (e.g. the ligand irreversibly binds to the exogenous receptor).

In certain embodiments of the compositions of the disclosure, the cell may be a prokaryotic cell. Prokaryotic cells of the disclosure include, but are not limited to, bacteria and

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archaea. For example, bacteria of the disclosure include, but are not limited to, *Listeria monocytogenes*.

In certain embodiments of the compositions of the disclosure, the cell may be a eukaryotic cell. Eukaryotic cells of the disclosure include, but are not limited to, yeast, plants, algae, insects, mammals, amphibians, birds, reptiles, marsupials, rodents, and humans. Preferred eukaryotic cells of the disclosure include, but are not limited to, human cells. Exemplary human cells of the disclosure include but are not limited to, immune cells (e.g. T cells), myeloid cells and bone marrow cells (e.g. hematopoietic stem cells (HSCs)).

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises an endogenous receptor with respect to the genomic sequence of the cell. Exemplary receptors include, but are not limited to, intracellular receptors, cell-surface receptors, transmembrane receptors, ligand-gated ion channels, and G-protein coupled receptors.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the non-naturally occurring receptor is a synthetic, modified, recombinant, mutant or chimeric receptor. In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a T-cell receptor (TCR). In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a scaffold protein. In certain embodiments, including those wherein the non-naturally occurring receptor does not comprise a transmembrane domain, the non-naturally occurring receptor interacts with a second transmembrane, membrane-bound and/or an intracellular receptor that, following contact with the non-naturally occurring receptor, transduces an intracellular signal.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the non-naturally occurring receptor is a synthetic, modified, recombinant, mutant or chimeric receptor. In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a T-cell receptor (TCR). In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a scaffold protein. In certain embodiments, the non-naturally occurring receptor comprises a transmembrane domain. In certain embodiments, the non-naturally occurring receptor interacts with an intracellular receptor that transduces an intracellular signal. In certain embodiments, the non-naturally occurring receptor comprises an intracellular signalling domain. In certain embodiments, the non-naturally occurring receptor is a chimeric ligand receptor (CLR). In certain embodiments, the CLR is a chimeric antigen receptor.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the CLR is a chimeric antigen receptor. In certain embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In certain embodiments, the ectodomain of (a) further comprises a signal peptide. In certain embodiments, the ectodomain of (a) further comprises a hinge between the ligand recognition region and the transmembrane domain. In certain embodiments, the signal

peptide comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1BB or GM-CSFR signal peptide. In certain embodiments, the signal peptide comprises a sequence encoding a human CD8 α signal peptide. In certain embodiments, the signal peptide comprises an amino acid sequence comprising MALPVTALLPLALLLHAARP (SEQ ID NO:17000). In certain embodiments, the signal peptide is encoded by a nucleic acid sequence comprising aggcactgcccagt- caccgcctgctgtgcctgtggctgtgcgtcagcagtagatcca (SEQ ID NO:17001). In certain embodiments, the transmembrane domain comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1BB or GM-CSFR transmembrane domain. In certain embodiments, the transmembrane domain comprises a sequence encoding a human CD8 α transmembrane domain. In certain embodiments, the transmembrane domain comprises an amino acid sequence comprising IYI-WAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 17002). In certain embodiments, the transmembrane domain is encoded by a nucleic acid sequence comprising atctacatggcac- cactggccgggacctgtggagtgtgcgtgcgtggcatcacactgtactgc (SEQ ID NO: 17003). In certain embodiments, the endodomain comprises a human CD3 ζ endodomain. In certain embodiments, the at least one costimulatory domain comprises a human 4-1BB, CD28, CD3 ζ , CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. In certain embodiments, the at least one costimulatory domain comprises a human CD3 ζ and/or a 4-1BB costimulatory domain. In certain embodiments, the CD3 ζ costimulatory domain comprises an amino acid sequence comprising RVKFSRSADAPAYKQQQNQLYNELNLRREEY-DVLDKRRGRDPREMGGKPRRKNPQ EGLYNELQDK-MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY-DALHMQALP PR (SEQ ID NO: 17004). In certain embodiments, the CD3 costimulatory domain is encoded by a nucleic acid sequence comprising cgctgtcaaggatggc- gatcagcagatgccccagctt- caaacaggagacaaccagctgtataacgagctgaatcgccggcga gag- gaatatgcgtgtggataagcggagaggacgcgacccggaaatggg- aggcaagcccaggcgeaaaacccctcaggagg ctgtataacgagctgcagaaggacaaaatggcagaaggcattctgagatcg- catgaaggggggacgcacggagggcaagg gcac- gatgggcgtaccaggactgagccaccccaaaaggacacccatgtatctg- catatgcaggactgcctccaagg (SEQ ID NO: 17005). In certain embodiments, the 4-1BB costimulatory domain comprises an amino acid sequence comprising KRGRKKLLY-IFKQPMPRVQTTQEEDGCSCRFPPEEEGGCEL (SEQ ID NO: 17006). In certain embodiments, the 4-1BB costimulatory domain is encoded by a nucleic acid sequence comprising aagagaggcaggaagaaactgtgtatatttcacacggcc- catgcgcggcgtcagactacccaggaggaagacgggtctcc tgtcgat- tccctgaggaagggaaaggcgggtgtgagct (SEQ ID NO: 17007). In certain embodiments, the 4-1BB costimulatory domain is located between the transmembrane domain and the CD3 ζ costimulatory domain. In certain embodiments, the hinge comprises a sequence derived from a human CD8 α , IgG4, and/or CD4 sequence. In certain embodiments, the hinge comprises a sequence derived from a human CD8 α sequence. In certain embodiments, the hinge comprises an amino acid sequence comprising

In certain embodiments, the hinge is encoded by a nucleic acid sequence comprising actaccacaccaggcacctgatggacc- caactccagtcacaccatcgcgagtcaaggccctgagtcgatggacct- gggctgtcaggcc agctgcaggag- gagctgtgcacaccaggccgtggacttcgcgtgcac (SEQ ID NO: 17028). In certain embodiments, the hinge is encoded by a nucleic acid sequence comprising ACCACAACCCCTGCCCCCAGACCTCC- CACACCCGCCCTTACCATCGCGAGTCAGC CCCT- 10 GAGTCTGAGACT- GAGGCCTGCAGGCCAGCTGCAGGAGGAGCTG- TGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 17009). In certain embodiments, the at least one protein scaffold specifically binds the ligand.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the CLR is a chimeric antigen receptor. In certain embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In certain embodiments, the at least one protein scaffold comprises an antibody, an antibody fragment, a single domain antibody, a single chain antibody, an antibody mimetic, or a Centyrin. In certain embodiments, the ligand recognition region comprises one or more of an antibody, an antibody fragment, a single domain antibody, a single chain antibody, an antibody mimetic, and a Centyrin. In certain embodiments, the single domain antibody comprises or consists of a VHH. In certain embodiments, the antibody mimetic comprises or consists of an affibody, an affilin, an affimer, an affitin, an alphabody, an anticalin, an avimer, a DARPin, a Fynomeric, a Kunitz domain peptide or a monobody. In certain embodiments, the Centyrin comprises or consists of a consensus sequence of at least one fibronectin type III (FN3) domain.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the CLR is a chimeric antigen receptor. In certain embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In certain embodiments, the Centyrin comprises or consists of a consensus sequence of at least one fibronectin type III (FN3) domain. In certain embodiments, the at least one fibronectin type III (FN3) domain is derived from a human protein. In certain embodiments, the human protein is Tenascin-C. In certain embodiments, the consensus sequence comprises LPAPKNLV-SEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGE- AINLTVPGSERSYDL

TGLKPGTEYTVSIYGVKGGRSNPLSAEFTT (SEQ ID NO: 17010). In certain embodiments, the consensus sequence comprises MLPAPKNLVSEVTED- SLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGS- ERSYD LTGLKPGTEYTVSIYGVKGGRSNPLSAEFTT (SEQ ID NO: 17011). In certain embodiments, the consensus sequence is modified at one or more positions within (a) a A-B loop comprising or consisting of the amino acid residues TEDS at positions 13-16 of the consensus sequence; (b) a B-C loop comprising or consisting of the amino acid residues TAPDAAF at positions 22-28 of the consensus sequence; (c) a C-D loop comprising or consisting of the amino acid residues SEKVGE at positions 38-43

of the consensus sequence; (d) a D-E loop comprising or consisting of the amino acid residues GSER at positions 51-54 of the consensus sequence; (e) a E-F loop comprising or consisting of the amino acid residues GLKPG at positions 60-64 of the consensus sequence; (f) a F-G loop comprising or consisting of the amino acid residues KGGRHRSN at positions 75-81 of the consensus sequence; or (g) any combination of (a)-(f). In certain embodiments, the Centryrin comprises a consensus sequence of at least 5 fibronectin type IT (FN3) domains. In certain embodiments, the Centryrin comprises a consensus sequence of at least 10 fibronectin type III (FN3) domains. In certain embodiments, the Centryrin comprises a consensus sequence of at least 15 fibronectin type III (FN3) domains. In certain embodiments, the scaffold binds an antigen with at least one affinity selected from a K_D of less than or equal to 10^{-9} M, less than or equal to 10^{-10} M, less than or equal to 10^{-11} M, less than or equal to 10^{-12} M, less than or equal to 10^{-13} M, less than or equal to 10^{-14} M, and less than or equal to 10^{-15} M. In certain embodiments, the K_D is determined by surface plasmon resonance. In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the CLR is a chimeric antigen receptor. In certain embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least a VHH antibody; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In certain embodiments, the VHH is camelid. Alternatively, or in addition, in certain embodiments, the VHH is humanized. In certain embodiments, the sequence comprises two heavy chain variable regions of an antibody, wherein the complementarity-determining regions (CDRs) of the VHH are human sequences.

In certain embodiments of the compositions of the disclosure, the sequence encoding the constitutive promoter of (b) comprises a sequence encoding an EF1 α promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the constitutive promoter of (b) comprises a sequence encoding a CMV promoter, a U6 promoter, a SV40 promoter, a PGK1 promoter, a Ubc promoter, a human beta actin promoter, a CAG promoter, or an EF1 α promoter.

In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an NF κ B promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an interferon (IFN) promoter or a sequence encoding an interleukin-2 promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding a nuclear receptor subfamily 4 group A member 1 (NR4A1; also known as NUR77) promoter or a sequence encoding a NR4A1 promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding a T-cell surface glycoprotein CD5 (CD5) promoter or a sequence encoding a CD5 promoter. In certain embodiments, the interferon (IFN) promoter is an IFN γ promoter. In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a cytokine or a chemokine. In certain embodiments, the cytokine or chemokine comprises IL2, IL3, IL4, IL5, IL6, IL10, IL12, IL13, IL17A/F, IL21, IL22, IL23, transforming growth factor beta (TGF β), colony stimulating

factor 2 (GM-CSF), interferon gamma (IFN γ), Tumor necrosis factor (TNF α), LT α , perforin, Granzyme C (Gzmc), Granzyme B (Gzmb), C-C motif chemokine ligand 5 (CCL5), C-C motif chemokine ligand 4 (CCL4), C-C motif chemokine ligand 3 (CCL3), X-C motif chemokine ligand 1 (XCL1) and LIF interleukin 6 family cytokine (Lif).

In certain embodiments of the compositions of the disclosure, including those wherein the sequence encoding the inducible promoter of (a) comprises a sequence encoding a NR4A1 promoter or a sequence encoding a NR4A1 promoter, the NR4A1 promoter is activated by T-cell Receptor (TCR) stimulation in T cells and by B-cell Receptor (BCR) stimulation in B cells, therefore, inducing expression of any sequence under control of the NR4A1 promoter upon activation of a T-cell or B-cell of the disclosure through a TCR or BCR, respectively.

In certain embodiments of the compositions of the disclosure, including those wherein the sequence encoding the inducible promoter of (a) comprises a sequence encoding a CD5 promoter or a sequence encoding a CD5 promoter, the CD5 promoter is activated by T-cell Receptor (TCR) stimulation in T cells, therefore, inducing expression of any sequence under control of the CD5 promoter upon activation of a T-cell of the disclosure through a TCR.

In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene comprising a surface protein involved in cell differentiation, activation, exhaustion and function. In certain embodiments, the gene comprises CD69, CD71, CTLA4, PD-1, TIGIT, LAG3, TIM-3, GITR, MHCII, COX-2, FASL and 4-1BB.

In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene involved in CD metabolism and differentiation. In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of Nr4a1, Nr4a3, Tnfrsf9 (4-1BB), Sema7a, Zfp3612, Gadd45b, Dusp5, Dusp6 and Neto2.

In certain embodiments of the compositions of the disclosure, the transgene comprises a sequence that is endogenous with respect to the genomic sequence of the cell.

In certain embodiments of the compositions of the disclosure, the transgene comprises a sequence that is exogenous with respect to the genomic sequence of the cell. In certain embodiments, the exogenous sequence is a sequence variant of an endogenous sequence within the genome of the cell. In certain embodiments, the exogenous sequence is a wild type sequence of gene that is entirely or partially absent in the cell, and wherein the gene is entirely present in the genome of a healthy cell. In certain embodiments, the exogenous sequence is a synthetic, modified, recombinant, chimeric or non-naturally occurring sequence with respect to the genome of the cell. In certain embodiments, the transgene encodes a secreted protein. In certain embodiments, the secreted protein is produced and/or secreted from the cell at a level that is therapeutically effective to treat a disease or disorder in a subject in need thereof.

In certain embodiments of the compositions of the disclosure, a first transposon comprises the inducible transgene construct of (a) and a second transposon comprises the receptor construct of (b). In certain embodiments of the compositions of the disclosure, a first vector comprises the first transposon and a second vector comprises the second transposon. In certain embodiments of the compositions of the disclosure, a vector comprises the first transposon and the second transposon. In certain embodiments, the first

transposon and the second transposon are oriented in the same direction. In certain embodiments, the first transposon and the second transposon are oriented in opposite directions. In certain embodiments, the vector is a plasmid. In certain embodiments, the vector is a nanoplasmid.

In certain embodiments of the compositions of the disclosure, the vector is a viral vector. Viral vectors of the disclosure may comprise a sequence isolated or derived from a retrovirus, a lentivirus, an adenovirus, an adeno-associated virus or any combination thereof. The viral vector may comprise a sequence isolated or derived from an adeno-associated virus (AAV). The viral vector may comprise a recombinant AAV (rAAV). Exemplary adeno-associated viruses and recombinant adeno-associated viruses of the disclosure comprise two or more inverted terminal repeat (ITR) sequences located in cis next to a sequence encoding a construct of the disclosure. Exemplary adeno-associated viruses and recombinant adeno-associated viruses of the disclosure include, but are not limited to all serotypes (e.g. AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, and AAV9). Exemplary adeno-associated viruses and recombinant adeno-associated viruses of the disclosure include, but are not limited to, self-complementary AAV (scAAV) and AAV hybrids containing the genome of one serotype and the capsid of another serotype (e.g. AAV2/5, AAV-DJ and AAV-DJ8). Exemplary adeno-associated viruses and recombinant adeno-associated viruses of the disclosure include, but are not limited to, rAAV-LK03 and AAVs with the NP-59 and NP-84 capsid variants.

In certain embodiments of the compositions of the disclosure, the vector is a nanoparticle. Exemplary nanoparticle vectors of the disclosure include, but are not limited to, nucleic acids (e.g. RNA, DNA, synthetic nucleotides, modified nucleotides or any combination thereof), amino acids (L-amino acids, D-amino acids, synthetic amino acids, modified amino acids, or any combination thereof), polymers (e.g. polymersomes), micelles, lipids (e.g. liposomes), organic molecules (e.g. carbon atoms, sheets, fibers, tubes), inorganic molecules (e.g. calcium phosphate or gold) or any combination thereof. A nanoparticle vector may be passively or actively transported across a cell membrane.

In certain embodiments of the compositions of the disclosure, first transposon or the second transposon is a piggyBac transposon. In certain embodiments, the first transposon and the second transposon is a piggyBac transposon. In certain embodiments, the composition further comprises a plasmid or a nanoplasmid comprising a sequence encoding a transposase enzyme. In certain embodiments, the sequence encoding a transposase enzyme is an mRNA sequence. In certain embodiments, the transposase is a piggyBac transposase. In certain embodiments, the piggyBac transposase comprises an amino acid sequence comprising SEQ ID NO: 1. In certain embodiments, the piggyBac transposase is a hyperactive variant and wherein the hyperactive variant comprises an amino acid substitution at one or more of positions 30, 165, 282 and 538 of SEQ ID NO: 1. In certain embodiments, the amino acid substitution at position 30 of SEQ ID NO: 1 is a substitution of a valine (V) for an isoleucine (I) (130V). In certain embodiments, the amino acid substitution at position 165 of SEQ ID NO: 1 is a substitution of a serine (S) for a glycine (G) (G165S). In certain embodiments, the amino acid substitution at position 282 of SEQ ID NO: 1 is a substitution of a valine (V) for a methionine (M) (M282V). In certain embodiments, the amino acid substitution at position 538 of SEQ ID NO: 1 is a substitution of a lysine (K) for an asparagine (N) (N538K). In certain embodiments, the transposase is a Super piggyBac

(SPB) transposase. In certain embodiments, the Super piggyBac (SPB) transposase comprises an amino acid sequence comprising SEQ ID NO: 2.

In certain embodiments 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:

(SEQ ID NO: 17029)

1 MGSSLDDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ
SDTEEAFIDE VHEVQPTSSG

61 SEILDEQNVI EQPGSSLASRN RILTLQRTI RGKNKHCWST
SKSTRRSRVS ALNIVRSQRG

121 PTRMCRNIYD PLDCFKLFFT DEIISEIVKW TNAEISLKKR
ESMTGATFRD TNEDEIYAFF

181 GILVMTAVRK DHNMSTDLF DRSLSMVYVS VMSRDRFDL
IRCLRMDDKS IRPTLRENDV

241 FTPVRKIWDL FIHQCIQNYT PQAHLTIDEQ LLGFRQRQPF
RMYIPNKPSK YQIKILMMCD

301 SGYKYMINGM PYLGRGTQTN GVRLGEYYVK ELSKPVHGSC
RNITCDNWPT SIPLAKNLLQ

361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMPCFDGP
LTLVSYKPKP AKMVYLLSSC

421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QCMSVMTCSR
KTNRWRMALL YGMINIACIN

481 SFIIYSHNVS SKGEKVQSRK KFMRNLMLYSL TSSFMRKRLE
APTLKRYLRD NISNILPNEV

541 PGTSDDSTEE PVMMKKRTYCT YCPSKIRRKA NASCKKCKV
ICREHNIDMC QSCF.

In certain embodiments of the disclosure, the transposase enzyme is a piggyBac™ (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at one or more of positions 30, 165, 282, or 538 of the sequence:

(SEQ ID NO: 17029)

1 MGSSLDDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ
SDTEEAFIDE VHEVQPTSSG

61 SEILDEQNVI EQPGSSLASRN RILTLQRTI RGKNKHCWST
SKSTRRSRVS ALNIVRSQRG

121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKKR
ESMTGATFRD TNEDEIYAFF

181 GILVMTAVRK DHNMSTDLF DRSLSMVYVS VMSRDRFDL
IRCLRMDDKS IRPTLRENDV

241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF
RMYIPNKPSK YGIKILMMCD

301 SGYKYMINGM PYLGRGTQTN GPVLGEYYVK ELSKPVHGSC
RNITCDNWPT SIPLAKNLLQ

361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMPCFDGP
LTLVSYKPKP AKMVYLLSSC

421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QCMSVMTCSR
KTNRWRPMALL YGMINIACIN

481 SFIIYSHNVS SKGEKVQSRK KFMRNLMLYSL TSSFMRKRLE
APTLKRYLRD NISNILPNEV

541 PGTSDDSTEE PVMMKKRTYCT YCPSKIRRKA NASCKKCKV
ICREHNIDMC QSCF.

In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at two or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 1. In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at three or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 1. In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at each of the following positions 30, 165, 282, and 538 of the sequence of SEQ ID NO: 1. In certain embodiments, the amino acid substitution at position 30 of the sequence of SEQ ID NO: 1 is a substitution of a valine (V) for an isoleucine (I). In certain embodiments, the amino acid substitution at position 165 of the sequence of SEQ ID NO: 1 is a substitution of a serine (S) for a glycine (G). In certain embodiments, the amino acid substitution at position 282 of the sequence of SEQ ID NO: 1 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 538 of the sequence of SEQ ID NO: 1 is a substitution of a lysine (K) for an asparagine (N).

In certain embodiments of the disclosure, the transposase enzyme is a Super piggyBacTM (SPB) transposase enzyme. In certain embodiments, the Super piggyBacTM (SPB) transposase enzymes of the disclosure may comprise or consist of the amino acid sequence of the sequence of SEQ ID NO: 1 wherein the amino acid substitution at position 30 is a substitution of a valine (V) for an isoleucine (I), the amino acid substitution at position 165 is a substitution of a serine (S) for a glycine (G), the amino acid substitution at position 282 is a substitution of a valine (V) for a methionine (M), and the amino acid substitution at position 538 is a substitution of a lysine (K) for an asparagine (N). In certain embodiments, the Super piggyBacTM (SPB) 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:

(SEQ ID NO: 17030)

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1 MGSSLDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ
SDTEEAFIGE VHEVQPTSSG

61 SEILDEQNVI EQPGSSLASN RILTLPORTI RGKNKHCWST
SKSTRRSRV ALNIVRSQRG

121 PTRMCRNIIYD PLLCFKLFFT DEIISEIVKW TNAEISLKR
ESMTSATFRD TNEDEIYAFF

181 GILVMTAVRK DNHMSTDDLF DPSLSMVYVS VMSRDRDFL
IRCLRMDDKS IRPLTRENDV

241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF
RVYIPNPKSK YGIKILMMCD

301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK ELSKPVHGSC
RNITCDNWFT SIPLAKNLLQ

361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP
LTLVSYKPKP AKMVYLLSSC

421 DEDASINEST GKPQMVMYNN QTKGGVDTLD QMCSVMTCSR
KTNRWPMLL YGMINIACIN

481 SFIIYSHNVS SKGEKVOSRK KFMRNLYMSL TSSFMRKRLE
APTLKRYLRD NISNLPKEV

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-continued

541 PGTSDDSTE PVMKKRTYCT YCRSKIRRKA NASCKKCKV
ICREHNIDMC QSCF.

In certain embodiments of the disclosure, including those 5 embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more 10 of positions 3, 46, 82, 103, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 258, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 486, 503, 552, 570 and 591 of the sequence of SEQ ID NO: 1 or SEQ ID 15 NO: 2. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more 20 of positions 46, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 485, 503, 552 and 570. In certain 25 embodiments, the amino acid substitution at position 3 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an asparagine (N) for a serine (S). In certain embodiments, the amino acid substitution at position 46 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a serine (S) for an alanine (A). In certain 30 embodiments, the amino acid substitution at position 46 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a threonine (T) for an alanine (A). In certain 35 embodiments, the amino acid substitution at position 82 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a tryptophan (W) for an isoleucine (I). In certain 40 embodiments, the amino acid substitution at position 103 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a proline (P) for a serine (S). In certain 45 embodiments, the amino acid substitution at position 119 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a proline (P) for an arginine (R). In certain 50 embodiments, the amino acid substitution at position 125 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an alanine (A) or a cysteine (C). In certain 55 embodiments, the amino acid substitution at position 125 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a cysteine (C). In certain 60 embodiments, the amino acid substitution at position 177 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a lysine (K) for a tyrosine (Y). In certain 65 embodiments, the amino acid substitution at position 177 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a histidine (H) for a tyrosine (Y). In certain 70 embodiments, the amino acid substitution at position 180 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a phenylalanine (F). In certain 75 embodiments, the amino acid substitution at position 180 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an isoleucine (I) for a phenylalanine (F). In certain 80 embodiments, the amino acid substitution at position 180 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a valine (V) for a phenylalanine (F). In certain 85 embodiments, the amino acid substitution at position 185 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a methionine (M). In certain 90 embodiments, the amino acid substitution at position 187 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a glycine (G) for an alanine (A). In certain 95 embodiments, the amino acid substitution at position 200 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a tryptophan (W) for a phenylalanine (F). In certain 100 embodiments, the amino acid substitution at position 207 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a proline (P) for a valine (V). In certain

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embodiments, the amino acid substitution at position 209 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a phenylalanine (F) for a valine (V). In certain embodiments, the amino acid substitution at position 226 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a phenylalanine (F) for a methionine (M). In certain embodiments, the amino acid substitution at position 235 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an arginine (R) for a leucine (L). In certain embodiments, the amino acid substitution at position 240 of SEQ ID NO: 1 or SEQ ID NO: 1 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at position 241 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 243 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a lysine (K) for a proline (P). In certain embodiments, the amino acid substitution at position 258 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a tryptophan (W) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a tyrosine (Y) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a phenylalanine (F) for a leucine (L). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an alanine (A) for a methionine (M). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an isoleucine (I) for a proline (P). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a valine (V) for a proline (P). In certain embodiments, the amino acid substitution at position 315 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a lysine (K) for an arginine (R). In certain embodiments, the amino acid substitution at position 319 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a glycine (G) for a threonine (T). In certain embodiments, the amino acid substitution at position 327 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an arginine (R) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 328 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a valine (V) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a glycine (G) for a cysteine (C). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a cysteine (C). In certain embodiments, the amino acid substitution at position 421 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a histidine (H) for the aspartic acid (D). In certain embodiments, the amino acid substitution at position 436 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an isoleucine (I) for a valine (V). In certain embodiments, the amino acid substitution at position 456 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a tyrosine (Y) for a methionine (M). In certain embodiments, the amino acid substitution at position 470 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a phenylalanine (F) for a leucine (L).

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In certain embodiments, the amino acid substitution at position 485 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a lysine (K) for a serine (S). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an isoleucine (I) for a methionine (M). In certain embodiments, the amino acid substitution at position 552 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a threonine (T) for an alanine (A). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a proline (P) for a glutamine (Q). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an arginine (R) for a glutamine (Q). In certain embodiments of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 1 or SEQ ID NO: 2. In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at two, three, four, five, six or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 1 or SEQ ID NO: 2. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 1 or SEQ ID NO: 2. In certain embodiments, the amino acid substitution at position 103 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a proline (P) for a serine (S). In certain embodiments, the amino acid substitution at position 194 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 372 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an alanine (A) for an arginine (R). In certain embodiments, the amino acid substitution at position 375 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an alanine (A) for a lysine (K). In certain embodiments, the amino acid substitution at position 450 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of an asparagine (N) for an aspartic acid (D). In certain embodiments, the amino acid substitution at position 509 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a glycine (G) for a serine (S). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 1 or SEQ ID NO: 2 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the piggyBacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 1. In certain embodiments, including those embodiments wherein the piggyBacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 1, the piggyBacTM transposase

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enzyme may further comprise an amino acid substitution at positions 372, 375 and 450 of the sequence of SEQ ID NO: 1 or SEQ ID NO: 2. In certain embodiments, the piggyBac™ transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 1, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 1, and a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 1. In certain embodiments, the piggyBac™ transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 1, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 1, a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 1 and a substitution of an asparagine (N) for an aspartic acid (D) at position 450 of SEQ ID NO: 1.

In certain embodiments of the disclosure, the transposase enzyme is a Sleeping Beauty transposase enzyme (see, for example, U.S. Pat. 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% identical to:

(SEQ ID NO: 17031)
MGKSKEISQDLRKIVDLHKSGSSLGAISKRLKVRSSVQTIVRKYKHHG
TTQPSYRGRRYLSPRDERTLVRKVQINPRTTAKDLVKMLEETGKVS1
STVKRVLYRHNLKGRSARKKPLLQNRHKKARLRFATAHGDKDRTFWRNVL
WSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSIMLWGCFAA
GGTGALHKIDGIMRKENYVDILQHLKTSVRKLKLGRWKWPQMDNDPKHT
SKVVAWLKDNDKVKVLEWPSQSPDLNPIENLWAELKKRVRARRPTNLTQL
HQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY.

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 75% identical to:

(SEQ ID NO. 17032)
MGKSKEISQDLRKIVDLHKSGSSLGAISKRLAVPRSSVQTIVRKYKHHG
TTQPSYRGRRYLSPRDERTLVRKVQINPRTTAKDLVKMLEETGKVS1
STVKRVLYRHNLKGHSARKKPLLQNRHKKARLRFATAHGDKDRTFWRNVL
WSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSIMLWGCFAA
GGTGALHKIDGIMDAVQYVDILQHLKTSVRKLKLGRWKWPQHDNDPKHT
SKVVAWLKDNDKVKVLEWPSQSPDLNPIENLWAELKKRVRARRPTNLTQL
HQLCQEEWAKIHPNYCGKLVEGYPKRLTQVKQFKGNATKY.

In certain embodiments of the compositions of the disclosure, the first transposon and/or the second transposon further comprises a selection gene. In certain embodiments, the selection gene comprises neo, DHFR (Dihydrofolate Reductase), TYMS (Thymidylate Synthetase), MGMT (O(6)-methylguanine-DNA methyltransferase), multidrug resistance gene (MDR1), ALDH1 (Aldehyde dehydrogenase 1 family, member A1), FRANCF, RAD51C (RAD51 Paralog C), GCS (glucosylceramide synthase), NKX2.2 (NK2 Homeobox 2) or any combination thereof. In certain embodiments, the selection gene comprises DHFR

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In certain embodiments of the compositions of the disclosure, the first transposon and/or the second transposon comprises an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 polypeptide, wherein the inducible caspase polypeptide does not comprise a non-human sequence. In certain embodiments, the non-human sequence is a restriction site. In certain embodiments, the ligand binding region inducible caspase polypeptide comprises a FK506 binding protein 12 (FKBP12) polypeptide. In certain embodiments, the amino acid sequence of the FK506 binding protein 12 (FKBP12) polypeptide comprises a modification at position 36 of the sequence. In certain embodiments, the modification is a substitution of valine (V) for phenylalanine (F) at position 36 (F36V). In certain embodiments, the FKBP12 polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTPKRGQTCVVHYTGMLEDGK-KVDSSRDRNKPFKMLGKQEV1
RGWEEGVQAQMSVGQRALKTISPDYAYGATGHPGIIP-PHATLVFDVELLKLE (SEQ ID NO: 17012). In certain embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17013)
GGGTCCAGGTCGAGACTATTACACCAGGGATGGCGAACATTCTCAA
AAGGGGCCAGACTTGCCTCGTCGATTACACCGGGATGCTGGAGGACGGGA
AGAAAGTGGACAGCTCAGGGATCGAACAAAGCCCTCAAGTTCATGCTG
GGAAAGCAGGAAGTGTCCAGGGATGGGAGGAAGGCGTGGCACAGATGTC
AGTCGGCCAGCGGGCAAAGTGACCATTAGCCCTGACTACGCTTATGGAG
CAACAGGCCACCCAGGGATCATTCCCCCTCATGCCACCTGGCTTCGAT
GTGGAAGTGTGAAGCTGGAG.

In certain embodiments, the linker region of the inducible proapoptotic polypeptide is encoded by an amino acid comprising GGGGS (SEQ ID NO: 17014). In certain embodiments, the linker region of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 17015).

In certain embodiments, the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. In certain embodiments, the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In certain embodiments, the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by an amino acid comprising GFGDV-GALESLRGNADLAYILSMEPCGHCLI-INNVNFRCESGLRTRTGSNICEKLRR-RFSSLHFMEVKGDLTAKKMVLALLE-LAQQDHGALDCVVVILSHGCQASHLQFPG-AVYGTGCPVS-VEKIVNIFNGTSCPSLGGKPKLFFIQACCGGEQKDHGFE-VASTSPEDE-SPGSNPEPDATPFQEGLRTFDQL-DAISSLPTPSDFIVSYSTFPGFVSWRDPKSGSWYVE-TLDDIFEQWAHSEDLQSLLRVA-NAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 17016). In certain embodiments, the truncated caspase 9

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poly peptide of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17017)
 TTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAATGCCGATCTGGC
 TTACATCCTGAGCATGGAACCCCTGCGGCCACTGTCTGATCATTAACAATG
 TGAACTTCTGCAGAGAAAAGCGGACTGCGAACACGGACTGGCTCCAATATT
 GACTGTGAGAAGCTGCGGAGAAGGTTCTCTAGTCTGCACTTATGGTCGA
 AGTGAAAGGGATCTGACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGC
 TGGCTCAGCAGGACCAGTGGAGCTCTGGATTCTGCGTGGTCGTGATCCCTG
 TCCCACGGGTGCCAGGCTTCTCATCTGCAGTTCCCGGAGCAGTGTACGG
 AACAGACGGCTGTCCTGTCAGCGTGGAGAAGATCGTCAACATCTCAACG
 GCACATTCTGCCTAGTCTGGGGAAAGCAAAATGTTCTTATCCAG
 GCCTGTGGCGGGAAACAGAAAGATCACGGCTTCGAGGTGGCCAGCACCAG
 CCCTGAGGACGAATCACCAAGGGAGCACCCCTGAACCAAGATGCAACTCCAT
 TCCAGGAGGGACTGAGGACCTTGACCAGCTGGATGCTATCTCAAGCCTG
 CCCACTCTAGTGACATTTCTGTCTTACAGTACCTTCCCAGGCTTGT
 CTGATGGCGCATCCAAAGTCAGGGAGCTGTCAGTGGAGACACTGGACG
 ACATCTTGAAACAGTGGGCCATTAGAGGACCTGCGAGAGCCTGCTGCTG
 CGAGTGGCAAACGCTGTCTGTGAAGGGCATCTACAAACAGATGCCCGG
 GTGCTTCATTCTGAGAAAGAAACTGTTCTTAAGACTTCC.

In certain embodiments, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTPKRGQTCVHYTGMLEDGK-KVDSSRDRNPKFKMLGKQEVI RGWEEGVAQMSVGQRALKTISPDYAYGATGHPGIIP-PHATLVDVELLKLEGGGS GFGDVGALESLRG-NADLAYILSMEPCGHCLIINNVNCRESGLRTRTG-SNIIDCEKLRR RFSSLHFMVVKGDTTAKKMVLALLE-LAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVS-VEKIVNIFNGTSCPSLGGKPFLFIQACGGEQKDHGFE-VASTSPED E SPGSNPEPDATPFQEGLRTFDQL-DAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQLSLLRVA-NAVSVKGIYKQMPGCFNRLKKLFFKTS (SEQ ID NO: 17018) In certain embodiments, the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17019)
 Ggggtccaggcgagactatccaccaggggatggcgaaacattccaaa aaggggccagacttgcgtcgattacacccggatgctggaggacggga agaaagtggacactccaggatcgcaacaaggccctaagttcatgtcg gaaagcaggaagtgtccaggatgggaggaaggcggtggcacagatgtc agtcggccagccggcaactgaccattagccctgactacgccttatggag caacaggccaccaggatcatccccctcatgccaccctggcttcgat gtggaaactgtcgaaatggggggggggatccggatttggggacgt gggggccctggagtcttcgaggaaatcccgatctggcttacatccgt

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-continued

gcatggaaacctgcggccactgtctgatcattaacaatgtgaacttcgc agagaaagcgactgcgaacacggactggctccaatattgactgtgagaa 5 gtcgcccggagaaggttctctagtcgcactttatggcgaagtggaaagggg atctgaccgccaagaaaatggctggccctgctggactggctcagcag gaccatggagactctggattgtcgctggcgtgatccgtccacgggtg 10 ccaggcttcatctgcagttcccccggagcagtgacggaaacagacggct gtccctgtcagcgtggagaagatcgtaacatctcaacggacttcgc cctagtcggggggaaaggccaaactgttcttacccaggccgtggcg 15 ggaacagaaagatcacggcttcgagggtggccagcaccaggccctgaggacg aatcaccaggcgaccaacctgaaaccagatgcaacttcattccaggaggga ctgaggaccccttgcaccatgtggatgtctatctcaagectgcccactcttag 20 tgacatttcgtgtttacagtaccttccaggcttgcattggcg atcccaagtccaggagctggatgtggagacactggacgacatcttcaa cagtgcccttcagaggacactgcagagccgtctgtcgagttggcaaa cgctgtctctgtgaaggccatctacaaacagatgcccgggtgtttcaatt 25 ttctgagaaagaaactgttcttaagacttcc.

In certain embodiments of the compositions of the disclosure, the first transposon and/or the second transposon comprises at least one self-cleaving peptide. In certain embodiments, the at least one self-cleaving peptide comprises a T2A peptide, a GSG-T2A peptide, an E2A peptide, a GSG-E2A peptide, an F2A peptide, a GSG-F2A peptide, a P2A peptide, or a GSG-P2A peptide. In certain embodiments, the at least one self-cleaving peptide comprises a T2A peptide. In certain embodiments, the T2A peptide comprises an amino acid sequence comprising EGRGSLLTCDVVEENPGP (SEQ ID NO: 17020). In certain embodiments, the GSG-T2A peptide comprises an amino acid sequence comprising GSGEGRGSLLTCDVVEENPGP (SEQ ID NO: 17021). In certain embodiments, the E2A peptide comprises an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 17022). In certain embodiments, the GSG-E2A peptide comprises an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 17023). In certain embodiments, the F2A peptide comprises an amino acid sequence comprising VKQTLNF DLLKLAGDVESNPGP (SEQ ID NO: 17024). In certain embodiments, the GSG-F2A peptide comprises an amino acid sequence comprising GSGVKQTLNF DLLKLAGDVESNPGP (SEQ ID NO: 17025). In certain embodiments, the P2A peptide comprises an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 17026). In certain embodiments, the GSG-P2A peptide comprises an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 17027). In certain embodiments, the at least one self-cleaving peptide is positioned between (a) the selection gene and the inducible transgene construct or (b) the inducible transgene construct and the inducible caspase polypeptide. In certain embodiments, the at least one self-cleaving peptide is positioned between (a) the selection gene and the reporter construct or (b) the reporter construct and the inducible caspase polypeptide.

The disclosure provides a cell comprising the composition of the disclosure.

The disclosure provides a method of inducing conditional gene expression in a cell comprising (a) contacting the cell with a composition of the disclosure, under conditions suitable to allow for integration of the inducible transgene construct into the genome of the cell and for the expression of the exogenous reporter and (b) contacting the exogenous receptor and a ligand that specifically binds thereto, to transduce an intracellular signal that targets the inducible promoter, thereby modifying gene expression. In certain embodiments, the cell is *in vivo*, *ex vivo*, *in vitro* or *in situ*. In certain embodiments, the cell is an immune cell. In certain embodiments, the immune cell is a T-cell, a Natural Killer (NK) cell, a Natural Killer (NK)-like cell, a hematopoietic progenitor cell, a peripheral blood (PB) derived T cell or an umbilical cord blood (UCB) derived T-cell. In certain embodiments, the immune cell is a T-cell. In certain embodiments, the cell is autologous. In certain embodiments, the cell is allogeneic.

The disclosure provides a method of treating a disease or disorder in a subject in need thereof, comprising administering to the subject a composition of the disclosure, under conditions suitable to allow for integration of the inducible transgene construct into the genome of the cell and for the expression of the exogenous reporter, and administering a ligand to which the exogenous receptor selectively binds, wherein the binding of the ligand to the exogenous receptor transduces an intracellular signal to target the inducible promoter controlling the transgene, wherein the transgene is expressed, and wherein the product of the transgene is therapeutically-effective for treating the disease or disorder. In certain embodiments, the product of the transgene is a secreted protein. In certain embodiments, the secreted protein is a clotting factor. In certain embodiments, the clotting factor is factor IX. In certain embodiments, the disease or disorder is a clotting disorder.

In certain embodiments of the methods of the disclosure, conditions suitable to allow for integration of the inducible transgene construct into the genome of the cell and for the expression of the exogenous reporter comprise *in vivo* conditions. In certain embodiments, conditions suitable to allow for integration of the inducible transgene construct into the genome of the cell and for the expression of the exogenous reporter comprise a temperature substantially similar to an internal temperature of a human body, a CO₂ level substantially similar to an internal CO₂ levels of a human body, an O₂ level substantially similar to an internal O₂ levels of a human body, an aqueous or saline environment with a level of electrolytes substantially similar to a level of electrolytes of an interior of a human body.

In certain embodiments of the compositions and methods of the disclosure, the ligand to which the exogenous receptor specifically binds is non-naturally occurring. In certain embodiments, the ligand is a nucleic acid, an amino acid, a polymer, an organic small molecule, an inorganic small molecule, or a combination thereof. Exemplary ligands include, but are not limited to, synthetic, modified, recombinant, mutant, chimeric, endogenous or non-naturally occurring, proteins (soluble or membrane-bound), steroid hormones, gas particles, nucleic acids, growth factors, neurotransmitters, vitamins, and minerals.

The disclosure provides a composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a ligand construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous ligand, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic

sequence of a cell, the exogenous ligand is expressed, and wherein the exogenous ligand, upon binding a receptor, transduces an intracellular signal that targets the inducible promoter of (a) to modify gene expression. In certain embodiments, the ligand comprises a non-natural or synthetic sequence. In certain embodiments, the ligand comprises a fusion protein. In certain embodiments, the ligand is bound to the surface of the cell. In certain embodiments, the ligand comprises an intracellular domain. In certain embodiments, the intracellular domain transduces a signal in the cell expressing the ligand. In certain embodiments, the structure of the ligand is substantially similar to the structure of the receptor of the compositions of the disclosure. In certain embodiments, the signal transduced by the ligand and the signal transduced by the receptor comprise a bi-directional signal.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A-B is a pair of schematic diagrams depicting NF-KB inducible vectors for expression in T-cells. Two T cell activation NF-KB inducible vectors were developed; one with the gene expression system (GES) in the forward orientation (A) and the other in the complementary direction (B), both preceding the constitutive EF1a promoter. These vectors also direct expression of a CAR molecule and a DHFR selection gene, separated by a T2A sequence. Both the conditional NF-KB inducible system and the EF1a directed genes are a part of a piggyBac transposon which can be permanently integrated into T cells using electroporation (EP). Once integrated into the genome, the T cells will constitutively express the CAR on the membrane surface and the DHFR within the cell, while expression of the NF-KB inducible gene, GFP, will be expressed to the highest level only upon T cell activation.

FIG. 2 is a pair of graphs depicting NF-KB inducible expression of GFP in activated T cells. T cells were nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR murein gene under control of an EF1a promoter along with the absence (No GES control) or presence of an NF-KB inducible expression system driving GFP expression in either the forward (pNFKB-GFP forward) or reverse orientation (pNFKB-GFP reverse). Cells were cultured in the presence of methotrexate selection until the cells were almost completely resting (Day 19) and GFP expression was assessed at Day 5 and Day 19. At Day 5, all T cells are proliferating and highly stimulated, with cells harboring the NF-KB inducible expression cassette producing high levels of GFP due to strong NF κ B activity. The No GES control cells did not express detectable levels of GFP. By Day 19, the GES T cells were almost fully resting and GFP expression was significantly lower than Day 5 (~1/8 MFI), since NF κ B activity is lower. GFP expression is still observed at Day 19, which may be due to the long half-life of GFP protein (~30 hr), or, basal level of NF κ B activity through, for example, a TCR, a CAR, a cytokine receptor, or a growth factor receptor signal.

FIG. 3 is a series of graphs depicting anti-BCMA CAR-mediated activation of NF-KB inducible expression of GFP in presence of BCMA+ tumor cells. T cells were either unmodified (Mock T cells) or nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR murein gene under control of an EF1a promoter along with the absence (No GES control) or presence of an NF-KB inducible expression system driving GFP expression in either the forward (pNFKB-GFP forward) or reverse orientation (pNFKB-GFP reverse). All cells were cultured for 22 days,

either with or without methotrexate selection (Mock T cells), until the cells were almost completely resting. Cells were then stimulated for 3 days in the absence (No stimulation) or presence of BCMA- (K562), BCMA+ (RPMI 8226), or positive control anti-CD3 anti-CD28 activation reagent (CD3/28 stimulation). GFP expression was undetectable under all conditions with the No GES control or Mock T cells. However, while pNFKB-GFP forward- and reverse-transposed cells exhibited little GFP expression over the No stimulation control when cultured with BCMA- K562 cells, they both demonstrated dramatic upregulation of gene expression either in the presence of BCMA+ tumor cells or under positive control conditions. Little difference in GFP expression was observed between the pNFKB-GFP forward- and reverse-transposed cells that were cocultured with BCMA+ tumor cells.

FIG. 4 is a series of graphs demonstrating that the Expression level of inducible gene can be regulated by number of response elements preceding the promoter T cells were nucleofected with a piggyBac vector encoding an anti-BCMA CARTyrin followed by a selection gene, both under control of a human EF1a promoter. Further, vectors either additionally encoded the conditional NF-KB inducible gene expression system driving expression of a truncated CD19 protein (dCD19) and included a number of NFKB response elements (RE) varying from 0-5, no GES (No GES), or received an electroporation pulse but no piggyBac nucleic acid (Mock). Data are shown for only the GES in the reverse (opposite) direction/orientation. All cells were cultured for 18 days and included selection for piggy-Bac-modified T cells using methotrexate addition. Cells were then stimulated for 3 days using anti-CD3 anti-CD28 bead activation reagent and dCD19 surface expression was assessed by FACS at Days 0, 3 and 18, and data are shown as FACS histograms and MF of target protein staining. Surface dCD19 expression was detected at low levels at Day 0 in all T cells transposed with vectors encoding the GES. At 3 days post-stimulation, dramatic upregulation of dCD19 expression was observed for all T cells expressing the GES, with a greater fold increase in surface expression in those with higher numbers of REs. Thus, surface dCD19 expression was directly proportional with the number of REs encoded in the GES. No dCD19 was detected on the surface of T cells that did not harbor the GES: No GES and Mock controls.

FIG. 5 is a schematic diagram showing the human coagulation pathway leading to blood clotting. Contact activation, for example by damaging an endothelium, activates an intrinsic clotting pathway. Tissue factors activate an extrinsic clotting pathway, for example following trauma Both pathways converge onto the conversion of Prothrombin into Thrombin, which catalyzes the conversion of fibrinogen into fibrin. Polymerized fibrin together with platelets forms a clot. In the absence of Factor IX (circled), clotting is defective. Factor VII (FVIII) deficiency leads to development of Hemophilia A. Factor IX (FIX) deficiency leads to development of Hemophilia B. Prior to the compositions and methods of the disclosure, the standard treatment for hemophilia B involved an infusion of recombinant FIX every 2 to 3 days, at an expense of approximately \$250,000 per year. In sharp contrast to this standard treatment option, T cells of the disclosure are maintained in humans for several decades.

FIG. 6 is a series of Fluorescence-Activated Cell Sorting (FACS plots) depicting FIX-secreting T cells. T cells encoding a human Factor IX transgene showed a T-cell phenotype in approximately 80% of cells. The 6 panels are described in

order from left to right. (1) Forward scatter (FSC) on the x-axis versus side scatter (SSC) on the y-axis. The x-axis is from 0 to 250 thousand (abbreviated k) in increments of 50k, the y-axis is for 0 to 250k, in increments of 50k. (2) FSC on the x-axis versus the cell viability marker 7 aminoactinomycin D (7AAD). The x-axis is labeled from 0 to 250k in increments of 50k. The y-axis reads, from top to bottom, -10^3 , 0, 10^3 , 10^4 , 10^5 . (3) On the x-axis is shown anti-CD56-APC conjugated to a Cy7 dye (CDC156-APC-Cy7), units from 0 to 10^5 incrementing in powers of 10. On the y-axis is shown anti-CD3 conjugated to phycoerythrin (PE), units from 0 to 10^5 incrementing in powers of 10. (4) On the x-axis is shown anti-CD8 conjugated to fluorescein isothiocyanate (FITC), units from 0 to 10^5 incrementing in powers of 10. On the y-axis is shown anti-CD4 conjugated to Brilliant Violet 650 dye (BV650), units from 0 to 10^5 incrementing in powers of 10. (5) On the x-axis is shown an anti CD62L antibody conjugated to a Brilliant Violet 421 dye (BV421), units from 0 to 10^5 incrementing in powers of 10. On the y-axis is shown an anti-CD45RA antibody conjugated to PE and Cy7, units from 0 to 10^5 incrementing in powers of 10. This panel is boxed. (6) On the x-axis is shown an anti-CCR7 antibody conjugated to Brilliant Violet 786 (BV786), units from 0 to 10 incrementing in powers of 10. On the y-axis is shown anti-CD45RA conjugated to PE and Cy7, units from 0 to 10^5 incrementing in powers of 10.

FIG. 7A is a graph showing human Factor IX secretion during production of modified T cells of the disclosure. On the y-axis, Factor IX concentration in nanograms (ng) per milliliter (mL) from 0 to 80 in increments of 20. On the x-axis are shown 9 day and 12 day T cells.

FIG. 7B is a graph showing the clotting activity of the secreted Factor IX produced by the T cells. On the y-axis is shown percent Factor IX activity relative to human plasma, from 0 to 8 in increments of 2. On the x-axis are 9 and 12 day T cells.

FIG. 8 is a series of graphs demonstrating that the expression level of inducible gene can be regulated by number of response elements preceding the promoter in CD4 positive cells. Truncated CD19 (dCD19) expressing CAR-T cells were stimulated by BCMA+ H929 multiple myeloma cells at 2:1 CAR-T:H929 ratio. The expression of dCD19 was driven by the minimal promoter that enhanced by 0, 1, 2, 3, 4 or 5 repeats of the NF-kB response element. The expression of BCMA CAR was driven by human elongation factor- α (EF-1 α) promoter, a constitutive promoter that is commonly used for gene expression in human T cells. Before tumor cell stimulation, the expression of CAR and dCD19 were both at basal levels compared to mock T cell control. The expression levels of CAR and dCD19 were both upregulated upon tumor stimulation (day 3) and then subsequently downregulated (day 9, 14) and eventually reached their respective basal levels when the cells resume a fully rested status again (day 20). However, CAR surface expression was equivalently up- or down-regulated in all the CAR-T cell samples during cell activation and resting process, while the expression levels of dCD19 were directly proportional to the number of NF-kB response elements (day 3, 9, 14). Data are shown as FACS histograms and MFI of target protein staining. Thus, surface dCD19 expression was directly proportional with the number of REs encoded in the GES. No dCD19 was detected on the surface of T cells that did not harbor the GES: No GES and Mock controls.

FIG. 9 is a series of graphs demonstrating that the expression level of inducible gene can be regulated by number of response elements preceding the promoter in

CD8 positive cells. Truncated CD19 (dCD19) expressing CAR-T cells were stimulated by BCMA+ H929 multiple myeloma cells at 2:1 CAR-T:H929 ratio. The expression of dCD19 was driven by the minimal promoter that enhanced by 0, 1, 2, 3, 4 or 5 repeats of the NF- κ B response element. The expression of BCMA CAR was driven by human elongation factor-1 α (EF-1 α) promoter, a constitutive promoter that is commonly used for gene expression in human T cells. Before tumor cell stimulation, the expression of CAR and dCD19 were both at basal levels compared to mock T cell control. The expression levels of CAR and dCD19 were both upregulated upon tumor stimulation (day 3) and then subsequently downregulated (day 9, 14) and eventually reached their respective basal levels when the cells resume a fully rested status again (day 20). However, CAR surface expression was equivalently up- or downregulated in all the CAR-T cell samples during cell activation and resting process, while the expression levels of dCD19 were directly proportional to the number of NF- κ B response elements (day 3, 9, 14). Data are shown as FACS histograms and MFI of target protein staining. Thus, surface dCD19 expression was directly proportional with the number of REs encoded in the GES. No dCD19 was detected on the surface of T cells that did not harbor the GES: No GES and Mock controls.

FIG. 10 is a bar graph depicting the knock out efficiency of targeting various checkpoint signaling proteins that could be used to armor T-cells. Cas-CLOVER was used to knock-out the checkpoint receptors. PD-1, TGFBR2, LAG-3, TIM-3 and CTLA-4 in resting primary human pan T cells. Percent knock-out is shown on the y-axis. Gene editing resulted in 30-70% loss of protein expression at the cell surface as measured by flow cytometry.

FIG. 11 is a series of schematic diagrams of wildtype, null and switch receptors and their effects on intracellular signaling, either inhibitory or stimulatory, in primary T-cells. Binding of the wildtype inhibitory receptor expressed endogenously on a T-cell with its endogenous ligand results in transmission of an inhibitory signal which, in part, reduces T-cell effector function. However, mutation (Mutated null) or deletion (Truncated null) of the intracellular domain (ICD) of a checkpoint receptor protein, such as PD1 (top panel) or TGFBRII (bottom panel), reduces or eliminates its signaling capability when cognate ligand(s) is bound. Thus, expression of engineered mutated or truncated null receptors on the surface of modified T cells results in a competition with endogenously-expressed wildtype receptors for binding of the free endogenous ligand(s), effectively reducing or eliminating delivery of inhibitory signals by endogenously-expressed wildtype receptors. Specifically, any binding by a mutated or null receptor sequesters the endogenous ligand(s) from binding the wildtype receptor and results in dilution of the overall level of checkpoint signaling effectively delivered to the modified T-cell, thereby reducing or blocking checkpoint inhibition and functional exhaustion of the modified T cells. A switch receptor is created by replacement of the wildtype ICD with an ICD from either a co-stimulatory molecule (such as CD3z, CD28, 4-1BB) or a different inhibitory molecule (such as CTLA4, PD1, Lag3). In the former case, binding of the endogenous ligand(s) by the modified switch receptor results in the delivery of a positive signal to the T-cells, thereby helping to enhance stimulation of the modified T cell and potentially enhance target tumor cell killing. In the latter case, binding of the endogenous ligand(s) by the modified switch receptor results in the delivery of a negative signal to the T-cells, thereby eliminating stimulation of the modified

T cell and potentially reducing target tumor cell killing. The signal peptide (purple arrow), extracellular domain (ECD) (bright green), transmembrane domain (yellow), intracellular signaling domain (ICD)(orange), and replacement ICD (green) are displayed in the receptor diagrams. “*” indicates a mutated ICD. “+” indicates the presence of a checkpoint signal. “-” indicates the absence of a checkpoint signal.

FIG. 12 is a schematic diagram showing an example of the design of null receptors with specific alterations that may help to increase expression of the receptor on the surface of modified T cells. Examples are shown for PD1 and TGFBRII null receptors and the signal peptide domain (SP), transmembrane domain (TM) and extracellular domain (ECD) of truncated null receptors for PD1 (top panel) and TGFBRII (bottom panel) are displayed. The first of the top four molecules is the wildtype PD-1 receptor, which encodes the wildtype PD-1 SP and TM. For the PD1 null receptor, replacement of PD1 wildtype SP or TM domain (green; light green) with the SP or TM domain of a human T cell CD8a receptor (red) is depicted. The second molecule encodes the CD8a SP along with the native PD-1 TM, the third encodes the wildtype PD-1 SP and the alternative CD8a TM, and the fourth encodes both the alternative CD8a SP and TM. Similarly, for the null receptor of TGF β RII, replacement of the wildtype TGFBRII SP (pink) with a SP domain of a human T cell CD8a receptor (red). The names of the constructs and the amino acid lengths (aa) of each construct protein is listed on the left of the diagram.

FIG. 13 is a series of histograms depicting the expression of the PD1 and TGFBRII null Receptors on the surface of modified primary human T cells as determined by flow cytometry. Each of the six truncated null constructs from FIG. 12 were expressed on the surface of primary human T cells. T cells were stained with either anti-PD1 (top; blue histograms) or anti-TGF β RII (bottom; blue histograms), or isotype control or secondary only (gray histograms). Cells staining positive for PD-1 or TGF β RII expression were gated (frequency shown above gate) and mean fluorescence intensity (MFI) value is displayed above each positive histogram. The names of the null receptor constructs are depicted above each plot. Both null receptor gene strategies, replacement of the wildtype SP with the alternative CD8a were successfully expressed. 02.8aSP-PD- and 02.8aSP-TGF β RII resulted in the highest level of expression at the T-cell surface. 02.8aSP-PD-1 null receptor exhibited an MFI of 43,680, which is 177-fold higher than endogenous T cell PD-1 expression and 2.8-fold higher than the wildtype PD-1 null receptor. 02.8aSP-TGF β RII null receptor exhibited an MFI of 13,809, which is 102-fold higher than endogenous T cell TGF β RII expression and 1.8-fold higher than the wildtype TGF β RII null receptor. Replacement of wildtype SP with the alternative CD8a SP for both PD1 and TGRBRII results in enhanced surface expression of the null or Switch receptor, which may help to maximize reduction or blockage of checkpoint inhibition upon binding and sequestration of the endogenous ligand(s).

FIG. 14 is a schematic depiction of the Csy4-T2A-Clo051-G4Slinker-dCas9 construct map (Embodiment 2).

FIG. 15 is a schematic depiction of the pRT-Clo051-dCas9 Double NLS construct map (Embodiment 1).

FIG. 16 is a pair of graphs comparing the efficacy of knocking out expression of either B2M on the surface of Pan T-cells (left) or the α -chain of the T-cell Receptor on the surface of Jurkat cells (right) for either Embodiment 1 (pRT1-Clo051-dCas9 Double NLS, as shown in FIG. 15) or Embodiment 2 (Csy4-T2A-Clo051-G4Slinker-dCas9, as shown in FIG. 14) of a Cas-Clover fusion protein of the

disclosure. For the right-hand graph, the fusion protein is provided at either 10 µg or 20 µg, as indicated.

FIG. 17 is a photograph of a gel electrophoresis analysis of mRNA encoding each of Embodiment 1 (Lane 2; pRT1-Clo051-dCas9 Double NLS, as shown in FIG. 15) or Embodiment 2 (Lane 3; Csy4-T2A-Clo051-G4SLinker-dCas9, as shown in FIG. 14). In addition, a previous preparation (“old version”) of mRNA encoding Embodiment 2 is included (Lane 4) for comparison. As shown, all mRNA samples encoding the two different embodiments migrate as distinct bands within the gel, are of high quality, and are similar in size, as expected.

DETAILED DESCRIPTION

The disclosure provides a composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a receptor construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous receptor, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic sequence of a cell, the exogenous reporter is expressed, and wherein the exogenous reporter, upon binding a ligand, transduces an intracellular signal that targets the inducible promoter of (a) to modify gene expression.

Exogenous Receptors

Exogenous receptors of the disclosure may comprise a non-naturally occurring receptor. In certain embodiments, the non-naturally occurring receptor is a synthetic, modified, recombinant, mutant or chimeric receptor. In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a T-cell receptor (TCR). In certain embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a scaffold protein. In certain embodiments, the non-naturally occurring receptor comprises a transmembrane domain. In certain embodiments, the non-naturally occurring receptor interacts with an intracellular receptor that transduces an intracellular signal. In certain embodiments, the non-naturally occurring receptor comprises an intracellular signaling domain. In certain embodiments, the non-naturally occurring receptor is a chimeric ligand receptor (CLR). In certain embodiments, the CLR is a chimeric antigen receptor.

In certain embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In certain embodiments, the CLR is a chimeric antigen receptor. In certain embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain.

The disclosure provides chimeric receptors comprising at least one Centyrrin. Chimeric ligand/antigen receptors (CLRs/CARs) of the disclosure may comprise more than one Centyrrin, referred to herein as a CARTyrrin.

The disclosure provides chimeric receptors comprising at least one VHHL. Chimeric ligand/antigen receptors (CLRs/CARs) of the disclosure may comprise more than one VHHL, referred to herein as a VCAR.

Chimeric receptors of the disclosure may comprise a signal peptide of human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR. A hinge/spacer domain of the disclosure may comprise a hinge/spacer/stalk of human CD8α, IgG4, and/or CD4. An intra-

cellular domain or endodomain of the disclosure may comprise an intracellular signaling domain of human CD3ζ and may further comprise human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. Exemplary transmembrane domains include, but are not limited to a human CD2, CD36, CD3e, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR transmembrane domain.

The disclosure provides genetically modified cells, such as T cells, NK cells, hematopoietic progenitor cells, peripheral blood (PB) derived T cells (including T cells from G-CSF-mobilized peripheral blood), umbilical cord blood (UCB) derived T cells rendered specific for one or more ligands or antigens by introducing to these cells a CLR/CAR, CARTyrrin and/or VCAR of the disclosure. Cells of the disclosure may be modified by electrotransfer of a transposon of the disclosure and a plasmid or a nanoplasmid comprising a sequence encoding a transposase of the disclosure (preferably, the sequence encoding a transposase of the disclosure is an mRNA sequence).

In some embodiments, the armored T-cell comprises a composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a receptor construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous receptor, such as a CLR or CAR, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic sequence of a cell, the exogenous receptor is expressed, and wherein the exogenous receptor, upon binding a ligand or antigen, transduces an intracellular signal that targets directly or indirectly the inducible promoter regulating expression of the inducible transgene (a) to modify gene expression.

Chimeric Receptors

Chimeric antigen receptors (CARs) and/or chimeric ligand receptors (CLRs) of the disclosure may comprise (a) an ectodomain comprising an antigen/ligand recognition region, (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In certain embodiments, the ectodomain may further comprise a signal peptide. Alternatively, or in addition, in certain embodiments, the ectodomain may further comprise a hinge between the antigen/ligand recognition region and the transmembrane domain. In certain embodiments of the CARs of the disclosure, the signal peptide may comprise a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR signal peptide. In certain embodiments of the CARs of the disclosure, the signal peptide may comprise a sequence encoding a human CD8α signal peptide. In certain embodiments, the transmembrane domain may comprise a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR transmembrane domain. In certain embodiments of the CARs of the disclosure, the transmembrane domain may comprise a sequence encoding a human CD8α transmembrane domain. In certain embodiments of the CARs/CLRs of the disclosure, the endodomain may comprise a human CD3ζ endodomain.

In certain embodiments of the CARs/CLRs of the disclosure, the at least one costimulatory domain may comprise a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. In certain embodiments of the CARs of the disclosure, the at least one costimulatory domain may comprise a CD28 and/or a 4-1BB costimulatory domain. In certain embodiments of the CARs of the disclosure, the hinge may comprise a sequence

derived from a human CD8 α , IgG4, and/or CD4 sequence. In certain embodiments of the CARs/CLRs of the disclosure, the hinge may comprise a sequence derived from a human CD8 α sequence.

The CD28 costimulatory domain may comprise an amino acid sequence comprising RVKFSRSADAPAYKQQQNQLYNELNLGRREEYDVLKDERRGRDKPRRNPKQ EGLYNELQDKDMAEAYSEIGMKGERRRGKGHDGLYQGLSIATKDTYDALHMQ-ALP PR (SEQ ID NO: 17004) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising RVKFSRSADAPAYKQQQNQLYNELNLGRREEYDVLKDERRGRDKPRRNPKQ EGLYNELQDKDMAEAYSEIGMKGERRRGKGHDGLYQGLSIATKDTYDALHMQ-ALP PR (SEQ ID NO: 17004). The CD28 costimulatory domain may be encoded by the nucleic acid sequence comprising cccgtgaatgttttcgatcggatcgatgcaggatgttgcataacggatctggccggccga gag-gaatatgcgtgtggataagcgaggagggcggatccggccaaatggag-geaagecccgaggcggccaaaacccctcaggaggatcgatcgatgcaggatggggggggcgacggaggaggcaagg gcac-gatgggctgtaccaggactgaggccaccccaaggacacccatgtatgcctgcatatgcaggcactgcctccaagg (SEQ ID NO: 17005). The 4-1BB costimulatory domain may comprise an amino acid sequence comprising KRGRKKLLY-IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 17006) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising

(SEQ ID NO: 17006)
KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB costimulatory domain may be encoded by the nucleic acid sequence comprising aagagaggcaggaaactctgttatatttcaaacagcccttcatgcgccccgtgcagac-tacccaggagggaaagacgggtgcctc tgcgttgcattccctgaggaagagaaggcgggtgcgt (SEQ ID NO: 17007) The 4-1BB costimulatory domain may be located between the transmembrane domain and the CD28 costimulatory domain.

In certain embodiments of the CARs/CLRs of the disclosure, the hinge may comprise a sequence derived from a human CD8 α , IgG4, and/or CD4 sequence. In certain embodiments of the CARs/CLRs of the disclosure, the hinge may comprise a sequence derived from a human CD8 α sequence. The hinge may comprise a human CD8 α amino acid sequence comprising TTTPAPRPPPTPAPTIA-SQPLSLRPEACRPAAGGAHVTRGLDFACD (SEQ ID NO: 17008) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising

(SEQ ID NO: 17008)
TTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAHVTRGLDFACD.

The human CD8 α hinge amino acid sequence may be encoded by the nucleic acid sequence comprising

(SEQ ID NO: 17028)
actaccacaccagcacctagaccaccaactccagtcacccatc
gcgagtccggccctcgatctcgatccgcggccatgcaggccagtc
gcaggaggagctgtgcacaccaggcccggacttcgcctgcgac.

ScFv

The disclosure provides single chain variable fragment (scFv) compositions and methods for use of these compositions to recognize and bind to a specific target protein. ScFv compositions comprise a heavy chain variable region and a light chain variable region of an antibody. ScFv compositions may be incorporated into an antigen/ligand recognition region of a CAR or CLR of the disclosure. An antigen/ligand recognition region of a CAR or CLR of the disclosure may comprise an ScFv or an ScFv composition of the disclosure. In some embodiments, ScFvs comprise fusion proteins of the variable regions of the heavy (VH) and light (VL) chains of an immunoglobulin, wherein the VH and VL domains are connected with a linker. ScFvs retain the specificity of the original immunoglobulin, despite removal of the constant regions and the introduction of the linker. An exemplary linker comprises a sequence of GGGGGGGGGGGGGGS (SEQ ID NO: 17033).

Centyrins

Centyrins of the disclosure specifically bind to an antigen or a ligand of the disclosure. CARs and/or CLRs of the disclosure comprising one or more Centyrins that specifically bind an antigen may be used to direct the specificity of a cell, (e.g. a cytotoxic immune cell) towards a cell expressing the specific antigen. Alternatively or in addition, CLRs of the disclosure comprising a Centyrin that specifically binds a ligand antigen may transduce a signal intracellularly to induce expression of a sequence under the control of an inducible promoter.

Centyrins of the disclosure may comprise a protein scaffold, wherein the scaffold is capable of specifically binding an antigen or a ligand. Centyrins of the disclosure may comprise a protein scaffold comprising a consensus sequence of at least one fibronectin type III (FN3) domain, wherein the scaffold is capable of specifically binding an antigen or a ligand. The at least one fibronectin type III (FN3) domain may be derived from a human protein. The human protein may be Tenascin-C. The consensus sequence may comprise

(SEQ ID NO: 17010)
LPAPKNLVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAI
NLTVPGSERSYDLTGLKPGTEYTVSIYGVKGHHRSNPLSAEFTT
or
(SEQ ID NO: 17011)
MLPAPKNLVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEA
INLTVPGSERSYDLTGLKPGTEYTVSFYGVKGHHRSNPLSAEFTT.

A Centyrin may comprise an amino sequence having at least 50%, 55%, 60% 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or any percentage in between of identity to the sequence of

(SEQ ID NO: 17010)
LPAPKNLVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAI
NLTVPGSERSYDLTGLKPGTEYTVSIYGVKGHHRSNPLSAEFTT
or
(SEQ ID NO: 17011)
MLPAPKNLVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEA
INLTVPGSERSYDLTGLKPGTEYTVSIYGVKGHHRSNPLSAEFTT.

A Centyrin may comprise an amino sequence having at least 74% identity to the sequence of

(SEQ_ID_NO: 17010)
LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYOESEKVGAEI

NLTVPGSERSYDLTGLKPGTEYTVSIYGVKGGRSNPLSAEFTT
or

(SEQ ID NO: 17011)
MLPAPKNLVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEE
INLTVPGSGERSYDLTGLKGPTETYTVSIYGVKGGHRSNPLSAEFTT.

The consensus sequence may be encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17034)
atgctgcctgcaccaaagaacacctgggtgtctcatgtgacagagg
atagtgccagactgtcatggactgctcccacgcagcggcttcgatag
tttatcatcggtaccgggagaacatcgaaacccggcgaggccatt
gtcctgacagtgcgcagggtccgaacgctttatgacctgacagatc
tgaagccccggaacttgagtactatgtgcagatcgccggcgtcaaagg
aggcaatatacgatccctgtccggatcttaccaca.

The consensus sequence may be modified at one or more positions within (a) a A-B loop comprising or consisting of the amino acid residues TEDS (SEQ ID NO: 17035) at positions 13-16 of the consensus sequence; (b) a B-C loop comprising or consisting of the amino acid residues TAP-DAAF (SEQ ID NO: 17036) at positions 22-28 of the consensus sequence; (c) a C-D loop comprising or consisting of the amino acid residues SEKVGE (SEQ ID NO: 17037) at positions 38-43 of the consensus sequence; (d) a D-E loop comprising or consisting of the amino acid residues GSER (SEQ ID NO: 17038) at positions 51-54 of the consensus sequence; (e) a E-F loop comprising or consisting of the amino acid residues GLKPG (SEQ ID NO: 17039) at positions 60-64 of the consensus sequence; (f) a F-G loop comprising or consisting of the amino acid residues KGGHRSN (SEQ ID NO: 17040) at positions 75-81 of the consensus sequence; or (g) any combination of (a)-(f). Centyrins of the disclosure may comprise a consensus sequence of at least 5 fibronectin type III (FN3) domains, at least 10 fibronectin type III (FN3) domains or at least 15 fibronectin type III (FN3) domains.

The Centryrin may bind an antigen or a ligand with at least one affinity selected from a K_D of less than or equal to $10^{-9}M$, less than or equal to $10^{-10}M$, less than or equal to $10^{-11}M$, less than or equal to $10^{-12}M$, less than or equal to $10^{-13}M$, less than or equal to $10^{-14}M$, and less than or equal to $10^{-15}M$. The K_D may be determined by surface plasmon resonance.

Antibody Mimetic

The term "antibody mimetic" is intended to describe an organic compound that specifically binds a target sequence and has a structure distinct from a naturally-occurring antibody. Antibody mimetics may comprise a protein, a nucleic acid, or a small molecule. The target sequence to which an antibody mimetic of the disclosure specifically binds may be an antigen. Antibody mimetics may provide superior properties over antibodies including, but not limited to, superior solubility, tissue penetration, stability towards heat and enzymes (e.g. resistance to enzymatic degradation), and lower production costs. Exemplary antibody mimetics

include, but are not limited to, an affibody, an affilin, an affimer, an affitin, an alphabody, an anticalin, and avimer (also known as avidity multimer), a DARPin (Designed Ankyrin Repeat Protein), a Fynomer, a Kunitz domain peptide, and a monobody.

Affibody molecules of the disclosure comprise a protein scaffold comprising or consisting of one or more alpha helix without any disulfide bridges. Preferably, affibody molecules of the disclosure comprise or consist of three alpha helices.

10 For example, an affibody molecule of the disclosure may comprise an immunoglobulin binding domain. An affibody molecule of the disclosure may comprise the Z domain of protein A.

Affilin molecules of the disclosure comprise a protein scaffold produced by modification of exposed amino acids of, for example, either gamma-B crystallin or ubiquitin. Affilin molecules functionally mimic an antibody's affinity to antigen, but do not structurally mimic an antibody. In any protein scaffold used to make an affilin, those amino acids that are accessible to solvent or possible binding partners in a properly-folded protein molecule are considered exposed amino acids. Any one or more of these exposed amino acids may be modified to specifically bind to a target sequence or antigen.

antigen.

25 Affimer molecules of the disclosure comprise a protein scaffold comprising a highly stable protein engineered to display peptide loops that provide a high affinity binding site for a specific target sequence. Exemplary affimer molecules of the disclosure comprise a protein scaffold based upon a

30 cystatin protein or tertiary structure thereof. Exemplary affimer molecules of the disclosure may share a common tertiary structure of comprising an alpha-helix lying on top of an anti-parallel beta-sheet.

Affitin molecules of the disclosure comprise an artificial protein scaffold, the structure of which may be derived, for example, from a DNA binding protein (e.g. the DNA binding protein Sac7d). Affitins of the disclosure selectively bind a target sequence, which may be the entirety or part of an antigen. Exemplary affitins of the disclosure are manufactured by randomizing one or more amino acid sequences on the binding surface of a DNA binding protein and subjecting the resultant protein to ribosome display and selection. Target sequences of affitins of the disclosure may be found, for example, in the genome or on the surface of a peptide, protein, virus, or bacteria. In certain embodiments of the disclosure, an affitin molecule may be used as a specific inhibitor of an enzyme. Affitin molecules of the disclosure may include heat-resistant proteins or derivatives thereof.

Alphabody molecules of the disclosure may also be referred to as Cell-Penetrating Alphabodies (CPAB). Alphabody molecules of the disclosure comprise small proteins (typically of less than 10 kDa) that bind to a variety of target sequences (including antigens). Alphabody molecules are capable of reaching and binding to intracellular target sequences. Structurally, alphabody molecules of the disclosure comprise an artificial sequence forming single chain alpha helix (similar to naturally occurring coiled-coil structures). Alphabody molecules of the disclosure may comprise a protein scaffold comprising one or more amino acids that are modified to specifically bind target proteins. Regardless of the binding specificity of the molecule, alphabody molecules of the disclosure maintain correct folding and thermostability.

Anticalin molecules of the disclosure comprise artificial proteins that bind to target sequences or sites in either proteins or small molecules. Anticalin molecules of the disclosure may comprise an artificial protein derived from a

human lipocalin. Anticalin molecules of the disclosure may be used in place of, for example, monoclonal antibodies or fragments thereof. Anticalin molecules may demonstrate superior tissue penetration and thermostability than monoclonal antibodies or fragments thereof. Exemplary anticalin molecules of the disclosure may comprise about 180 amino acids, having a mass of approximately 20 kDa. Structurally, anticalin molecules of the disclosure comprise a barrel structure comprising antiparallel beta-strands pairwise connected by loops and an attached alpha helix. In preferred embodiments, anticalin molecules of the disclosure comprise a barrel structure comprising eight antiparallel beta-strands pairwise connected by loops and an attached alpha helix.

Avimer molecules of the disclosure comprise an artificial protein that specifically binds to a target sequence (which may also be an antigen). Avimers of the disclosure may recognize multiple binding sites within the same target or within distinct targets. When an avimer of the disclosure recognize more than one target, the avimer mimics function of a bi-specific antibody. The artificial protein avimer may comprise two or more peptide sequences of approximately 30-35 amino acids each. These peptides may be connected via one or more linker peptides. Amino acid sequences of one or more of the peptides of the avimer may be derived from an A domain of a membrane receptor. Avimers have a rigid structure that may optionally comprise disulfide bonds and/or calcium. Avimers of the disclosure may demonstrate greater heat stability compared to an antibody.

DARPins (Designed Ankyrin Repeat Proteins) of the disclosure comprise genetically-engineered, recombinant, or chimeric proteins having high specificity and high affinity for a target sequence. In certain embodiments, DARPins of the disclosure are derived from ankyrin proteins and, optionally, comprise at least three repeat motifs (also referred to as repetitive structural units) of the ankyrin protein. Ankyrin proteins mediate high-affinity protein-protein interactions. DARPins of the disclosure comprise a large target interaction surface.

Fynomers of the disclosure comprise small binding proteins (about 7 kDa) derived from the human Fyn SH3 domain and engineered to bind to target sequences and molecules with equal affinity and equal specificity as an antibody.

Kunitz domain peptides of the disclosure comprise a protein scaffold comprising a Kunitz domain. Kunitz domains comprise an active site for inhibiting protease activity. Structurally, Kunitz domains of the disclosure comprise a disulfide-rich alpha+beta fold. This structure is exemplified by the bovine pancreatic trypsin inhibitor. Kunitz domain peptides recognize specific protein structures and serve as competitive protease inhibitors. Kunitz domains of the disclosure may comprise Ecallantide (derived from a human lipoprotein-associated coagulation inhibitor (LACI)).

Monobodies of the disclosure are small proteins (comprising about 94 amino acids and having a mass of about 10 kDa) comparable in size to a single chain antibody. These genetically engineered proteins specifically bind target sequences including antigens. Monobodies of the disclosure may specifically target one or more distinct proteins or target sequences. In preferred embodiments, monobodies of the disclosure comprise a protein scaffold mimicking the structure of human fibronectin, and more preferably, mimicking the structure of the tenth extracellular type III domain of fibronectin. The tenth extracellular type III domain of fibronectin, as well as a monobody mimetic thereof, contains

seven beta sheets forming a barrel and three exposed loops on each side corresponding to the three complementarity determining regions (CDRs) of an antibody. In contrast to the structure of the variable domain of an antibody, a monobody lacks any binding site for metal ions as well as a central disulfide bond. Multispecific monobodies may be optimized by modifying the loops BC and FG. Monobodies of the disclosure may comprise an adnectin. VHH

In certain embodiments of the compositions and methods of the disclosure, a CAR or a CLR comprises a single domain antibody (SdAb). In certain embodiments, the SdAb is a VHH.

The disclosure provides a CAR or a CLR comprising an antigen or ligand recognition region, respectively, that comprises at least one VHH (to produce a "VCAR" or "VCLR"). CARs and CLRs of the disclosure may comprise more than one VHH. For example, a bi-specific VCAR or VCLR may comprise two VHHs. In some embodiments of the bi-specific VCAR or VCLR, each VHH specifically binds a distinct antigen.

VHH proteins of the disclosure specifically bind an antigen or a ligand. CARs of the disclosure comprising one or more VHHs that specifically bind an antigen may be used to direct the specificity of a cell, (e.g. a cytotoxic immune cell) towards a target cell expressing the specific antigen. CLRs of the disclosure comprising one or more VHHs that specifically bind an antigen may transduce an intracellular signal upon binding a ligand of either VHH to activate expression of a sequence under the control of an inducible promoter.

Sequences encoding a VHH of the disclosure can be altered, added and/or deleted to reduce immunogenicity or reduce, enhance or modify binding, affinity, on-rate, off-rate, avidity, specificity, half-life, stability, solubility or any other suitable characteristic, as known in the art.

Optionally, VHH proteins can be engineered with retention of high affinity for the antigen or ligand and other favorable biological properties. To achieve this goal, the VHH proteins can be optionally prepared by a process of analysis of the parental sequences and various conceptual engineered products using three-dimensional models of the parental and engineered sequences. Three-dimensional models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate sequences and can measure possible immunogenicity (e.g., Immunofilter program of Xencor, Inc. of Monrovia, Calif.). Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate sequence, i.e., the analysis of residues that influence the ability of the candidate VHH protein to bind its antigen/ligand. In this way, residues can be selected and combined from the parent and reference sequences so that the desired characteristic, such as affinity for the target antigen(s)/ligand(s), is achieved. Alternatively, or in addition to, the above procedures, other suitable methods of engineering can be used.

VH

In certain embodiments of the compositions and methods of the disclosure, a CAR or a CLR comprises a single domain antibody (SdAb). In certain embodiments, the SdAb is a VH.

The disclosure provides CARs/CLRs comprising a single domain antibody (to produce a "VCAR" or a "VCLR", respectively). In certain embodiments, the single domain antibody comprises a VH. In certain embodiments, the VH

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is isolated or derived from a human sequence. In certain embodiments, VH comprises a human CDR sequence and/or a human framework sequence and a non-human or humanized sequence (e.g. a rat Fc domain). In certain embodiments, the VH is a fully humanized VH. In certain embodiments, the VH is neither a naturally occurring antibody nor a fragment of a naturally occurring antibody. In certain embodiments, the VH is not a fragment of a monoclonal antibody. In certain embodiments, the VH is a UniDabTM antibody (TeneoBio).

In certain embodiments, the VH is fully engineered using the UniRatTM (TeneoBio) system and “NGS-based Discovery” to produce the VH. Using this method, the specific VH are not naturally-occurring and are generated using fully engineered systems. The VH are not derived from naturally-occurring monoclonal antibodies (mAbs) that were either isolated directly from the host (for example, a mouse, rat or human) or directly from a single clone of cells or cell line (hybridoma). These VHs were not subsequently cloned from said cell lines. Instead, VH sequences are fully-engineered using the UniRatTM system as transgenes that comprise human variable regions (VH domains) with a rat Fc domain, and are thus human/rat chimeras without a light chain and are unlike the standard mAb format. The native rat genes are knocked out and the only antibodies expressed in the rat are from transgenes with VH domains linked to a Rat Fc (UniAbs). These are the exclusive Abs expressed in the UniRat. Next generation sequencing (NGS) and bioinformatics are used to identify the full antigen-specific repertoire of the heavy-chain antibodies generated by UniRatTM after immunization. Then, a unique gene assembly method is used to convert the antibody repertoire sequence information into large collections of fully-human heavy-chain antibodies that can be screened in vitro for a variety of functions. In certain embodiments, fully humanized VH are generated by fusing the human VH domains with human Fcs in vitro (to generate a non-naturally occurring recombinant VH antibody). In certain embodiments, the VH are fully humanized, but they are expressed in vivo as human/rat chimera (human VH, rat Fc) without a light chain. Fully humanized VHs are expressed in vivo as human/rat chimera (human VH, rat Fc) without a light chain are about 80 kDa (vs 150 kDa).

VCARs/VCLRs of the disclosure may comprise at least one VH of the disclosure. In certain embodiments, the VH of the disclosure may be modified to remove an Fc domain or a portion thereof. In certain embodiments, a framework sequence of the VH of the disclosure may be modified to, for example, improve expression, decrease immunogenicity or to improve function.

Transposons/Transposases

Exemplary transposon/transposase systems of the disclosure include, but are not limited to, piggyBac transposons and transposases, Sleeping Beauty transposons and transposases, Helraiser transposons and transposases and Tol2 transposons and transposases.

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 certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBacTM or a Super piggyBacTM (SPB) transposase. In certain embodiments, and, in particular, those embodiments wherein the transposase is a Super piggyBacTM (SPB) transposase, the sequence encoding the transposase is an mRNA sequence.

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In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBacTM (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:

(SEQ ID NO: 14487)

10 1 MGSSLDEHI LSALLQSDDE LVGEDSDSEI
SDHVSEDDVQ SDTEEAFFIDE VHEVQPTSSG
5 61 SEILDEQNVT EQPGSSLASN RILTLQRTI
RGKNCWST SKSTRRSRV ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW
TNAEISLKKR ESMTGATFRD TNEDEIYAFF
101 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS
VMSRDRFDPL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLT1DEQ
LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK
ELSKPVHGSC RNITCDNWFT SIPIAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNNSRSPV
GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD
QMCVMTCSR KTNRWPMLL YGMINIAICIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL
TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA
NASCKKCKKV ICREHNIDMC QSCF.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at one or more of positions 30, 165, 282, or 538 of the sequence:

(SEQ ID NO: 14487)

50 1 MGSSLDEHI LSALLQSDDE LVGEDSDSEI
SDHVSEDDVQ SDTEEAFFIDE VHEVQPTSSG
55 61 SEILDEQNVI EQPGSSLASN RILTLQRTI
RGKNCWST SKSTRRSRV ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW
TNAEISLKKR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS
VMSRDRFDPL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLT1DEQ
LLGFRGRCPF RMYIPNKPSK YGIKILMMCD

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-continued

301	SGTKYMINGM PYLGRGTQTN GVLGEYYVK
	ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361	EPYKLTIVGT VRSNKREIPE VLKNRSRPV
	GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421	DEDASINEST GKPQMVMYYN QTKGGVDTLD
	QMCsvMTCSR KTNRWPMLL YGMINIACIN
481	SFIISYHNVs SKGEKVQSRK KFMRNLYMSL
	TSSFMRKRLE APTLKRYLRD NISNILPNEV
541	PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA
	NASCKKCKKV ICREHNIDMC QSCF.

In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at two or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at three or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the transposase enzyme is a piggyBacTM (PB) transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at each of the following positions 30, 165, 282, and 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the amino acid substitution at position 30 of the sequence of SEQ ID NO: 14487 is a substitution of a valine (V) for an isoleucine (I). In certain embodiments, the amino acid substitution at position 165 of the sequence of SEQ ID NO: 14487 is a substitution of a serine (S) for a glycine (G). In certain embodiments, the amino acid substitution at position 282 of the sequence of SEQ ID NO: 14487 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 538 of the sequence of SEQ ID NO: 14487 is a substitution of a lysine (K) for an asparagine (N).

In certain embodiments of the methods of the disclosure, the transposase enzyme is a Super piggyBacTM (SPB) transposase enzyme. In certain embodiments, the Super piggyBacTM (SPB) transposase enzymes of the disclosure may comprise or consist of the amino acid sequence of the sequence of SEQ ID NO: 14487 wherein the amino acid substitution at position 30 is a substitution of a valine (V) for an isoleucine (I), the amino acid substitution at position 165 is a substitution of a serine (S) for a glycine (G), the amino acid substitution at position 282 is a substitution of a valine (V) for a methionine (M), and the amino acid substitution at position 538 is a substitution of a lysine (K) for an asparagine (N). In certain embodiments, the Super piggyBacTM (SPB) 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:

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-continued

61	SEILDEQNVI EQPGSSLASN RILTLPORTI
	RGKNCWST SKSTRRSRVs ALNIVRSQRG
121	PTRMCRNYYD PLLCFKLFFT DEIISEIVKW
	TNAEISLKR EsMTSATFRD TNEDEIYAFF
181	GILVMTAVRK DNHMSTDDLF DRSLSMVYVS
	VMSRDRDFDL IRCLRMDDKS IRPTLRENDV
241	FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ
	LLGFRGRCPF RVYIPNPKSK YGIKILMMCD
301	SGTKYMINGM PYLGRGTQTN GVLGEYYVK
	ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361	EPYKLTIVGT VRSNKREIPE VLKNRSRPV
	GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421	DEDASINEST GKPQMVMYYN QTKGGVDTLD
	QMCsvMTCSR KTNRWPMLL YGMINIACIN
481	SFIISYHNVs SKGEKVQSRK KFMRNLYMSL
	TSSFMRKRLE APTLKRYLRD NISNILPKEV
541	PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA
	NASCKKCKKV ICREHNIDMC QSCF.

In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more of positions 3, 46, 82, 103, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 258, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 486, 503, 552, 570 and 591 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more of positions 46, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 485, 503, 552 and 570. In certain embodiments, the amino acid substitution at position 3 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an asparagine (N) for a serine (S). In certain embodiments, the amino acid substitution at position 46 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an alanine (A). In certain embodiments, the amino acid substitution at position 46 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a threonine (T) for an alanine (A). In certain embodiments, the amino acid substitution at position 82 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for an isoleucine (I). In certain embodiments, the amino acid substitution at position 103 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a serine (S). In certain embodiments, the amino acid substitution at position 119 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for an arginine (R). In certain embodiments, the amino acid substitution at position 125 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) a cysteine (C). In certain embodiments, the amino acid sub-

(SEQ ID NO: 14484)

1 MGSSLDEHI LSALLQSDDE LVGEDSDSEV

SDHVSEDDVQ SDTEEA FIDE VHEVQPTSSG

sition at position 125 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a cysteine (C). In certain embodiments, the amino acid substitution at position 177 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 177 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a histidine (H) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 185 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 187 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for an alanine (A). In certain embodiments, the amino acid substitution at position 200 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 207 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a valine (V). In certain embodiments, the amino acid substitution at position 209 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a valine (V). In certain embodiments, the amino acid substitution at position 226 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a methionine (M). In certain embodiments, the amino acid substitution at position 235 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a leucine (L). In certain embodiments, the amino acid substitution at position 240 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at position 241 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 243 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a proline (P). In certain embodiments, the amino acid substitution at position 258 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tyrosine (Y) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a leucine (L). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) for a methionine (M). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a proline (P). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a methionine (M).

a proline (P). In certain embodiments, the amino acid substitution at position 315 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for an arginine (R). In certain embodiments, the amino acid substitution at position 319 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a threonine (T). In certain embodiments, the amino acid substitution at position 327 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 328 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a cysteine (C). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a cysteine (C). In certain embodiments, the amino acid substitution at position 421 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a histidine (H) for the aspartic acid (D). In certain embodiments, the amino acid substitution at position 436 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a valine (V). In certain embodiments, the amino acid substitution at position 456 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tyrosine (Y) for a methionine (M). In certain embodiments, the amino acid substitution at position 470 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a leucine (L). In certain embodiments, the amino acid substitution at position 485 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a serine (S). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a methionine (M). In certain embodiments, the amino acid substitution at position 552 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a threonine (T) for an alanine (A). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a glutamine (Q). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a glutamine (Q).

In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at two, three, four, five, six or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an

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amino acid substitution at positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, the amino acid substitution at position 103 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a serine (S). In certain embodiments, the amino acid substitution at position 194 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 372 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) for an arginine (R). In certain embodiments, the amino acid substitution at position 375 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) for a lysine (K). In certain embodiments, the amino acid substitution at position 450 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an asparagine (N) for an aspartic acid (D). In certain embodiments, the amino acid substitution at position 509 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a serine (S). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the piggy-BacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487. In certain embodiments, including those embodiments wherein the piggyBacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, the piggyBacTM transposase enzyme may further comprise an amino acid substitution at positions 372, 375 and 450 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, the piggyBacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 14487, and a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 14487. In certain embodiments, the piggyBacTM transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 14487, a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 14487 and a substitution of an asparagine (N) for an aspartic acid (D) at position 450 of SEQ ID NO: 14487.

The sleeping beauty 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 various embodiments, SB transposon-mediated gene transfer, or gene transfer using any of a number of similar transposons, may be used in the compositions and methods of the disclosure.

In certain embodiments, and, in particular, those embodiments wherein the transposon is a Sleeping Beauty transposon, the transposase is a Sleeping Beauty transposase or a hyperactive Sleeping Beauty transposase (SB100X).

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In certain embodiments of the methods of the disclosure, 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:

(SEQ ID NO: 14485)
 1 MGKSKEISQD LRKKIVDLHK SGSSLGAISK
 5 RLKVPRSSVQ TIVRXYKHG TTQPSYRSGR
 10 61 RRVLSPRDER TLVRKVQINP RTTAKDLVKM
 LEETGTKVSI STVKRVLYRH NLKGRSARKK
 15 121 PLLQNRHKKA RLRFATAHGD KDRTFWRNVL
 WSDETKIELF GHNDHRYVWR KKGEACKPKN
 20 181 TIPTVKHGGG SIMLGCFAA GGTGALHKID
 GIMRKENYVD ILKQHLKTSV RKLKLGKWW
 25 241 FQMDNDPKHT SKVVAWLKD NKVKVLEWPS
 QSPDLPNIEN LWAELKKRVR ARRPTNLTLQ
 30 301 HQLCQEEWAK IHPNYCGKLV EGYPKRLTQV
 KQFKGNATKY.

In certain embodiments of the methods of the disclosure, the hyperactive Sleeping Beauty (SB100X) transposase enzyme comprises an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14486)
 1 KGKSKEISQD LRKRIVDLHK SGSSLGAISK
 5 RLAVPRSSVQ TIVRKYKHG TTQPSYRSGR
 10 61 RRVLSPRDER TLVRKVQINP RTTAKDLVKM
 LEETGTKVSI STVKRVLYRH NLKGHSARKK
 15 121 PLLQNRHKKA RLRFATAHGD KDRTFWRNVL
 WSDETKIELF GHNDHRYVWR KKGEACKPKN
 20 181 TIPTVKHGGG SIMLGCFAA GGTGALHKID
 GIMDAVQYVD ILKQHLKTSV RKLKLGKWW
 25 241 FQHDNDPKHT SKVVAWLKD NKVKVLEWPS
 QSPDLPNIEN LWAELKKRVR ARRPTNLTLQ
 30 301 HQLCQEEWAK IHPNYCGKLV EGYPKRLTQV
 KQFKGNATKY.

The Helraiser transposon is transposed by the Helitron transposase. Helitron transposases mobilize the Helraiser transposon, an ancient element from the bat genome that was active about 30 to 36 million years ago. An exemplary Helraiser transposon of the disclosure includes Helibat1, which comprises a nucleic acid sequence comprising:

(SEQ ID NO: 14652)
 1 TCCTATATAA TAAAAGAGAA ACATGCAAAT TGACCATCCC TCCGCTACGC TCAAGGCCAG
 5 61 CCCACCAGCC AATCAGAAGT GACTATGCAA ATTAACCAA CAAAGATGGC AGTTAAATT
 10 121 GCATACGCAG GTGTCAAGCG CCCCAGGAGG CAACGGCGGC CGCGGGCTCC CAGGACCTTG

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181 GCTGGCCCCG GGAGGGGAGG CCGGCCGCGC CTAGCCACAC CCGCGGGCTC CCGGGACCTT
 241 CGCCAGCAGA GAGCAGAGCG GGAGAGCGGG CGGAGAGCGG GAGGTTTGGA GGACTTGGCA
 301 GAGCAGGAGG CCGCTGGACA TAGAGCAGAG CGAGAGAGAG GGTGGCTTGG AGGGCGTGGC
 361 TCCCTCTGTC ACCCCAGCTT CCTCATCACA GCTGTGAAA CTGACAGCAG GGAGGAGGAA
 421 GTCCCACCCC CACAGAATCA GCCAGAATCA GCCGTTGGTC AGACAGCTCT CAGCGGCCTG
 481 ACAGCCAGGA CTCTCATTCA CCTGCATCTC AGACCGTGAC AGTAGAGAGG TGGGACTATG
 541 TCTAAAGAAC AACTGTTGAT ACAACGTAGC TCTGCAGCCG AAAGATGCCG GCGTTATCGA
 601 CAGAAAATGT CTGCAGAGCA ACGTGCCTCT GATCTTGAAA GAAGGCGGCG CCTGCAACAG
 661 AATGTATCTG AAGAGCAGCT ACTGGAAAAA CGTCGCTCTG AAGCCGAAAA ACAGCGGCGT
 721 CATCGACAGA AAATGTCATA AGACCAACGT GCCTTGAAAG TTGAAAGAAG GCGGTGGCGA
 781 CGACAGAATA TGTCTAGAGA ACAGTCATCA ACAAGTACTA CCAATACCGG TAGGAACATGC
 841 CTTCTCAGCA AAAATGGAGT ACATGAGGAT GCAATTCTCG AACATAGTTG TGGTGGAAATG
 901 ACTGTTCGAT GTGAATTTG CCTATCACTA AATTCTCTG ATGAAAAACC ATCCGATGGG
 961 AAATTTACTC GATGTTGTAG CAAAGGGAAA GTCTGTCAA ATGATATACA TTTTCCAGAT
 1021 TACCCGGCAT ATTTAAAAG ATTAATGACA AACGAAGATT CTGACAGTAA AAATTCATG
 1081 GAAAATATTC GTTCCATAAA TAGTTCTTT GCTTTGCTT CCATGGGTGC AAATATTGCA
 1141 TCGCCATCAG GATATGGGCC ATACTGTTT AGAATACACG GACAAGTTA TCACCGTACT
 1201 GGAACTTTAC ATCCTTCGGA TGGTGTTCCT CGGAAGTTG CTCAACTCTA TATTTGGAT
 1261 ACAGCCGAAG CTACAAGTAA AAGATTAGCA ATGCCAGAAA ACCAGGGCTG CTCAGAAAGA
 1321 CTCATGATCA ACATCAACAA CCTCATGCAT GAAATAATG AATTAAGAAA ATCGTACAAG
 1381 ATGCTACATG AGGTAGAAAA GGAAGCCAA TCTGAAGCAG CAGCAAAAGG TATTGCTCCC
 1441 ACAGAAGTAA CAATGGCGAT TAAATACGAT CGTAACAGTG ACCCAGGTAG ATATAATTCT
 1501 CCCCGTGTAA CCGAGGGTGC TGTCATATTG TAAACCGAT CCCAATAATC CAAATGCCAC TAAAATGAAA
 1561 AGGGACTTGC TCATTCAATTG TAAACCGAT CCCAATAATC CAAATGCCAC TAAAATGAAA
 1621 CAAATCAGTA TCCTGTTCC TACATTAGAT GCAATGACAT ATCCTATTCT TTTTCCACAT
 1681 GGTGAAAAAG GCTGGGGAAC AGATATTGCA TTAAGACTCA GAGACAACAG TGTAAATCGAC
 1741 AATAATACTA GACAAAATGT AAGGACACGA GTCACACAAA TGCAGTATTAA TGGATTTCAT
 1601 CTCTCTGTGC GGGACACGTT GAATCCTATT TAAATGCAG GAAAATTAAC TCAACAGTTT
 1861 ATTGTGGATT CATATTCAAA AATCGAGGCC AATCGGATAA ATTCATCAA AGCAAACCAA
 1921 TCTAAGTTGA GAGTTGAAAA ATATAGTGGT TTGATGGATT ATCTCAAATC TAGATCTGAA
 1981 AATGACAATG TGCCGATTGG TAAAATGATA ATACTTCCAT CATCTTTGA GGGTAGTCCC
 2041 AGAAATATGC AGCAGCGATA TCAGGATGCT ATGGCAATTG TAACGAAGTA TGGCAAGCCC
 2101 GATTATTCA TAACCATGAC ATGCAACCCC AAATGGGCAG ATATTACAAA CAATTACAA
 2161 CGCTGGCAAA AAGTTGAAAA CAGACCTGAC TTGGTAGCCA GAGTTTTAA TATTAAGCTG
 2221 AATGCTCTT TAAATGATAT ATGAAATTC CATTATTGTT GGAAAGTAAT AGCTAAAATT
 2281 CATGTCATTG AATTCAGAA ACGCGGACTG CCTCACGCTC ACATATTATT GATATTAGAT
 2341 AGTGAGTCCA AATTACGTTC AGAAGATGAC ATTGACCGTA TAGTTAAGGC AGAAATTCCA
 2401 GATGAAGACC AGTGTCTCG ACTTTTCAA ATTGAAAAT CAAATATGGT ACATGGACCA
 2461 TGTGGAATAC AAAATCGAAA TAGTCCATGT ATGGAAAATG GAAAATGTC AAAGGGATAT
 2521 CCAAAAGAAT TTCAAAATGC GACCA1TGGA AATATTGATG GATATCCGAA ATACAAACGA
 2581 AGATCTGGTA GCACCATGTC TATTGAAAT AAAGTTGTCG ATAACACTTG GATTGTCCCT

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2641 TATAACCCGT ATTTGTGCCT TAAATATAAC TGTCATATAA ATGTTGAAGT CTGTGCATCA
 2701 ATTAAAAGTG TCAAATATTG ATTTAAATAC ATCTATAAAG GGCACGATTG TGCAAATATT
 2761 CAAATTCCTG AAAAAAATAT TATCAATCAT GACGAAGTAC AGGACTTCAT TGACTCCAGG
 2821 TATGTGAGCG CTCCCTGAGGC TGTTGGAGA CTTTTGCAA TGCAGATGCA TGACCAATCT
 2881 CATGCATCA CAAGATTAGC TATTCAATTG CCAAATGATC AGAATTGTA TTTTCATACC
 2941 GATGATTGTTG CTGAAGTTT AGATAGGGCT AAAAGGCATA ACTCGACTTT GATGGCTTGG
 3001 TTCTTATTGA ATAGAGAAGA TTCTGATGCA CGTAATTATT ATTATTGGGA GATTCCACAG
 3061 CATTATGCT TTAATAATTG TTTGTGGACA AAACGCCAA AGGGTGGGAA TAAAGTATTA
 3121 GGTAGACTGT TCACTGTGAG CTTTAGAGAA CCAGAACGAT ATTAGCTTAG ACTTTGCTT
 3181 CTGCATGTA AAGGTGCGAT AAGTTTGAG GATCTGCGAA CTGTAGGAGG TGTAACTTAT
 3241 GATACATTTC ATGAAGCTGC TAAACACCGA GGATTATTAC TTGATGACAC TATCTGGAAA
 3301 GATACGATTG ACGATGCAAT CATCCTTAAT ATGCCAAAC AACTACGGCA ACTTTTGCA
 3361 TATATATGTC TGTTGGATG TCCTCTGCT GCAGACAAAT TATGGATGA GAATAATCT
 3421 CATTTTATTG TTGATTCTG TTGGAAATTA CACCGAAGAG AAGGTGCCTG TGTGAACGT
 3481 GAAATGCATG CCCTTAACGA AATTCAAGG GTATTCACAT TGCATGGAAT GAAATGTTCA
 3541 CATTCTAACAC TTCCGGACTA TCCTTTATTA ATGAATGCAAA ATACATGTGA TCAATTGTC
 3601 GAGCAACAAAC AGGCAGAGGT TTTGATAAAT TCTCTGAATG ATGAACAGTT GGCAGCCTT
 3661 CAGACTATAA CTTCAGCCAT CGAAGATCAA ACTGTACACC CCAAATGCTT TTCTGGAT
 3721 GGTCCAGGTG GTAGTGGAAA AACATATCTG TATAAAGTT TAACACATTA TATTAGAGGT
 3781 CGTGGTGGTA CTGTTTACCA CACAGCATCT ACAGGAATTG CTGAAATTT ACTTCTGGT
 3841 GGAAGAACCT TTGATCCCCA ATATAAATTAA CCAATTCCAT TAAATGAAAC TTCAATTCTT
 3901 AGACTCGATA TAAAGAGTGA AGTTGCTAAA ACCATTTAAA AGGCCAACT TCTCATTATT
 3961 GATGAATGCA CCATGGCATC CAGTCATGCT ATAAACGCCA TAGATAGATT ACTAAGAGAA
 4021 ATTATGAATT TGAATGTTGC ATTTGGTGGG AAAGTTCTCC TTCTCGGAGG GGATTTGCA
 4081 CAATGTCCTCA GTATTGTACC ACATGCTATG CGATCGGCCA TAGTACAAAC GAGTTAAAG
 4141 TACTGTAATG TTTGGGGATG TTTCAAGAAA TTGCTCTTTA AAACAAATAT GAGATCAGAG
 4201 GATTCTGCTT ATAGTGAATG GTTAGTAAAA CTTGGAGATG GCAAACCTGA TAGCAGTTT
 4261 CATTAGGAA TGGATATTAT TGAAATCCCC CATGAAATGA TTTGTAACCC ATCTATTATT
 4321 GAAGCTACCT TTGGAAATAG TATATCTATA GATAATTTA AAAATATATC TAAACGTGCA
 4381 ATTCTTGTC CAAAAAATGA GCATGTTCAA AAATTAATG AAGAAATTTT GGATATACTT
 4441 GATGGAGATT TTCACACATA TTTGAGTGAT GATTCCATTG ATTCAACAGA TGATGCTGAA
 4501 AAGGAAATTT CTCCTCGA ATTTCTTAAT AGTATTACTC CTTCGGGAAT GCCGTGTCA
 4561 AAATTAATG TGAAAGTGGG TGCAATCATC ATGCTATTGA GAAATCTAA TAGTAAATGG
 4621 GGTCTTGTA ATGGTACTAG ATTATTATC AAAAGATTAC GACCTAACAT TATCGAAGCT
 4681 GAAAGTATTAA CAGGATCTGC AGAGGGAGAG GTTGGTCTGA TTCCAAGAAT TGATTTGTCC
 4741 CCATCTGACA CTGGCCTCCC ATTTAAATTA ATTCGAAGAC AGTTCCCGT GATGCCAGCA
 4801 TTTGCGATGA CTATTAATAA ATCACAAAGGA CAAACTCTAG ACAGAGTAGG AATATTCTA
 4861 CCTGAACCCG TTTTCCACA TGGTCAGTTA TATGTTGCTT TCTCTCGAGT TCGAAGAGCA
 4921 TGTGACGTTA AAGTAAAGT TGTAATACT TCATCACAAG GGAAATTAGT CAAGCACTCT
 4981 GAAAGTGTGTT TTACTCTTAA TGTGGTATAC AGGGAGATAT TAGAATAAGT TTAATCACTT

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5041 TATCAGTCAT TGTTTGCATC AATGTTGTTT TTATATCATG TTTTGTTGT TTTTATATCA
 5101 TGTCTTGTT GTTGTATAT CATGTTGTTA TTGTTATTAT ATTAATAAAAT TTATGTATTA
 5161 TTTTCATATA CATTTCATC ATTCCTTTC ATCTCTACA CTTCTATTAT AGAGAAAGGG
 5221 CAAATAGCAA TATTAATAAATA TTTCCCTCAA TTAATTCCCT TTCAATGTGC ACGAATTTCG
 5281 TGCACCGGGC CACTAG.

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. 15

An exemplary Helitron transposase of the disclosure comprises an amino acid sequence comprising:

(SEQ ID NO: 14501) 20
 1 MSKEQLLXQR SSAEERCRRY RQKMSAEQRA
 SDLERRRRLQ QKVSEEQOLLE KKRSEAEKQR
 61 RHRQKMSKDQ RAPEVERRRW RRQNMSREQS 25
 STSTTNTRGRN CLLSKNGVHE DAILEHSCGG
 121 MTVRCEFCLS LNFSDEKPSD GKFTTRCCSKG
 KVCPNDIHPP DYPAYLKRLM TNEDSDSKNF
 181 MENIRSINSS FAFASMGANI ASPSGYGPYC 30
 FRIHGQVYHR TGTLHPSDGV SRKFAQLYIL
 241 DTAEATSKRL AMPENQGCSE RLMININNLM
 HEINELTKSY KMLHEVEKEA QSEAAAKGIA 35
 301 PTEVTMAIKY DRNSDPGRYN SPRVTEAVI
 FRNEDGEPPP ERDLLIHCKP DPNNPNATKM
 361 KQISILFPTL DAMTYPILFP HGEKGWGTDI 40
 ALRLRDNSVI DKNTRQMVRT RVTQMQYYGF
 421 HLSVRDTFNP IILNAGKLTQQ FIVDSYSKME
 ANRINFIIKAN QSKLRVKEKYS GLMDYLKSRS 45
 481 ENDNPIGKMI ILPSSFEGS PRNMQQRQYQD
 AMAIVTKYSK PDLFITMTCN PKWADITNNL
 541 QRWQKVENRP DLVARVFNPK LNALLNDICK 50
 FHLFGKVIAK IHVIEFQKRG LPHAHILLIL
 601 DSESKLRS8ED DIDRIYKAEI PDEDQCPRLF
 QIVKSMMVHG PCGIQNPNSP CMENGKCSKG
 661 YPKEFQNATI GNIDGYPKYK RRSGSTMSIG
 NKVVDTNTWIV PYNPYLCLKY NCHINVEVCA
 721 SIKSVKYLFK YIYKGHDCAI IQISEKNIIN 60
 HDEVQDFIDS RYVSAPEAVW RLFAMRMHDQ
 781 SHAITRLAIH LPMDQMLYFH TDDFAEVLDR
 AKRHNSTLMA WFLLNREDSD ARNYYWEP

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841 QHYVFNNSLW TKRRKGGMKV LGRLFTVSFR
 EPERYYLRLL LLHVKGAIKF EDLRTVGGVT
 901 YDTDFHEAAKH RGLLLDDTIW KDTIDDAIIL
 NMVKQLRQLF AYICVFGCPS AADKLWDENK
 561 SHFIEDFCWK LHRREGACVN CEMHALNEIQ
 EVFTLHGMKC SHFKLPDYPL LMNANTCDQL
 1021 YEQQQAEVLI NSLMDEQLAA FQTITSAIED
 QTVHPKCFPL DGPGGSGKTY LYKVLTHYIR
 1081 GRGGTVLPTA STGIAANLLL GGRTFHQSQYK
 LPIPLNETSI SRLDIKSEVA KTIKKAQLLI
 1141 IDECTMASSH AINAIDRLLR EXMNLNVAFG
 GKVLLLGGDF RQCLSVIPHA MRSAlVQTSI
 1201 KYCNVWGCPR KLSLKTNmRS EDSAYSEWLW
 KLGDGKLDSS FHLGMDIIEI PHEMICNGSI
 1261 IEATFGNSIS IDNIKNISK RAILCPKNEHV
 QKLNNEEILDI LDGDFHTYLS DDSIDSTDDA
 1321 EKENFPIEFL NSITPSGMPC HKLKLKVGA
 IMLLRLNLSK WGLCNGTRET IKRLRPNIIE
 1381 AEVLGSAEG EVVLIPRIDL SPSPDTGLPFK
 LIRRQFPVMP AFAMTIMKSQ GQTLDRVGIF
 1441 LPEPVFAHGQ LYVAFSRVRR ACDVKVKVNN
 TSSQGKLVKH SESVFTLNVV YREILE.

In Helitron transpositions, a hairpin close to the 3' end of the transposon functions as a terminator. However, this hairpin can be bypassed by the transposase, resulting in the transduction of flanking sequences. In addition, Helraiser transposition generates covalently closed circular intermediates. Furthermore, Helitron transpositions can lack target site duplications. In the Helraiser sequence, the transposase is flanked by left and right terminal sequences termed LTS and RTS. These sequences terminate with a conserved 5'-TC/CTAG-3' motif. A 19 bp palindromic sequence with the potential to form the hairpin termination structure is located 11 nucleotides upstream of the RTS and consists of the sequence

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(SEQ ID NO: 14500)
 GTGCACGAATTCGTCGACCGGGCCACTAG.

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

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kilobases and contain a gene encoding the Tol2 transposase, which contains four exons. An exemplary Tol2 transposase

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of the disclosure comprises an amino acid sequence comprising the following:

(SEQ ID NO: 14502)
1 MEEVCDSSAA ASSTVQNQPQ DQEHPWPYLR EFFSLSGVNK DSFKMKCVLC LDLNKEISAF
61 KSSPSNLRKH IERMHPNYLK NYSKLTAQKR KIGTSTHASS SKQLKVDSVF PVKHSVPTV
121 NKAILRYIIQ GLHPFSTVDL PSFKELISTL QPGISVITRP TLRSKIAEAA LIMKQKVTA
181 MSEVEWIATT TDCWTARRKS FIGVTAHWIN PGSLERHSAA LACKRLMGSH TFEVLASAMN
241 DIHSEYEIRD KVVCTTDSG SNFMKAFRVF GVENNDIETE ARRCESDDTD SEGCGEGLSDG
301 VEFQDASRVL DQDDGPEFQL PKHQKCACHL LNLVSSVDAQ KALSNEHYKK LYRSVFGKQ
361 ALWNKSSRSA LAAEAVESES RLQLLRPNQT RWNSTFMAVD RILQICKEAG EGALRNICTS
421 LEVPMFNPAE MLFLTEWANT MRPVAKVLDI LQAETNTQLG WLLPSVHQLS LKLQRLHHSL
481 RYCDPLVDAL QQGIQTRFKH MFEDPEIIAA AILLPKFRTS WTNDETIICKR GMDYIRVHLE
541 PLDHKKELAN SSSDDEDFFA SLKPTTHEAS KELDGYLACV SDTRESLLTF PAICSLSIKT
601 NTPLTASAAC ERLFSTAGLL FSPKRARLDT NNFNENQLLK LNLREYNFE

An exemplary Tol2 transposon of the disclosure, including inverted repeats, subterminal sequences and the Tol2 transposase, is encoded by a nucleic acid sequence comprising the following:

(SEQ ID NO: 17041)
1 CAGAGGTGTA AAGTACTTGA GTAATTTAC TTGATTACTG TACTTAAGTA TTATTTTG
61 GGATTTTAC TTTACTTGAG TACAATTAAA AATCAATACT TTTACTTTA CTTAATTACA
121 TTTTTTAGA AAAAAAGTA CTTTTTACTC CTTACAATTT TATTTACAGT CAAAAAGTAC
181 TTATTTTTG GAGATCACTT CATTCTATT TCCCTTGCTA TTACCAAACC AATTGAATTG
241 CGCTGATGCC CAGTTAATT TAAATGTTAT TTATTCTGCC TATGAAAATC GTTTTCACAT
301 TATATGAAAT TGGTCAGACA TGTTCATGG TCCTTTGGAA GTGACGTCAT GTCACATCTA
361 TTACCCACAAT GCACAGCACCC TTGACCTGGA AATTAGGGAA ATTATAACAG TCAATCAGTG
421 GAAGAAAATG GAGGAAGTAT GTGATTCACTC AGCAGCTGCG AGCAGCACAG TCCAAATCA
481 GCCACAGGAT CAAGAGCACCC CGTGGCCGTA CTCTCGCGAA TTCTTTCTT TAAGTGGTGT
541 AAATAAAAGAT TCATTCAAGA TGAAATGTGT CCTCTGTCTC CCGCTTAATA AAGAAATATC
601 GGCCTTCAAA AGTCGCCAT CAAACCTAAG GAAGCATATT GAGGTAAGT CATTAAGTAT
661 TTTGTTTAC TGATAGTTT TTTTTTTTT TTTTTTTTT TTTTTGGGT TGCAATTTT
721 GACGTTGATG GCGCGCCTT TATATGTGTA GTAGGCCTAT TTTCACTAAT GCATGCGATT
781 GACAATATAA GGCTCACGTA ATAAAATGCT AAAATGCATT TGTAATTGGT AACGTTAGGT
841 CCACGGAAA TTGGCGCCTT ATTGCGACCTT TGAATAATCA TTATCATTCC GTGCTCTCAT
901 TGTGTTCAA TTCATGCAAA ACACAAGAAA ACCAAGCGAG AAATTTTTT CCAAACATGT
961 TGTATTGTCA AAACGGTAAC ACTTTACAAT GAGGTTGATT AGTTCATGTA TTAACATAACA
1021 TTAAATAACC ATGAGCAATA CATTGTTAC TGTATCTGTT AATCTTGTT AACGTTAGTT
1081 AATAGAAATA CAGATGTTCA TTGTTGTTTC ATGTTAGTTC ACAGTGCATT AACTAATGTT
1141 AACAAAGATAT AAAAGTATTAG TAAATGTTGA AATTAACATG TATACGTGCA GTTCATTATT
1201 AGTTCATGTT AACTAATGTA GTTAACTAAC GAACCTTATT GTAAAAGTGT TACCATCAAA
1261 ACTAATGTAA TGAAATCAAT TCACCCCTGTC ATGTCAGCCT TACAGTCCTG TGTTTTGTC
1321 AATATAATCA GAAATAAAAT TAATGTTGA TTGTCACTAA ATGCTACTGT ATTTCTAAAA

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1381 TCAACAAGTA TTTAACATTA TAAAGTGTGC AATTGGCTGC AAATGTCAGT TTTATTAAAG
 1141 GGTTAGTTCA CCCAAAAATG AAAATAATGT CATTAATGAC TCGCCCTCAT GTCGTTCCAA
 1501 GCCCGTAAGA CCTCCGTTCA TCTTCAGAAC ACAGTTAAG ATATTTAGA TTTAGTCCGA
 1561 GAGCTTCTG TGCCCTCATT GAGAATGTAT GTACGGTATA CTGTCATGT CCAGAAAGGT
 1621 AATAAAAACA TCAAAGTAGT CCATGTGACA TCAGTGGGTT AGTTAGAATT TTTGAAGCA
 1681 TCGAATACAT TTTGGTCCAA AAATAACAAA ACCTACGACT TTATTCGGCA TTGTATTCTC
 1741 TTCCGGGTCT GTTGTCAATC CGCGTTCACG ACTTCGCAGT GACGCTACAA TGCTGAATAA
 1801 AGTCGTAGGT TTTGTTATTT TTGGACAAA ATGTATTTTC GATGCTCAA ATAATTCTAC
 1861 CTAACCCACT GATGTCAGAT GGACTACTTT GATGTTTTA TTACCTTCT GGACATGGAC
 1921 AGTATACCGT ACATACATTT TCAGTGGAGG GACAGAAAGC TCTCGGACTA AATCTAAAAT
 1981 ATCTTAAACT GTGTTCCGAA GATGAACGGA GGTGTTACGG GCTTGGAAACG ACATGAGGGT
 2041 GAGTCATTAA TGACATCTTT TCATTTTGG GTGAACTAAC CCTTTAATGC TGTAATCAGA
 2101 GACTGTATGT GTAATTGTTA CATTATTCC ATACAATATA AATATTTATT TGTTGTTTT
 2161 ACAGAGAATG CACCCAAATT ACCTCAAAAA CTACTCTAAA TTGACAGCAC AGAAGAGAAA
 2221 GATCGGGACC TCCACCCATG CTTCAGCAG TAAGCAACTG AAAGTTGACT CAGTTTCCC
 2281 AGTCAAACAT GTGCTCCAG TCACTGTGAA CAAAGCTATA TTAAGGTACA TCATTCAAGG
 2341 ACTTCATCCT TTCAGCACTG TTGATCTGCC ATCATTAAA GAGCTGATTA GTACACTGCA
 2401 GCCTGGCATT TCTGTCATTA CAAGGCCTAC TTTACGCTCC AAGATAGCTG AAGCTGCTCT
 2461 GATCATGAAA CAGAAAGTGA CTGCTGCCAT GAGTGAAGTT GAATGGATTG CAACCACAAAC
 2521 GGATTGTTGG ACTGCACGTA GAAAGTCATT CATTGGTGT ACTGCTCACT GGATCAACCC
 2581 TGGAAAGTCTT GAAAGACATT CCGCTGCACT TGCCTGCAAAG ATTAATGG GCTCTCATAC
 2641 TTTTGAGGTA CTGGCCAGTG CCATGAATGA TATCCACTCA GAGTATGAAA TACGTGACAA
 2701 GGTGTTGC ACAACCACAG ACAGTGGTC CAACTTTATG AAGGCTTCA GAGTTTGG
 2761 TGTGGAAAAC AATGATATCG AGACTGAGGC AAGAAGGTGT GAAAGTGATG ACAGTGATTC
 2821 TGAAGGCTGT GGTGAGGGAA GTGATGGTGT GGAATTCCAA GATGCTCAG GAGTCCTGGA
 2881 CCAAGACGAT GGCTTCGAAT TCCAGCTACC AAAACATCAA AAGTGTGCCT GTCACTTACT
 2941 TAACCTAGTC TCAAGCGTT ATGCCAAAA AGCTCTCTCA AATGAACACT ACAAGAAACT
 3001 CTACAGATCT GTCTTGGCA AATGCCAAGC TTTATGGAAT AAAAGCAGCC GATCGGCTCT
 3061 AGCAGCTGAA GCTGTTGAAT CAGAAAGCCG GCTTCAGCTT TTAAGGCCAA ACCAAACGCG
 3121 GTGGAATTCA ACTTTATGG CTGTTGACAG AATTCTCAA ATTGCAAAG AAGCAGGAGA
 3181 AGGCGCACTT CGGAATATAT CCACCTCTCT TGAGGTTCCA ATGTAAGTGT TTTCCCCTC
 3241 TATCGATGTA AACAAATGTG GGTTGTTTT GTTTAATACT CTTTGATTAT GCTGATTCT
 3301 CCTGTAGGTT TAATCCAGCA GAAATGCTCT TCTTGACACCA CTCCGCCAAC ACAATCCGTC
 3361 CAGTTGCAAAG AGTACTCGAC ATCTTGCAAG CGGAAACGAA TACACAGCTG GGGTGGCTGC
 3421 TGCCTAGTGT CCATCAGTTA AGCTTGAAAC TTCAGCGACT CCACCATTCT CTCAGGTACT
 3481 GTGACCCACT TGTGGATGCC CTACAACAAG GAATCCAAAC ACGATTCAAG CATATGTTG
 3541 AAGATCCTGA GATCATAGCA GCTGCCATCC TTCTCCCTAA ATTCGGACC TCTTGGACAA
 3601 ATGATGAAAC CATCATAAAA CGAGGTTAAAT GAATGCAAGC AACATACACT TGACGAATTG

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3661 TAATCTGGGC AACCTTTGAG CCATACCAAA ATTATTCTTT TATTTATTAA TTTTGACT
3721 TTTAGGAAT GTTATATCCC ATCTTGGCT GTGATCTCAA TATGAATATT GNPGTAAAGT
3781 ATTCTTGCAG CAGGTTGTAG TTATCCCTCA GTGTTCTTG AAACCAACT CATATGTATG
3841 ATATGTGGTT TGGAAATGCA GTTAGATTTT ATGCTAAAAT AAGGGATTG CATGATTAA
3901 GATGTAGATG ACTGCACGTA AATGTAGTTA ATGACAAAAT CCATAAAATT TGTTCCAGT
3961 CAGAACCCCC TCAACCAAA TTTCTTGTG GTCTGCTCAC TGTGCTTGTAA GGATGGACT
4021 ACATCAGAGT GCATCTGGAG CCTTTGGACC ACAAGAAGGA ATTGGCAAC AGTCATCTG
4081 ATGATGAAGA TTTTTTCGCT TCTTGAAAC CGACACACAA TGAAGGCCAGC AAAGAGTTGG
4141 ATGGATATCT GCCCTGTGTT TCAGACACCA GGGAGTCTCT GCTCACGTTT CCTGCTATT
4201 GCAGCCTCTC TATCAAGACT AATACACCTC TTCCCGCATC GGCTGCCTGT GAGAGGCTTT
4261 TCAGCACTGC AGGATTGCTT TCAGGCCCA AAAGAGCTAG GCTTGACACT AACAATTTG
4321 AGAACATCAGCT TCTACTGAAG TAAATCTGA GGTTTACAA CTTTGAGTAG CGTGTACTGG
4381 CATTAGATTG TCTGTCTTAT AGTTTGATAA TAAATACAA ACAGTTCTAA AGCAGGATAA
4441 AACCTTGTAT GCATTCATT TAATGTTTT TGAGATTAAA AGCTTAAACA AGAATCTCTA
4501 GTTTCTTTC TTGCTTTAC TTTTACTTCC TTAATACTCA AGTACAATT TAATGGAGTA
4561 CTTTTTACT TTAATCTCAAG TAAGATTCTA GCCAGATACT TTTACTTTA ATTGAGTAAA
4621 ATTTCCCTA AGTACTTGTA CTTCACCTG AGTAAAATT TTGAGTACTT TTACACCTC
4681 TG.

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Exemplary transposon/transposase systems of the disclosure include, but are not limited to, piggyBac and piggyBac-like transposons and transposases.

PiggyBac and piggyBac-like transposases recognizes transposon-specific inverted terminal repeat sequences (ITRs) on the ends of the transposon, and moves the contents between the ITRs into TAA or TTAT chromosomal sites. The piggyBac or piggyBac-like transposon system has no payload limit for the genes of interest that can be included between the ITRs.

In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme.

35 In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or a piggyBac-like transposase enzyme. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14487)

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1 MGSSLDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEFIDE VHEVQPTSSG
61 SEILDEQNVII EQPGSSLASR RILTLPORTI RGKNKHCWST SKSTRRSRVs ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DHNMSTDDLF DRSLSMVYVS VMSRDRFDL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PAGAHLTIDEQ LLGFRGRCPF RMYIPNPKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK ELSKPVGSC RNITCDNWFT SIPLALNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNRSRSPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYNN QTKGGVDTLD QMC SVMTCR KTNRWPMLL YGMINIAINC
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKPYLRD NISNLPNEV
541 PGTSDDSTEE PVMKKRTYCT YCP SKIRKA NASCKKCKV ICREHNIDMC QSCF.

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transposase is a piggyBacTM, Super piggyBacTM (SPB) transposase. In certain embodiments, and, in particular, those embodiments wherein the transposase is a piggyBacTM, Super piggyBacTM (SPB), the sequence encoding the transposase is an mRNA sequence.

65 In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at one or more of positions 30, 165, 282, or 538 of the sequence:

(SEQ ID NO: 14487)

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1 MGSSLDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIGE VHEVQPTSSG
61 SEILDEQNVI EQPGSSLASN RILTLPORTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DHNMSTDDLF DRSLSMVYVS VMSRDRFDL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGERGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCVMTCSR KTNRWPMLL YGMINIAICIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNLPNEV
541 PGTSDDSTE PVMKKRTYCT YCPSKIRRKA NASCKKCKV ICREHNIDMC QSCF .

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In certain embodiments, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at two or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at three or more of positions 30, 165, 282, or 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme that comprises or consists of an amino acid sequence having an amino acid substitution at each of the following positions 30, 165, 282, and 538 of the sequence of SEQ ID NO: 14487. In certain embodiments, the amino acid substitution at position 30 of the sequence of SEQ ID NO: 14487 is a substitution of a valine (V) for an

20 the Super piggyBac™ (SPB) or piggyBac-like transposase enzyme of the disclosure may comprise or consist of the amino acid sequence of the sequence of SEQ ID NO: 14487 wherein the amino acid substitution at position 30 is a substitution of a valine (V) for an isoleucine (I), the amino acid substitution at position 165 is a substitution of a serine (S) for a glycine (G), the amino acid substitution at position 282 is a substitution of a valine (V) for a methionine (M), and the amino acid substitution at position 538 is a substitution of a lysine (K) for an asparagine (N). In certain 25 embodiments, the Super piggyBac™ (SPB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14484)

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1 MGSSLDEHI LSALLQSDSEV SDHVSEDDVQ SDTEEAFIGE VHEVQPTSSG
61 SEILDEQNVI EQPGSSLASN RILTLPORTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DHNMSTDDLF DRSLSMVYVS VMSRDRFDL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCVMTCSR KTNRWPMLL YGMINIAICIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNLPKEV
541 PGTSDDSTE PVMKKRTYCT YCPSKIRRKA NASCKKCKV ICREHNIDMC QSCF .

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isoleucine (I). In certain embodiments, the amino acid substitution at position 165 of the sequence of SEQ ID NO: 14487 is a substitution of a serine (S) for a glycine (G). In certain embodiments, the amino acid substitution at position 282 of the sequence of SEQ ID NO: 14487 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 538 of the sequence of SEQ ID NO: 14487 is a substitution of a lysine (K) for an asparagine (N).

In certain embodiments of the methods of the disclosure, the transposase enzyme is a Super piggyBac™ (SPB) or piggyBac-like transposase enzyme. In certain embodiments,

55 In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBac™, Super piggyBac™ or piggyBac-like transposase enzyme may further comprise an amino acid substitution at one or more of positions 3, 46, 82, 103, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 258, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 486, 503, 552, 570 and 591 of the 60 sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at

positions 30, 165, 282 and/or 538, the piggyBacTM, Super piggyBacTM or piggyBac-like transposase enzyme may further comprise an amino acid substitution at one or more of positions 46, 119, 125, 177, 180, 185, 187, 200, 207, 209, 226, 235, 240, 241, 243, 296, 298, 311, 315, 319, 327, 328, 340, 421, 436, 456, 470, 485, 503, 552 and 570. In certain embodiments, the amino acid substitution at position 3 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an asparagine (N) for a serine (S). In certain embodiments, the amino acid substitution at position 46 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an alanine (A). In certain embodiments, the amino acid substitution at position 46 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a threonine (T) for an alanine (A). In certain embodiments, the amino acid substitution at position 82 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for an isoleucine (I). In certain embodiments, the amino acid substitution at position 103 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a serine (S). In certain embodiments, the amino acid substitution at position 119 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for an arginine (R). In certain embodiments, the amino acid substitution at position 125 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) a cysteine (C). In certain embodiments, the amino acid substitution at position 125 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a cysteine (C). In certain embodiments, the amino acid substitution at position 177 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 177 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a histidine (H) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 180 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 185 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 187 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for an alanine (A). In certain embodiments, the amino acid substitution at position 200 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 207 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a valine (V). In certain embodiments, the amino acid substitution at position 209 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a valine (V). In certain embodiments, the amino acid substitution at position 226 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a methionine (M). In certain embodiments, the amino acid substitution at position 235 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a leucine (L). In certain embodiments, the amino acid substitution at position 240 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at

position 241 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a phenylalanine (F). In certain embodiments, the amino acid substitution at position 243 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a proline (P). In certain embodiments, the amino acid substitution at position 258 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the amino acid substitution at position 2% of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tryptophan (W) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tyrosine (Y) for a leucine (L). In certain embodiments, the amino acid substitution at position 296 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a leucine (L). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) for a methionine (M). In certain embodiments, the amino acid substitution at position 298 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a proline (P). In certain embodiments, the amino acid substitution at position 311 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine for a proline (P). In certain embodiments, the amino acid substitution at position 315 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for an arginine (R). In certain embodiments, the amino acid substitution at position 319 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a threonine (T). In certain embodiments, the amino acid substitution at position 327 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 328 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a tyrosine (Y). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a cysteine (C). In certain embodiments, the amino acid substitution at position 340 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a cysteine (C). In certain embodiments, the amino acid substitution at position 421 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a histidine (H) for the aspartic acid (D). In certain embodiments, the amino acid substitution at position 436 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an isoleucine (I) for a valine (V). In certain embodiments, the amino acid substitution at position 456 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a tyrosine (Y) for a methionine (M). In certain embodiments, the amino acid substitution at position 470 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a phenylalanine (F) for a leucine (L). In certain embodiments, the amino acid substitution at position 485 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a serine (S). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a leucine (L) for a methionine (M). In certain embodiments, the amino acid substitution at position 503 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an

isoleucine (I) for a methionine (M). In certain embodiments, the amino acid substitution at position 552 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a lysine (K) for a valine (V). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a threonine (T) for an alanine (A). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a glutamine (Q). In certain embodiments, the amino acid substitution at position 591 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an arginine (R) for a glutamine (Q).

In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or piggyBac-like transposase enzyme or may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at one or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments of the methods of the disclosure, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or piggyBac-like transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at two, three, four, five, six or more of positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, including those embodiments wherein the transposase comprises the above-described mutations at positions 30, 165, 282 and/or 538, the piggyBacTM or piggyBac-like transposase enzyme may comprise or the Super piggyBacTM transposase enzyme may further comprise an amino acid substitution at positions 103, 194, 372, 375, 450, 509 and 570 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In certain embodiments, the amino acid substitution at position 103 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a proline (P) for a serine (S). In certain embodiments, the amino acid substitution at position 194 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a valine (V) for a methionine (M). In certain embodiments, the amino acid substitution at position 372 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an alanine (A) for a lysine (K). In certain embodiments, the amino acid substitution at position 450 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of an asparagine (N) for an aspartic acid (D). In certain embodiments, the amino acid substitution at position 509 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a glycine (G) for a serine (S). In certain embodiments, the amino acid substitution at position 570 of SEQ ID NO: 14487 or SEQ ID NO: 14484 is a substitution of a serine (S) for an asparagine (N). In certain embodiments, the piggyBacTM or piggyBac-like transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487. In certain embodiments, including those embodiments wherein the piggyBacTM or piggyBac-like transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, the piggyBacTM or piggyBac-like transposase enzyme may further comprise an amino acid substitution at positions 372, 375 and 450 of the sequence of SEQ ID NO: 14487 or SEQ ID NO: 14484. In

certain embodiments, the piggyBacTM or piggyBac-like transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 14487, and a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 14487. In certain embodiments, the piggyBacTM or piggyBac-like transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, a substitution of an alanine (A) for an arginine (R) at position 372 of SEQ ID NO: 14487, a substitution of an alanine (A) for a lysine (K) at position 375 of SEQ ID NO: 14487 and a substitution of an asparagine (N) for an aspartic acid (D) at position 450 of SEQ ID NO: 14487.

In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from an insect. In certain embodiments, the insect is *Trichoplusia ni* (GenBank Accession No. AAA87375; SEQ ID NO: 17083), *Argyrogramma agnata* (GenBank Accession No. GU477713; SEQ ID NO: 17084, SEQ ID NO: 17085), *Anopheles gambiae* (GenBank Accession No. XP_312615 (SEQ ID NO: 17086); GenBank Accession No. XP_320414 (SEQ ID NO: 17087); GenBank Accession No. XP_310729 (SEQ ID NO: 17088)), *Aphis gossypii* (GenBank Accession No. GU329918; SEQ ID NO: 17089, SEQ ID NO: 17090), *Acyrthosiphon pisum* (GenBank Accession No. XP_001948139; SEQ ID NO: 17091), *Agrotis ipsilon* (GenBank Accession No. GU477714; SEQ ID NO: 17092, SEQ ID NO: 17093), *Bombyx mori* (GenBank Accession No. BAD11135; SEQ ID NO: 17094), *Chilo suppressalis* (GenBank Accession No. JX294476; SEQ ID NO: 17095, SEQ ID NO: 17096), *Drosophila melanogaster* (GenBank Accession No. AAL39784; SEQ ID NO: 17097), *Helicoverpa armigera* (GenBank Accession No. ABS18391; SEQ ID NO: 17098), *Heliothis virescens* (GenBank Accession No. ABD76335; SEQ ID NO: 17099) *Macdunnoughia crassisigna* (GenBank Accession No. EU287451; SEQ ID NO: 17100, SEQ ID NO: 17101), *Pectinophora gossypiella* (GenBank Accession No. GU270322; SEQ ID NO: 17102, SEQ ID NO: 17103), *Tribolium castaneum* (GenBank Accession No. XP_001814566; SEQ ID NO: 17104), *Ctenoplusia agnata* (also called *Argyrogramma agnata*), *Messour bouvieri*, *Megachile rotundata*, *Bombus impatiens*, *Mamestra brassicae*, *Mayetiola destructor* or *Apis mellifera*.

In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from an insect. In certain embodiments, the insect is *Trichoplusia ni* (AAA87375).

In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from an insect. In certain embodiments, the insect is *Bombyx mori* (BAD11135).

In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from a crustacean. In certain embodiments, the crustacean is *Daphnia pulicaria* (AAM76342, SEQ ID NO: 17105).

In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from a vertebrate. In certain embodiments, the vertebrate is *Xenopus tropicalis* (GenBank Accession No. BAF82026; SEQ ID NO: 17106), *Homo sapiens* (GenBank Accession No. NP_689808; SEQ ID NO: 17107), *Mus musculus* (GenBank Accession No. NP_741958; SEQ ID NO: 17108), *Macaca fascicularis* (GenBank Accession No. AB179012; SEQ ID NO: 17108, SEQ ID NO: 17109), *Rattus norvegicus* (GenBank Accession No. XP_220453; SEQ ID NO: 17110) or *Myotis lucifugus*.

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In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from a urochordate. In certain embodiments, the urochordate is *Ciona intestinalis* (GenBank Accession No. XP_002123602; SEQ ID NO: 17111).

In certain embodiments, the piggyBac or piggyBac-like transposase inserts a transposon at the sequence 5'-TTAT-3' within a chromosomal site (a TTAT target sequence).

In certain embodiments, the piggyBac or piggyBac-like transposase inserts a transposon at the sequence 5'-TTAA-3' within a chromosomal site (a TTAA target sequence).

In certain embodiments, the target sequence of the piggy Bac or piggyBac-like transposon comprises or consists of 5'-CTAA-3', 5'-TTAG-3', 5'-ATAA-3', 5'-TCAA-3', 5'AGTT-3', 5'-ATTA-3', 5'-GTTA-3', 5'-TTGA-3', 5'-TTTA-3', 5'-TTAC-3', 5'-ACTA-3', 5'-AGGG-3', 5'-CTAG-3',

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5'-TGAA-3', 5'-AGGT-3', 5'-ATCA-3', 5'-CTCC-3', 5'-TAAA-3', 5'-TCTC-3', 5'-TGAA-3', 5'-AAAT-3', 5'-AATC-3', 5'-ACAA-3', 5'-ACAT-3', 5'-ACTC-3', 5'-AGTG-3', 5'-ATAG-3', 5'-CAAA-3', 5'-CAC-3', 5'-CATA-3', 5'-CCAG-3', 5'-CCCA-3', 5'-CGTA-3', 5'-GTCC-3', 5'-TAAG-3', 5'-TCTA-3', 5'-TGAG-3', 5'-TGTT-3', 5'-TTCA-3' 5'-TTCT-3' and 5'-TTTT-3'.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Bombyx mori*. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14504)

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1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIALLYL AGLIKSNRQS LKDLWRDGT GVDIFRTTMS LQRFQFLQNN
241 IFRDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FDVVNLLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHD NSIDEESTGEK QKPEMITFYN STKAGVDVVD ELSANYNVSR
481 NSKRPWMTLF YGVLNMAAIN ACIIYRANKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPTYKKDRKT KHSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90° %, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14505)

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1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIALLYL AGLIKSNRQS LKDLWRDGT GVDIFRTTMS LQRFQFLQNN
241 IFRDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FYVVNLLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHD NSIDEESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRPWMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPTYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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In certain embodiments, the piggyBac or piggyBac-like transposase is fused to a nuclear localization signal. In certain embodiments, the amino acid sequence of the pig-

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gyBac or piggyBac-like transposase fused to a nuclear localization signal is encoded by a polynucleotide sequence comprising.

(SEQ ID NO: 14629)

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1 atggcaccca aaaagaaaacg taaaagtgtatc gacattgaaat gacaggaaaga aagaatcagg
61 gcgatgctcg aagaagaact gagcgactac tccgacgaat cgtcatcaga ggtatgaaacc
121 gaccactgtta gcgagcatga ggttaactac gacaccgagg aggagagaat cgactctgtg
181 gatgtgcctt ccaactcactg ccaagaagag gccaatgcaa ttatcgaaa cgaatcgac
241 agcgatccag acgtatgttc gccactgtcc ctctgtcgcc agcgcccgac cgcttcgaga
301 caagtgtca gttccattcta cacttcaag gacggcacta aatgttataaa gaattggccag
361 cgacctaactg ttagactccg ctccgagaat atcgatgtcc aacaggctca ggtcaagaat
421 atcgcccccg acgcctcgac tgagtgacg tggttggata ttttctgtac ttccggacatg
481 ctgcaagaaa ttctgacgca cacaacacg tcgatttaggc atcgccagac caagactgca
541 ggggagaact catcgcccgaa aaccccttc tatatgcaag agactactct gtgcgaaactg
601 aaggcgctga ttgcactgtt gtacttggcc ggcttcatca aatcaaatacg gcagagcctc
661 aaagatctctt ggagaacggta tggaaacttggta gtggatatct ttccggacgac tatgagctt
721 cagcggttcc agtttctgca aaacaatatac agattcgacg acaagtccac ccgggacgaa
781 aggaaacaga ctgacaacat ggctgcgttc cggtaatat tctgtatcgat ttgtgcgtgc
841 tgccaaaacg cttatagccc atcgaaattt ctgaccatcg acgaaatgtt tctctccctc
901 cggggggcgct ggctgttccg agtgtacatc ccgaacaacgc cggctaaata cggaaatcaa
961 atccctggccc tgggtggacgc caagaatttc tacgtcgtta atctcgaaatgtt gtacgcagga
1021 aagcaaccgtt cggggaccgtt cggctgttccg aaccggccgtt ttgttggatcgat ttgttggatcg
1081 attcagcggtt tggccagatc ccaccgcaat gttacccttgc acaatttgggtt caccggctac
1141 gagctgtatgc ttcacccatgaa gacgttgcac cggctcaactt gctgtggggac tggatcgatgg
1201 aacaagcgcc agatcccaga atcccttcatac cgcaccgacc gccagctaa ctcgtccgtt
1261 ttccggatttc aaaaggatatac caccgttgc tggatcgccc ccaagaaaaaa caaggatcgat
1321 gtctgtatgc gcaccatgca tcacgacaac agcatcgacg agtcaaccgg agaaaagcaa
1381 aagccccgaga tgateacccatc ctacaattca actaaggccg cggctcgatgtt cgtggatggaa
1441 ctgtgcgcga actataacgtt gtcccgaaatc tctaaggccg ggcctatgac tctttctac
1501 ggagtgctga atatggccgc aatcaacgcg tggatcgatcc accgcacccaa caagaacgtt
1561 accatcaaggc gcaccgatgtt catcgatcg ctgggtttgc gcatgtatca cggccaccc
1621 cattcacggaa acaagaagaa gaatatccctt acttacgttgc ggcacgttat cggatcgatgg
1681 ttggggagaac caagcccccgcc ccacgttgcac gttccggggcc gctacgttgc gttggccaaat
1741 tgcccgatca aaaaggaccg caaaaacccaa agatcgatgttgc acgcgttgc caaacccatc
1801 tgcatggatgc atgcaccaattt tctgtgttgc aattgttgcgtt aactcgatcc tccctgtt.

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In certain 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 certain embodiments, the hyperactive piggyBac or piggyBac-like transposase enzyme is isolated or derived from

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Bombyx mori. In certain embodiments, the piggyBac or piggyBac-like transposase is a hyperactive variant of SEQ ID NO: 14505. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to:

(SEQ ID NO: 14576)

1	MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
61	EANAIIANES DSDPDDDLPL SLVRQRASAS RQMSGPHYTS KDGTKWYKNC QRPNVRLRSE
121	NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAATS
181	FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLQNN
241	IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301	IPNPKAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361	NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421	VSYARKKNKV VVVMSTMHHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVS
481	NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541	PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCOPYKKDRKT KRSCNACAKP ICMEHAKFLC
601	ENCAELDSHL.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14576. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14630)

1	MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
61	EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121	NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAATS
181	FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLNN
241	IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301	IPNPKAKYGI KILALVDAKN FYVHNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361	NVTFDNWFTG YEVMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VEGFQKDITL
421	VSYAPKKNKV VVVMSTMHHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVS
481	NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541	PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCOPYKKDRKT KRSCNACAKP ICMEHAKFLC
601	ENCAHLD.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14631)

1	MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
61	EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121	NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAATS
181	FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLNN
241	IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301	IPNPKAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361	NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL

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421 VSYAPKKNV VVVMSTMHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541 PTYLQRRIAM QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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(SEQ ID NO: 14632)
1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS VDVPSNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKTQIPENF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNV VVVMSTMHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELQANYNVSR
481 NSKRWPMLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541 PTYLQRRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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(SEQ ID NO: 14633)
1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS VDVPSNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNV VVVMSTMHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKNI
541 PTYLQRRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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In certain embodiments, the hyperactive piggyBac or 55
piggyBac-like transposase comprises a sequence of:

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(SEQ ID NO: 14634)
1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS VDVPSNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIALLYL AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY

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- continued

301 IPNPKPAKYGI KILALVDAKN DYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
 361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNS VFGFQKDITL
 421 VSYAPKKNKV VVVMSTMHD NSIDEESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
 481 NSKRWPMTLF YGVLNMAAIN ACIYRTNKN VTIKPTEFIR SLGLSMIYEH LHSRNKKNI
 541 PTYLRQRIEK QLGEPSSRHV NVKGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
 601 ENCAELDSSL.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase is more active than the transposase of SEQ ID NO: 14505. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase is at least 90%, at least 95%, at least 9%, at least 97%, at least 98%, or at least 99% or any percentage in between identical to SEQ ID NO: 14505.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises an amino acid substitution at a position selected from 92, 93, 96, 97, 165, 178, 189, 196, 200, 201, 211, 215, 235, 238, 246, 253, 258, 261, 263, 271, 303, 321, 324, 330, 373, 389, 399, 402, 403, 404, 448, 473, 484, 507, 523, 527, 528, 543, 549, 550, 557, 601, 605, 607, 609, 610 or a combination thereof (relative to SEQ ID NO: 14505). In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises an amino acid substitution of Q92A, V93L, V93M, P96G, F97H, F97C, H165E, H165W, E178S, E178H, C189P, A196G, L200I, A201Q, L211A, W215Y, G219S, Q235Y, Q235G, Q238L, K246I, K253V, M258V, F261L, S263K, C271S, N303R, F321W, F321D, V324K, V324H, A330V, L373C, L373V, V389L, S399N, R402K, T403L, D404Q, D404S, D404M, N441R, G448W, E449A, V469T, C473Q, R484K, T507C, G523A, I527M, Y528K, Y543I, E549A, K550M, P557S, E601V, E605H, E605W, D607H, S609H, L610I or any combination thereof. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises an amino acid substitution of Q92A, V93L, V93M, P96G, F97H, F97C, H165E, H165W, E178S, E178H, C189P, A196G, L200I, A201Q, L211A, W215Y, G219S, Q235Y, Q235G, Q238L, K246I, K253V, M258V, F261L, S263K, C271S, N303R, F321W, F321D, V324K, V324H, A330V, L373C, L373V, V389L, S399N, R402K, T403L, D404Q, D404S, D404M, N441R, G448W, E449A, V469T, C473Q, R484K, T507C, G523A, I527M, Y528K, Y543I, E549A, K550M, P557S, E601V, E605H, E605W, D607H, S609H and L610I.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises one or more substitutions of an amino acid that is not wild type, wherein the one or more substitutions a for wild type amino acid comprises a substitution of E4X, A12X, M13X, L14X, E15X, D20X, E24X, S25X, S26X, S27X, D32X, H33X, E36X, E44X, E45X, E46X, I48X, D49X, R58X, A62X, N63X, A64X, I65X, I66X, N68X, E69X, D71X, S72X, D76X, P79X, R84X, Q85X, A87X, S88X, Q92X, V93X, S94X, G95X, P96X, F97X, Y98X, T99X, I145X, S149X, D150X, L152X, E154X, T157X, N160X, S161X, S162X, H165X, R166X, T168X, K169X, T170X, A171X, E173X, S175X, S176X, E178X, T179X, M183X, Q184X, T186X, T187X, L188X, C189X, L194X, I195X, A196X, L198X, L200X, A201X, L203X, I204X, K205X, A206X, N207X, Q209X, S210X, L211X, K212X, D213X, L214X, W215X, R216X, T217X, G219X, V222X, D223X, I224X, T227X, M229X, Q235X,

L237X, Q238X, N239X, N240X, P302X, N303X, P305X, A306X, K307X, Y308X, I310X, K311X, I312X, L313X, A314X, L315X, V316X, D317X, A318X, K319X, N320X, F321X, Y322X, V323X, V324X, L326X, E327X, V328X, A330X, Q333X, P334X, S335X, G336X, P337X, A339X, V340X, S341X, N342X, R343X, P344X, F345X, E346X, V347X, E349X, I352X, Q353X, V355X, A356X, R357X, N361X, D365X, W367X, T369X, G370X, L373X, M374X, L375X, H376X, N379X, E380X, R382X, V386X, V389X, N392X, R394X, Q395X, S399X, F400X, I401X, R402X, T403X, D404X, R405X, Q406X, P407X, N408X, S409X, S410X, V411X, F412X, F414X, Q415X, I418X, T419X, L420X, N428X, V432X, M434X, D440X, N441X, S442X, I443X, D444X, E445X, G448X, E449X, Q451X, K452X, M455X, I456X, T457X, F458X, S461X, A464X, V466X, Q468X, V469X, E471X, L472X, C473X, A474X, K483X, W485X, T488X, L489X, Y491X, G492X, V493X, M496X, I499X, C502X, I503X, T507X, K509X, N510X, V511X, T512X, I513X, R515X, E517X, S521X, G523X, L524X, S525X, I527X, Y528X, E529X, H532X, S533X, N535X, K536X, K537X, N539X, I540X, T542X, Y543X, Q546X, E549X, K550X, Q551X, G553X, E554X, P555X, S556X, P557X, R558X, H559X, V560X, N561X, V562X, P563X, G564X, R565X, Y566X, V567X, Q570X, D571X, P573X, Y574X, K576X, K581X, S583X, A586X, A588X, E594X, F598X, L599X, E601X, N602X, C603X, A604X, E605X, L606X, D607X, S608X, S609X or L610X (relative to SEQ ID NO: 14505). A list of hyperactive amino acid substitutions can be found in U.S. Pat. No. 10,041,077, the contents of which are incorporated herein by reference in their entirety.

In certain embodiments, the piggyBac or piggyBac-like transposase is integration deficient. In certain 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. In certain embodiments, the piggyBac or piggyBac-like transposase is an integration deficient variant of SEQ ID NO: 14505.

In certain embodiments, the excision competent, integration deficient piggyBac or piggyBac-like transposase comprises one or more substitutions of an amino acid that is not wild type, wherein the one or more substitutions a for wild type amino acid comprises a substitution of R9X, A12X, M13X, D20X, Y21K, D23X, E24X, S25X, S26X, S27X, E28X, E30X, D32X, H33X, E36X, H37X, A39X, Y41X, D42X, T43X, E44X, E45X, E46X, R47X, D49X, S50X, S55X, A62X, N63X, A64X, I66X, A67X, N68X, E69X, D70X, D71X, S72X, D73X, P74X, D75X, D76X, D77X, I78X, S81X, V83X, R84X, Q85X, A7X, S88X, A89X, S90X, R91X, Q92X, V93X, S94X, G95X, P96X, F97X, Y98X, T99X, W012X, G103X, Y107X, K108X, L117X, I122X, Q128X, I312X, D135X, S137X, E139X, Y140X,

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I145X, S149X, D150X, Q153X, E154X, T157X, S61X, S162X, R164X, H165X, R166X, Q167X, T168X, K169X, T170X, A171X, A172X, E173X, R174X, S175X, S176X, A177X, E178X, T179X, S180X, Y182X, Q184X, E185X, T187X, L188X, C189X, L194X, I195X, A196X, L198X, L200X, A201X, L203X, I204X, K205X, N207X, Q209X, L21X, D213X, L214X, W215X, R216X, T217X, G219X, T220X, V222X, D223X, I224X, T227X, T228X, F234X, Q235X, L237X, Q238X, N239X, N240X, N303X, K304X, I310X, I312X, L313X, A314X, L315X, V316X, D317X, A318X, K319X, N320X, F321X, Y322X, V323X, V324X, N325X, L326X, E327X, V328X, A330X, G331X, K332X, Q333X, S335X, P337X, P344X, F345X, E349X, H359X, N361X, V362X, D365X, F368X, Y371X, E372X, L373X, H376X, E380X, R382X, R382X, V386X, G387X, T388X, V389X, K391X, N392X, R394X, Q395X, E398X, S399X, F400X, I401X, R402X, T403X, D404X, R405X, Q406X, P407X, N408X, S409X, S410X, Q415X, K416X, A424X, K426X, N428X, V430X, V432X, V433X, M434X, D436X,

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D440X, N441X, S442X, I443X, D444X, E445X, S446X, 0,447X, G448X, E449X, K450X, Q451X, E454X, M455X, I456X, T457X, F458X, S461X, A464X, V466X, Q468X, V469X, C473X, A474X, N475X, N477X, K483X, R484X, P486X, T488X, L489X, G492X, V493X, M496X, I499X, I503X, Y505X, T507X, N510X, V511X, T512X, I513X, K514X, T516X, E517X, S521X, G523X, L524X, S525X, I527X, Y528X, L531X, H532X, S533X, N535X, I540X, T542X, Y543X, R545X, Q546X, E549X, L552X, G553X, E554X, P555X, S556X, P557X, R558X, H559X, V560X, N561X, V562X, P563X, G564X, V567X, Q570X, D571X, P573X, Y574X, K575X, K576X, N585X, A586X, M593X, K596X, E60X, N602X, A604X, E605X, L606X, D607X, S608X, S609X or L610X (relative to SEQ ID NO: 14505).
A list of integration deficient amino acid substitutions can be found in U.S. Pat. No. 10,041,077, the contents of which are incorporated by reference in their entirety.

In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14606)

1 MDIERQEERI RAMLEEEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS DVVPNSRQE
61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSSPFYTS KDGTWKYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIALLYL AGLIKSNRQS LKDLWRKDGT GVDIFRTTMS LQRFQFLNN
241 IRFPDDISTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FYVVNLLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMYYEH LHSRNKKNI
541 PTYLQRRIEK QLGEPVPRHV NYPGRYVRCQ DCPTYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

40 In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14607)

1 MDIERQEERI RAMLEEEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS DVVPNSRQE
61 EANAIIANES DSDPDDDLPL SDVRQRASAS RQVSGPFYTS KDGTWKYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYL AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFYFLQNN
241 IRFDDKSTLD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN FYVVNLLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKWPMTLF YGVLNMAAIN ACIIYPTNKN VTIKRTEFIR SLGLSMYYEH LHSRNKKNI
541 PTYLQRRIEK QLGEPSPRHV NYPGRYVRCQ DCPTYKKDRKT KRSCNACAKP ICMEHAKFLC
601 VNCAELDSSL.

In certain embodiments, the piggyBac or piggyBac-like transposase that is integration deficient comprises a sequence of:

(SEQ ID NO: 14608)

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1 MDIERQEERI RAMLEELSD YSDESSSEDE TDHCSEHEVN YDTEERIDS DVVPSNSRQE
61 EANAIIANES DSDPDDLPL SLVPQRASAS RQVSGPFYTS KDGTKWYKNC QPPNVLRRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIALYL AGLIKSNRQS LKDLWRKDGT GVDIFRTTMS LQRFQFLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNPKAKYGI KILALVDAKN DYVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YECMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDEESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
421 NSKKWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIKEH LHSRNKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYRKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL.

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In certain embodiments, the integration deficient transposase comprises a sequence that is at least 90% identical to SEQ ID NO: 14608.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Bombyx mori*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14506)

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1 ttatccggc gagcatgagg cagggtatct cataccatgg taaaatttta aagttgtgta
61 ttttataaaa ttttcgtctg acaacactag cgcgctcagt agctggaggc aggagcgtgc
121 gggagggat agtggcgtga tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc
181 aaacctgtt cgggtatgtt ataccctgcc tcattgtta cgtatttttt ttatgttaatt
241 tttccgatta ttaattcaa ctgttttatt ggtatttta tgttatccat tggttttttt
301 ttatgattna ctgtatcggt tgttttcgt tccttagtt gagtttttt ttattattna
361 cagtttttga tcaaa.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

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1 tcataaaaa agttaaaaa aataattata tgtttataa tgaaaagaat ctcattatct
61 ttcagtatta ggttgattta tattccaaag aataatattt ttgttaatt gtgtattnn
121 gtaaacctct aatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
181 taataatttc ataattaaaa acttcttca ttgaatgcca ttaaataaac cattattna
241 caaaataaga tcaacataat tgagtaata ataataagaa caatattata gtacaacaaa
301 atatgggtat gtcataccct gccacattct tgatgtaact tttttcacc tcatgctcgc
361 cgggttat

```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14508)

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1 ttatccggc gagcatgagg cagggtatct cataccctgg taaaattta aagttgtgt
61 ttttataaaa ttttggtctg acaacactag cgcgctcagt aggtggaggc aggagcgtgg
121 gggagggat agtggcgtga tggcagtgtg gcacggaca ccggcgagat attcgtgtgc
181 aaacctgttt cgggtatgtt ataccctgcc tcat.

```

In certain embodiments, the piggyBac™ (PB) or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14509)

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1 taaataataa taatttcata attaaaaact tcttcattt aatgccatta aataaaccat
61 tattttacaa aataagatca acataattga gtaaataata ataagaacaa tattatagta
121 caacaaata tgggtatgtc ataccctgcc acattcttga tgtaactttt tttcacctca
181 tgctcgccgg gttat.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a left sequence corresponding to SEQ ID NO: 14506 and a right sequence corresponding to SEQ ID NO: 14507. In certain embodiments, one piggyBac or piggyBac-like transposon end is at least 85%, at least 90%, at least 95%, at least 98%, at least 99% identical or any percentage in between identical to SEQ ID NO: 14506 and the other piggyBac or piggyBac-like transposon end is at least 85%, at least 90%, at least 95%, at least 98%, at least 99% or any percentage in between identical to SEQ ID NO: 14507. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14506 and SEQ ID NO: 14507 or SEQ ID NO: 14509. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14508 and SEQ ID NO: 14507 or SEQ ID NO: 14509. In certain embodiments, the left and right transposon ends share a 16 bp repeat sequence at their ends of CCCGGCGAGCATGAGG (SEQ ID NO: 14510) immediately adjacent to the 5'-TTAT-3' target insertion site, which is

comprising the reverse complement of this sequence: 5'-CCTCATGCTGCCGGGTTAT-3' (SEQ ID NO: 14512).

In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end comprising at least 14, 16, 18, 20, 30 or 40 contiguous nucleotides of SEQ ID NO: 14506 or SEQ ID NO: 14508. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end comprising at least 14, 16, 18, 20, 30 or 40 contiguous nucleotides of SEQ ID NO: 14507 or SEQ ID NO: 14509. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end with at least 90% identity to SEQ ID NO: 14506 or SEQ ID NO: 14508. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end with at least 90% identity to SEQ ID NO: 14507 or SEQ ID NO: 14509.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14515)

```

1 ttaacccggc gagcatgagg cagggtatct cataccctgg taaaattta aagttgtgt
61 ttttataaaa ttttggtctg acaacactag cgcgctcagt aggtggaggc aggagcgtgg
121 gggagggat agtggcgtga tggcagtgtg gcacggaca ccggcgagat attcgtgtgc
181 aaacctgttt cgggtatgtt ataccctgcc tcattgttgc cgtatTTTT ttatgttaatt
241 ttcccgatta ttaattcaa ctgtttatt ggtatTTTT tgttatccat tgTTTttttt
301 ttatgattta ctgtatcggt tggatTTTcggt tccttagttt gagTTTTTT ttattatTTT
361 cagTTTTGA tcAAA.

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inverted in the orientation in the two ends. In certain embodiments, left transposon end begins with a sequence

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14516)

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1 tcataTTTT agtttaaaaa aataattata tgTTTTaaTG gaaaAGAAT ctcattatct
61 ttcaGTTATTa ggTTGATTa TATTCCAAAG aataatTTT TTGTaaATT gTTGATTTT
121 gtaaacCTCT aataTTTGC TGCTAAATT ACTGTGTTA AGAAAAAGAT TAATAATAA
181 taataattTC ATAATTAAA ACTTCTTCA TTGAATGCCA TTAATAATT CATTATTTA
241 caaaATAAGA TCAACATAAC TGAGTAAATA ATAATAAGAA CAATATTATA GTACAACAAA

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301 atatgggtat gtcataccct tttttttttt tttttttttt ttctttcggg tagagggccg
361 aacctcctac gaggtccccg cgcaaaaaggg gcgcgcgggg tatgtgagac tcaacgatct
421 gcatggtgtt gtgagcagac cgcggggcca aggattttag agcccaccca ctaaacgact
481 cctctgcact cttacacccg acgtccgatc ccctccgagg tcagaacccg gatgaggttag
541 gggggctacc ggggtcaaca ctacaaccag acggcgccgc tcaccccaag gacgcccagc
601 cgacggagcc ttccggggcga atcgaaggct ctgaaacgtc ggccgtctcg gtacggcagc
661 ccgtcggggcc gcccagacgg tgccgttggt gtcccgaaat accccgctgg accagaacca
721 gcctgcccggg tcggggacggc atacaccgtc gaccgggtcgcc tccaatcaact ccacggcagc
721 gcgctagagt gctggta.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of CCCGGCGAGCAT-GAGG (SEQ ID NO: 14510). In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of SEQ ID NO: 14510. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTATCCCGGCGAGCATGAGG (SEQ ID NO: 14511). In certain embodiments, the piggyBac or piggyBac-like transposon comprises at least 16 contiguous nucleotides from SEQ ID NO: 14511. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of CCTCATGCTCGCCGGTTAT (SEQ ID NO: 14512). In certain embodiments, the piggyBac or piggyBac-like transposon comprises at least 16 contiguous nucleotides from SEQ ID NO: 14512. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end comprising at least 16 contiguous nucleotides from SEQ ID NO: 14511 and one end comprising at least 16 contiguous nucleotides from SEQ ID NO: 14512. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14511 and SEQ ID NO: 14512. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCCGGCGAGCATGAGG (SEQ ID NO 14513). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of CCT-CATGCTGCCGGTTAA (SEQ ID NO: 14514).

In certain embodiments, the piggyBac or piggyBac-like transposon may have ends comprising SEQ ID NO: 14506 and SEQ ID NO: 14507, or a variant of either or both of these having at least 90% sequence identity to SEQ ID NO: 14506 or SEQ ID NO: 14507, and the piggyBac or piggyBac-like transposase has the sequence of SEQ ID NO: 14504 or SEQ ID NO: 14505, or a sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identity to SEQ ID NO: 14504 or SEQ ID NO: 14505. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a heterologous polynucleotide inserted between a pair of inverted repeats, where the transposon is capable of transposition by a piggyBac or piggyBac-like transposase having at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identity to SEQ ID NO: 14504 or SEQ ID NO: 14505. In certain embodiments, the transposon comprises two transposon ends, each of which comprises SEQ ID NO: 14510 in inverted orientations in the two transposon ends. In certain embodiments, each inverted terminal repeat (ITR) is at least 90% identical to SEQ ID NO: 14510.

In certain 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 certain embodiments, one end of the piggyBac or piggyBac-like transposon comprises at least 16 contiguous nucleotides from SEQ ID NO: 14506 and the other transposon end comprises at least 16 contiguous nucleotides from SEQ ID NO: 14507. In certain embodiments, one end of the piggyBac or piggyBac-like transposon comprises at least 17, at least 18, at least 19, at least 20, at least 22, at least 25, at least 30 contiguous nucleotides from SEQ ID NO: 14506 and the other transposon end comprises at least 17, at least 18, at least 19, at least 20, at least 22, at least 25, at least 30 contiguous nucleotides from SEQ ID NO: 14507.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises transposon ends (each end comprising an ITR) corresponding to SEQ ID NO: 14506 and SEQ ID NO: 14507, and has a target sequence corresponding to 5'-TTAT3'. In certain embodiments, the piggyBac or piggyBac-like transposon also comprises a sequence encoding a transposase (e.g. SEQ ID NO: 14505). In certain embodiments, the piggyBac or piggyBac-like transposon comprises one transposon end corresponding to SEQ ID NO: 14506 and a second transposon end corresponding to SEQ ID NO: 14516. SEQ ID NO: 14516 is very similar to SEQ ID NO: 14507, but has a large insertion shortly before the ITR. Although the ITR sequences for the two transposon ends are identical (they are both identical to SEQ ID NO: 14510), they have different target sequences: the second transposon has a target sequence corresponding to 5'-TTAA-3', providing evidence that no change in ITR sequence is necessary to modify the target sequence specificity. The piggyBac or piggyBac-like transposase (SEQ ID NO: 14504), which is associated with the 5'-TTAA-3' target site differs from the 5'-TTAT-3'-associated transposase (SEQ ID NO: 14505) by only 4 amino acid changes (D322Y, S473C, A507T, H582R). In certain embodiments, the piggyBac or piggyBac-like transposase (SEQ ID NO: 14504), which is associated with the 5'-TTAA-3' target site is less active than the 5'-TTAT-3'-associated piggyBac or piggyBac-like transposase (SEQ ID NO: 14505) on the transposon with 5'-TTAT-3' ends. In certain embodiments, piggyBac or piggyBac-like transposons with 5'-TTAA-3' target sites can be converted to piggyBac or piggyBac-like transposases with 5'-TTAT-3 target sites by replacing 5'-TTAA-3' target sites with 5'-TTAT-3'. Such transposons can be used either with a piggyBac or piggyBac-like transposase such as SEQ ID NO: 14504 which recognizes the 5'-TTAT-3' target sequence, or with a variant of a transposase originally associated with the

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5'-TTAA-3' transposon. In certain embodiments, the high similarity between the 5'-TTAA-3' and 5'-TTAT-3' piggyBac or piggyBac-like transposases demonstrates that very few changes to the amino acid sequence of a piggyBac or piggyBac-like transposase alter target sequence specificity. In certain embodiments, modification of any piggyBac or piggyBac-like transposon-transposase gene transfer system, in which 5'-TTAA-3' target sequences are replaced with 5'-TTAT-3'-target sequences, the ITRs remain the same, and the transposase is the original piggyBac or piggyBac-like transposase or a variant thereof resulting from using a low-level mutagenesis to introduce mutations into the trans-

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posase. In certain embodiments, piggyBac or piggyBac-like transposon transposase transfer systems can be formed by the modification of a 5'-TTAT-3'-active piggyBac or piggyBac-like transposon-transposase gene transfer systems in which 5'-TTAT-3' target sequences are replaced with 5'-TTAA-3'-target sequences, the ITRs remain the same, and the piggyBac or piggyBac-like transposase is the original transposase or a variant thereof.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Bombyx mori*. In 10 certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14577)
 1 cccggcgagc atgaggcagg gatatctata ccctggtaaa attttaagt tgtgtatccc
 61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
 121 ggggatagtg gcggtatcgc agtgtggcac gggacaccgg cgagatattc gtgtgaaac
 181 ctgtttcggg tatgttatac cctgcctcat tggacgta t.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14578)
 1 tttaaaaaaa agattaataa ataataataa tttcataatt aaaaacttct ttcatatgtat
 61 gccattaaat aaaccattat tttacaaaat aagatcaaca taattgagta aataataata
 121 agaacaatata tatagtacaa caaaatatgg gatgtcata ccctgcacca ttcttgatgt
 181 aactttttt cacctcatgc tcgccccgg.

In certain embodiments, the transposon comprises at least 16 35 contiguous bases from SEQ ID NO: 14577 and at least 16 contiguous bases from SEQ ID NO: 14578, and inverted terminal repeats that are at least 87% identical to CCCGGCGAGCATGAGG (SEQ ID NO: 14510). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14595)
 1 cccggcgagc atgaggcagg gatatctata ccctggtaaa attttaagt tgtgtatccc
 61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
 121 ggggatagtg gcggtatcgc agtgtggcac gggacaccgg cgagatattc gtgtgaaac
 181 ctgtttcggg tatgttatac cctgcctcat tggacgta ttttttttat gtaattttt
 241 cgattattaa ttcaactgt ttatggta ttttatgtt atccattgtt ctttttttat
 301 gatttactgt atcggttgc ttgcgtcct ttagttgagt ttttttttat tattttcagt
 361 ttttgcataa a.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14596)
 1 tcataattttt agtttaaaaaa aataattata ttgtttataa tgaaaagaat ctcattatct
 61 ttcaatgttta ggttgcattta tattccaaag aataatattt ttgttaattt gttgatcccc
 121 gtaaacctct aaatgtttgt tgctaaaatt actgtgttta agaaaaagat taataataaa
 181 taataatttc ataattaaaaa acttcttca ttgaatgcc ttaataaac cattattttt
 241 caaaaataaga tcaacataat tggatcaaata ataataagaa caatattata gtacaacaaa

-continued

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301 atatgggtat gtcataccct gccacattct ttagttaact tttttcacc tcatacgctgc
361 cggg.
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In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14595 and SEQ ID NO: 14596, and is transposed by the piggyBac or piggyBac-like transposase of SEQ ID NO: 14505. In certain embodiments, 10 the ITRs of SEQ ID NO: 14595 and SEQ ID: 14596 are not flanked by a 5'-TTAA-3' sequence. In certain embodiments, the ITRs of SEQ ID NO: 14595 and SEQ ID: 14596 are flanked by a 5'-TTAT-3' sequence.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

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(SEQ ID NO: 14597)
1 cccggcgagc atgaggcagg gatatctata ccctggtaaa attttaaagt tgtgtatccc
61 ataaaaatccc cgtctgacaa cactagcgcg ctcaatgtat ggaggcagga gcgtgcgggg
121 ggggataatgc gcgtgtatgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
181 ctgtttcggg tatgttatac cctgcctcat tgttgacgta tttttttat gtaattttc
241 cgattattaa ttcaactgc ttatggta ttttatgtt atccattgtt cttttttat
301 g.
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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

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(SEQ ID NO: 14598)
1 cagggtatct cataccctgg taaaatcca aagttgtgtat ttttataaaa ttttcgtctg
61 acaacactag cgcgctcagt agtggaggc aggagcgtgc gggagggat agtggcgtga
121 tgcgtgtgc acggggaca cggggagat attcgtgtgc aaacctgttt cgggtatgtt
181 ataccctgcc tcattgttga cgtatcccc ttatgttaatt tttccgatta ttaatccaa
241 ctgttttatt ggtatcccc ttttatccat tgttttttt ttatg.
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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

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(SEQ ID NO: 14599)
1 cagggtatct cataccctgg taaaatcca aagttgtgtat ttttataaaa ttttcgtctg
61 acaacactag cgcgctcagt agtggaggc aggagcgtgc gggagggat agtggcgtga
121 tgcgtgtgc acggggaca cggggagat attcgtgtgc aaacctgttt cgggtatgtt
181 ataccctgcc tcattgttga cgtat.
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In certain embodiments, the left end of the piggyBac or piggyBac-like transposon comprises a sequence of SEQ ID 60 NO: 14577, SEQ ID NO: 14595, or SEQ ID NOs: 14597-14599. In certain embodiments, the left end of the piggyBac or piggyBac-like transposon is preceded by a left target sequence.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14600)

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1 tcatattttt agtttaaaaa aataattata tgtttataa taaaaagaat ctcattatct
61 ttcagtttta ggttgattt tattccaaag aataatattt ttgttaattt gtgttatttt
121 gtaaacctct aatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
181 taataatttc ataattaaaa acyttttca ttgaatgcc aataataaac cattatttt
241 caaaataaga tcaacataat tgagtaataa ataataagaa caatattata gtacaacaaa
301 atatgggtat gtcataccct gccacattct ttagttaact tttttcacc tcattgtcg
351 cggg.

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In certain embodiments the piggyBac or piggyBac-like transposon comprises a sequence of:

sequence that is at least 90%, at least 95% or at least 99% or any percentage in between identical to SEQ ID NO:

(SEQ ID NO: 14601)

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1 tttaagaaaa agattaataa ataataataa tttcataatt aaaaacttct ttcatgttat
61 gccattaaat aaaccattat tttacaaaat aagatcaaca taattgagta aataataata
121 agaacaatat tatagtacaa caaaatatgg gtatgtata ccctgcccata ttcttgatgt
181 aactttttt ca.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

14577 and one end that comprises a sequence that is at least 90%, at least 95% or at least 99% or any percentage in

(SEQ ID NO: 14602)

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1 cccggcgagg atgaggcagg gtatctata ccctggtaaa attttaaagt tgtgttatttt
61 ataaaatttt cgtctgacaa cactagcgcg ctctagtagct ggaggcagg gcgtgcggga
121 gggatagtg gcgtgatcgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
181 ctgttcqqq tatgttatac cctqcctcat tggacqta tttttttat gtaattttc
241 cgattattaa ttcaactgt ttatggta ttttatgtt atccattgtt cttttttat
301 gatttactgt atcggttgc ttctgttcc ttagttgagt tttttttat tattttcagt
361 ttttgatcaa a.

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In certain embodiments, the right end of the piggyBac or piggyBac-like transposon comprises a sequence of SEQ ID NO: 14578, SEQ ID NO: 14596, or SEQ ID NOS: 14600-45 14601. In certain embodiments, the right end of the piggy-Bac or piggyBac-like transposon is followed by a right target sequence. In certain embodiments, the transposon is transposed by the transposase of SEQ ID NO: 14505. In certain 50 embodiments, the left and right ends of the piggyBac or piggyBac-like transposon share a 16 bp repeat sequence of SEQ ID NO: 14510 in inverted orientation and immediately adjacent to the target sequence. In certain embodiments, the left transposon end begins with SEQ ID NO: 14510, and the right transposon end ends with the reverse complement of SEQ ID NO: 14510, 5'-CCTCATGCTGCCGGG-3' (SEQ ID NO: 14603). In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR with at least 93%, at least 87%, or at least 81% or any percentage in between identity to SEQ ID NO: 14510 or SEQ ID NO: 14603. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a target sequence followed by a left transposon end comprising a sequence selected from SEQ ID NOS: 88, 105 or 107 and a right transposon end comprising SEQ ID NO: 14578 or 106 followed by a target sequence, in certain embodiments, the piggyBac or piggy-Bac like transposon comprises one end that comprises a

between identical to SEQ ID NO: 14578. In certain embodiments, one transposon end comprises at least 14, at least 16, at least 18 or at least 20 contiguous bases from SEQ ID NO: 14577 and one transposon end comprises at least 14, at least 16, at least 18 or at least 20 contiguous bases from SEQ ID NO: 14578.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises two transposon ends wherein each transposon ends comprises a sequence that is at least 81% identical, at least 87% identical or at least 93% identical or any percentage in between identical to SEQ ID NO: 14510 in inverted orientation in the two transposon ends. One end may further comprise at least 14, at least 16, at least 18 or at least 20 contiguous bases from SEQ ID NO: 14599, and the other end may further comprise at least 14, at least 16, at least 18 or at least 20 contiguous bases from SEQ ID NO: 14601. The piggyBac or piggyBac-like transposon may be transposed by the transposase of SEQ ID NO: 14505, and the transposase may optionally be fused to a nuclear localization signal.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14595 and SEQ ID NO: 14596 and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14504 or SEQ ID NO: 14505. In certain 60 65 embodiments, the piggyBac or piggyBac-like transposon

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comprises SEQ ID NO: 14597 and SEQ ID NO: 14596 and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14504 or SEQ ID NO: 14505. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14595 and SEQ ID NO: 14578 and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14504 or SEQ ID NO: 14505. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14602 and SEQ ID NO: 14600 and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14504 or SEQ ID NO: 14505.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a left end comprising 1, 2, 3, 4, 5, 6, or 7 sequences selected from ATGAGGCAGGGTAT (SEQ ID NO: 14614), ATACCCTGCCTCAT (SEQ ID NO: 14615), GGCAGGGTAT (SEQ ID NO: 14616),

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ATACCCTGCC (SEQ ID NO: 14617), TAAAATITTA (SEQ ID NO: 14618), ATITUATAAAAT (SEQ ID NO: 14619), TCATACCCCTG (SEQ ID NO: 14620) and TAAATAATAATAA (SEQ ID NO: 14621). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a right end comprising 1, 2 or 3 sequences selected from SEQ ID NO: 14617. SEQ ID NO: 14620 and SEQ ID NO: 14621.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Xenopus tropicalis*. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14317)

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1   MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61  DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFV TVPGVKVDT NFEPIINFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY APAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNCIDE SLLLFKGRRLQ FRQYIPSRA RYGIKFYKLC ESSSGYT SYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPPLLQQGPHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIFK FDKNNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPREMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYPKCPN PNPGLCFKPCF EIYETQLHY.

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In some embodiments, the piggyBac or piggyBac-like transposase is a hyperactive variant of SEQ ID NO: 14517. In certain embodiments, the piggyBac or piggyBac-like transposase is an integration defective variant of SEQ ID NO: 14517. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14518)

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1   MAKRFYSAEE AAAHCMAPSS EEFSGSDSEY VRPASESDSS TEESWCSSST VSALEEPMEV
61  DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFV TVPGVKVDT NFEPIINFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWNNTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPDHD RLHKLRPLID
241 SLSERFAAVY TPCQNCIDE SLLLFKGRRLR FRQYIPSRA RYGIKFYKLC ESSSGYT SYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPPLLQQGPHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRTR KGLPRALLDK KLNRGETYAL RKNELLAIFK FDKNNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDP TDQL QHYYNATRKT SAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPLP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYPKCPN PNPGLCFKPCF EIYHTQLHY.

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In certain embodiments, the piggyBac or piggyBac-like transposase is isolated or derived from *Xenopus tropicalis*. In certain embodiments, the piggyBac or piggyBac-like transposase is a hyperactive piggyBac or piggyBac-like transposase. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence at least 90% identical to:

(SEQ ID NO: 14572)

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1  MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDT S NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRLID
241 SLSERFANVY TPCQNICIDE SLMLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDPTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAYPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPD SDNVARLIGK HFIDTLPPPT
541 GKQRQKGCK VCRKRGIRRD TRYCPKCPR NPGLCRKPCF EIYHTQLHY.

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In certain embodiments, piggyBac or piggyBac-like transposase is a hyperactive piggyBac or piggyBac-like transposase. 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 certain embodiments, a hyperactive piggyBac or piggyBac-like transposase is more active than the transposase of SEQ ID NO: 14517. In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14572)

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1  MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDT S NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRLID
241 SLSERFANVY TPCQNICIDE SLMLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDPTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAYPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPD SDNVARLIGK HFIDTLPPPT
541 GKQRQKGCK VCRKRGIRRD TRYCPKCPR NPGLCRKPCF EIYHTQLHY.

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In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14624)

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1  MAKRKYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61 DEDVDDLEQ EAGDRADAAA GGEPAWGPPC NFPPEIPPF TVPGVKVDTA NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVESAT MSRNRYQLLL RFLHENNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLSQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNREGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPKGCK VCRKRGIRRD TRYCPKCPR NPGLCRKPCF EIYHTQLHY.

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In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14625)

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1  MAKRKYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESVCSSST VSALEEPMEV
51 DEDVDDLEQ EAGDRADAAA GGEPAWGPPC NFPPEIPPF TVPGVKVDTA NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLKIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNICIDE SLLLIFKGRQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNREGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPKGCK VCRKRGIRRD TRYCPKCPR NPGLCRKPCF EIYHTQLHY.

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In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 14627)

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1  MAKRKYSAEE AAAHCMASSS EQTSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61 DEDVDDLEQ EAGDRADAAA GGEPAWGPPC NFPPEIPPF TVPCVKVDTA NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFANVY TPCQNICIDE SLLLIFKGRQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNREGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPKPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPKGCK VCRKRGIRRD TRYCPKCPR NPGLCRKPCF EIYHTQLHY.

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(SEQ ID NO: 14628)

1 MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPCP NFPPEIPPF TVPGVKVDTN NFEPINFFQL
 121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEKRFVGL TLAMGLIKAN
 181 SLESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRLPID
 241 SLSERFANVY TPCQNICIDE SLMLFKGRLO FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
 301 LIYEGKDSDL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
 361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKNVFMLT SIHDESVIRE
 421 QRVGRPPKNA PLCSKEYSKY MGGVDRTDQL QHYNNATRKRT RHWYKKVGIY LIQMALARNSY
 481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
 541 GKQRPKGCK VCRKRGIRRD TRYCPKPCR NPGLCRKPCF EIYHTQLHY.

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

(SEQ ID NO: 17042).

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises an amino acid substitution at a position selected from amino acid 6, 7, 16, 19, 20, 21, 22, 23, 24, 26, 28, 31, 34, 67, 73, 76, 77, 88, 91, 141, 145, 146, 148, 150, 157, 162, 179, 182, 189, 192, 193, 196, 198, 200, 210, 212, 218, 248, 263, 270, 294, 297, 308, 310, 333, 336, 354, 357, 358, 359, 377, 423, 426, 428, 438, 447, 450, 462, 469, 472, 498, 502, 517, 520, 523, 533, 534, 576, 577, 582, 583 or 587 (relative to SEQ ID NO: 14517). In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises an amino acid substitution of Y6C, S7G, M16S, S19G, S20Q, S20G, S20D, E21D, E22Q, F23T, F23P, S24Y, S26V, S28Q, V31K, A34E, L67A, G73H, A76V, D77N, P88A, N91D, Y141Q, Y141A, N145E, N145V, P146T, P146V, P146K, P148T, P148H, Y150G, Y150S, Y50C, H157Y, A162C, A179K, L182I, L182V, T189G, L192H, S193N, S193K, V1%, S198G, T200W, L210H, F212N, N218E, A248N, L263M, Q270L, S294T, T297M, S308R, L310R, L333M, Q336M, A354H, C357V, L358F, D359V, L377I, V423H, P426K, K428R, S438A, T447G, T447A, L450V, A462H, A462Q, I469V, I472L, Q498M, L502V, E517I, P520D, P520G, N523S, I533E, D534A, F576R, F576E, K577I, I582R, Y583F, L587Y or L587W, or any combination thereof including at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or all of these mutations (relative to SEQ ID NO: 14517).

In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises one or more substitutions of an amino acid that is not wild type, wherein the one or more substitutions a for wild type amino acid comprises a substitution of A2X, K3X, R4X, F5X, Y6X, S7X, A11X, A3X, C15X, M16X, A17X, S18X, S19X, S20X, E21X, E22X, F23X, S24X, G25X, 26X, D27X, S28X, E29X, E42X, E43X, S44X, C46X, S47X, S48X, S49X, T50X, V51X, S52X, A53X, L54X, E55X, E56X, P57X, M58X, E59X, E62X, D63X, V64X, D65X, D66X, L67X, E68X, D69X, Q70X, E71X, A72X, G73X, D74X, R75X, A76X, D77X, A78X, A79X, A80X, G81X, G82X, E83X, P84X, A85X, W86X, G87X, P88X, P89X, C90X, N91X, F92X, P93X, E95X, I96X, P97X, P98X, F99X, T100X, T101X, P103X, G104X, V105X, K106X, V107X, D108X, T109X, N111X, P114X, I115X, N116X, F117X, F118X, Q119X, M122X, T123X, E124X, A125X, I126X, L127X, Q128X, D129X, M130X, L132X, Y133X, V126X, Y127X, A138X, E139X, Q140X, Y141X, L142X, Q144X, N145X, P146X,

L147X, P148X, Y150X, A151X, A155X, H157X, P158X, I161X, A162X, V168X, T171X, L72X, A173X, M174X, I177X, A179X, L182X, D187X, T188X, T189X, T190X, L192X, S193X, I194X, P195X, V196X, S198X, A199X, T200X, S202X, L208X, L209X, L210X, R21X, F212X, F215X, N217X, N218X, A219X, T220X, A221X, V222X, P224X, D225X, Q226X, P227X, H229X, R231X, H233X, L235X, P237X, I239X, D240X, L242X, S243X, E244X, R244X, F246X, A247X, A248X, V249X, Y250X, T251X, P252X, C253X, Q254X, I256X, C257X, I258X, D259X, E260X, S261X, L262X, L263X, L264X, F265X, K266X, G267X, R268X, L269X, Q270X, F271X, R272X, Q273X, Y274X, I275X, P276X, S277X, K278X, R279X, A280X, R281X, Y282X, G283X, I284X, K285X, F286X, Y287X, K288X, L289X, C290X, E291X, S292X, S293X, S294X, G295X, Y296X, T297X, S298X, Y299X, F300X, E304X, L310X, P313X, G314X, P316X, P317X, D318X, L319X, T320X, V321X, K324X, E328X, I330X, S331X, P332X, L333X, L334X, G335X, Q336X, F338X, L340X, D343X, N344X, F345X, Y346X, S347X, L351X, F352X, A354X, L355X, Y356X, C357X, L358X, D359X, T360X, R422X, Y423X, G424X, P426X, K428X, N429X, K430X, P431X, L432X, S434X, K435X, E436X, S438X, K439X, Y440X, G443X, R446X, T447X, L450X, Q451X, N455X, T460X, R461X, A462X, K465X, V467X, G468X, I469X, Y470X, L471X, I472X, M474X, A475X, L476X, R477X, S479X, Y480X, V482X, Y483X, K484X, A485X, A486X, V487X, P488X, P490X, K491X, S493X, Y494X, Y495X, K496X, Y497I, Q498X, L499X, Q500X, I501X, L502X, P503X, A504X, L505X, L506X, F507X, G508X, G509X, V510X, E511X, E512X, Q513X, T514X, V515X, E517X, M518X, P519X, P520X, S521X, D522X, N523X, V524X, A525X, L527X, I528X, K530X, H531X, F532X, L533X, D534X, T535X, L536X, T539X, P540X, Q546X, K550X, R553X, K554X, R555X, G556X, I557X, R558X, R559X, D560X, T561X, Y564X, P566X, K567X, P569X, R570X, N571X, L574X, C575X, F576X, K577X, P578X, F580X, E581X, I582X, Y583X, T585X, Q586X, L587X, H588X or Y589X (relative to SEQ ID NO: 14517). A list of hyperactive amino acid substitutions can be found in U.S. Pat. No. 10,041,077, the contents of which are incorporated by reference in their entirety.

In certain embodiments, the piggyBac or piggyBac-like transposase is integration deficient. In certain 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 naturally occurring

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transposase. In certain embodiments, the piggyBac or piggyBac-like transposase is an integration deficient variant of SEQ ID NO: 14517. In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase is deficient relative to SEQ ID NO: 14517.

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In certain embodiments, the piggyBac or piggyBac-like transposase is active for excision but deficient in integration. In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

(SEQ ID NO: 14605)

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1   MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61  DEDVDDLEDQ EAGDRVDAAA GGEPAWGPPC NFPPEIPPF TVPGVKVDTN NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL KFLHFNNNEAT AVPPDQPGHD RLHKLRLPID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPPLLQQGPHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIF FDKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPREMPP SDNVARLIGK HFIDTLPPPT
541 GKQRQPQKGCK VCRKRGIRRD TRYCPKPCR NPGLCFKPCF EIYHTQLHYG RR.

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25 In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

(SEQ ID NO: 14604)

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1   MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61  DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPF TVPGVKVDTN NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLNPVFSAT MSRNRYQLLL RFLEFNNEAT AVPPDQPGHD RLHKLRLPID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPPLLQQGPHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIF FDKNVFMLT SIHDESVIRE
421 QPVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPREMPP SDNVARLIGK HFIDTLPPPT
541 GKQRQPQKGCK VCRKRGIRRD TRYCPKPCR NPGLCFKPCF EIYHTQLHY.

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In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

(SEQ ID NO: 14611)

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1   MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
61  DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPF TVPGVKVDTN NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNDAT AVPPDQPGHD RLHKLRLPID
241 SLTERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPPLLQQGPHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIF FDKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY

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- continued

481 IVYKAAVPGP KLSYYKYQLQ ILPALLEFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPPTP
 541 GKQRQKGCK VCRKRGIRRD TRYCPKCPR NPGLCFKPCF EIYHTQLHYG RR.

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In certain embodiments, the integration deficient piggy-Bac or piggyBac-like transposase comprises SEQ ID NO: 14611. In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

E21X, E22X, F23X, S24X, G25X, 26X, D27X, S28X, E29X, V31X, P32X, P33X, A34X, S35X, E36X, S37X, D38X, S39X, S40X, T41X, E42X, E43X, S44X, W45X, C46X, S47X, S48X, S49X, T50X, V51X, S52X, A53X, L54X, E55X, E56X, P57X, M58X, E59X, V60X, M122X,

(SEQ ID NO: 14612)

1 MAKRFYSAEE ALAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAP GGEPAWGPPC NFPPEIPPFPT TVPGVKVDTNS NFEPIINFFQL
 121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
 181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNEAT AVPPDQPGHD RLHKLRPLID
 241 SLSSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIYFYKLC ESSSGYTSYF
 301 LIYEGKDSKL DPPGCPDDL VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
 361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKNVFMLT SIHDESVIRE
 421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
 481 IVYKAAVPGP KLSYYKYQLQ ILPALLEFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPPTP
 541 GKQRQKGCK VCRKRGIRRD TRYCPKCPR NPGLCFKPCF EIYHTQLHYG RR.

In certain embodiments, the integration deficient piggy-Bac or piggyBac-like transposase comprises SEQ ID NO: 14612. In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of

T123X, E124X, A125X, L127X, Q128X, D129X, L132X, Y133X, V126X, Y127X, E139X, Q140X, Y141X, L142X, T43X, Q144X, N145X, P146X, L147X, P148X, R149X, Y150X, A151X, H154X, H157X, P158X, T159X, D160X, I161X, A162X, E163X, M164X, K165X, R166X, F167X,

(SEQ ID NO: 14613)

1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFPT TVPGVKVDTNS NFEPIINFFQL
 121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
 181 SLESYWDTTT VLNIIPVFSAT MSRNRYQLLL RFLEFNNNAT AVPPDQPGHD RLHKLRPLID
 241 SLSSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
 301 LIYEGKDSKL DPPGCPDDL VSGKIVWELI SPLLGQGFHL YVDNEYSSIP LFTALYCLDT
 361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKNVFMLT SIHDESVIRE
 421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
 481 IVYKAAVPGP KLSYYKYQLQ ILPALLEFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPPTP
 541 GKQRQKGCK VCRKRGIRRD TRYCPKCPR NPGLCFKPCF EIYHTQLHYG RR.

In certain embodiments, the integration deficient piggy-Bac or piggyBac-like transposase comprises SEQ ID NO: 14613. In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises an amino acid substitution wherein the Asn at position 218 is replaced by a Glu or an Asp (N218D or N218E) (relative to SEQ ID NO: 14517).

In certain embodiments, the excision competent, integration deficient piggyBac or piggyBac-like transposase comprises one or more substitutions of an amino acid that is not wild type, wherein the one or more substitutions a for wild type amino acid comprises a substitution of A2X, K3X, R4X, F5X, Y6X, S7X, A8X, E9X, E10X, A11X, A12X, A13X, H14X, C15X, M16X, A17X, S18X, S19X, S20X,

V168X, G169X, L170X, T171X, L172X, A173X, M174X, G175X, L176X, I177X, K178X, A179X, N180X, S181X, L182X, S184X, Y185X, D187X, T188X, T89X, T190X, V191X, L192X, S193X, I194X, P195X, V196X, F197X, S198X, A199X, T200X, M201X, S202X, R203X, N204X, R205X, Y206X, Q207X, L208X, L209X, L210X, R211X, F212X, L213X, H241X, F215X, N216X, N217X, N218X, A219X, T220X, A221X, V222X, P223X, P224X, D225X, Q226X, P227X, G228X, H229X, D230X, R231X, H233X, K234X, L235X, R236X, L238X, I239X, D240X, L242X, S243X, E244X, R244X, F246X, A247X, A248X, V249X, Y250X, T251X, P252X, C253X, Q254X, N255X, I256X, C257X, I258X, D259X, E260X, S261X, L262X, L263X, L264X, F265X, K266X, G267X, R268X, L269X, Q270X,

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F271X, R272X, Q273X, Y274X, I275X, P276X, S277X, K278X, R279X, A280X, R281X, Y282X, G283X, I284X, K285X, F286X, Y287X, K288X, L289X, C290X, E291X, S292X, S293X, S294X, G295X, Y296X, T297X, S298X, Y299X, F300X, I302X, E304X, G305X, K306X, D307X, S308X, K309X, L310X, D311X, P312X, P313X, G314X, C315X, P316X, P317X, D318X, L319X, T320X, V321X, S322X, G323X, K324X, I325X, V326X, W327X, E328X, L329X, I330X, S331X, P332X, L333X, L334X, G335X, Q336X, F338X, H339X, L340X, V342X, N344X, F345X, Y346X, S347X, S348X, I349X, L351X, T353X, A354X, Y356X, C357X, L358X, D359X, T360X, P361X, A362X, C363X, G364X, I366X, N367X, R368X, D369X, K371X, G372X, L373X, R375X, A376X, L377X, L378X, D379X, K380X, K381X, L382X, N383X, R384X, G385X, T387X, Y388X, A389X, L390X, K392X, N393X, E394X, A397X, K399X, F400X, F401X, D402X, N405X, L406X, L409X, R422X, Y423X, G424X, E425X, P426X, K428X, N429X, K430X, P431X, L432X, S434X, K435X, E436X, S438X, K439X, Y440X, G442X, G443X, V444X, R446X, T447X, L450X, Q451X, H452X, N455X, T457X, R458X, T460X, R461X, A462X, Y464X, K465X, V467X, G468X, I469X, L471X, I472X, Q473X, M474X, L476X, R477X, N478X, S479X, Y480X, V482XY483X, K484X, A485X, A486X,

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V487X, P488X, G489X, P490X, K491X, L492X, S493X, Y494X, Y495X, K496X, Q498X, L499X, Q500X, I501X, L502X, P503X, A504X, L505X, L506X, F507X, G508X, G509X, V510X, E511X, E512X, Q513X, T514X, V515X, E517X, M518X, P519X, P520X, S521X, D522X, N523X, V524X, A525X, L527X, I528X, G529X, K530X, F532X, J533X, D534X, T535X, L536X, P537X, P538X, T539X, P540X, G541X, F542X, Q543X, R544X, P545X, Q546X, K547X, G548X, C549X, K550X, V551 X, C552X, R553X, K554X, R555X, G556X, 1557X, R558X, R559X, D560X, T561X, R562X, Y563X, Y564X, C565X, P566X, K567X, C568X, P569X, R570X, N571X, P572X, G573X, L574X, C575X, F576X, K577X, P578X, C579X, F580X, E581X, I582X, Y583X, H584X, T585X, Q586X, L587X, H588X or Y589X (relative to SEQ ID NO: 14517). A list of excision competent, integration deficient amino acid substitutions can be found in U.S. Pat. No. 10,041,077, the contents of which are incorporated by reference in their entirety.

In certain embodiments, the piggyBac or piggyBac-like transposase is fused to a nuclear localization signal. In certain embodiments, SEQ ID NO: 14517 or SEQ ID NO: 14518 is fused to a nuclear localization signal. In certain embodiments, the amino acid sequence of the piggyBac or piggyBac like transposase fused to a nuclear localization signal is encoded by a polynucleotide sequence comprising:

(SEQ ID NO: 14626)

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1 atggcaccca aaaagaaaacg taaaagtgtat gccaaaagat ttcatcagcgc cgaagaagca
61 gcagcacatt gcatggcatt gtcatccgaa gaattctcggtt ggagcgatc cgaatatgtc
121 ccaccggcct cggaaaagcga ttgcgactt gaggagtcgtt ggccgttccctc ctcaacttgtc
181 tcggcttttgg aggagccgac ggaagtggat gaggatgtgg acgacttgga ggaccaggaa
241 gcccggagaca gggccgacgc tgccgcggga gggggagccgc cgccggggacc tccatgcata
301 tttccctcccg aaatccaccat gttcaactact gtgccggggag tgaagggtcga cacgtccaa
361 ttcaaccgcg tcaatttctc tcaactcttc atgactgaag cgatcctgca agatatggtg
421 ctctacacta atgtgtacgc cgagcagtttact ctgactcaaa acccgctgcc tcgctacgcg
481 agagcgcattt cgtggcaccc gaccgatata gcggagatga agcggttcgtt gggactgacc
541 ctgcgaatgg gcctgtatcaa ggccaaacgcg ctcgagttcat accgggatatac caccgtatgt
601 cttagcattt cgggtttctc cgcttaccatg tcccgtaacc gccaccaact cctgtcgccg
661 ttccctccact tcaacaacaa tgccgaccgt gtgccacctg accagccagg acacgcacaga
721 ctccacaaggc tgccgcattt gatcgactcg ctgagcgacgc gactcgccgc ggtgtacacc
781 ctttgccaaa acatttgcaaa cgacgatcg cttctgtgtt taaaaggccgc gtttcagttc
841 cgccaggatca tccccatcgaa gccgcgtcg tatggatca aattctacaa actctgcgag
901 tcgtccagcg gtcacacgttca atacttcttgc atctacgagg ggaaggactc taagctggac
951 ccaccggggtt gtccaccggaa tcttactgttcc tccggaaaaaa tcgtgtggaa actcatctca
1021 cttctccatcg gacaagggttca tcatctcttac gtcgacaaattt tccactcatc gatccctctg
1081 ttcaaccgcctt tctactgtccc ggataacttcca gctgtggaa ccattaacag aaaccggaaag
1141 ggtctgcgaa gggactgttttcc ggataagaag ttgaacaggag gagagactt cgcgtgaga
1201 aagaacgaac tcctcgccat caaatcttc gacaagaaaa atgtgtttat gtcacccctcc
1321 ctgtgtctta aggaataactc caagttatcg ggggggtgtcc accggaccgc tcagctgcag
1381 cattactaca acggccacttag aaagacccgg gcctgttaca agaaagtccgg catctacatcg
1441 atccaaatgg cactgaggaa ttcgttatattt gtctacaagg ctgcccgttcc gggccggaaa

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- continued

1501 ctgtcatact acaagtagtacca gcttcaaattc ctggccggcgc tgctgttcgg tggagtggaa
1561 gaacagactg tgccccgagat gccggccatcc gacaacgtgg cccgggttgat cgaaaaagcac
1621 ttcatgtata ccctgcgtcc gagcgcgttga aagcagcgcc cacagaaggg atgcaaagg
1681 tgccgcgaagc gggaaatacg gcgcgatacc cgctactatt gcccgaagtg ccccccgaat
1741 cccggacttgt gtttcaagcc ctgttttgaa atctaccaca cccagttgc a ttac.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Xenopus tropicalis*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

10

(SEQ ID NO: 14519)

1	ttaaccttt tactgccaat gacgcattggg atacgtcggt gcagtaaaag ggcttaaatg
61	ccaaacgacgc gtccccatacg ttgttggcat ttttaagtctt ctatctgcag cggcagcgtt
121	tgccgcgcgt gcagagagtt tcttagcgatg acagccccctc tgggcaacga gccgggggggg
181	cttgt.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14519)

(SEQ ID NO: 14520)
1 tttgcatttt tagacattta gaaggctata tcttgttaca gaattggaa tacacaaaaa
61 ttctaccata ttttggaaagc ttaggttgaa ctgaaaaaaaa caatatatgg ttttcctggg
121 taaaactaaaa gtcggccctcgaa gggaaaggcccc cttaaagtgaa acagtgcacaa acgttcaaaa
181 actgtctggc aatacaagtt ccactttgc caaaacggct gggcgttaaaa gggtttaa.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14519 and SEQ ID NO: 14520. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

35

(SEQ ID NO: 14521)
1 ttaacccttt gcctgccaat cacgcatttggg atacgtcggt gcaagtaaaagg ggcttaaatgg
61 ccaacgacgc gtcccatatcg ttgttggcat tttaagtctt ctctctgcag cggcagcatg
121 tgccgcgcgt gcagagatgt tctagcgatg acagccccctc tgggcaacga gccccgggggg
181 ctgtc.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14522)

```
1 tttgcatttt tagacattta gaagcctata tcctgttaca gaattggaa tacacaaaaa  
61 ttctaccata ttttgaagc ttaggttgtt ctgaaaaaaaa caatatatgg ttttcctggg  
121 taaaactaaaa gtcggctcgaa ggaaaggccc ctaaagtgaa acagtgc当地 acgttcaaaa  
181 actgtctggc aatacaagtt ccactttggg acaaatcgcc tggcagtgaa agggttaa.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
(SEQ ID NO: 14523)
1 ttaaccttt tactgccaat gacgcattggg atacgtcggt gcagtaaaag ggcttaaatg
61 ccaacgacgc gtcccatatcg ttgttggcat tttatttc ctctctgcag cggcagcatg
121 tgccggcgct gcagagagtt tctagcgatg acagccccctc tgggcaacga gcccgggggg
181 ctgtc.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14520 and SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14522 and SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end comprising at least 14, 16, 18, 20, 30 or 40 contiguous nucleotides from SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end comprising at least 14, 16, 18, 20, 30 or 40 contiguous nucleotides from SEQ ID NO: 14520 or SEQ ID NO: 14522. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end with at least 90% identity to SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523. In certain embodiments, the piggyBac or piggyBac-like transposon comprises one end with at least 90% identity to SEQ ID NO: 14520 or SEQ ID NO: 14522. In one embodiment, one transposon end is at least 90% identical to SEQ ID NO: 14519 and the other transposon end is at least 90% identical to SEQ ID NO: 14520.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCTTT-TACTGCCA (SEQ ID NO: 14524). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCCTTGCTGCCA (SEQ ID NO: 14526). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCYTTT-TACTGCCA (SEQ ID NO: 14527). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TGGCAGTAAAAGGGTTAA (SEQ ID NO: 14529). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TGGCAGT-GAAAGGGTTAA (SEQ ID NO: 14531). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCYTITKMCTGCCA (SEQ ID NO: 14533). In certain embodiments, one end of the piggyBac or piggyBac-like transposon comprises a sequence selected from SEQ ID NO: 14524, SEQ ID NO: 14526 and SEQ ID NO: 14527. In certain embodiments, one end of the piggyBacTM (PB) or piggyBac-like transposon comprises a sequence selected from SEQ ID NO: 14529 and SEQ ID NO: 14531. In certain embodiments, each inverted terminal repeat of the piggyBac or piggyBac-like transposon comprises a sequence of ITR sequence of CCYTTTKMCTGCCA (SEQ ID NO: 14563). In certain embodiments, each end of the piggyBacTM (PB) or piggyBac-like transposon comprises SEQ ID NO: 14563 in inverted orientations. In certain embodiments, one ITR of the piggyBac or piggyBac-like transposon comprises a sequence selected from SEQ ID NO: 14524, SEQ ID NO: 14526 and SEQ ID NO: 14527. In certain embodiments, one ITR of the piggyBac or piggyBac-like transposon comprises

a sequence selected from SEQ ID NO: 14529 and SEQ ID NO: 14531. In certain embodiments, the piggyBac or pig-

gyBac like transposon comprises SEQ ID NO: 14533 in inverted orientation in the two transposon ends.

In certain embodiments, the piggyBac or piggyBac-like transposon may have ends comprising SEQ ID NO: 14519 and SEQ ID NO: 14520 or a variant of either or both of these having at least 90% sequence identity to SEQ ID NO: 14519 or SEQ ID NO: 14520, and the piggyBac or piggyBac-like transposase has the sequence of SEQ ID NO: 14517 or a variant showing at least %, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between sequence identity to SEQ ID NO: 14517 or SEQ ID NO: 14518. In certain embodiments, one piggyBac or piggyBac-like transposon end comprises at least 14 contiguous nucleotides from SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523, and the other transposon end comprises at least 14 contiguous nucleotides from SEQ ID NO: 14520 or SEQ ID NO: 14522. In certain embodiments, one transposon end comprises at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 22, at least 25, at least 30 contiguous nucleotides from SEQ ID NO: 14519, SEQ ID NO: 14521 or SEQ ID NO: 14523, and the other transposon end comprises at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 22, at least 25 or at least 30 contiguous nucleotides from SEQ ID NO: 14520 or SEQ ID NO: 14522.

In certain embodiments, the piggyBac or piggyBac-like transposase recognizes a transposon end with a left sequence corresponding to SEQ ID NO: 14519, and a right sequence corresponding to SEQ ID NO: 14520. It will excise the transposon from one DNA molecule by cutting the DNA at the 5'-TTAA-3' sequence at the left end of one transposon end to the 5'-TTAA-3' at the right end of the second transposon end, including any heterologous DNA that is placed between them, and insert the excised sequence into a second DNA molecule. In certain embodiments, truncated and modified versions of the left and right transposon ends will also function as part of a transposon that can be transposed by the piggyBac or piggyBac-like transposase. For example, the left transposon end can be replaced by a sequence corresponding to SEQ ID NO: 14521 or SEQ ID NO: 14523, the right transposon end can be replaced by a shorter sequence corresponding to SEQ ID NO: 14522. In certain embodiments, the left and right transposon ends share an 18 bp almost perfectly repeated sequence at their ends (5'-TTAACCYTITKMCTGCCA: SEQ ID NO: 14533) that includes the 5'-TTAA-3' insertion site, which sequence is inverted in the orientation in the two ends. That is in SEQ ID NO: 14519 and SEQ ID NO: 14523 the left transposon end begins with the sequence 5'-TTAACCTT-TACTGCCA-3' (SEQ ID NO: 14524), or in SEQ ID NO: 14521 the left transposon end begins with the sequence 5'-TTAACCTTGCTGCCA-3' (SEQ ID NO: 14526); the right transposon ends with approximately the reverse

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complement of this sequence: in SEQ ID NO: 14520 it ends 5' TGGCAGTAAAAGGGTTAA-3' (SEQ ID NO: 14529), in SEQ ID NO: 14522 it ends 5'-TGGCAGTGAAAGGGT-TAA-3' (SEQ ID NO: 14531.) One embodiment of the invention is a transposon that comprises a heterologous polynucleotide inserted between two transposon ends each comprising SEQ ID NO: 14533 in inverted orientations in the two transposon ends. In certain embodiments, one transposon end comprises a sequence selected from SEQ ID

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NOS: 14524, SEQ ID NO: 14526 and SEQ ID NO: 14527. In some embodiments, one transposon end comprises a sequence selected from SEQ ID NO: 14529 and SEQ ID NO: 14531.

⁵ In certain embodiments, the piggyBacTM (PB) or piggyBac-like transposon is isolated or derived from *Xenopus tropicalis*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14573)

```

1   ccctttgcct gccaatcacg catggatac gtcgtggcag taaaaggct taaatgcaa
61   cgacgcgtcc catacggtt.

```

15

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14574)

```

1   cctggtaaa ctaaaagtcc cctcgaggaa aggcccctaa agtgaacacg tgcaaaacgt
61   tcaaaaaactg tctggcaata caagttccac tttggacaa atcggctggc agtgaaggg.

```

25

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at least 16 contiguous bases from SEQ ID NO: 14573 or SEQ ID NO: 14574, and inverted terminal repeat of CCYTTTBMCCTGCCA (SEQ ID NO: 14575).

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14579)

```

1   ccctttgcct gccaatcacg catggatac gtcgtggcag taaaaggct taaatgcaa
61   cgacgcgtcc catacggtt tggcatttttta agtcttctct ctgcagcggc agcatgtgcc
121  gcccgtgcag agagtttcta gcgtacacag cccctctggg caacgacccg ggggggctgt
181  c.

```

40

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14580)

```

1   ccttttact gccaatgacg catggatac gtcgtggcag taaaaggct taaatgcaa
61   cgacgcgtcc catacggtt tggcatttttta attcttctct ctgcagcggc agcatgtgcc
121  gcccgtgcag agagtttcta gcgtacacag cccctctggg caacgacccg ggggggctgt
181  c.

```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14581)

```

1   ccttttact gccaatgacg catggatac gtcgtggcag taaaaggct taaatgcaa
61   cgacgcgtcc catacggtt tggcatttttta agtcttctct ctgcagcggc agcatgtgcc
121  gcccgtgcag agagtttcta gcgtacacag cccctctggg caacgacccg ggggggctgt
181  c.

```

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14582)
1 ccttttact gccaatgacg catggatac gtcgtggcag taaaaggcg taaatgccaa
61 cgaegcgtcc catacggtt tggcattta agtcttctct ctgcagcggc agcatgtgcc
121 qccqctqcaq aqaq.

10

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14583)
1 ccttttact gccaatgacg catgggatac gtcgtggcag taaaaggcgt taaaatgcca
61 cgacggcgatcc catacggttg tggcattta agtctt

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14584)
1 ccctttgcct gccaaatcacg catgggatac gtcgtggcag taaaaggcgt taaatgccaa
61 cgacgcgtcc catacgatgt tggcatttt agtctt .

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14585)
1 ttatcccttt tactgccaat gacgcataggg atacgtcggt gcagtaaaaag ggctttaaatg
61 ccaacgacgc gtccccatacg ttgttggcat tttaagtctt ctctctgcag cggcagcatg
121 tgccgcgcgt gcagagagt tctagcgatg acagccccctc tgggcaacga gcccgggggg
131 ctqtc.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14586)
1 tttgcatttt tagacatTTA gaagcctata tcttgTTaca gaattggaaT tacacaaaaa
61 ttctaccata ttttggaaAGC ttaggttGTT ctgaaaaaaaa caatatATTG ttttcctggg
121 taaaactaaaaa gttccCTCGA ggaaaggccc ctaaagtGAA acagtGAAA acgttcaaaa
161 actgtctqqc aatacaaaqTT ccactttqqq acaaattcqC tqqcaqtqaa aqqq.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a left transposon end sequence selected from SEQ ID NO: 14573 and SEQ ID NOS: 14579-14585. In certain embodiments, the left transposon end sequence is preceded by a left target sequence. In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

(SEQ ID NO: 14587)
1 tttgcatttt tagacattta gaaggctata tcttgttaca gaattggaa tacacaaaa
61 ttctaccata ttttgaagc tttaggttgtt ctgaaaaaaaa caatataattg ttttcctgg
121 taaaactaaaa gtcccccgt gggaaaggccc ctaaagtgaa acagtgcaaa acggtcaaaa
181 actqtctqqc aataacaqtt ccactttqac caaaacqgqt qqcaqtaaaa qqq.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
(SEQ ID NO: 14588)
1 ttgttctgaa aaaaacaata tatttttc ctggtaaac taaaagtccc ctcgaggaaa
61 ggccctaaa gtgaaacagt gcaaaacgtt caaaaactgt ctggcaatac aagttccact
121 ttgacaaaaa cggctggcag taaaaggg.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
(SEQ ID NO: 14589)
1 tttgcattt tagacattta gaagcctata tcttgtaaca gaattggat tacacaaaaaa
61 ttctaccata tttgaaagc ttaggtgtt ctgaaaaaaaaa caatatattt tttctggg
121 taaaactaaa gtcgcctcgaa ggaaaggccc ctaaagtgaa acagtgc当地 acgttcaaaa
181 actgtctggc aatacaagtt ccacttgac caaaacggct ggcagtaaaa gggttat.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
(SEQ ID NO: 14590)
1 ttgttctgaa aaaaacaata tatttttc ctggtaaac taaaagtccc ctcgaggaaa
61 ggccctaaa gtgaaacagt gcaaaacgtt caaaaactgt ctggcaatac aagttccact
121 ttgggacaaa tcggctggca gtgaaaggg.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a right transposon end sequence selected from SEQ ID NO: 14574 and SEQ ID NOs: 35 14587-14590. In certain embodiments, the right transposon end sequence is followed by a right target sequence. In certain embodiments, the left and right transposon ends share a 14 repeated sequence inverted in orientation in the 40 two ends (SEQ ID NO: 14575) adjacent to the target sequence. In certain embodiments, the piggyBac or piggy-Bac-like transposon comprises a left transposon end comprising a target sequence and a sequence that is selected 45 from SEQ ID NOs: 14582-14584 and 14573, and a right transposon end comprising a sequence selected from SEQ ID NOs: 14588-14590 and 14574 followed by a right target sequence.

In certain embodiments, the left transposon end of the 50 piggyBac or piggyBac-like transposon comprises

```
(SEQ ID NO: 14591)
1 atcacgcatg ggatacgtcg tggcagtaaa agggcttaaa tgccaaacgac gcgtccccata
61 cgtt,
```

and an ITR. In certain embodiments, the left transposon end comprises

```
(SEQ ID NO: 14592)
1 atgacgcatg ggatacgtcg tggcagtaaa agggcttaaa tgccaaacgac gcgtccccata
61 cgttgttggc atttaagtc tt
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and an ITR. In certain embodiments, the right transposon end of the piggyBac or piggyBac-like transposon comprises

(SEQ ID NO: 14593)

```

1 cctgggtaaa ctaaaagtcc cctcgaggaa aggccccta aagtggaaacag tgcaaaacgta
61 tcaaaaaactg tctggcaata caagttccac ttggggacaa atcggc

```

and an ITR. In certain embodiments, the right transposon end comprises

(SEQ ID NO: 14594)

```

1 ttgttctgaa aaaaacaata tatttttc ctgggtaaac taaaagtccc ctcgaggaaa
61 ggccccctaaa gtgaaacagt gcaaaacgtt caaaaaactgt ctggcaatac aagttccact
121 ttgaccaaaa cggc

```

and an ITR.

In certain embodiments, one transposon end comprises a sequence that is at least 90%, at least 95%, at least 99% or any percentage in between identical to SEQ ID NO: 14573 and the other transposon end comprises a sequence that is at least 90%, at least 95%, at least 99% or any percentage in between identical to SEQ ID NO: 14574. In certain embodiments, one transposon end comprises at least 14, at least 16, at least 18, at least 20 or at least 25 contiguous nucleotides from SEQ ID NO: 14573 and one transposon end comprises at least 14, at least 16, at least 18, at least 20 or at least 25 contiguous nucleotides from SEQ ID NO: 14574. In certain embodiments, one transposon end comprises at least 14, at least 16, at least 18, at least 20 from SEQ ID NO: 14591, and the other end comprises at least 14, at least 16, at least 18, at least 20 from SEQ ID NO: 14593. In certain embodiments, each transposon end comprises SEQ ID NO: 14575 in inverted orientations.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence selected from of SEQ ID

20 NO: 14573, SEQ ID NO: 14579, SEQ ID NO: 14581, SEQ ID NO: 14582, SEQ ID NO: 14583, and SEQ ID NO: 14588, and a sequence selected from SEQ ID NO: 14587, SEQ ID NO: 14588, SEQ ID NO: 14589 and SEQ ID NO: 14586 and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14517 or SEQ ID NO: 14518.

25 In certain embodiments, the piggyBac or piggyBac-like transposon comprises ITRs of CCCTITGCCTGCCA (SEQ ID NO: 14622) (left ITR) and TGGCAGTGAAAGGG (SEQ ID NO: 14623) (right ITR) adjacent to the target sequences.

30 In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Helicoverpa armigera*. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30% 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14525)

```

1 MASRQRLNHD EIATILEND DYSPLDSESE KEDCVVEDDV WSDNEDAIVD FVEDTSAQED

61 PDNNNIASRES PNLEVTSLTS HRIITLPQRS IRGKNNHVWS TTKGRTTGRT SAINIIRTNR

121 GPTRMCRNIV DPLLCFQLFI TDEIIHEIVK WTNVEIIVKR QNLKDISASY RDTNTMEIWA

181 LVGILTLTAV MKDNHLSTDE LFADATFSGTR YVSVMSRERF EFLIRCIRMD DKTLRPTLRS

241 DDAAPLPVRKI WEIFINQCRO NHVPGSNLTV DEQLLGFRGR CPFRMYIPNK PKYGYIKFPM

301 MCAAATKYMIDAIPIYLGKST KTNGPLGEF YVKDLTKTVH GTNRNITCDN WFTSIPLAKN

361 MLQAPYNLTI VGTIRSNKRE MPEEIKNSRS RPVGSSMFCF DGPLTLVSYK PKPSKMVFLL

421 SSCDENAVIN ESNGKPDMIL FYNQTKGGVD SFDQMCKSMS ANRKTNRWPM AVFYGMLNMA

481 FVNSYIIYCH NKINKQEKPISRKEFMKKLS IQLTTPWMQE RLQAPTLKRT LRDNITNVLK

541 NVVPASSENI SNEPEPKKRR YCGVC SYKKR RMTKAQCCKC KKAICGEHNI DVCQDCI.

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In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Helicoverpa armigera*.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14570)
 1 ttaaccctag aagcccaatc tacgtaaatt tgacgtatac cgccgcgaaa tatctctgtc
 61 tcttcatgt ttaccgtcg atcgccgcta acttctgaac caactcagta gccattggaa
 121 cctcgcagga cacagttcg tcatctcggt aagtgcgc acatcttatt
 161 acaacacacg tcacgtcagc tcggtgcacg tcattttgac gtataattgg gctttgtgt
 241 actttgaat ttgttcaaa tttttatgt ttgtgattta ttggatata tcgtattgtt
 301 tcgttacatt ttcatataa taataatatt ttcaggttgta gtacaaa.

15

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14528)
 1 agactgtttt ttgttaagag acttctaaaa tattattacg agttgatata attttatgaa
 61 aacatttaaa actagtttat ttttttata attacataat tttaagaaaa agtgttagag
 121 gcttgatttt ttgttgatt tttctaaaga ttgtttaaa gtccataat agtattaata
 181 aagagtttt tttaactaa aatgtatattt atttattaaat taaaacttca attatgataa
 241 ctcatgcataa aatatagttc attaacagaa aaaaatagga aaactttgaa gttttgttt
 301 tacacgtcat ttgttacgtat gattggcatt tatacgat taaaatgtat tgggcttcta
 361 gggtaa.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Pectinophora gossypiella*. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14530)
 1 MDLRKQDEKI RQWLEQDIEE DSKGESDNSS SETEDIVEME VHKNNTSSESE VSSESVDYEPV
 61 CPSKRQRTQI IESEESDNSE SIRPSRRQTS RVIDSDETDE DVMSSTPQNI PRNPVNVIQPS
 121 SRFLYGKNKH KWSSAAKPSS VRTSRRNIIH FIPGPKERAR EVSEPIDIFS LFISEDMLOQQ
 181 VVTFTNAEML IRKNKYKTET FTVSPTNLEE IRALLGLFN AAAMKSNNLHP TRMLFNTHRS
 241 GTIFKACMSA ERLNFLIKCL RFDDKLTRNV RQRDDRFAPI RDLWQALISN FQKWYTPGSY
 301 ITVDEQLVGF RGRCSFRMYI PNKPNKYGIK LVMAADVNSK YIVNAIPYLG KGTDPQNQPL
 361 ATFFIKEITS TLHGTNRNIT MDNWFTSVPL ANELLMAPYN LTLVGLRSN KREIPEKLN
 421 SKSRAIGTSM FCYDGDKTLV SYKAKSNKVV FILSTIHDPQ DINQETGKPE MIHFYNSTKG
 481 AVDTVDQMC SISTNRKTQR WPLCVFYNML NLSIINAYVV YVYNNVRNNK KPMSSRDFVI
 541 KLGDQLMEPW LRQRLQTVTL RRDIKVMIQD ILGESSIONDEA PVPSVSNNRK IYYLCPSKAR
 601 RMTKHRCIKC KQAICGPHNI DICSRCIE.

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In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Pectinophora gossypiella*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
(SEQ ID NO: 14532)
1 ttaaccctag ataactaaac attcgtccgc tcgacgacgc gctatgccgc gaaattgaag
61 ttacattt attccgcgtc cccggcccc gcccgtttt ctatgttctt gatttgcaaa
121 atagtgcata gcgtgacacg ctcgaggta cacgacaatt aggtcgaaag ttacaggaat
181 ttcgtcgcc gtcgacgaa agtttagtaa ttacgttaat ttggcaaagg taagtgaatg
241 aagtatttt ttataattat tttaattt ttatagtga taacgttaagg ttatattaaa
301 ttattactt ttatagttac tttagccaatt gtataaatt ccttgttatt gctgaaaaat
361 ttgcctgttt tagtcaaat ttattaactt ttgcategtt ttttag.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
(SEQ ID NO: 14571)
1 ttcactaag taatttgtt cctatttgtt agataagtaa
25 cacataatta ttgtgatatt
61 caaaacttaa gaggtttat aaataataat aaaaaaaaaaa
25 tggttttat ttctgtatct
121 gctcgacgaa tgggtttttt ttacgttaacc gtgaatata
30 ttttagtgc tagggtaa.
```

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Ctenoplusia agnata*. The piggyBac or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

```
(SEQ ID NO: 14534)
1 MASRQHLYQD EIAAILENED DYSPHDTDSE MEDCVTQDDV
45 RSDVEDEMDV NINGTSPAS
61 RHEDPETPDP SSEASNLEVT LSSHRIIILP QRSIREKNNH
IWSTTKGQSS GRTAAINIVR
121 TNRGPTRMCR NIVDPPLCFO LFIKEEIVEE IVKWTNVEMV
45 QKRVNLKDIS ASYRDTNEME
181 IWAIISMLTL SAVMKDNHLS TDELFNVSYG TRYVSVMSRE
50 RFEFLRLRLR MGDKLRLPRL
241 RQEDAFTPVR KIWEIFINQC RLNYVPGTNL TVDEQLLGFR
GRCPFRMYIP NKPDKYGIKF
301 PMVCDAAATKY MVDAIPYLGK STKTQGLPLG EFYVKELTQT
55 VHGTNRNVTC DNWFTSVPLA
361 KSLLNSPYNL TLVGTIRSINK REIPEEVKNS RSRQVGSSMF
CFDGPLTLVS YKPKPSKMVF
421 LLSSCNEDAV VNQSNKPDM ILFYNQTKGG VDSFDQMCSS
MSTNRKTNRW PMAVFYGMNLN
481 MAFVNSYIIY CHNMLAKKEK PLSRKDFMKK LSTDLTTPSM
QKRLEAPTLK RSLPDNITNV
541 LKIVPQAAID TSFDEPEPKK RRYCGFCSYK KKRMKTQCF
KCKKPVCGEH NIDVCQDCI.
```

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In certain embodiments, the piggy Bac or piggyBac-like transposon is isolated or derived from *Ctenoplusia agnata*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
(SEQ ID NO: 14535)
1 ttaaccctag aagcccaatc tacgtcattc tgacgtgtat
gtcgccgaaa atactctgtc
61 tctttcttcc gcacgatcg attgcgcgca acgctcgatt
caacccagt ggccgcgaga
121 tctattggag gactgcggcg ttgattcggt aagtccgc
atttgtcat agtaacagta
181 ttgcacgtca gtttgacgta tatttggtt ttgtgttatt
tttgtaaattt ttcaacgtta
241 gtttattttt gcatctttt gttacattac tggtttattt
gcatgttata ctcaaatatt
301 atttttattt tagcgtagaa aataaca.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of

```
(SEQ ID NO: 14536)
1 agactgtttt ttttgtatcc gcattatata ttatattcta
45 aagtgttattt aattctaa
61 aaaacattaa aataagtttc tttttgtaaa atttaattaa
ttataagaaa aagttaatgt
121 tcatctcatt ttttataaaa atttgcaatg tttccaaagt
tattttgtta aaagaataaa
181 taaaagtaaa ctgagttta attgtatgtt tattatata
ttataactata tattacttaa
241 ataaaacaat aactgaatgt atttctaaaa ggaatcacta
50 gaaaatatacg tcatcaaaaa
301 ttacacgtc atttttgcgt atgattggc ttttaggtt
ctaaaaatata gattgggcct
361 ctagggttaa.
```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCCTAGAAGCCCAATC (SEQ ID NO: 14564).

In certain embodiments of the methods of the disclosure, 60 the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Agrotis ipsilon*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

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(SEQ ID NO: 14537)

1 MESPQLRNQD EIATILEND DYSPLSDSE AEDRVVVEDDV
WSDNEDAMID YVEDTSRQED

61 PDNNIASQES ANLEVTSLTS HRIISLPQRS ICGKNNHVWS
TTKGRTTGR T SAINIIRTNR

121 GPTTRMCRNIV DPLICFQLFI TDEIIHEIVK WTNVEMIVKR
QNLLDISASY RDTNTMEMWA

181 LVGILTLTAV MKDNHLSTDE LFDFATSGTR YVSVMSREPF
EFLIRCMRMD DKTLRPTLRS

241 DDAFIPVRKL WEIFINQCRL NYVPGGNLTV DEQLLGFRGR
CPFRMYIPNK PDKYGIREFPM

301 MCDAATKYM1 DAIPIYLGKST KTNGPLGEF YVKELTKTVH
GTNRNVTCDN WFTSIPLAKN

361 MLQAPYNLT1 VGTIRSNSKRE IPPEEIKNSRS RPVGSSMFCL
DGPLTLVSYK PKPSRMVFLL

421 SSCDENAVIN ESNQKPDML FYNQTKGGVD SFDQMCKSMS
ANRKTNRWPM AVFYGMNLNA

481 FVNSYIYCH NKINKQKKPI NRKEFMKNLS TDLTPWMQE
RLKAPTLKRT LRDNITNVLK

541 NVVPPSPANN SEEPGRKKRS YCGFCSYKKR RMTKTQFYKC
KKAICGEHNT DVCQDCV.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Agrotis ipsilon*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14538)

1 ttaaccctag aagcccaatc tacgtaaatt tgacgtatac
cgccggcaaa tatatatctgtc

61 tctttcacgt ttacccgtcg attcccgcta acttcggAAC
caactcgtca gcccattgaga

121 actccccagga cacagtgcg tcatctcggt aagtgcgc
attttgttgtt aatagacagg

181 ttgcacgtca tttgcacgtta taattgggtt ttgtgttaact
tttgcacgtca tttgcacgtta taattgggtt ttgtgttaact

241 ttatgtatgtt gattttttt agttaatcgt attgttttgtt
tacatttttc atatgtatatt

301 aatattttca gattgaatataaaa.

In certain embodiments, the piggyBac or piggy Bac-like transposon comprises a sequence of:

(SEQ ID NO: 14539)

1 agactgtttt ttttaaaagg ctataaagt attactatttg
cgtgatttaa ttttataaaaa

61 atatttaaaa ccagttgatt ttttaataaa ttacctaatt
ttaagaaaaa atgttagaa

121 cttgatattt ttagttgattt ttttctaaga tttgattaa
aggccataat tgtattaataa

181 aagagtattt ttaactcaa atttattttt ttttataatt
aaaacttcaa ttatgtataat

241 acatgcaaaa atatagttca tcaacagaaa aatataaggaa
aactctaataa gttttatttt

301 tacacgtcat ttttacgtat gattgggctt tatacgtagt
caaatatgtat tgggcttctca

351 gggttaa.

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In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Megachile rotundata*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14540)

1 MNGKDSLGEF YLDDLSDCLD CRSASSTDDE SDSSNIAIRK
RCRIPLIYSD SEDEDMNNNV

61 EDNNHFVKEES NRYHYQIVEK YKITSKTKW KDVTVTMKK
FLGLIILMQQ VKKDVLVLYDW

121 STDPSIETPF FSKVMSRNRF LQIMQSWHFY NNNDISPNSH
RLVKIQPVID YFKEKFNNVV

181 KSDQQLSLDE CLIPWRGRRLS IKTYNPAAKIT KYGILVRVLS
EARTGYVSNF CVYAADGKKI

241 EETVLSVIGP YKNMWHHVYQ DNYYNSVNIA KIFLKNKLRV
CGTIRKNRSL PQILQTVKLS

301 RGHQHQFLRNG HTLLEVWNNG KRNVNMISTI HSAQMAESRN
RSRTSDCPIQ KPISIIDYDNK

361 YMKGVDRADQ YLSYYISIFRK TKKWTKRVVM FFINCALFNS
FKVYTTLNQQ KITYKNFLHK

421 AALSЛИEDCG TEEQGTDLPN SEPTTTRRTS RVDHPGRIEN
FGKHKLBNV1N TSGQCKKPLR

481 QCRVCASKKK LSRTGFACKY CNVPLHKGDC FERYHSLKKY.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Megachile rotundata*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14541)

1 ttaaataatgc cccactctatc atgaacttaa cactttaccg
accggccgtc gattattcga

61 cgtttgcctt ccagcgctta ccgaccggcc atcgattatt
cgacgtttgc ttcccacgc

121 ttacccgaccg gtcatcgact tttgatcttt ccgttagatt
ttgttagtc agattgacaa

181 gtagcaagca tttcgcatc ttttattcaaa taatcggtca
ttttctaa gcttttagcooc

241 ttatgtatgtt gattttttt agttaatcgt attgttttgtt
tacatttttc atatgtatatt

55 In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14542)

1 acaacttctt ttttcaacaa atatgttat atggatttt
tattttatataa ttatgtat

61 gtagcaagca tttcgcatc ttttattcaaa taatcggtca
ttttctaa gcttttagcooc

121 gaaaacgattt gtaatagatg aaataaatat ttttttaaca
ctaatataat taaatgtat

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-continued

181 gatttaata aattcggtta ccctacaata acacgaagcg
tacaattta ccagagtta

241 ttaa.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Bombus impatiens*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14543)

1 MNEKNGIGEF YLDDLSDCPD SYSRNSGDE SDGSDTIRK
RGSVLPPRYS DSEDEINNV

61 EDNANNVENN DDIWSTNDEA IILEPPEGSP GLKIMPSSAE
SVDTNVNLFF GDDFFEHHLVR

121 ESNRYHYQVM EKYKIPSKAK KWTDITVPEM KKFLGLIVLM
GQIKKDVLYD YWSTDPSIET

181 PFPSSQVMSRN RFVQIMQSWH FCNNNDNIPH SHRLAKIQPV
IDYFRRKFND VYKPCQQLSL

241 DESIIPWPGR LSIKTYNPBK ITKYGILVRV LSEAVTGYVC
NEFDYAADGK KLEDTAVIEP

30 301 YKNIWHQIYQ DNYYNSVKMA RILLKNKVRV CGTIRKNRGL
PRSLKTQIQLS RGQYEFRRNH

361 QILLEVNWNNG RRNVNMISTI HSAQLMESRS KSKRSDVPIQ
KPNSIIDYNK YMKGVDRADQ

421 YLAYYSIFRK TKWTKTRVVM FFINCALFNS FRVYTILNGK
NITYKNFLHK VAVSWIEDGE

481 TNCTEQDDNL PNSEPTRRRAP RLDHPGRLSN YGKHKLINIV
TSGRSLKPKQR QCRVCAVQKK

541 RSRTCFVCKF CNVPLHKGDC FERYHTLKKY.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Bombus impatiens*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14544)

1 ttaatttttt aacattttac cgaccgatag ccgattaatc
gggttttgc cgctgacgt

50 61 taccgaccga taacctatta atccggcttt tgcgtcgaa
gcttaccaac ctatagccta

121 cctatagttt atccgggtgcc atggcgataa acaatcttc
tcatatatag agcagtaatt

181 tggttatitag tactaaggta ccttgctcaq ttgcgtcaq
tgcgttgctt tgtaagtc

241 cacagttta taccattcg aaaaacttac cgttcgcg.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of

(SEQ ID NO: 14545)

1 actatttcac attgaacta aaaaccgttg taatagataa
aataaatata atttagatt

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-continued

61 aatatttatgg aaacaaaaga ttttattcaa tttaattatc
ctatagtaac aaaaagcggc

121 caattttacat tgagcatacg aaaagcacag atactcccgc
ccgacagctt aaaccgaaac

181 agagccggcg ccagggagaa tctgcgcctg agcagccggt
cggcgtgc tttgctgttg

241 aaccgcgtat ggtcagtaaa ccagaaccag tcagtaagec
agtaactgt cagtttaacta

301 gattgtatag ttcaaatgtt acttaatcta gtttttaagc
gtatgaatgt tgtcttaactt

361 cgttatataat tatattctt ttaa.

15 In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Mamestra brassicae*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14546)

1 MFSFVPNKEQ TRTVLIFCFH LKTTAAESHR PLVEAFGEQV
PTVKTCEWRQ QRFKSGDFDV

30 61 DDKEHGKPPK RYEDAEQLAL LDEDDAQTKQ QLAQELEVSQ
QAVSNRLREG GKIQKVGRWV

121 PHELNERQRE RRKNTCEILL SRYKRKSFLH RIVTGEEKWI
FFVNPKRKKS YVDPGQPAT

181 TARPNRFGKK TRLCVWWDQS GVIYYELLKP GETVNTARYQ
QQLINLNRAL QRKRPEQKR

241 QHRVIFLHDN APSHTARAVR DTLETLNWEV LPHAYSPDL
APSDYHFLAS MGHALAEQRF

40 301 DSYESVEEWL DEWFAAKDDE FYWRGIIHKL P ERWDNCVASD
GKYFE.

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Mamestra brassicae*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14547)

1 ttatgggtt gccaaaaaag taattgcggta tttttcatat
acctgtctt taaacgtaca

61 tagggatcga actcagtaaa actttgaccc ttgtgaataaa
caaaatggac tgcaccaacca

121 ccatagttt ggcgcaattt agcgtcataa ttgttttgc
ttttgcactt caac.

In certain embodiments, the piggyBac or piggyBac-1e transposon comprises a sequence of:

(SEQ ID NO: 14548)

1 atgatttttt ctttttaaac caatttat

tagttaattt atataaaaat ccgcaattac

61 tttttggca acccaataa.

In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like

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transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Mayetiola destructor*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80% 85% 90%, 95% 99% or any percentage in between identical to:

(SEQ ID NO: 14549)

```

1 MENFENWRKR RHLREVLLLGH FFAKTTAES
      HRLLVEVYGE HALAKTQCFC WFQRFKSGDF
15 61 DTEDKERPGQ PKKFEDEELE ALLDEDCCQT
      QEELAKSLGV TQQAIISKRLK AAGYIQKQGN
20 121 WVPHELKPRD VERRFCMSEM LLQRHKKSF
      LSRIITGDEK WIHYDNSKRK KSYVKRGGRA
25 181 KSTPKSNLHG AKVMLCIKWD QRGVLYYELL
      EPGQTITGDL YRTQLIRLKQ ALAEKRPEYA
30 241 KRHGAVIFHH DNARPHVALP VKNYLENSGW
      EVLPHPYPSP DLAPPSDYHILF RSMQNNDLAGK
35 301 RFTSEQGIPK WLDSFLAAKP AKFFEKGHIHE
      LSERWEKVIA SDGQYFE.

```

In certain embodiments, the piggy ac or piggyBac-like transposon is isolated or derived from *Mayetiola destructor*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14550)

```

1 taagacttcc aaaatttcca cccgaacttt
      accttccccg cgcattatgt ctctcttttc
40 61 accctctgtat ccctggatt gttgtcgagc
      acgatttata ttgggtgtac aacttaaaaa
121 ccggaattgg acgctagatg tccacactaa
      cgaatagtgt aaaagcacaa attccatata
181 181 tacgtcattt tgaaggatca tttgacagct
      atcaaataatca gtcaataaaaa ctattctatc
241 tgtgtgcattc atatttttt attaact.

```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of

(seq ID NO: 14551)

```

1 tgcatttcatt cattttgtta tcgaaataaa
      gcattaattt ccactaaaaa attccggttt
60 61 ttaagttgtat caccaaatat catccttagt
      gacaattttc aaatggctt cccattgagc
121 tgaaaccgtg gctatagtaa gaaaaacgcc
      caaccggcgtca tcatatgcct tttttttctc
161 aacatccg.

```

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In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Apis mellifera*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

10 (SEQ ID NO: 14552)

```

1 MENQKEHYRH ILLFYFRKGK NASQAHKKLC
      AVYGDEALKR RQCQNWFDFK RSGDFSLKDE
15 61 KRSGRPVEVD DLLIKAIIDS DRHSTTREIA
      EKLHVSHSTCI ENHLKQLGYV QKLDTWVPHE
20 121 LKEKHLTQRI NSCDLLKKRN ENDPFLKRLI
      TGDEKWVVYN NIKRKRSWSR PREPAQTTSK
25 181 AGIHRKKVLL SVWWWDYKGIV YFELLPPNRT
      INSVVYIEQL TKLNNAVEEK RPELTNRKGIV
30 241 VFPHHDNARPH TSLVTRQKLL ELGWDVLPHP
      PYSPDLAPSD YFLFRSLQNS LNGKNFNND
35 301 DIKSYLIQFF ANKNQKFYER GIMMLPERWQ
      KVIDQNGQHI TE.

```

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Apis mellifera*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

35 (SEQ ID NO: 14553)

```

1 ttgggttggc aactaagtttta ttgcggattt
      cactcataga tggcttcagt tgaattttta
40 61 gtttgctgg cgtatgtccaa atgtaaaaaca
      cattttgtta tttgatagttt ggcacttcag
45 121 ctgtcaatca gtaaaaaaaaag tttttgtatc
      ggttgcgttag ttttcgtttt ggcgttcgttg
50 181 aaaa.

```

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

55 (SEQ ID NO: 14554)

```

1 agttattttag ttccatgaaa aaattgtctt
      tgattttctt aaaaaaatcc gcaattactt
60 61 agttgccaat ccaa.

```

In certain embodiments of the methods of the disclosure, 60 the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Messor bouvieri*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14555)

```

1 MSSFVPENVH LRHALLFLFH QKRAAESHR
      LLVETYGEHA PTIRTCETWF RQFKCGDFNV
      5       61 QDKERPGRPK TFEDAEQLQEL LDEDSTQTQK
      QLAEKLNVSRA VAICERLQAM GKIQKMGRWV
      10      121 PHELNDRQME NRKIVSEMLL QRYERKSFLH
      RIVTGDEKWI YFENPKRKKS WLSPGEAGPS
      15      181 TARPNNRFGRK TMLCVWWWDQI GVYYYELLKP
      GETVNNTDRYR QQMINLNCL IEKRPQYAQR
      20      241 HDKVILQHDN APSHTAKPVK EMLKSLGWEV
      LSHPPYSPDL APSDYHLFAS MGHALAEQHF
      25      301 ADFEEVKKWL DEWFSSKEKL FFWNGIHKLS
      ERWTKCIESN GQYFE.

```

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Messor bouvieri*. In 25 certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14556) 30

```

1 agtcagaaat gacacctcgta tcgacgacta
      atcgacgtct aatcgacgtc gattttatgt
      5       61 caaacatgtta ccagggtgtgt cggttaattcc
      tttccgggtt ttccggcaga tgtcaactagc
      10      121 cataagtatg aaatgttatg atttgataca
      tatgtcattt taftctactg acattaacct
      15      131 taaaactaca caagttacgt tccggccaaaa
      taacagcggtt atagatttat aattttttga
      20      241 aa.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14557) 50

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1 ataaatttga actatccatt ctaagtaacg
      tgttttttt aacgaaaaaaaaa ccggaaaaaaaa
      5       61 attaccgaca ctcctggtat gtaaacatgt
      tattttcgac attgaatcgc gtgcattcga
      10      121 agtcgatcga ggtgtcattt ctgact.

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In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme. In certain embodiments, the piggyBac or piggyBac-like transposase enzyme is isolated or derived from *Trichoplusia ni*. The piggyBac (PB) or piggyBac-like transposase enzyme may comprise or consist of an amino acid sequence at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 900%, 95%, 99% or any percentage in between identical to:

(SEQ ID NO: 14558)

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1 MGSSLDEHI LSALLQSDE LVGEDSDSEV
      SDHVSEDDVQ SDTEEAFIGE VHEVQPTSSG
      5       61 SEILDEQNVI EQPGSSLASN RILTLQPRTI
      RGKKNKHWCST SKSTRRSRVS ALNIVRSORG
      10      121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW
      TNAEISLKRR ESMTSATFRD TNEDEIYAFF
      15      181 GILVMTAVRK DNHMSTDLLF DRSLSMVYVS
      VMSRDRFDL IRCLRMDDKS IRPTLRENDV
      20      241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ
      LLGFRGRCPF RVYIPNPKSK YGIKILMMCD
      25      301 SGTKYMINGM PYLGRGTQTN GPVLGEYYVK
      ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
      30      361 EPYKLTTIVGT VRSNKREIPE VLKNSRSRPV
      GTSMECFDGP LTLVSYKPKP AKMVYLLSSC
      35      421 DEDASINEST GKPQMVMYYN QTKGVDLTD
      QMCCSVNTCSR KTNPWPMLL YGMINIACIN
      40      481 SFIIFYSHNVS SKGEKVQSRK KFMRNLYMSL
      TSSEMPEPIE APTLKRYLRD NISNILPKEV
      45      541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA
      NASCKKCKKV ICREHNIDMC QSCF.

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In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Trichoplusia ni*. In 45 certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14559)

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1 ttaaccctag aaagatagtc tgccgtaaaat
      tgacccatgc attcttggaaa tattgtctc
      5       61 tctttctaaa tagcgcaat ccgtcgctgt
      gcatttagga cacctcagtc gcccgttgg
      10      121 gctcccgat ggcgtgcttg tcaatgcgggt
      aagtgtcaact gatttgaac tataacgacc
      15      181 gcgtgagtca aatgacgca tgattatctt
      ttacgtgact tttaagattt aactcatacg
      20      241 ataattatata cgttattttca tggctactt
      acgtgataac ttattatata tatattttct
      25      301 tggatagat atc.

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In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14560) 5
 1 tttgttactt tatagaagaa atttgagtt
 tttgtttttt ttcaataaat aaataaacat
 61 aaataaaattg tttgttgaat ttattattag
 tatgttaagt taaaataat aaaacttaat
 121 atctattcaa attaataaat aaacctcgat
 atacagaccg ataaaacaca tgcccaatt
 181 tcacgcatttga ttatcttcaa cgtacgtcac
 aatatgatta tctttccagg gttaa

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14561)
 1 cccttagaaag atagtctcg taaaatttgc
 goatgcattt tcgttattt gcttcttctt
 61 tctaaatagc gcgaatccgt cgctgtgcatt
 ttaggacatc tcagtcgcgg ctggagetc
 121 cctgtggccg tgcttgcatt tgccgttaat
 gtcactgatt ttgttactata acgaccgct
 181 gagtcaaat gacgcattat tatcttttac
 gtgacttttta agatataact catacgataa
 241 ttatattgtt atttcatgtt ctacttacgt
 gataacttat tatataataa ttttcttgg
 301 atagatata.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14562) 45
 1 tttgttactt tatagaagaa atttgagtt
 tttgtttttt tttaataaat aaataaacat
 61 aaataaaattg tttgttgaat ttattattag
 tatgttaagt taaaataataaaacttaat
 121 atctattcaa attaataaat aaacctcgat
 atacagaccg ataaaacaca tgcccaatt
 181 ttacgcatttga ttatcttcaa cgtacgtcac
 aatatgatta tctttcttagg g.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14609)
 1 tctaaatagc gcgaatccgt cgctgtgcatt
 ttaggacatc tcagtcgcgg ctggagetc

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-continued
 61 ccgtgaggcg tgcttgcatt tgccgttaat
 gtcactgatt ttgttactata acgaccgct
 121 gagtcaaat gacgcattat tatcttttac
 gtgacttttta agatataact catacgataa
 181 ttatattgtt atttcatgtt ctacttacgt
 gataacttat tatataataa ttttcttgg
 241 atagatata.

In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

(SEQ ID NO: 14610)
 1 tttgttactt tatagaagaa atttgagtt
 tttgtttttt tttaataaat aaataaacat
 61 aaataaaattg tttgttgaat ttattattag
 tatgttaagt taaaataataaaacttaat
 121 atccattcaa attaataaat aaacctcgat
 atacagaccg ataaaacaca tgcccaatt
 181 ttacgcatttga ttatcttcaa cgtacgtcac
 aatatgatta tctttcttagg g

30 In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14561 and SEQ ID NO: 14562, and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14558. In certain embodiments, the piggyBac or piggyBac-like transposon comprises SEQ ID NO: 14609 and SEQ ID NO: 14610, and the piggyBac or piggyBac-like transposase comprises SEQ ID NO: 14558.

35 In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Aphis gossypii*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCTTCCAGCGGGCGCGC (SEQ ID NO: 14565).

In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Chilo suppressalis*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCCAGATTAGCCT (SEQ ID NO: 14566).

40 In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Heliothis virescens*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCCTTAAT-TACTCGCG (SEQ ID NO: 14567).

45 In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Pectinophora gossypiella*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCCTAGAA-TAACTAAC (SEQ ID NO: 14568).

50 In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Anopheles stephensi*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises an ITR sequence of CCCTAGAAA-GATA (SEQ ID NO: 14569).

Immune and Immune Precursor Cells

55 In certain embodiments, immune cells of the disclosure comprise lymphoid progenitor cells, natural killer (NK) cells, T lymphocytes (T-cell), stem memory T cells (T_{SCM} cells), central memory T cells (T_{CM}), stem cell-like T cells, B lymphocytes (B-cells), myeloid progenitor cells, neutro-

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phils, basophils, eosinophils, monocytes, macrophages, platelets, erythrocytes, red blood cells (RBCs), megakaryocytes or osteoclasts.

In certain embodiments, immune precursor cells comprise any cells which can differentiate into one or more types of immune cells. In certain embodiments, immune precursor cells comprise multipotent stem cells that can self renew and develop into immune cells. In certain embodiments, immune precursor cells comprise hematopoietic stem cells (HSCs) or descendants thereof. In certain embodiments, immune precursor cells comprise precursor cells that can develop into immune cells. In certain embodiments, the immune precursor cells comprise hematopoietic progenitor cells (HPCs). Hematopoietic Stem Cells (HSCs)

Hematopoietic stem cells (HSCs) are multipotent, self-renewing cells. All differentiated blood cells from the lymphoid and myeloid lineages arise from HSCs. HSCs can be found in adult bone marrow, peripheral blood, mobilized peripheral blood, peritoneal dialysis effluent and umbilical cord blood.

HSCs of the disclosure may be isolated or derived from a primary or cultured stem cell. HSCs of the disclosure may be isolated or derived from an embryonic stem cell, a multipotent stem cell, a pluripotent stem cell, an adult stem cell, or an induced pluripotent stem cell (iPSC).

Immune precursor cells of the disclosure may comprise an HSC or an HSC descendent cell. Exemplary HSC descendent cells of the disclosure include, but are not limited to, multipotent stem cells, lymphoid progenitor cells, natural killer (NK) cells, T lymphocyte cells (T-cells), B lymphocyte cells (B-cells), myeloid progenitor cells, neutrophils, basophils, eosinophils, monocytes, and macrophages.

HSCs produced by the methods of the disclosure may retain features of “primitive” stem cells that, while isolated or derived from an adult stem cell and while committed to a single lineage, share characteristics of embryonic stem cells. For example, the “primitive” HSCs produced by the methods of the disclosure retain their “stemness” following division and do not differentiate. Consequently, as an adoptive cell therapy, the “primitive” HSCs produced by the methods of the disclosure not only replenish their numbers, but expand *in vivo*. “Primitive” HSCs produced by the methods of the disclosure may be therapeutically-effective when administered as a single dose. In some embodiments, primitive HSCs of the disclosure are CD34+. In some embodiments, primitive HSCs of the disclosure are CD34+ and CD38-. In some embodiments, primitive HSCs of the disclosure are CD34+, CD38- and CD90+. In some embodiments, primitive HSCs of the disclosure are CD34+, CD38-, CD90+ and CD45RA-. In some embodiments, primitive HSCs of the disclosure are CD34+, CD38-, CD90+, CD45RA-, and CD49f+. In some embodiments, the most primitive HSCs of the disclosure are CD34+, CD38-, CD90+, CD45RA-, and CD49f+.

In some embodiments of the disclosure, primitive HSCs, HSCs, and/or HSC descendent cells may be modified according to the methods of the disclosure to express an exogenous sequence (e.g. a chimeric antigen receptor or therapeutic protein). In some embodiments of the disclosure, modified primitive HSCs, modified HSCs, and/or modified HSC descendent cells may be forward differentiated to produce a modified immune cell including, but not limited to, a modified T cell, a modified natural killer cell and/or a modified B-cell of the disclosure.

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T Cells

Modified T cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

Unlike traditional biologics and chemotherapeutics, modified-T cells of the disclosure possess the capacity to rapidly reproduce upon antigen recognition, thereby potentially obviating the need for repeat treatments. To achieve this, in some embodiments, modified-T cells of the disclosure not only drive an initial response, but also persist in the patient as a stable population of viable memory T cells to prevent potential relapses. Alternatively, in some embodiments, when it is not desired, modified-T cells of the disclosure do not persist in the patient.

Intensive efforts have been focused on the development of antigen receptor molecules that do not cause T cell exhaustion through antigen-independent (tonic) signaling, as well as of a modified-T cell product containing early memory T cells, especially stem cell memory (T_{SCM}) or stem cell-like T cells. Stem cell-like modified-T cells of the disclosure exhibit the greatest capacity for self-renewal and multipotent capacity to derive central memory (T_{CM}) T cells or T_{CM} like cells, effector memory (T_{EM}) and effector T cells (T_E), thereby producing better tumor eradication and long-term modified-T cell engraftment. A linear pathway of differentiation may be responsible for generating these cells: Naïve T cells (T_N) $> T_{SCM} > T_{CM} > T_{EM} > T_E > T_{TE}$, whereby T_N is the parent precursor cell that directly gives rise to T_{SCM} , which then, in turn, directly gives rise to T_{CM} , etc. Compositions of T cells of the disclosure may comprise one or more of each 30 parental T cell subset with T_{SCM} cells being the most abundant (e.g. $T_{SCM} > T_{CM} > T_{EM} > T_E > T_{TE}$).

In some embodiments of the methods of the disclosure, the immune cell precursor is differentiated into or is capable of differentiating into an early memory T cell, a stem cell 35 like T-cell, a Naïve T cells (T_N), a T_{SCM} , a T_{CM} , a T_{EM} , a T_E , or a T_{TE} . In some embodiments, the immune cell precursor is a primitive HSC, an HSC, or a HSC descendent cell of the disclosure.

In some embodiments of the methods of the disclosure, 40 the immune cell is an early memory T cell, a stem cell like T-cell, a Naïve T cells (T_N), a T_{SCM} , a T_{CM} , a T_{EM} , a T_E , or a T_{TE} .

In some embodiments of the methods of the disclosure, the immune cell is an early memory T cell.

In some embodiments of the methods of the disclosure, the immune cell is a stem cell like T-cell.

In some embodiments of the methods of the disclosure, the immune cell is a T_{SCM} .

In some embodiments of the methods of the disclosure, the immune cell is a T_{CM} .

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 55% 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of an early memory T cell. In certain embodiments, the plurality of modified early memory T cells comprises at least one modified stem cell-like T cell. In certain embodiments, the plurality of modified early memory T cells comprises at least one modified T_{SCM} . In certain embodiments, the plurality of modified early memory T cells comprises at least one modified T_{CM} .

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%,

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20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of a stem cell-like T cell. In certain embodiments, the plurality of modified stem cell-like T cells comprises at least one modified T_{SCM} . In certain embodiments, the plurality of modified stem cell-like T cells comprises at least one modified T_{CM} .

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of a stem memory T cell (T_{SCM}). In certain embodiments, the cell-surface markers comprise CD62L and CD45RA. In certain embodiments, the cell-surface markers comprise one or more of CD62L, CD45RA, CD28, CCR7, CD127, CD45RO, CD95, CD95 and IL-2R β . In certain embodiments, the cell-surface markers comprise one or more of CD45RA, CD95, IL-2R β , CCR7, and CD62L.

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of a central memory T cell (T_{CM}). In certain embodiments, the cell-surface markers comprise one or more of CD45RO, CD95, IL-2R β , CCR7, and CD62L.

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of a naïve T cell (T_N). In certain embodiments, the cell-surface markers comprise one or more of CD45RA, CCR7 and CD62L.

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of an effector T-cell (modified T_{EFF}). In certain embodiments, the cell-surface markers comprise one or more of CD45RA, CD95, and IL-2R β .

In some embodiments of the methods of the disclosure, the methods modify and/or the methods produce a plurality of modified T cells, wherein at least 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between of the plurality of modified T cells expresses one or more cell-surface marker(s) of a stem cell-like T cell, a stem memory T cell (T_{SCM}) or a central memory T cell (T_{CM}).

In some embodiments of the methods of the disclosure, a buffer comprises the immune cell or precursor thereof. The buffer maintains or enhances a level of cell viability and/or a stem-like phenotype of the immune cell or precursor thereof, including T-cells. In certain embodiments, the buffer maintains or enhances a level of cell viability and/or a stem-like phenotype of the primary human T cells prior to the nucleofection. In certain embodiments, the buffer maintains or enhances a level of cell viability and/or a stem-like

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phenotype of the primary human T cells during the nucleofection. In certain embodiments, the buffer maintains or enhances a level of cell viability and/or a stem-like phenotype of the primary human T cells following the nucleofection. In certain embodiments, the buffer comprises one or more of KCl, MgCl₂, ClNa, Glucose and Ca(NO₃)₂ in any absolute or relative abundance or concentration, and, optionally, the buffer further comprises a supplement selected from the group consisting of HEPES, Tris/HCl, and a phosphate buffer. In certain embodiments, the buffer comprises 5 mM KCl, 15 mM MgCl₂, 90 mM ClNa, 10 mM Glucose and 0.4 mM Ca(NO₃)₂. In certain embodiments, the buffer comprises 5 mM KCl, 15 mM MgCl₂, 90 mM ClNa, 10 mM Glucose and 0.4 mM Ca(NO₃)₂ and a supplement comprising 20 mM HEPES and 75 mM Tris/HCl. In certain embodiments, the buffer comprises 5 mM KCl, 15 mM MgCl₂, 90 mM ClNa, 10 mM Glucose and 0.4 mM Ca(NO₃)₂ and a supplement comprising 40 mM Na₂HPO₄/NaH₂PO₄ at pH 7.2. In certain embodiments, the composition comprising primary human T cells comprises 100 μ l of the buffer and between 5×10^6 and 25×10^6 cells. In certain embodiments, the composition comprises a scalable ratio of 250×10^6 primary human T cells per milliliter of buffer or other media during the introduction step.

In some embodiments of the methods of the disclosure, the methods comprise contacting an immune cell of the disclosure, including a T cell of the disclosure, and a T-cell expansion composition. In some embodiments of the methods of the disclosure, the step of introducing a transposon and/or transposase of the disclosure into an immune cell of the disclosure may further comprise contacting the immune cell and a T-cell expansion composition. In some embodiments, including those in which the introducing step of the methods comprises an electroporation or a nucleofection step, the electroporation or a nucleofection step may be performed with the immune cell contacting T-cell expansion composition of the disclosure.

In some embodiments of the methods of the disclosure, the T-cell expansion composition comprises, consists essentially of or consists of phosphorus; one or more of an octanoic acid, a palmitic acid, a linoleic acid, and an oleic acid; a sterol; and an alkane.

In certain embodiments of the methods of producing a modified T cell of the disclosure, the expansion supplement comprises one or more cytokine(s). The one or more cytokine(s) may comprise any cytokine, including but not limited to, lymphokines. Exemplary lymphokines include, but are not limited to, interleukin-2 (IL-2), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-6 (IL-6), interleukin-7 (IL-7), interleukin-15 (IL-15), interleukin-21 (IL-21), granulocyte-macrophage colony-stimulating factor (GM-CSF) and interferon-gamma (INF γ). The one or more cytokine(s) may comprise IL-2.

In some embodiments of the methods of the disclosure, the T-cell expansion composition comprises human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement. In certain embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid, nicotinamide, 2,4,7,9-tetramethyl-5-decyn-4,7-diol (TMDD), diisopropyl adipate (DIPA), n-butyl-benzene-sulfonamide, 1,2-benzenedicarboxylic acid, bis(2-methylpropyl) ester, palmitic acid, linoleic acid, oleic acid, stearic acid hydrazide, oleamide, a sterol and an alkane. In certain embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid, palmitic acid, linoleic acid, oleic acid and a sterol. In certain

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embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid at a concentration of between 0.9 mg/kg to 90 mg/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; oleic acid at a concentration of 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; and a sterol at a concentration of about 0.1 mg/kg to 10 mg/kg, inclusive of the endpoints. In certain embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid at a concentration of about 9 mg/kg, palmitic acid at a concentration of about 2 mg/kg, linoleic acid at a concentration of about 2 mg/kg, oleic acid at a concentration of about 2 mg/kg and a sterol at a concentration of about 1 mg/kg. In certain embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid at a concentration of between 6.4 μmol/kg and 640 μmol/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.7 μmol/kg and 70 μmol/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.75 μmol/kg and 75 μmol/kg, inclusive of the endpoints; oleic acid at a concentration of between 0.75 μmol/kg and 75 μmol/kg, inclusive of the endpoints; and a sterol at a concentration of between 0.25 μmol/kg and 25 μmol/kg, inclusive of the endpoints. In certain embodiments of this method, the T-cell expansion composition further comprises one or more of octanoic acid at a concentration of about 64 μmol/kg, palmitic acid at a concentration of about 7 μmol/kg, linoleic acid at a concentration of about 7.5 μmol/kg, oleic acid at a concentration of about 7.5 μmol/kg and a sterol at a concentration of about 2.5 μmol/kg.

In certain embodiments, the T-cell expansion composition comprises one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement to produce a plurality of expanded modified T-cells, wherein at least 2% of the plurality of modified T-cells expresses one or more cell-surface marker(s) of an early memory T cell, a stem cell-like T cell, a stem memory T cell (T_{SCM}) and/or a central memory T cell (T_{CM}). In certain embodiments, the T-cell expansion composition comprises or further comprises one or more of octanoic acid, nicotinamide, 2,4,7,9-tetramethyl-5-decyn-4,7-diol (TMDD), diisopropyl adipate (DIPA), n-butyl-benzenesulfonamide, 1,2-benzenedicarboxylic acid, bis(2-methylpropyl) ester, palmitic acid, linoleic acid, oleic acid, stearic acid hydrazide, oleamide, a sterol and an alkane. In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid, palmitic acid, linoleic acid, oleic acid and a sterol (e.g. cholesterol). In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of between 0.9 mg/kg to 90 mg/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; oleic acid at a concentration of 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; and a sterol at a concentration of about 0.1 mg/kg to 10 mg/kg, inclusive of the endpoints (wherein mg/kg=parts per million). In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of about 9 mg/kg, palmitic acid at a concentration of about 2 mg/kg, linoleic acid at a concentration of about 2 mg/kg, oleic acid at a concentration of about 2 mg/kg, and a sterol at a concentration of about 1 mg/kg (wherein mg/kg=parts per

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million). In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of 9.19 mg/kg, palmitic acid at a concentration of 1.86 mg/kg, linoleic acid at a concentration of about 2.12 mg/kg, oleic acid at a concentration of about 2.13 mg/kg, and a sterol at a concentration of about 1.01 mg/kg (wherein mg/kg=parts per million). In certain embodiments, the T-cell expansion composition comprises octanoic acid at a concentration of 9.19 mg/kg, palmitic acid at a concentration of 1.86 mg/kg, linoleic acid at a concentration of 2.12 mg/kg, oleic acid at a concentration of about 2.13 mg/kg, and a sterol at a concentration of 1.01 mg/kg (wherein mg/kg=parts per million). In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of between 6.4 μmol/kg and 640 μmol/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.7 μmol/kg and 70 μmol/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.75 μmol/kg and 75 μmol/kg, inclusive of the endpoints; oleic acid at a concentration of between 0.75 μmol/kg and 75 μmol/kg, inclusive of the endpoints; and a sterol at a concentration of between 0.25 μmol/kg and 25 μmol/kg, inclusive of the endpoints. In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of about 64 μmol/kg, palmitic acid at a concentration of about 7 μmol/kg, linoleic acid at a concentration of about 7.5 μmol/kg, oleic acid at a concentration of about 7.5 μmol/kg and a sterol at a concentration of about 2.5 μmol/kg. In certain embodiments, the T-cell expansion composition comprises one or more of octanoic acid at a concentration of about 63.75 μmol/kg, palmitic acid at a concentration of about 7.27 μmol/kg, linoleic acid at a concentration of about 7.57 μmol/kg, oleic acid at a concentration of about 7.56 μmol/kg and a sterol at a concentration of about 2.61 μmol/kg. In certain embodiments, the T-cell expansion composition comprises octanoic acid at a concentration of about 63.75 μmol/kg, palmitic acid at a concentration of about 7.27 μmol/kg, linoleic acid at a concentration of about 7.57 μmol/kg, oleic acid at a concentration of about 7.56 μmol/kg and a sterol at a concentration of 2.61 μmol/kg.

As used herein, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement at 37° C. Alternatively, or in addition, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of phosphorus, an octanoic fatty acid, a palmitic fatty acid, a linoleic fatty acid and an oleic acid. In certain embodiments, the media comprises an amount of phosphorus that is 10-fold higher than may be found in, for example, Iscove’s Modified Dulbecco’s Medium (IMDM); available at ThermoFisher Scientific as Catalog number 12440053).

As used herein, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, Iscove’s MDM, and an expansion supplement at 37° C. Alternatively, or in addition, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of the following elements: boron, sodium, magnesium, phosphorus, potassium, and calcium. In certain embodiments, the

terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following elements present in the corresponding average concentrations: boron at 3.7 mg/L, sodium at 3000 mg/L, magnesium at 18 mg/L, phosphorus at 29 mg/L, potassium at 15 mg/L and calcium at 4 mg/L.

As used herein, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement at 37° C. Alternatively, or in addition, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following components: octanoic acid (CAS No. 124-07-2), nicotinamide (CAS No. 98-92-0), 2,4,7,9-tetramethyl-5-decyn-4,7-diol (TMDD) (CAS No. 126-86-3), diisopropyl adipate (DIPA) (CAS No. 6938-94-9), n-butyl-benzenesulfonamide (CAS No. 3622-84-2), 1,2-benzenedicarboxylic acid, bis(2-methylpropyl) ester (CAS No. 84-69-5), palmitic acid (CAS No. 57-10-3), linoleic acid (CAS No. 60-33-3), oleic acid (CAS No. 112-80-1), stearic acid hydrazide (CAS No. 4130-54-5), oleamide (CAS No. 3322-62-1), sterol (e.g., cholesterol) (CAS No. 57-88-5), and alkanes (e.g., nonadecane) (CAS No. 629-92-5). In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following components: octanoic acid (CAS No. 124-07-2), nicotinamide (CAS No. 98-92-0), 2,4,7,9-tetramethyl-5-decyn-4,7-diol (TMDD) (CAS No. 126-86-3), diisopropyl adipate (DIPA) (CAS No. 6938-94-9), n-butyl-benzenesulfonamide (CAS No. 3622-84-2), 1,2-benzenedicarboxylic acid, bis(2-methylpropyl) ester (CAS No. 84-69-5), palmitic acid (CAS No. 57-10-3), linoleic acid (CAS No. 60-33-3), oleic acid (CAS No. 112-80-1), stearic acid hydrazide (CAS No. 4130-54-5), oleamide (CAS No. 3322-62-1), sterol (e.g., cholesterol) (CAS No. 57-88-5), alkanes (e.g., nonadecane) (CAS No. 629-92-5), and phenol red (CAS No. 143-74-8). In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following components: octanoic acid (CAS No. 124-07-2), nicotinamide (CAS No. 98-92-0), 2,4,7,9-tetramethyl-5-decyn-4,7-diol (TMDD) (CAS No. 126-86-3), diisopropyl adipate (DIPA) (CAS No. 6938-94-9), n-butyl-benzenesulfonamide (CAS No. 3622-84-2), 1,2-benzenedicarboxylic acid, bis(2-methylpropyl) ester (CAS No. 84-69-5), palmitic acid (CAS No. 57-10-3), linoleic acid (CAS No. 60-33-3), oleic acid (CAS No. 112-80-1), stearic acid hydrazide (CAS No. 4130-54-5), oleamide (CAS No. 3322-62-1), phenol red (CAS No. 143-74-8) and lanolin alcohol.

In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement at 37° C. Alternatively, or in addition, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following ions: sodium, ammonium, potassium, magnesium, calcium, chloride, sulfate and phosphate.

As used herein, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, and an expansion supplement at 37° C. Alternatively, or in addition, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following free amino acids, histidine, asparagine, serine, glutamate, arginine, glycine, aspartic acid, glutamic acid, threonine, alanine, proline, cysteine, lysine, tyrosine, methionine, valine, isoleucine, leucine, phenylalanine and tryptophan. In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following free amino acids in the corresponding average mole percentages: histidine (about 1%), asparagine (about 0.5%), serine (about 1.5%), glutamine (about 67%), arginine (about 1.5%), glycine (about 1.5%), aspartic acid (about 1%), glutamic acid (about 2%), threonine (about 2%), alanine (about 1%), proline (about 1.5%), cysteine (about 1.5%), lysine (about 3%), tyrosine (about 1.5%), methionine (about 1%), valine (about 3.5%), isoleucine (about 3%), leucine (about 3.5%), phenylalanine (about 1.5%) and tryptophan (about 0.5%). In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of the following free amino acids in the corresponding average mole percentages: histidine (about 0.78%), asparagine (about 0.4%), serine (about 1.6%), glutamine (about 67.01%), arginine (about 1.67%), glycine (about 1.72%), aspartic acid (about 1.00%), glutamic acid (about 1.93%), threonine (about 2.38%), alanine (about 1.11%), proline (about 1.49%), cysteine (about 1.65%), lysine (about 2.84%), tyrosine (about 1.62%), methionine (about 0.85%), valine (about 3.45%), isoleucine (about 3.14%), leucine (about 3.3%), phenylalanine (about 1.64%) and tryptophan (about 0.37%).

As used herein, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of human serum albumin, recombinant human insulin, human transferrin, 2-Mercaptoethanol, Iscove's MDM, and an expansion supplement at 37° C. Alternatively, or in addition, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of phosphorus, an octanoic fatty acid, a palmitic fatty acid, a linoleic fatty acid and an oleic acid. In certain embodiments, the media comprises an amount of phosphorus that is 10-fold higher than may be found in, for example, Iscove's Modified Dulbecco's Medium ((IMDM); available at ThermoFisher Scientific as Catalog number 12440053).

In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of octanoic acid, palmitic acid, linoleic acid, oleic acid and a sterol (e.g. cholesterol). In certain embodiments, the terms "supplemented T-cell expansion composition" or "T-cell expansion composition" may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of between 0.9 mg/kg to 90 mg/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; oleic acid at a

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concentration of 0.2 mg/kg to 20 mg/kg, inclusive of the endpoints; and a sterol at a concentration of about 0.1 mg/kg to 10 mg/kg, inclusive of the endpoints (wherein mg/kg=parts per million). In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of about 9 mg/kg, palmitic acid at a concentration of about 2 mg/kg, linoleic acid at a concentration of about 2 mg/kg, oleic acid at a concentration of about 2 mg/kg, and a sterol at a concentration of about 1 mg/kg (wherein mg/kg=parts per million). In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of 9.19 mg/kg, palmitic acid at a concentration of 1.86 mg/kg, linoleic acid at a concentration of about 2.12 mg/kg, oleic acid at a concentration of about 2.13 mg/kg, and a sterol at a concentration of about 1.01 mg/kg (wherein mg/kg=parts per million). In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of 9.19 mg/kg, palmitic acid at a concentration of 1.86 mg/kg, linoleic acid at a concentration of about 2.12 mg/kg, oleic acid at a concentration of about 2.13 mg/kg, and a sterol at a concentration of 1.01 mg/kg (wherein mg/kg=parts per million). In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of between 6.4 μ mol/kg and 640 μ mol/kg, inclusive of the endpoints; palmitic acid at a concentration of between 0.7 μ mol/kg and 70 μ mol/kg, inclusive of the endpoints; linoleic acid at a concentration of between 0.75 μ mol/kg and 75 μ mol/kg, inclusive of the endpoints; oleic acid at a concentration of between 0.75 μ mol/kg and 75 μ mol/kg, inclusive of the endpoints; and a sterol at a concentration of between 0.25 μ mol/kg and 25 μ mol/kg, inclusive of the endpoints. In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of about 64 μ mol/kg, palmitic acid at a concentration of about 7 μ mol/kg, linoleic acid at a concentration of about 7.5 μ mol/kg, oleic acid at a concentration of about 7.5 μ mol/kg and a sterol at a concentration of about 7.5 μ mol/kg.

In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of about 63.75 μ mol/kg, palmitic acid at a concentration of about 7.27 μ mol/kg, linoleic acid at a concentration of about 7.57 μ mol/kg, oleic acid at a concentration of about 7.56 μ mol/kg and a sterol at a concentration of about 2.61 μ mol/kg. In certain embodiments, the terms “supplemented T-cell expansion composition” or “T-cell expansion composition” may be used interchangeably with a media comprising one or more of octanoic acid at a concentration of about 63.75 μ mol/kg, palmitic acid at a concentration of about 7.27 μ mol/kg, linoleic acid at a concentration of about 7.57 μ mol/kg, oleic acid at a concentration of 7.56 μ mol/kg and a sterol at a concentration of 2.61 μ mol/kg.

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a T_{CM}) of the disclosure, the method comprises contacting a

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modified T cell and an inhibitor of the PI3K-Akt-mTOR pathway. Modified T-cells of the disclosure, including modified stem cell-like T cells, T_{SCM} and/or T_{CM} of the disclosure, may be incubated, cultured, grown, stored, or otherwise, combined at any step in the methods of the procedure with a growth medium comprising one or more inhibitors a component of a PI3K pathway. Exemplary inhibitors a component of a PI3K pathway include, but are not limited to, an inhibitor of GSK30 such as TWS119 (also known as 10 GSK 3B inhibitor XII; CAS Number 601514-19-6 having a chemical formula $C_{18}H_{14}N_4O_2$). Exemplary inhibitors of a component of a PI3K pathway include, but are not limited to, bb007 (BLUEBIRDBIOTM). Additional Exemplary inhibitors of a component of a PI3K pathway include, but are not limited to, an allosteric Akt inhibitor VIII (also referred to as Akti-1/2 having Compound number 10196499), ATP competitive inhibitors (Orthosteric inhibitors targeting the ATP-binding pocket of the protein kinase B (Akt)), Isoquinoline-5-sulfonamides (H-8, H-89, and 15 NL-71-101), Azepane derivatives (A series of structures derived from (-)-balanol), Aminofurazans (GSK690693). Heterocyclic rings (7-azaindole, 6-phenylpurine derivatives, pyrrolo[2,3-d]pyrimidine derivatives, CCT128930, 3-amino-pyrrolidine, anilinotriazole derivatives, spiroindoline derivatives, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, and A-443654). Phenylpyrazole derivatives (AT7867 and AT13148), Thiophenecarboxamide derivatives (Afuresertib (GSK2110183), 2-pyrimidyl-5-amidothiophene derivative (DC120), uprosertib (GSK2141795)), 20 Allosteric inhibitors (Superior to orthosteric inhibitors providing greater specificity, reduced side-effects and less toxicity). 2,3-diphenylquinoxaline analogues (2,3-diphenylquinoxaline derivatives, triazolo[3,4-f][1,6]naphthyridin-3 (2H)-one derivative (MK-2206)), Alkylphospholipids 25 Edelfosine (1-O-octadecyl-2-O-methyl-rac-glycero-3-phosphocholine, ET-8-OCH₃) ilmofosine (BM 41.440), miltefosine (hexadecylphosphocholine, HePC), perifosine (D-21266), erucylphosphocholine (ErPC), erufosine (ErPC3, erucylphosphohomocholine), Indole-3-carbinol analogues (Indole-3-carbinol, 3-chloroacetylindole, diindolylmethane, diethyl 6-methoxy-5,7-dihydroindolo [2,3-b] carbazole-2,10-dicarboxylate (SR13668), OSU-A9), Sulfonylamine derivatives (PH-316 and PHT-427), Thiourea derivatives (PIT-1, PIT-2, DM-PIT-1, N-[1-methyl-1H-pyrazol-4-yl]carbonyl]-N'-(3-bromophenyl)-thiourea), Purine derivatives (Triciribine (TCN, NSC 154020), triciridine mono-phosphate active analogue (TCN-P), 4-amino-pyrido[2,3-d]pyrimidine derivative API-1, 3-phenyl-3H-imidazo[4,5-b]pyridine derivatives, ARQ 092). BAY 30 1125976, 3-methyl-xanthine, quinoline-4-carboxamide and 2-[4-(cyclohexa-1,3-dien-1-yl)-1H-pyrazol-3-yl]phenol, 3-oxo-tirucalllic acid, 3 α - and 3 β -acetoxy-tirucalllic acids, acetoxy-tirucalllic acid, and irreversible inhibitors (antibiotics, Lactoquinomycin, Frenolicin B, kalafungin, medermycin, Boc-Phe-vinyl ketone, 4-hydroxynonenal (4-HNE), 1,6-naphthyridinone derivatives, and imidazo-1,2-pyridine derivatives).

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a T_{CM}) of the disclosure, the method comprises contacting a modified T cell and an inhibitor of T cell effector differentiation. Exemplary inhibitors of T cell effector differentiation include, but are not limited to, a BET inhibitor (e.g. JQ1, a hienotriazolodiazepine) and/or an inhibitor of the BET family of proteins (e.g. BRD2, BRD3, BRD4, and BRDT).

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a

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T_{CM}) of the disclosure, the method comprises contacting a modified T cell and an agent that reduces nucleo-cytoplasmic Acetyl-CoA. Exemplary agents that reduce nucleo-cytoplasmic Acetyl-CoA include, but are not limited to, 2-hydroxy-citrate (2-HC) as well as agents that increase expression of Acss1.

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a T_{CM}) of the disclosure, the method comprises contacting a modified T cell and a composition comprising a histone deacetylase (HDAC) inhibitor. In some embodiments, the composition comprising an HDAC inhibitor comprises or consists of valproic acid, Sodium Phenylbutyrate (NaPB) or a combination thereof. In some embodiments, the composition comprising an HDAC inhibitor comprises or consists of valproic acid. In some embodiments, the composition comprising an HDAC inhibitor comprises or consists of Sodium Phenylbutyrate (NaPB).

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a T_{CM}) of the disclosure, the activation supplement may comprise one or more cytokine(s). The one or more cytokine(s) may comprise any cytokine, including but not limited to, lymphokines. Exemplary lymphokines include, but are not limited to, interleukin-2 (IL-2), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-6 (IL-6), interleukin-7 (IL-7), interleukin-15 (IL-15), interleukin-21 (IL-21), granulocyte-macrophage colony-stimulating factor (GM-CSF) and interferon-gamma (INF γ). The one or more cytokine(s) may comprise IL-2.

In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a T_{SCM} and/or a T_{CM}) of the disclosure, the activation supplement may comprise one or more activator complexes. Exemplary and nonlimiting activator complexes may comprise a monomeric, dimeric, trimeric or tetrameric antibody complex that binds one or more of CD3, CD28, and CD2. In some embodiments, the activation supplement comprises or consists of an activator complex that comprises a human, a humanized or a recombinant or a chimeric antibody. In some embodiments, the activation supplement comprises or consists of an activator complex that binds CD3 and CD28. In some embodiments, the activation supplement comprises or consists of an activator complex that binds CD3, CD28 and CD2.

Natural Killer (NK) Cells

In certain embodiments, the modified immune or immune precursor cells of the disclosure are natural killer (NK) cells. In certain embodiments, NK cells are cytotoxic lymphocytes that differentiate from lymphoid progenitor cells.

Modified NK cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

In certain embodiments, non-activated NK cells are derived from CD3-depleted leukopheresis (containing CD14/CD19/CD56+ cells).

In certain embodiments, NK cells are electroporated using a Lonza 4D nucleofector or BTX ECM 830 (500V, 700 usec pulse length, 0.2 mm electrode gap, one pulse). All Lonza 4D nucleofector programs are contemplated as within the scope of the methods of the disclosure.

In certain embodiments, 5 \times 10E6 cells were electroporated per electroporation in 100 μ L P3 buffer in cuvettes. However, this ratio of cells per volume is scalable for commercial manufacturing methods.

In certain embodiments, NK cells were stimulated by co-culture with an additional cell line. In certain embodiments,

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the additional cell line comprises artificial antigen presenting cells (aAPCs). In certain embodiments, stimulation occurs at day 1, 2, 3, 4, 5, 6, or 7 following electroporation. In certain embodiments, stimulation occurs at day 2 following electroporation.

In certain embodiments, NK cells express CD56. B Cells

In certain embodiments, the modified immune or immune precursor cells of the disclosure are B cells. B cells are a type of lymphocyte that express B cell receptors on the cell surface. B cell receptors bind to specific antigens.

Modified B cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

In certain embodiments, HSPCs are modified using the methods of the disclosure, and then primed for B cell differentiation in presence of human IL-3, Flt3L, TPO, SCF, and G-CSF for at least 3 days, at least 4 days, at least 5 days, at least 6 days or at least 7 days. In certain embodiments, HSPCs are modified using the methods of the disclosure, and then primed for B cell differentiation in presence of human IL-3, Flt3L, TPO, SCF, and G-CSF for 5 days.

In certain embodiments, following priming, modified HSPC cells are transferred to a layer of feeder cells and fed bi-weekly, along with transfer to a fresh layer of feeders once per week. In certain embodiments, the feeder cells are MS-5 feeder cells.

In certain embodiments, modified HSPC cells are cultured with MS-5 feeder cells for at least 7, 14, 21, 28, 30, 33, 35, 42 or 48 days. In certain embodiments, modified HSPC cells are cultured with MS-5 feeder cells for 33 days.

Methods of Cell Modification

In some embodiments of the methods of the disclosure, a composition comprises a scalable ratio of 250 \times 10 6 primary human T cells per milliliter of buffer or other media during a delivery or an introduction step.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced to a cell by electroporation or nucleofection. In some embodiments, a delivery or introduction step comprises electroporation or nucleofection.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced to a cell by a method other than electroporation or nucleofection.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced by one or more of topical delivery, adsorption, absorption, electroporation, spinfection, co-culture, transfection, mechanical delivery, sonic delivery, vibrational delivery, magnetofection or by nanoparticle-mediated delivery. In some embodiments, a delivery or introduction step comprises one or more of topical delivery, adsorption, absorption, electroporation, spinfection, co-culture, transfection, mechanical delivery, sonic delivery, vibrational delivery, magnetofection or by nanoparticle-mediated delivery.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced by liposomal transfection, calcium phosphate transfection, fugene transfection, and dendrimer-mediated transfection. In some embodiments, a delivery or introduction step comprises one or more of liposomal transfection, calcium phosphate transfection, fugene transfection, and dendrimer-mediated transfection.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced by mechanical transfection comprises cell squeezing, cell bombardment, or gene gun techniques. In some embodiments, a delivery or intro-

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duction step comprises one or more of mechanical transfection comprises cell squeezing, cell bombardment, or gene gun techniques.

In some embodiments of the methods of the disclosure, a composition is delivered or introduced by nanoparticle-mediated transfection comprises liposomal delivery, delivery by micelles, and delivery by polymerosomes. In some embodiments, a delivery or introduction step comprises one or more of liposomal delivery, delivery by micelles, and delivery by polymerosomes.

Non-Transposition Methods of Delivery

In some embodiments of the compositions and methods of the disclosure, a modified cell of the disclosure may be produced by introducing a sequence into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure. The introducing step may comprise delivery of a sequence and/or a gene editing composition via a non-transposition delivery system. The introduction step may be performed ex vivo, in vivo, in vitro or in situ.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprises one or more of topical delivery, adsorption, absorption, electroporation, spin-fection, co-culture, transfection, mechanical delivery, sonic delivery, vibrational delivery, magnetofection and nanoparticle-mediated delivery.

In some embodiments of the compositions and methods of the disclosure, introducing a nucleic acid sequence and/or a gene editing construct into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprises liposomal transfection, calcium phosphate transfection, fugene transfection, and dendrimer-mediated transfection.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure by mechanical transfection comprises cell squeezing, cell bombardment, or gene gun techniques.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure by nanoparticle-mediated transfection comprises one or more of a liposome, a micelle, a polymer and a polymerosome.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprises a non-viral vector. In some embodiments, the non-viral vector comprises the sequence and/or the gene editing composition. In some embodiments, the non-viral vector comprises plasmid DNA, linear double-stranded DNA (dsDNA), linear single-stranded DNA (ssDNA). DoggyBone™ DNA, nanoplasmids, minicircle DNA, single-stranded oligodeoxynucleotides (ssODN), DDNA oligonucleotides, single-stranded mRNA (ssRNA), and double-stranded mRNA (dsRNA).

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprises a viral vector. In some embodiments, the viral vector is a non-integrating and/or non-chromosomal vector.

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Exemplary non-integrating non-chromosomal vectors include, but are not limited to, adeno-associated virus (AAV), adenovirus, and herpes viruses. In some embodiments, the viral vector is an integrating chromosomal vector.

5 Integrating chromosomal vectors include, but are not limited to, adeno-associated vectors (AAV), Lentiviruses, and gamma-retroviruses. In some embodiments, the viral vector comprises the sequence and/or the gene editing composition.

In some embodiments of the compositions and methods of

10 the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprises a combination of vectors of the disclosure. Exemplary, non-limiting vector combinations include: viral and non-viral vectors, a plurality of non-viral vectors, or a plurality of viral vectors. Exemplary but non-limiting vectors combinations include: a combination of a DNA-derived and an RNA-derived vector, a combination of non-viral expression vector and a viral delivery vector, a combination of a non-viral expression vector and a nanoparticle delivery vector, a combination of two distinct non-viral expression vectors, a combination of a non-viral expression vector and a mechanical or chemical method of transfection.

In some embodiments of the compositions and methods of

25 the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure stably integrates a sequence, transiently integrates a sequence, produces site-specific integration of a sequence, or produces a biased integration of a sequence. In some embodiments, the sequence is a nucleic acid sequence. In some embodiments, the nucleic acid sequence comprises a transgene.

In some embodiments of the compositions and methods of

30 the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure stably integrates a sequence. In some embodiments, the sequence is a nucleic acid sequence. In some embodiments, the stable chromosomal integration can be a random integration, a site-specific integration, or a biased integration. In some embodiments, the site-specific integration can be non-assisted or assisted. In some embodiments, the assisted site-specific integration is co-delivered with a site-directed nuclease. In some embodiments, the site-directed nuclease comprises a transgene with 5' and 3' nucleotide sequence extensions that contain a percentage homology to upstream and downstream regions of the site of genomic integration.

In some embodiments, the transgene with homologous 35 nucleotide extensions enable genomic integration by homologous recombination, microhomology-mediated end joining, or nonhomologous end-joining. In some embodiments the site-specific integration occurs at a safe harbor site. Genomic safe harbor sites are able to accommodate the

40 45 50 55 integration of new genetic material in a manner that ensures that the newly inserted genetic elements function reliably (for example, are expressed at a therapeutically effective level of expression) and do not cause deleterious alterations to the host genome that cause a risk to the host organism.

Potential genomic safe harbors include, but are not limited to, intronic sequences of the human albumin gene, the adeno-associated virus site 1 (AAVS1), a naturally occurring site of integration of AAV virus on chromosome 19, the site of the chemokine (C-C motif) receptor 5 (CCR5) gene and the site of the human ortholog of the mouse Rosa26 locus.

In some embodiments, the site-specific transgene integration occurs at a site that disrupts expression of a target gene.

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In some embodiments, disruption of target gene expression occurs by site-specific integration at introns, exons, promoters, genetic elements, enhancers, suppressors, start codons, stop codons, and response elements. In some embodiments, exemplary target genes targeted by site-specific integration include but are not limited to TRAC, TRAB, PD1, any immunosuppressive gene, and genes involved in allo-rejection.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure site-specific transgene integration occurs at a site that results in enhanced expression of a target gene. In some embodiments, enhancement of target gene expression occurs by site-specific integration at introns, exons, promoters, genetic elements, enhancers, suppressors, start codons, stop codons, and response elements.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure enzymes may be used to create strand breaks in the host genome to facilitate delivery or integration of the transgene. In some embodiments, enzymes create single-strand breaks. In some embodiments, enzymes create double-strand breaks. In some embodiments, examples of break-inducing enzymes include but are not limited to: transposases, integrases, endonucleases, CRISPR-Cas9, transcription activator-like effector nucleases (TALEN), zinc finger nucleases (ZFN), Cas-CLOVER™, and CPF1. In some embodiments, break-inducing enzymes can be delivered to the cell encoded in DNA, encoded in mRNA, as a protein, as a nucleoprotein complex with a guide RNA (gRNA).

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure site-specific transgene integration is controlled by a vector-mediated integration site bias. In some embodiments vector-mediated integration site bias is controlled by the chosen lentiviral vector. In some embodiments vector-mediated integration site bias is controlled by the chosen gammaretroviral vector.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure site-specific transgene integration site is a non-stable chromosomal insertion. In some embodiments, the integrated transgene may become silenced, removed, excised, or further modified.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure genome modification comprises a non-stable integration of a transgene. In some embodiments, the non-stable integration can be a transient non-chromosomal integration, a semi-stable non chromosomal integration, a semi-persistent non-chromosomal insertion, or a non-stable chromosomal insertion. In some embodiments, the transient non-chromosomal insertion can be epi-chromosomal or cytoplasmic.

In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure

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the transient non-chromosomal insertion of a transgene does not integrate into a chromosome and the modified genetic material is not replicated during cell division.

5 In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure genome modification comprises a semi-stable or persistent non-chromosomal integration of a transgene. In some 10 embodiments, a DNA vector encodes a Scaffold/matrix attachment region (S-MAR) module that binds to nuclear matrix proteins for episomal retention of a non-viral vector allowing for autonomous replication in the nucleus of dividing cells.

15 In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure genome modification is a non-stable chromosomal integration of a transgene. In some embodiments, the integrated transgene may become silenced, removed, excised, or further modified.

20 In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure genome modification to the genome by transgene insertion can occur via host cell-directed double-strand breakage repair (homology-directed repair) by homologous recombination (HR), microhomology-mediated end joining (MMEJ), nonhomologous end joining (NHEJ), transposase enzyme-mediated modification, integrase enzyme-mediated modification, endonuclease enzyme-mediated modification, or recombinant enzyme-mediated modification. In some embodiments, the modification to the genome by transgene insertion can occur via CRISPR-Cas9, TALEN, ZFNs, Cas-CLOVER, and cpf1.

Nanoparticle Delivery

25 35 40 In some embodiments of the compositions and methods of the disclosure, introducing a sequence and/or a gene editing composition into an HSC, an HSC descendent cell, an immune cell or an immune precursor cell of the disclosure comprise a nanoparticle vector. Nanoparticle vectors may encapsulate a composition of the disclosure. Alternatively, or in addition, a surface of a nanoparticle vector may comprise a composition of the disclosure. In some embodiments, the surface is an interior surface. In some embodiments, the surface is an exterior surface. In some embodiments, the surface comprises a composition of the disclosure integrated therein or thereon.

45 50 55 Nonlimiting examples of nanoparticle vectors of the disclosure may comprise one or more of a hydrophilic block, a hydrophobic block, and a charged block. In some embodiments, the hydrophilic block may be poly(ethylene oxide) (PEO), and the charged block may be poly(L-histidine).

The disclosure provides nanoparticle vectors comprising di-block and tri-block co-polymers. Exemplary di-block co-polymers may comprise one or more of a hydrophilic block, a hydrophobic block, and a charged block. In some 60 65 embodiments, the hydrophilic block may be poly(ethylene oxide) (PEO), and the charged block may be poly(L-histidine). Exemplary tri-block co-polymers may comprise one or more of a hydrophilic block, a hydrophobic block, and a charged block. In some embodiments, the hydrophilic block may be poly(ethylene oxide) (PEO), and the charged block may be poly(L-histidine).

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An exemplary tri-block copolymer that may be used in various embodiments is a PEO-b-PLA-b-PHIS, with variable numbers of repeating units in each block varying by design.

Poly(histidine) (i.e., poly(L-histidine)), is a pH-sensitive polymer due to the imidazole ring providing an electron lone pair on the unsaturated nitrogen. That is, poly(histidine) has amphoteric properties through protonation-deprotonation. The various embodiments enable intracellular delivery of compositions of the disclosure, including gene editing compositions, by, for example, complexing with poly(histidine)-based micelles.

Diblock copolymers that may be used as intermediates for making triblock copolymers of the embodiment micelles may have hydrophilic biocompatible poly(ethylene oxide) (PEO), which is chemically synonymous with PEG, coupled to various hydrophobic aliphatic poly(anhydrides), poly(nucleic acids), poly(esters), poly(ortho esters), poly(peptides), poly(phosphazenes) and poly(saccharides), including but not limited by poly(lactide) (PLA), poly(glycolide) (PLGA), poly(lactic-co-glycolic acid) (PLGA), poly(ϵ -caprolactone) (PCL), and poly(trimethylene carbonate) (PTMC).

Polymeric micelles comprised of 100% PEGylated surfaces possess improved in vitro chemical stability, augmented in vivo bioavailability, and prolonged blood circulatory half-lives. For example, aliphatic polyesters, constituting the polymeric micelle's membrane portions, are degraded by hydrolysis of their ester linkages in physiological conditions such as in the human body. Because of their biodegradable nature, aliphatic polyesters have received a great deal of attention for use as implantable biomaterials in drug delivery devices, bioresorbable sutures, adhesion barriers, and as scaffolds for injury repair via tissue engineering.

Without wishing to be bound by a particular theory, it is believed that believed that in the micelles that are formed by the various embodiment triblock copolymers, the hydrophobic blocks aggregate to form a core, leaving the hydrophilic blocks and poly(histidine) blocks on the ends to form one or more surrounding layer.

Scaffold Proteins

Protein scaffolds of the disclosure may be derived from a fibronectin type III (FN3) repeat protein, encoding or complementary nucleic acids, vectors, host cells, compositions, combinations, formulations, devices, and methods of making and using them. In a preferred embodiment, the protein scaffold is comprised of a consensus sequence of multiple FN3 domains from human Tenascin-C (hereinafter "Tenascin"). In a further preferred embodiment, the protein scaffold of the present disclosure is a consensus sequence of 15 FN3 domains. The protein scaffolds of the disclosure can be designed to bind various molecules, for example, a cellular target protein. In a preferred embodiment, the protein scaffolds of the disclosure can be designed to bind an epitope of a wild type and/or variant form of a ligand or an antigen.

Protein scaffolds of the disclosure may include additional molecules or moieties, for example, the Fc region of an antibody, albumin binding domain, or other moiety influencing half-life. In further embodiments, the protein scaffolds of the disclosure may be bound to a nucleic acid molecule that may encode the protein scaffold.

The disclosure provides at least one method for expressing at least one protein scaffold based on a consensus sequence of multiple FN3 domains, in a host cell, comprising culturing a host cell as described herein under conditions

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wherein at least one protein scaffold is expressed in detectable and/or recoverable amounts.

The disclosure provides at least one composition comprising (a) a protein scaffold based on a consensus sequence of multiple FN3 domains and/or encoding nucleic acid as described herein; and (b) a suitable and/or pharmaceutically acceptable carrier or diluent.

The disclosure provides a method of generating libraries of a protein scaffold based on a fibronectin type III (FN3) repeat protein, preferably, a consensus sequence of multiple FN3 domains and, more preferably, a consensus sequence of multiple FN3 domains from human Tenascin. The library is formed by making successive generations of scaffolds by altering (by mutation) the amino acids or the number of amino acids in the molecules in particular positions in portions of the scaffold, e.g., loop regions. Libraries can be generated by altering the amino acid composition of a single loop or the simultaneous alteration of multiple loops or additional positions of the scaffold molecule. The loops that are altered can be lengthened or shortened accordingly. Such libraries can be generated to include all possible amino acids at each position, or a designed subset of amino acids. The library members can be used for screening by display, such as in vitro or CIS display (DNA, RNA, ribosome display, etc.), yeast, bacterial, and phage display.

Protein scaffolds of the disclosure provide enhanced biophysical properties, such as stability under reducing conditions and solubility at high concentrations; they may be expressed and folded in prokaryotic systems, such as *E. coli*, in eukaryotic systems, such as yeast, and in in vitro transcription/translation systems, such as the rabbit reticulocyte lysate system.

The disclosure provides a method of generating a scaffold molecule that binds to a particular target by panning the scaffold library of the invention with the target and detecting binders. In other related aspects, the disclosure comprises screening methods that may be used to generate or affinity mature protein scaffolds with the desired activity, e.g., capable of binding to target proteins with a certain affinity. Affinity maturation can be accomplished by iterative rounds of mutagenesis and selection using systems, such as phage display or in vitro display. Mutagenesis during this process may be the result of site directed mutagenesis to specific scaffold residues, random mutagenesis due to error-prone PCR, DNA shuffling, and/or a combination of these techniques.

The disclosure provides an isolated, recombinant and/or synthetic protein scaffold based on a consensus sequence of fibronectin type III (FN3) repeat protein, including, without limitation, mammalian-derived scaffold, as well as compositions and encoding nucleic acid molecules comprising at least one polynucleotide encoding protein scaffold based on the consensus FN3 sequence. The disclosure further includes, but is not limited to, methods of making and using such nucleic acids and protein scaffolds, including diagnostic and therapeutic compositions, methods and devices.

The protein scaffolds of the disclosure offer advantages over conventional therapeutics, such as ability to administer locally, orally, or cross the blood-brain barrier, ability to express in *E. Coli* allowing for increased expression of protein as a function of resources versus mammalian cell expression ability to be engineered into bispecific or tandem molecules that bind to multiple targets or multiple epitopes of the same target, ability to be conjugated to drugs, polymers, and probes, ability to be formulated to high concentrations, and the ability of such molecules to effectively penetrate diseased tissues and tumors.

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Moreover, the protein scaffolds possess many of the properties of antibodies in relation to their fold that mimics the variable region of an antibody. This orientation enables the FN3 loops to be exposed similar to antibody complementarity determining regions (CDRs). They should be able to bind to cellular targets and the loops can be altered, e.g., affinity matured, to improve certain binding or related properties.

Three of the six loops of the protein scaffold of the disclosure correspond topologically to the complementarity determining regions (CDRs 1-3), i.e., antigen-binding regions, of an antibody, while the remaining three loops are surface exposed in a manner similar to antibody CDRs. These loops span at or about residues 13-16, 22-28, 38-43, 51-54, 60-64, and 75-81 of the consensus sequence. Preferably, the loop regions at or about residues 22-28, 51-54, and 75-81 are altered for binding specificity and affinity. One or more of these loop regions are randomized with other loop regions and/or other strands maintaining their sequence as backbone portions to populate a library and potent binders can be selected from the library having high affinity for a particular protein target. One or more of the loop regions can interact with a target protein similar to an antibody CDR interaction with the protein.

Discovery of Antigen/Ligand Recognition Region Sequences

The disclosure provides a method of generating libraries of antigen/ligand recognition region (ARR/LRR) sequences for binding antigens and/or ligands of the disclosure. The library is formed by making successive generations of ARR/LRR sequences by altering (by mutation) the amino acids or the number of amino acids in the sequences at particular positions of the ARR/LRR. In some embodiments, the ARR/LRR comprises one or more of a protein scaffold, an antibody mimetic, a Centyrin, a single chain antibody (scFv), a single domain antibody, a VHH and a VH of the disclosure. In some embodiments, the library is formed by making successive generations of ARR/LRR sequences by altering (by mutation) the amino acids or the number of amino acids in the sequences at particular positions of an antibody, an ScFv, VHH or VH, e.g., one or more complementarity determining regions (CDR) and/or framework regions of a variable domain.

Libraries can be generated by altering the amino acid composition of a single CDR or the simultaneous alteration of multiple CDRs or additional positions of an antibody, an scFv, VHH or VH (e.g. a framework sequence of the variable region). The CDR and/or framework sequence of the variable domain that are altered can be lengthened or shortened accordingly.

Libraries can be generated by altering the amino acid composition of a loop of a scaffold protein or a Centyrin. The loop sequences that are altered can be lengthened or shortened accordingly.

Libraries can be generated by altering the amino acid composition of an antigen or ligand-binding or specificity-determining region of an antibody mimetic.

Such libraries can be generated to include all possible amino acids at each position, or a designed subset of amino acids. The library members can be used for screening by display, such as in vitro or CIS display (DNA, RNA, ribosome display, etc.), yeast, bacterial, and phage display.

ARRs/LRRs of the disclosure provide enhanced biophysical properties, such as stability under reducing conditions and solubility at high concentrations; they may be expressed and folded in prokaryotic systems, such as *E. coli*, in

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eukaryotic systems, such as yeast, and in in vitro transcription/translation systems, such as the rabbit reticulocyte lysate system.

The disclosure provides a method of generating an ARR/LRR or a portion thereof that binds to a particular target by panning a library of the invention with the target and detecting binders. In other related aspects, the disclosure comprises screening methods that may be used to generate or affinity mature ARRs/LRRs with the desired activity. e.g., capable of binding to target proteins with a certain affinity. Affinity maturation can be accomplished by iterative rounds of mutagenesis and selection using systems, such as phage display or in vitro display. Mutagenesis during this process may be the result of site directed mutagenesis to specific protein residues, random mutagenesis due to error-prone PCR, DNA shuffling, and/or a combination of these techniques.

The disclosure provides an isolated, recombinant and/or synthetic protein scaffold comprising at least one VHH. The disclosure further includes, but is not limited to, methods of making and using such nucleic acids and protein scaffolds, including diagnostic and therapeutic compositions, methods and devices.

The compositions of the disclosure offer advantages over conventional therapeutics, such as ability to administer locally, orally, or cross the blood-brain barrier, ability to express in *E. Coli* allowing for increased expression of protein as a function of resources versus mammalian cell expression ability to be engineered into bispecific or tandem molecules that bind to multiple targets or multiple epitopes of the same target, ability to be conjugated to drugs, polymers, and probes, ability to be formulated to high concentrations, and the ability of such molecules to effectively penetrate diseased tissues and tumors.

Production and Generation of Proteins

Proteins of the disclosure can be optionally produced by a cell line, a mixed cell line, an immortalized cell or clonal population of immortalized cells, as well known in the art. See, e.g., Ausubel, et al., ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc., NY, N.Y. (1987-2001); Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor, N.Y. (1989); Harlow and Lane, *Antibodies, a Laboratory Manual*, Cold Spring Harbor, N.Y. (1989); Colligan, et al., eds., *Current Protocols in Immunology*, John Wiley & Sons, Inc., NY (1994-2001); Colligan et al., *Current Protocols in Protein Science*, John Wiley & Sons, NY, N.Y., (1997-2001).

Amino acids encoding a protein can be altered, added and/or deleted to reduce immunogenicity or reduce, enhance or modify binding, affinity, on-rate, off-rate, avidity, specificity, half-life, stability, solubility or any other suitable characteristic, as known in the art.

Proteins can be engineered with retention of high affinity for an antigen or a ligand as well as other favorable biological properties. To achieve this goal, the proteins can be optionally prepared by a process of analysis of the parental sequences and various conceptual engineered products using three-dimensional models of the parental and engineered sequences. Three-dimensional models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate sequences and can measure possible immunogenicity (e.g., Immunofilter program of Xencor, Inc. of Monrovia, Calif.). Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate sequence, i.e., the analysis of residues that

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influence the ability of the protein to bind its antigen. In this way, residues can be selected and combined from the parent and reference sequences so that the desired characteristic, such as affinity for the target antigen(s)/ligand(s), is achieved. Alternatively, or in addition to, the above procedures, other suitable methods of engineering can be used.

Screening of ARR/LRRs

Screening protein ARR/LRRs or any portion thereof for specific binding to similar proteins or fragments can be conveniently achieved using nucleotide (DNA or RNA display) or peptide display libraries, for example, in vitro display. This method involves the screening of large collections of peptides for individual members having the desired function or structure. The displayed nucleotide or peptide sequences can be from 3 to 5000 or more nucleotides or amino acids in length, frequently from 5-100 amino acids long, and often from about 8 to 25 amino acids long. In addition to direct chemical synthetic methods for generating peptide libraries, several recombinant DNA methods have been described. One type involves the display of a peptide sequence on the surface of a bacteriophage or cell. Each bacteriophage or cell contains the nucleotide sequence encoding the particular displayed peptide sequence. Such methods are described in PCT Patent Publication Nos. 91/17271, 91/18980, 91/19818, and 93/08278.

Other systems for generating libraries of peptides have aspects of both in vitro chemical synthesis and recombinant methods. See, PCT Patent Publication Nos. 92/05258, 92/14843, and 96/19256. See also, U.S. Pat. Nos. 5,658,754; and 5,643,768. Peptide display libraries, vector, and screening kits are commercially available from such suppliers as Invitrogen (Carlsbad, Calif.), and Cambridge Antibody Technologies (Cambridgeshire, UK). See, e.g., U.S. Pat. Nos. 4,704,692, 4,939,666, 4,946,778, 5,260,203, 5,455, 030, 5,518,889, 5,534,621, 5,656,730, 5,763,733, 5,767,260, 5,856,456, assigned to Enzon; U.S. Pat. Nos. 5,223,409, 5,403,484, 5,571,698, 5,837,500, assigned to Dyax, U.S. Pat. Nos. 5,427,908, 5,580,717, assigned to Affymax; U.S. Pat. No. 5,885,793, assigned to Cambridge Antibody Technologies; U.S. Pat. No. 5,750,373, assigned to Genentech, U.S. Pat. Nos. 5,618,920, 5,595,898, 5,576,195, 5,698,435, 5,693,493, 5,698,417, assigned to Xoma, Colligan, supra; Ausubel, *supra*; or Sambrook, *supra*.

The ARR/LRRs of the disclosure comprising one or more of a protein scaffold, an antibody, an ScFv, a Centyrin, a single domain antibody, a VHH or a VH of the disclosure can bind human or other mammalian proteins with a wide range of affinities (KD). In a preferred embodiment, at least one ARR/LRR can optionally bind to a target protein with high affinity, for example, with a KD equal to or less than about 10^{-7} M, such as but not limited to, 0.1-9.9 (or any range or value therein) $\times 10^{-8}$, 10^{-9} , 10^{-10} , 10^{-11} , 10^{-12} , 10^{-13} , 10^{-14} , 10^{-15} or any range or value therein, as determined by surface plasmon resonance or the Kineka method, as practiced by those of skill in the art. In a preferred embodiment, at least one protein scaffold, antibody, ScFv, Centyrin, single domain antibody, VHH or VH of the

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disclosure can optionally bind to a target protein with high affinity, for example, with a KD equal to or less than about 10^{-7} M, such as but not limited to, 0.1-9.9 (or any range or value therein) $\times 10^{-8}$, 10^{-9} , 10^{-10} , 10^{-11} , 10^{-12} , 10^{-13} , 10^{-14} , 10^{-15} or any range or value therein, as determined by surface plasmon resonance or the Kineka method, as practiced by those of skill in the art.

The affinity or avidity of a protein scaffold, an antibody, an ScFv, a Centyrin, a single domain antibody, a VHH or a VH of the disclosure for an antigen/ligand can be determined experimentally using any suitable method. (See, for example, Berzofsky, et al., "Antibody-Antigen Interactions," In Fundamental Immunology. Paul, W. E., Ed., Raven Press: New York, N.Y. (1984); Kuby, Janis Immunology, W.H. Freeman and Company: New York, N.Y. (1992); and methods described herein). The measured affinity of a particular protein-antigen/ligand interaction can vary if measured under different conditions (e.g., salt concentration, pH). Thus, measurements of affinity and other antigen-binding parameters (e.g., KD, K_{on} , K_{off}) are preferably made with standardized solutions of protein scaffold (e.g. VHH) and antigen, and a standardized buffer, such as the buffer described herein.

Competitive assays can be performed with the protein scaffold, antibody, ScFv, Centyrin, single domain antibody, VHH or VH of the disclosure in order to determine what proteins, antibodies, and other antagonists compete for binding to a target protein and/or share the epitope region. These assays as readily known to those of ordinary skill in the art evaluate competition between antagonists or ligands for a limited number of binding sites on a protein. The protein and/or antibody is immobilized or insolubilized before or after the competition and the sample bound to the target protein is separated from the unbound sample, for example, by decanting (where the protein/antibody was preinsolubilized) or by centrifuging (where the protein/antibody was precipitated after the competitive reaction). Also, the competitive binding may be determined by whether function is altered by the binding or lack of binding of the protein scaffold, antibody, ScFv, Centyrin, single domain antibody, VHH or VH to the target protein, e.g., whether protein scaffold, antibody, ScFv, Centyrin, single domain antibody, VHH or VH inhibits or potentiates the enzymatic activity of, for example, a label. ELISA and other functional assays may be used, as well known in the art.

Therapeutic Proteins

In certain embodiments of the disclosure, T cells are modified to express therapeutic proteins, including secreted human proteins. These secreted proteins may be used as a monotherapy or in combination with another therapy in the treatment or prevention of any disease or disorder. These secreted proteins may be used as a monotherapy or in combination with another therapy for enzyme replacement and/or administration of biologic therapeutics. A database of human secreted proteins can be found at proteinatlas.org/search/protein_class:Predicted%20secreted%20proteins, the contents of which are incorporated herein by reference. Exemplary human therapeutic proteins can be found, but are not limited to the human proteins in Table 1.

TABLE 1

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.		
Gene Name	Gene Description	Protein SEQ ID NO
A1BG	Alpha-1-B glycoprotein	SEQ ID NOS: 1-2
A2M	Alpha-2-macroglobulin	SEQ ID NOS: 3-6

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
A2ML1	Alpha-2-macroglobulin-like 1	SEQ ID NOS: 7-12
A4GNT	Alpha-1,4-N-acetylglucosaminyltransferase	SEQ ID NO: 13
AADACL2	Arylacetamide deacetylase-like 2	SEQ ID NOS: 14-15
AANAT	Aralkylamine N-acetyltransferase	SEQ ID NOS: 16-19
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	SEQ ID NOS: 20-26
ABHD1	Abhydrolase domain containing 1	SEQ ID NOS: 27-31
ABHD10	Abhydrolase domain containing 10	SEQ ID NOS: 32-35
ABHD14A	Abhydrolase domain containing 14A	SEQ ID NOS: 36-40
ABHD15	Abhydrolase domain containing 15	SEQ ID NO: 41
ABI3BP	ABI family, member 3 (NESH) binding protein	SEQ ID NOS: 42-63
FAM175A	Family with sequence similarity 175, member A	SEQ ID NOS: 64-71
LA16c-380H5.3		SEQ ID NO: 72
AC008641.1		SEQ ID NO: 73
CTB-60B18.6		SEQ ID NOS: 74-75
AC009133.22		SEQ ID NO: 76
AC009491.2		SEQ ID NO: 77
RP11-977G19.10		SEQ ID NOS: 78-80
CTD-2370N5.3		SEQ ID NOS: 81-84
RP11-196G11.1		SEQ ID NOS: 85-87
AC136352.5		SEQ ID NO: 88
RP11-812E19.9		SEQ ID NO: 89
AC145212.4	MaFF-interacting protein	SEQ ID NO: 90
AC233755.1		SEQ ID NO: 91
AC011513.3		SEQ ID NOS: 92-93
ACACB	Acetyl-CoA carboxylase beta	SEQ ID NOS: 94-100
ACAN	Aggrecan	SEQ ID NOS: 101-108
ACE	Angiotensin I converting enzyme	SEQ ID NOS: 109-121
ACHE	Acetylcholinesterase (Yt blood group)	SEQ ID NOS: 122-134
ACP2	Acid phosphatase 2, lysosomal	SEQ ID NOS: 135-142
ACP5	Acid phosphatase 5, tartrate resistant	SEQ ID NOS: 143-151
ACP6	Acid phosphatase 6, lysophosphatidic acid	SEQ ID NOS: 152-158
PAPL	Iron/zinc purple acid phosphatase-like protein	SEQ ID NOS: 159-162
ACPP	Acid phosphatase, prostate	SEQ ID NOS: 163-167
ACR	Acrosin	SEQ ID NOS: 168-169
ACRBP	Acrosin binding protein	SEQ ID NOS: 170-174
ACRV1	Acrosomal vesicle protein 1	SEQ ID NOS: 175-178
ACSF2	Acyl-CoA synthetase family member 2	SEQ ID NOS: 179-187
ACTL10	Actin-like 10	SEQ ID NO: 188
ACVR1	Activin A receptor, type I	SEQ ID NOS: 189-197
ACVR1C	Activin A receptor, type IC	SEQ ID NOS: 198-201
ACVRL1	Activin A receptor type II-like 1	SEQ ID NOS: 202-207
ACYP1	Acylphosphatase 1, erythrocyte (common) type	SEQ ID NOS: 208-213
ACYP2	Acylphosphatase 2, muscle type	SEQ ID NOS: 214-221
CECR1	Cat eye syndrome chromosome region, candidate 1	SEQ ID NOS: 222-229
ADAM10	ADAM metallopeptidase domain 10	SEQ ID NOS: 230-237
ADAM12	ADAM metallopeptidase domain 12	SEQ ID NOS: 238-240
ADAM15	ADAM metallopeptidase domain 15	SEQ ID NOS: 241-252
ADAM17	ADAM metallopeptidase domain 17	SEQ ID NOS: 253-255
ADAM18	ADAM metallopeptidase domain 18	SEQ ID NOS: 256-260
ADAM22	ADAM metallopeptidase domain 22	SEQ ID NOS: 261-269
ADAM28	ADAM metallopeptidase domain 28	SEQ ID NOS: 270-275
ADAM29	ADAM metallopeptidase domain 29	SEQ ID NOS: 276-284
ADAM32	ADAM metallopeptidase domain 32	SEQ ID NOS: 285-291
ADAM33	ADAM metallopeptidase domain 33	SEQ ID NOS: 292-296
ADAM7	ADAM metallopeptidase domain 7	SEQ ID NOS: 297-300
ADAM8	ADAM metallopeptidase domain 8	SEQ ID NOS: 301-305
ADAM9	ADAM metallopeptidase domain 9	SEQ ID NOS: 306-311
ADAMDEC1	ADAM-like, decysin 1	SEQ ID NOS: 312-314
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	SEQ ID NOS: 315-318
ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	SEQ ID NOS: 319-324
ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	SEQ ID NOS: 325-327

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif, 13	SEQ ID NOS: 328-335
ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	SEQ ID NOS: 336-337
ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif, 15	SEQ ID NO: 338
ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif, 16	SEQ ID NOS: 339-340
ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17	SEQ ID NOS: 341-344
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	SEQ ID NOS: 345-348
ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif, 19	SEQ ID NOS: 349-352
ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	SEQ ID NOS: 353-355
ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif, 20	SEQ ID NOS: 356-359
ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	SEQ ID NOS: 360-361
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	SEQ ID NO: 362
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif, 6	SEQ ID NOS: 363-364
ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	SEQ ID NO: 365
ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	SEQ ID NO: 366
ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	SEQ ID NOS: 367-371
ADAMTSL1	ADAMTS-like 1	SEQ ID NOS: 372-382
ADAMTSL2	ADAMTS-like 2	SEQ ID NOS: 383-385
ADAMTSL3	ADAMTS-like 3	SEQ ID NOS: 386-387
ADAMTSL4	ADAMTS-like 4	SEQ ID NOS: 388-391
ADAMTSL5	ADAMTS-like 5	SEQ ID NOS: 392-397
ADCCK1	AarF domain containing kinase 1	SEQ ID NOS: 398-402
ADCYAP1	Adenylate cyclase activating polypeptide 1 (pituitary)	SEQ ID NOS: 403-404
ADCYAP1R1	Adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	SEQ ID NOS: 405-411
ADGRA3	Adhesion G protein-coupled receptor A3	SEQ ID NOS: 412-416
ADGRB2	Adhesion G protein-coupled receptor B2	SEQ ID NOS: 417-425
ADGRD1	Adhesion G protein-coupled receptor D1	SEQ ID NOS: 426-431
ADGRE3	Adhesion G protein-coupled receptor E3	SEQ ID NOS: 432-436
ADGRE5	Adhesion G protein-coupled receptor E5	SEQ ID NOS: 437-442
ADGRF1	Adhesion G protein-coupled receptor F1	SEQ ID NOS: 443-447
ADGRG1	Adhesion G protein-coupled receptor G1	SEQ ID NOS: 448-512
ADGRG5	Adhesion G protein-coupled receptor G5	SEQ ID NOS: 513-515
ADGRG6	Adhesion G protein-coupled receptor G6	SEQ ID NOS: 516-523
ADGRV1	Adhesion G protein-coupled receptor V1	SEQ ID NOS: 524-540
ADI1	Acireductone dioxygenase 1	SEQ ID NOS: 541-543
ADIG	Adipogenin	SEQ ID NOS: 544-547
ADIPOQ	Adiponectin, C1Q and collagen domain containing	SEQ ID NOS: 548-549
ADM	Adrenomedullin	SEQ ID NOS: 550-557
ADM2	Adrenomedullin 2	SEQ ID NOS: 558-559
ADM5	Adrenomedullin 5 (putative)	SEQ ID NO: 560
ADPGK	ADP-dependent glucokinase	SEQ ID NOS: 561-570
ADPRHL2	ADP-ribosylhydrolase like 2	SEQ ID NO: 571
AEBP1	AE binding protein 1	SEQ ID NOS: 572-579
LACE1	Lactation elevated 1	SEQ ID NOS: 580-583
AFM	Afamin	SEQ ID NO: 584
AFP	Alpha-fetoprotein	SEQ ID NOS: 585-586
AGA	Aspartylglucosaminidase	SEQ ID NOS: 587-589
AGER	Advanced glycosylation end product-specific receptor	SEQ ID NOS: 590-600
AGK	Acylglycerol kinase	SEQ ID NOS: 601-606
AGPS	Alkylglycerone phosphate synthase	SEQ ID NOS: 607-610
AGR2	Anterior gradient 2, protein disulphide isomerase family member	SEQ ID NOS: 611-614
AGR3	Anterior gradient 3, protein disulphide isomerase family member	SEQ ID NOS: 615-617

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
AGRН	Agrin	SEQ ID NOS: 618-621
AGRР	Agouti related neuropeptide	SEQ ID NO: 622
AGT	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	SEQ ID NO: 623
AGTPBP1	ATP/GTP binding protein 1	SEQ ID NOS: 624-627
AGTRAP	Angiotensin II receptor-associated protein	SEQ ID NOS: 628-635
AHCYL2	Adenosylhomocysteinase-like 2	SEQ ID NOS: 636-642
AHSG	Alpha-2-HS-glycoprotein	SEQ ID NOS: 643-644
AIG1	Androgen-induced 1	SEQ ID NOS: 645-653
AK4	Adenylate kinase 4	SEQ ID NOS: 654-657
AKAP10	A kinase (PRKA) anchor protein 10	SEQ ID NOS: 658-666
AKR1C1	Aldo-keto reductase family 1, member C1	SEQ ID NOS: 667-669
RP4-576H24.4		SEQ ID NOS: 670-672
SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	SEQ ID NO: 673
RP11-14J7.7		SEQ ID NOS: 674-675
RP11-903H12.5		SEQ ID NO: 676
AL356289.1		SEQ ID NO: 677
AL589743.1		SEQ ID NO: 678
XXbac-BPG116M5.17		SEQ ID NOS: 679-680
XXbac-BPG181M17.5		SEQ ID NO: 681
XXbac-BPG32J3.20		SEQ ID NO: 682
RP11-350O14.18		SEQ ID NO: 683
ALAS2	5'-aminolevulinate synthase 2	SEQ ID NOS: 684-691
ALB	Albumin	SEQ ID NOS: 692-701
ALDH9A1	Aldehyde dehydrogenase 9 family, member A1	SEQ ID NO: 702
ALDOA	Aldolase A, fructose-bisphosphate	SEQ ID NOS: 703-717
ALG1	ALG1, chitobiosyldiphospholichol beta-mannosyltransferase	SEQ ID NOS: 718-723
ALG5	ALG5, dolichyl-phosphate beta-glucosyltransferase	SEQ ID NOS: 724-725
ALG9	ALG9, alpha-1,2-mannosyltransferase	SEQ ID NOS: 726-736
FAM150A	Family with sequence similarity 150, member A	SEQ ID NOS: 737-738
FAM150B	Family with sequence similarity 150, member B	SEQ ID NOS: 739-745
ALKBH1	AlkB homolog 1, histone H2A dioxygenase	SEQ ID NOS: 746-748
ALKBH5	AlkB homolog 5, RNA demethylase	SEQ ID NOS: 749-750
ALP1	Alkaline phosphatase, intestinal	SEQ ID NOS: 751-752
ALPL	Alkaline phosphatase, liver/bone/kidney	SEQ ID NOS: 753-757
ALPP	Alkaline phosphatase, placental	SEQ ID NO: 758
ALPPL2	Alkaline phosphatase, placental-like 2	SEQ ID NO: 759
AMBN	Ameloblastin (enamel matrix protein)	SEQ ID NOS: 760-762
AMBP	Alpha-1-microglobulin/bikunin precursor	SEQ ID NOS: 763-765
AMELX	Amelogenin, X-linked	SEQ ID NOS: 766-768
AMELY	Amelogenin, Y-linked	SEQ ID NOS: 769-770
AMH	Anti-Müllerian hormone	SEQ ID NO: 771
AMPD1	Adenosine monophosphate deaminase 1	SEQ ID NOS: 772-774
AMTN	Amelotin	SEQ ID NOS: 775-776
AMY1A	Amylase, alpha 1A (salivary)	SEQ ID NOS: 777-779
AMY1B	Amylase, alpha 1B (salivary)	SEQ ID NOS: 780-783
AMY1C	Amylase, alpha 1C (salivary)	SEQ ID NO: 784
AMY2A	Amylase, alpha 2A (pancreatic)	SEQ ID NOS: 785-787
AMY2B	Amylase, alpha 2B (pancreatic)	SEQ ID NOS: 788-792
ANG	Angiogenin, ribonuclease, RNase A family, 5	SEQ ID NOS: 793-794
ANGEL1	Angel homolog 1 (<i>Drosophila</i>)	SEQ ID NOS: 795-798
ANGPT1	Angiopoietin 1	SEQ ID NOS: 799-803
ANGPT2	Angiopoietin 2	SEQ ID NOS: 804-807
ANGPT4	Angiopoietin 4	SEQ ID NO: 808
ANGPTL1	Angiopoietin-like 1	SEQ ID NOS: 809-811
ANGPTL2	Angiopoietin-like 2	SEQ ID NOS: 812-813
ANGPTL3	Angiopoietin-like 3	SEQ ID NO: 814
ANGPTL4	Angiopoietin-like 4	SEQ ID NOS: 815-822
ANGPTL5	Angiopoietin-like 5	SEQ ID NOS: 823-824
ANGPTL6	Angiopoietin-like 6	SEQ ID NOS: 825-827
ANGPTL7	Angiopoietin-like 7	SEQ ID NO: 828
C19orf80	Chromosome 19 open reading frame 80	SEQ ID NOS: 829-832
ANK1	Ankyrin 1, erythrocytic	SEQ ID NOS: 833-843
ANKDD1A	Ankyrin repeat and death domain containing 1A	SEQ ID NOS: 844-850

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ANKRD54	Ankyrin repeat domain 54	SEQ ID NOS: 851-859
ANKRD60	Ankyrin repeat domain 60	SEQ ID NO: 860
ANO7	Anoctamin 7	SEQ ID NOS: 861-864
ANOS1	Anosmin 1	SEQ ID NO: 865
ANTXR1	Anthrax toxin receptor 1	SEQ ID NOS: 866-869
AOAH	Acyloxyacyl hydrolase (neutrophil)	SEQ ID NOS: 870-874
AOC1	Amine oxidase, copper containing 1	SEQ ID NOS: 875-880
AOC2	Amine oxidase, copper containing 2 (retina-specific)	SEQ ID NOS: 881-882
AOC3	Amine oxidase, copper containing 3	SEQ ID NOS: 883-889
AP000721.4		SEQ ID NO: 890
APBB1	Amyloid beta (A4) precursor protein-binding, family B, member I (Fe65)	SEQ ID NOS: 891-907
APCDD1	Adenomatous polyposis coli down-regulated 1	SEQ ID NOS: 908-913
APCS	Amyloid P component, serum	SEQ ID NO: 914
APELA	Apelin receptor early endogenous ligand	SEQ ID NOS: 915-917
APLN	Apelin	SEQ ID NO: 918
APLP2	Amyloid beta (A4) precursor-like protein 2	SEQ ID NOS: 919-928
APOA1	Apolipoprotein A-I	SEQ ID NOS: 929-933
APOA2	Apolipoprotein A-II	SEQ ID NOS: 934-942
APOA4	Apolipoprotein A-IV	SEQ ID NO: 943
APOA5	Apolipoprotein A-V	SEQ ID NOS: 944-946
APOB	Apolipoprotein B	SEQ ID NOS: 947-948
APOC1	Apolipoprotein C-I	SEQ ID NOS: 949-957
APOC2	Apolipoprotein C-II	SEQ ID NOS: 958-962
APOC3	Apolipoprotein C-III	SEQ ID NOS: 963-966
APOC4	Apolipoprotein C-IV	SEQ ID NOS: 967-968
APOC4-APOC2	APOC4-APOC2 readthrough (NMD candidate)	SEQ ID NOS: 969-970
APOC2		
APOD	Apolipoprotein D	SEQ ID NOS: 971-974
APOE	Apolipoprotein E	SEQ ID NOS: 975-978
APOF	Apolipoprotein F	SEQ ID NO: 979
APOH	Apolipoprotein H (beta-2-glycoprotein I)	SEQ ID NOS: 980-983
APOL1	Apolipoprotein L, 1	SEQ ID NOS: 984-994
APOL3	Apolipoprotein L, 3	SEQ ID NOS: 995-1009
APOM	Apolipoprotein M	SEQ ID NOS: 1010-1012
APOOL	Apolipoprotein O-like	SEQ ID NOS: 1013-1015
ARCN1	Archain 1	SEQ ID NOS: 1016-1020
ARFIP2	ADP-ribosylation factor interacting protein 2	SEQ ID NOS: 1021-1027
ARHGAP36	Rho GTPase activating protein 36	SEQ ID NOS: 1028-1033
HMHA1	Histocompatibility (minor) HA-1	SEQ ID NOS: 1034-1042
ARHGAP6	Rho GTPase activating protein 6	SEQ ID NOS: 1043-1048
ARIGEF4	Rho guanine nucleotide exchange factor (GEF) 4	SEQ ID NOS: 1049-1059
ARL16	ADP-ribosylation factor-like 16	SEQ ID NOS: 1060-1068
ARMC5	Armadillo repeat containing 5	SEQ ID NOS: 1069-1075
ARNTL	Aryl hydrocarbon receptor nuclear translocator-like	SEQ ID NOS: 1076-1090
ARSA	Arylsulfatase A	SEQ ID NOS: 1091-1096
ARSB	Arylsulfatase B	SEQ ID NOS: 1097-1100
ARSE	Arylsulfatase E (chondrodysplasia punctata 1)	SEQ ID NOS: 1101-1104
ARSG	Arylsulfatase G	SEQ ID NOS: 1105-1108
ARSI	Arylsulfatase family, member I	SEQ ID NOS: 1109-1111
ARSK	Arylsulfatase family, member K	SEQ ID NOS: 1112-1116
ARTS	ADP-ribosyltransferase 3	SEQ ID NOS: 1117-1124
ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	SEQ ID NOS: 1125-1128
ART5	ADP-ribosyltransferase 5	SEQ ID NOS: 1129-1133
ARTN	Artemin	SEQ ID NOS: 1134-1144
ASAHI	N-acylsphingosine amidohydrolase (acid ceramidase) 1	SEQ ID NOS: 1145-1195
ASAHI2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	SEQ ID NOS: 1196-1201
ASCL1	Achaete-scute family bHLH transcription factor 1	SEQ ID NO: 1202
ASIP	Agouti signaling protein	SEQ ID NOS: 1203-1204
ASPN	Asporin	SEQ ID NOS: 1205-1206
ASTL	Astacin-like metallo-endopeptidase (M12 family)	SEQ ID NO: 1207
ATAD5	ATPase family, AAA domain containing 5	SEQ ID NOS: 1208-1209
ATAT1	Alpha tubulin acetyltransferase 1	SEQ ID NOS: 1210-1215
ATG2A	Autophagy related 2A	SEQ ID NOS: 1216-1218
ATG5	Autophagy related 5	SEQ ID NOS: 1219-1227
ATMIN	ATM interactor	SEQ ID NOS: 1228-1231
ATP13A1	ATPase type 13A1	SEQ ID NOS: 1232-1234
ATP5F1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit B1	SEQ ID NOS: 1235-1236
ATP6AP1	ATPase, H ⁺ transporting, lysosomal accessory protein 1	SEQ ID NOS: 1237-1244

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ATP6AP2	ATPase, H ⁺ transporting, lysosomal accessory protein 2	SEQ ID NOS: 1245-1267
ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	SEQ ID NOS: 1268-1278
AUH	AU RNA binding protein/enoyl-CoA hydratase	SEQ ID NOS: 1279-1280
AVP	Arginine vasopressin	SEQ ID NO: 1281
AXIN2	Axin 2	SEQ ID NOS: 1282-1289
AZGP1	Alpha-2-glycoprotein 1, zinc-binding	SEQ ID NOS: 1290-1292
AZU1	Azurocidin 1	SEQ ID NOS: 1293-1294
B2M	Beta-2-microglobulin	SEQ ID NOS: 1295-1301
B3GALNT1	Beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	SEQ ID NOS: 1302-1314
B3GALNT2	Beta-1,3-N-acetylgalactosaminyltransferase 2	SEQ ID NOS: 1315-1317
B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	SEQ ID NO: 1318
B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	SEQ ID NO: 1319
B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	SEQ ID NOS: 1320-1324
B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	SEQ ID NO: 1325
B3GAT3	Beta-1,3-glucuronidyltransferase 3	SEQ ID NOS: 1326-1330
B3GLCT	Beta 3-glucosyltransferase	SEQ ID NO: 1331
B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	SEQ ID NOS: 1332-1335
B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	SEQ ID NOS: 1336-1339
B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	SEQ ID NOS: 1340-1341
B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	SEQ ID NO: 1342
B3GNT8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	SEQ ID NO: 1343
B3GNT9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	SEQ ID NO: 1344
B4GALNT1	Beta-1,4-N-acetyl-galactosaminyl transferase 1	SEQ ID NOS: 1345-1356
B4GALNT3	Beta-1,4-N-acetyl-galactosaminyl transferase 3	SEQ ID NOS: 1357-1358
B4GALNT4	Beta-1,4-N-acetyl-galactosaminyl transferase 4	SEQ ID NOS: 1359-1361
B4GALT4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	SEQ ID NOS: 1362-1375
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	SEQ ID NO: 1376
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	SEQ ID NOS: 1377-1380
B4GAT1	Beta-1,4-glucuronidyltransferase 1	SEQ ID NO: 1381
B9D1	B9 protein domain 1	SEQ ID NOS: 1382-1398
BACE2	Beta-site APP-cleaving enzyme 2	SEQ ID NOS: 1399-1401
BAGE5	B melanoma antigen family, member 5	SEQ ID NO: 1402
BCAM	Basal cell adhesion molecule (Lutheran blood group)	SEQ ID NOS: 1403-1406
BCAN	Brevican	SEQ ID NOS: 1407-1413
BCAP29	B-cell receptor-associated protein 29	SEQ ID NOS: 1414-1426
BCAR1	Breast cancer anti-estrogen resistance 1	SEQ ID NOS: 1427-1444
BCHE	Butyrylcholinesterase	SEQ ID NOS: 1445-1449
BCKDHB	Branched chain keto acid dehydrogenase E1, beta polypeptide	SEQ ID NOS: 1450-1452
BDNF	Brain-derived neurotrophic factor	SEQ ID NOS: 1453-1470
BGLAP	Bone gamma-carboxyglutamate (gla) protein	SEQ ID NO: 1471
BGN	Biglycan	SEQ ID NOS: 1472-1473
BLVRB	Biliverdin reductase B	SEQ ID NOS: 1474-1478
BMP1	Bone morphogenetic protein 1	SEQ ID NOS: 1479-1490
BMP10	Bone morphogenetic protein 10	SEQ ID NO: 1491
BMP15	Bone morphogenetic protein 15	SEQ ID NO: 1492
BMP2	Bone morphogenetic protein 2	SEQ ID NO: 1493
BMP3	Bone morphogenetic protein 3	SEQ ID NO: 1494
BMP4	Bone morphogenetic protein 4	SEQ ID NOS: 1495-1502
BMP6	Bone morphogenetic protein 6	SEQ ID NO: 1503
BMP7	Bone morphogenetic protein 7	SEQ ID NOS: 1504-1507
BMP8A	Bone morphogenetic protein 8a	SEQ ID NO: 1508
BMP8B	Bone morphogenetic protein 8b	SEQ ID NO: 1509
BMPER	BMP binding endothelial regulator	SEQ ID NOS: 1510-1513
BNC1	Basonuclin 1	SEQ ID NOS: 1514-1515
BOC	BOC cell adhesion associated, oncogene regulated	SEQ ID NOS: 1516-1526
BOD1	Biorientation of chromosomes in cell division 1	SEQ ID NOS: 1527-1531

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
BOLA1	BolA family member 1	SEQ ID NOS: 1532-1534
BPI	Bactericidal/permeability-increasing protein	SEQ ID NOS: 1535-1538
BPIFA1	BPI fold containing family A, member 1	SEQ ID NOS: 1539-1542
BPIFA2	BPI fold containing family A, member 2	SEQ ID NOS: 1543-1544
BPIFA3	BPI fold containing family A, member 3	SEQ ID NOS: 1545-1546
BPIFB1	BPI fold containing family B, member 1	SEQ ID NOS: 1547-1548
BPIFB2	BPI fold containing family B, member 2	SEQ ID NO: 1549
BPIFB3	BPI fold containing family B, member 3	SEQ ID NO: 1550
BPIFB4	BPI fold containing family B, member 4	SEQ ID NOS: 1551-1552
BPIFB6	BPI fold containing family B, member 6	SEQ ID NOS: 1553-1554
BPIFC	BPI fold containing family C	SEQ ID NOS: 1555-1558
BRF1	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	SEQ ID NOS: 1559-1574
BRINP1	Bone morphogenetic protein/retinoic acid inducible neural-specific 1	SEQ ID NOS: 1575-1576
BRINP2	Bone morphogenetic protein/retinoic acid inducible neural-specific 2	SEQ ID NO: 1577
BRINP3	Bone morphogenetic protein/retinoic acid inducible neural-specific 3	SEQ ID NOS: 1578-1580
BSG	Basigin (Ok blood group)	SEQ ID NOS: 1581-1591
BSPH1	Binder of sperm protein homolog 1	SEQ ID NO: 1592
BST1	Bone marrow stromal cell antigen 1	SEQ ID NOS: 1593-1597
BTBD17	BTB (POZ) domain containing 17	SEQ ID NO: 1598
BTD	Biotinidase	SEQ ID NOS: 1599-1608
BTN2A2	Butyrophilin, subfamily 2, member A2	SEQ ID NOS: 1609-1622
BTN3A1	Butyrophilin, subfamily 3, member A1	SEQ ID NOS: 1623-1629
BTN3A2	Butyrophilin, subfamily 3, member A2	SEQ ID NOS: 1630-1640
BTN3A3	Butyrophilin, subfamily 3, member A3	SEQ ID NOS: 1641-1649
RP4-	Complement factor H-related protein 2	SEQ ID NO: 1650
608O15.3		
C10orf99	Chromosome 10 open reading frame 99	SEQ ID NO: 1651
C11orf1	Chromosome 11 open reading frame 1	SEQ ID NOS: 1652-1656
C11orf24	Chromosome 11 open reading frame 24	SEQ ID NOS: 1657-1659
C11orf45	Chromosome 11 open reading frame 45	SEQ ID NOS: 1660-1661
C11orf94	Chromosome 11 open reading frame 94	SEQ ID NO: 1662
C12orf10	Chromosome 12 open reading frame 10	SEQ ID NOS: 1663-1666
C12orf49	Chromosome 12 open reading frame 49	SEQ ID NOS: 1667-1670
C12orf73	Chromosome 12 open reading frame 73	SEQ ID NOS: 1671-1680
C12orf76	Chromosome 12 open reading frame 76	SEQ ID NOS: 1681-1688
C14orf93	Chromosome 14 open reading frame 93	SEQ ID NOS: 1689-1704
C16orf89	Chromosome 16 open reading frame 89	SEQ ID NOS: 1705-1707
C16orf90	Chromosome 16 open reading frame 90	SEQ ID NOS: 1708-1709
C17orf67	Chromosome 17 open reading frame 67	SEQ ID NO: 1710
C17orf75	Chromosome 17 open reading frame 75	SEQ ID NOS: 1711-1719
C17orf99	Chromosome 17 open reading frame 99	SEQ ID NOS: 1720-1722
C18orf54	Chromosome 18 open reading frame 54	SEQ ID NOS: 1723-1727
C19orf47	Chromosome 19 open reading frame 47	SEQ ID NOS: 1728-1735
C19orf70	Chromosome 19 open reading frame 70	SEQ ID NOS: 1736-1739
C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1	SEQ ID NOS: 1740-1744
C1orf127	Chromosome 1 open reading frame 127	SEQ ID NOS: 1745-1748
C1orf159	Chromosome 1 open reading frame 159	SEQ ID NOS: 1749-1761
C1orf198	Chromosome 1 open reading frame 198	SEQ ID NOS: 1762-1766
C1orf54	Chromosome 1 open reading frame 54	SEQ ID NOS: 1767-1769
C1orf56	Chromosome 1 open reading frame 56	SEQ ID NO: 1770
C1QA	Complement component 1, q subcomponent, A chain	SEQ ID NOS: 1771-1773
C1QB	Complement component 1, q subcomponent, B chain	SEQ ID NOS: 1774-1777
C1QC	Complement component 1, q subcomponent, C chain	SEQ ID NOS: 1778-1780
C1QL1	Complement component 1, q subcomponent-like 1	SEQ ID NO: 1781
C1QL2	Complement component 1, q subcomponent-like 2	SEQ ID NO: 1782
C1QL3	Complement component 1, q subcomponent-like 3	SEQ ID NOS: 1783-1784
C1QL4	Complement component 1, q subcomponent-like 4	SEQ ID NO: 1785
C1QTNF1	C1q and tumor necrosis factor related protein 1	SEQ ID NOS: 1786-1795
FAM132A	Family with sequence similarity 132, member A	SEQ ID NO: 1796
C1QTNF2	C1q and tumor necrosis factor related protein 2	SEQ ID NO: 1797
C1QTNF3	C1q and tumor necrosis factor related protein 3	SEQ ID NOS: 1798-1799
C1QTNF4	C1q and tumor necrosis factor related protein 4	SEQ ID NOS: 1800-1801
C1QTNF5	C1q and tumor necrosis factor related protein 5	SEQ ID NOS: 1802-1804
C1QTNF7	C1q and tumor necrosis factor related protein 7	SEQ ID NOS: 1805-1809
C1QTNF8	C1q and tumor necrosis factor related protein 8	SEQ ID NOS: 1810-1811
C1QTNF9	C1q and tumor necrosis factor related protein 9	SEQ ID NOS: 1812-1813

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
C1QTNF9B	C1q and tumor necrosis factor related protein 9B	SEQ ID NOS: 1814-1816
C1R	Complement component 1, r subcomponent	SEQ ID NOS: 1817-1825
C1RL	Complement component 1, r subcomponent-like	SEQ ID NOS: 1826-1834
C1S	Complement component 1, s subcomponent	SEQ ID NOS: 1835-1844
C2	Complement component 2	SEQ ID NOS: 1845-1859
C21orf33	Chromosome 21 open reading frame 33	SEQ ID NOS: 1860-1868
C21orf62	Chromosome 21 open reading frame 62	SEQ ID NOS: 1869-1872
C22orf15	Chromosome 22 open reading frame 15	SEQ ID NOS: 1873-1875
C22orf46	Chromosome 22 open reading frame 46	SEQ ID NO: 1876
C2CD2	C2 calcium-dependent domain containing 2	SEQ ID NOS: 1877-1879
C2orf40	Chromosome 2 open reading frame 40	SEQ ID NOS: 1880-1882
C2orf66	Chromosome 2 open reading frame 66	SEQ ID NO: 1883
C2orf69	Chromosome 2 open reading frame 69	SEQ ID NO: 1884
C2orf78	Chromosome 2 open reading frame 78	SEQ ID NO: 1885
C3	Complement component 3	SEQ ID NOS: 1886-1890
C3orf33	Chromosome 3 open reading frame 33	SEQ ID NOS: 1891-1895
C3orf58	Chromosome 3 open reading frame 58	SEQ ID NOS: 1896-1899
C4A	Complement component 4A (Rodgers blood group)	SEQ ID NOS: 1900-1901
C4B	Complement component 4B (Chido blood group)	SEQ ID NOS: 1902-1903
C4BPA	Complement component 4 binding protein, alpha	SEQ ID NOS: 1904-1906
C4BPB	Complement component 4 binding protein, beta	SEQ ID NOS: 1907-1911
C4orf48	Chromosome 4 open reading frame 48	SEQ ID NOS: 1912-1913
C5	Complement component 5	SEQ ID NO: 1914
C5orf46	Chromosome 5 open reading frame 46	SEQ ID NOS: 1915-1916
C6	Complement component 6	SEQ ID NOS: 1917-1920
C6orf120	Chromosome 6 open reading frame 120	SEQ ID NO: 1921
C6orf15	Chromosome 6 open reading frame 15	SEQ ID NO: 1922
C6orf58	Chromosome 6 open reading frame 58	SEQ ID NO: 1923
C7	Complement component 7	SEQ ID NO: 1924
C7orf57	Chromosome 7 open reading frame 57	SEQ ID NOS: 1925-1929
C8A	Complement component 8, alpha polypeptide	SEQ ID NO: 1930
C8B	Complement component 8, beta polypeptide	SEQ ID NOS: 1931-1933
C8G	Complement component 8, gamma polypeptide	SEQ ID NOS: 1934-1935
C9	Complement component 9	SEQ ID NO: 1936
C9orf47	Chromosome 9 open reading frame 47	SEQ ID NOS: 1937-1939
CA10	Carbonic anhydrase X	SEQ ID NOS: 1940-1946
CA11	Carbonic anhydrase XI	SEQ ID NOS: 1947-1948
CA6	Carbonic anhydrase VI	SEQ ID NOS: 1949-1953
CA9	Carbonic anhydrase IX	SEQ ID NOS: 1954-1955
CABLES1	Cdk5 and Abl enzyme substrate 1	SEQ ID NOS: 1956-1961
CABP1	Calcium binding protein 1	SEQ ID NOS: 1962-1965
CACNA2D1	Calcium channel, voltage-dependent, alpha 2/delta subunit 1	SEQ ID NOS: 1966-1969
CACNA2D4	Calcium channel, voltage-dependent, alpha 2/delta subunit 4	SEQ ID NOS: 1970-1983
CADM3	Cell adhesion molecule 3	SEQ ID NOS: 1984-1986
CALCA	Calcitonin-related polypeptide alpha	SEQ ID NOS: 1987-1991
CALCB	Calcitonin-related polypeptide beta	SEQ ID NOS: 1992-1994
CALCR	Calcitonin receptor	SEQ ID NOS: 1995-2001
CALCRL	Calcitonin receptor-like	SEQ ID NOS: 2002-2006
FAM26D	Family with sequence similarity 26, member D	SEQ ID NOS: 2007-2011
CALR	Calreticulin	SEQ ID NOS: 2012-2015
CALR3	Calreticulin 3	SEQ ID NOS: 2016-2017
CALU	Calumenin	SEQ ID NOS: 2018-2023
CAMK2D	Calcium/calmodulin-dependent protein kinase II delta	SEQ ID NOS: 2024-2035
CAMP	Cathelicidin antimicrobial peptide	SEQ ID NO: 2036
CANX	Calnexin	SEQ ID NOS: 2037-2051
CARM1	Coactivator-associated arginine methyltransferase 1	SEQ ID NOS: 2052-2059
CARNS1	Carnosine synthase 1	SEQ ID NOS: 2060-2062
CARTPT	CART prepropeptide	SEQ ID NO: 2063
CASQ1	Calsequestrin 1 (fast-twitch, skeletal muscle)	SEQ ID NOS: 2064-2065
CASQ2	Calsequestrin 2 (cardiac muscle)	SEQ ID NO: 2066
CATSPERG	Catsper channel auxiliary subunit gamma	SEQ ID NOS: 2067-2074
CBLN1	Cerebellin 1 precursor	SEQ ID NOS: 2075-2077
CBLN2	Cerebellin 2 precursor	SEQ ID NOS: 2078-2081
CBLN3	Cerebellin 3 precursor	SEQ ID NOS: 2082-2083
CBLN4	Cerebellin 4 precursor	SEQ ID NO: 2084
CCBE1	Collagen and calcium binding EGF domains 1	SEQ ID NOS: 2085-2087
CCDC112	Coiled-coil domain containing 112	SEQ ID NOS: 2088-2091
CCDC129	Coiled-coil domain containing 129	SEQ ID NOS: 2092-2099
CCDC134	Coiled-coil domain containing 134	SEQ ID NOS: 2100-2101

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CCDC149	Coiled-coil domain containing 149	SEQ ID NOS: 2102-2105
CCDC3	Coiled-coil domain containing 3	SEQ ID NOS: 2106-2107
CCDC80	Coiled-coil domain containing 80	SEQ ID NOS: 2108-2111
CCDC85A	Coiled-coil domain containing 85A	SEQ ID NO: 2112
CCDC88B	Coiled-coil domain containing 88B	SEQ ID NOS: 2113-2115
CCER2	Coiled-coil glutamate-rich protein 2	SEQ ID NOS: 2116-2117
CCK	Cholecystokinin	SEQ ID NOS: 2118-2120
CCL1	Chemokine (C-C motif) ligand 1	SEQ ID NO: 2121
CCL11	Chemokine (C-C motif) ligand 11	SEQ ID NO: 2122
CCL13	Chemokine (C-C motif) ligand 13	SEQ ID NOS: 2123-2124
CCL14	Chemokine (C-C motif) ligand 14	SEQ ID NOS: 2125-2128
CCL15	Chemokine (C-C motif) ligand 15	SEQ ID NOS: 2129-2130
CCL16	Chemokine (C-C motif) ligand 16	SEQ ID NOS: 2131-2133
CCL17	Chemokine (C-C motif) ligand 17	SEQ ID NOS: 2134-2135
CCL18	Chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	SEQ ID NO: 2136
CCL19	Chemokine (C-C motif) ligand 19	SEQ ID NOS: 2137-2138
CCL2	Chemokine (C-C motif) ligand 2	SEQ ID NOS: 2139-2140
CCL20	Chemokine (C-C motif) ligand 20	SEQ ID NOS: 2141-2143
CCL21	Chemokine (C-C motif) ligand 21	SEQ ID NOS: 2144-2145
CCL22	Chemokine (C-C motif) ligand 22	SEQ ID NO: 2146
CCL23	Chemokine (C-C motif) ligand 23	SEQ ID NOS: 2147-2149
CCL24	Chemokine (C-C motif) ligand 24	SEQ ID NOS: 2150-2151
CCL25	Chemokine (C-C motif) ligand 25	SEQ ID NOS: 2152-2155
CCL26	Chemokine (C-C motif) ligand 26	SEQ ID NOS: 2156-2157
CCL27	Chemokine (C-C motif) ligand 27	SEQ ID NO: 2158
CCL28	Chemokine (C-C motif) ligand 28	SEQ ID NOS: 2159-2161
CCL3	Chemokine (C-C motif) ligand 3	SEQ ID NO: 2162
CCL3L3	Chemokine (C-C motif) ligand 3-like 3	SEQ ID NO: 2163
CCL4	Chemokine (C-C motif) ligand 4	SEQ ID NOS: 2164-2165
CCL4L2	Chemokine (C-C motif) ligand 4-like 2	SEQ ID NOS: 2166-2175
CCL5	Chemokine (C-C motif) ligand 5	SEQ ID NOS: 2176-2178
CCL7	Chemokine (C-C motif) ligand 7	SEQ ID NOS: 2179-2181
CCL8	Chemokine (C-C motif) ligand 8	SEQ ID NO: 2182
CCNB1IP1	Cyclin B1 interacting protein 1, E3 ubiquitin protein ligase	SEQ ID NOS: 2183-2194
CCNL1	Cyclin L1	SEQ ID NOS: 2195-2203
CCNL2	Cyclin L2	SEQ ID NOS: 2204-2211
CD14	CD14 molecule	SEQ ID NOS: 2212-2216
CD160	CD160 molecule	SEQ ID NOS: 2217-2221
CD164	CD164 molecule, sialomucin	SEQ ID NOS: 2222-2227
CD177	CD177 molecule	SEQ ID NOS: 2228-2230
CD1E	CD1e molecule	SEQ ID NOS: 2231-2244
CD2	CD2 molecule	SEQ ID NOS: 2245-2246
CD200	CD200 molecule	SEQ ID NOS: 2247-2253
CD200R1	CD200 receptor 1	SEQ ID NOS: 2254-2258
CD22	CD22 molecule	SEQ ID NOS: 2259-2276
CD226	CD226 molecule	SEQ ID NOS: 2277-2284
CD24	CD24 molecule	SEQ ID NOS: 2285-2291
CD276	CD276 molecule	SEQ ID NOS: 2292-2307
CD300A	CD300a molecule	SEQ ID NOS: 2308-2312
CD300LB	CD300 molecule-like family member b	SEQ ID NOS: 2313-2314
CD300LF	CD300 molecule-like family member f	SEQ ID NOS: 2315-2323
CD300LG	CD300 molecule-like family member g	SEQ ID NOS: 2324-2329
CD3D	CD3d molecule, delta (CD3-TCR complex)	SEQ ID NOS: 2330-2333
CD4	CD4 molecule	SEQ ID NOS: 2334-2336
CD40	CD40 molecule, TNF receptor superfamily member 5	SEQ ID NOS: 2337-2340
CD44	CD44 molecule (Indian blood group)	SEQ ID NOS: 2341-2367
CD48	CD48 molecule	SEQ ID NOS: 2368-2370
CD5	CD5 molecule	SEQ ID NOS: 2371-2372
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	SEQ ID NOS: 2373-2383
CD59	CD59 molecule, complement regulatory protein	SEQ ID NOS: 2384-2394
CD5L	CD5 molecule-like	SEQ ID NO: 2395
CD6	CD6 molecule	SEQ ID NOS: 2396-2403
CD68	CD68 molecule	SEQ ID NOS: 2404-2407
CD7	CD7 molecule	SEQ ID NOS: 2408-2413
CD79A	CD79a molecule, immunoglobulin-associated alpha	SEQ ID NOS: 2414-2416
CD80	CD80 molecule	SEQ ID NOS: 2417-2419
CD86	CD86 molecule	SEQ ID NOS: 2420-2426
CD8A	CD8a molecule	SEQ ID NOS: 2427-2430
CD8B	CD8b molecule	SEQ ID NOS: 2431-2436

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CD99	CD99 molecule	SEQ ID NOS: 2437-2445
CDC23	Cell division cycle 23	SEQ ID NOS: 2446-2450
CDC40	Cell division cycle 40	SEQ ID NOS: 2451-2453
CDC45	Cell division cycle 45	SEQ ID NOS: 2454-2460
CDCP1	CUB domain containing protein 1	SEQ ID NOS: 2461-2462
CDCP2	CUB domain containing protein 2	SEQ ID NOS: 2463-2464
CDH1	Cadherin 1, type 1	SEQ ID NOS: 2465-2472
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)	SEQ ID NOS: 2473-2482
CDH13	Cadherin 13	SEQ ID NOS: 2483-2492
CDH17	Cadherin 17, LI cadherin (liver-intestine)	SEQ ID NOS: 2493-2497
CDH18	Cadherin 18, type 2	SEQ ID NOS: 2498-2504
CDH19	Cadherin 19, type 2	SEQ ID NOS: 2505-2509
CDH23	Cadherin-related 23	SEQ ID NOS: 2510-2525
CDH5	Cadherin 5, type 2 (vascular endothelium)	SEQ ID NOS: 2526-2533
CDHR1	Cadherin-related family member 1	SEQ ID NOS: 2534-2539
CDHR4	Cadherin-related family member 4	SEQ ID NOS: 2540-2544
CDHR5	Cadherin-related family member 5	SEQ ID NOS: 2545-2551
CDKN2A	Cyclin-dependent kinase inhibitor 2A	SEQ ID NOS: 2552-2562
CONF	Cerebral dopamine neurotrophic factor	SEQ ID NOS: 2563-2564
CDON	Cell adhesion associated, oncogene regulated	SEQ ID NOS: 2565-2572
CDSN	Corneodesmosin	SEQ ID NO: 2573
CEACAM16	Carcinoembryonic antigen-related cell adhesion molecule 16	SEQ ID NOS: 2574-2575
CEACAM18	Carcinoembryonic antigen-related cell adhesion molecule 18	SEQ ID NO: 2576
CEACAM19	Carcinoembryonic antigen-related cell adhesion molecule 19	SEQ ID NOS: 2577-2583
CEACAM5	Carcinoembryonic antigen-related cell adhesion molecule 5	SEQ ID NOS: 2584-2591
CEACAM7	Carcinoembryonic antigen-related cell adhesion molecule 7	SEQ ID NOS: 2592-2594
CEACAM8	Carcinoembryonic antigen-related cell adhesion molecule 8	SEQ ID NOS: 2595-2596
CEL	Carboxyl ester lipase	SEQ ID NO: 2597
CELA2A	Chymotrypsin-like elastase family, member 2A	SEQ ID NO: 2598
CELA2B	Chymotrypsin-like elastase family, member 2B	SEQ ID NOS: 2599-2600
CELA3A	Chymotrypsin-like elastase family, member 3A	SEQ ID NOS: 2601-2603
CELA3B	Chymotrypsin-like elastase family, member 3B	SEQ ID NOS: 2604-2606
CEMIP	Cell migration inducing protein, hyaluronan binding	SEQ ID NOS: 2607-2611
CEP89	Centrosomal protein 89 kDa	SEQ ID NOS: 2612-2617
CER1	Cerberus 1, DAN family BMP antagonist	SEQ ID NO: 2618
CERCAM	Cerebral endothelial cell adhesion molecule	SEQ ID NOS: 2619-2626
CERS1	Ceramide synthase 1	SEQ ID NOS: 2627-2631
CES1	Carboxylesterase 1	SEQ ID NOS: 2632-2637
CES3	Carboxylesterase 3	SEQ ID NOS: 2638-2642
CES4A	Carboxylesterase 4A	SEQ ID NOS: 2643-2648
CES5A	Carboxylesterase 5A	SEQ ID NOS: 2649-2656
CETP	Cholestryl ester transfer protein, plasma	SEQ ID NOS: 2657-2659
CCDC108	Coiled-coil domain containing 108	SEQ ID NOS: 2660-2669
CFB	Complement factor B	SEQ ID NOS: 2670-2674
CFC1	Cripto, FRL-1, cryptic family 1	SEQ ID NOS: 2675-2677
CFC1B	Cripto, FRL-1, cryptic family 1B	SEQ ID NOS: 2678-2680
CFD	Complement factor D (adipsin)	SEQ ID NOS: 2681-2682
CFDP1	Craniofacial development protein 1	SEQ ID NOS: 2683-2686
CFH	Complement factor H	SEQ ID NOS: 2687-2689
CFHR1	Complement factor H-related 1	SEQ ID NOS: 2690-2691
CFHR2	Complement factor H-related 2	SEQ ID NOS: 2692-2693
CFHR3	Complement factor H-related 3	SEQ ID NOS: 2694-2698
CFHR4	Complement factor H-related 4	SEQ ID NOS: 2699-2702
CFHR5	Complement factor H-related 5	SEQ ID NO: 2703
CFI	Complement factor I	SEQ ID NOS: 2704-2708
CFP	Complement factor properdin	SEQ ID NOS: 2709-2712
CGA	Glycoprotein hormones, alpha polypeptide	SEQ ID NOS: 2713-2717
CGB1	Chorionic gonadotropin, beta polypeptide 1	SEQ ID NOS: 2718-2719
CGB2	Chorionic gonadotropin, beta polypeptide 2	SEQ ID NOS: 2720-2721
CGB	Chorionic gonadotropin, beta polypeptide	SEQ ID NO: 2722
CGB5	Chorionic gonadotropin, beta polypeptide 5	SEQ ID NO: 2723
CGB7	Chorionic gonadotropin, beta polypeptide 7	SEQ ID NOS: 2724-2726
CGB8	Chorionic gonadotropin, beta polypeptide 8	SEQ ID NO: 2727
CGREF1	Cell growth regulator with EF-hand domain 1	SEQ ID NOS: 2728-2735
CHAD	Chondroadherin	SEQ ID NOS: 2736-2738
CHADL	Chondroadherin-like	SEQ ID NOS: 2739-2741
CHEK2	Checkpoint kinase 2	SEQ ID NOS: 2742-2763

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CHGA	Chromogranin A	SEQ ID NOS: 2764-2766
CHGB	Chromogranin B	SEQ ID NOS: 2767-2768
CHI3L1	Chitinase 3-like 1 (cartilage glycoprotein-39)	SEQ ID NOS: 2769-2770
CHI3L2	Chitinase 3-like 2	SEQ ID NOS: 2771-2784
CHIA	Chitinase, acidic	SEQ ID NOS: 2785-2793
CHID1	Chitinase domain containing 1	SEQ ID NOS: 2794-2812
CHIT1	Chitinase 1 (chitotriosidase)	SEQ ID NOS: 2813-2816
CHL1	Cell adhesion molecule L1-like	SEQ ID NOS: 2817-2825
CHN1	Chimerin 1	SEQ ID NOS: 2826-2836
CHPF	Chondroitin polymerizing factor	SEQ ID NOS: 2837-2839
CHPF2	Chondroitin polymerizing factor 2	SEQ ID NOS: 2840-2843
CHRD	Chordin	SEQ ID NOS: 2844-2849
CHRDL1	Chordin-like 1	SEQ ID NOS: 2850-2854
CHRDL2	Chordin-like 2	SEQ ID NOS: 2855-2863
CHRNA2	Cholinergic receptor, nicotinic, alpha 2 (neuronal)	SEQ ID NOS: 2864-2872
CHRNA5	Cholinergic receptor, nicotinic, alpha 5 (neuronal)	SEQ ID NOS: 2873-2876
CHRNBI	Cholinergic receptor, nicotinic, beta 1 (muscle)	SEQ ID NOS: 2877-2882
CHRND	Cholinergic receptor, nicotinic, delta (muscle)	SEQ ID NOS: 2883-2888
CHST1	Carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	SEQ ID NO: 2889
CHST10	Carbohydrate sulfotransferase 10	SEQ ID NOS: 2890-2897
CHST11	Carbohydrate (chondroitin 4) sulfotransferase 11	SEQ ID NOS: 2898-2902
CHST13	Carbohydrate (chondroitin 4) sulfotransferase 13	SEQ ID NOS: 2903-2904
CHST4	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	SEQ ID NOS: 2905-2906
CHST5	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	SEQ ID NOS: 2907-2908
CHST6	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	SEQ ID NOS: 2909-2910
CHST7	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	SEQ ID NO: 2911
CHST8	Carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 8	SEQ ID NOS: 2912-2915
CHSY1	Chondroitin sulfate synthase 1	SEQ ID NOS: 2916-2917
CHSY3	Chondroitin sulfate synthase 3	SEQ ID NO: 2918
CHTF8	Chromosome transmission fidelity factor 8	SEQ ID NOS: 2919-2929
CLIP	Cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	SEQ ID NO: 2930
CLIP2	Cartilage intermediate layer protein 2	SEQ ID NOS: 2931-2932
CKLF	Chemokine-like factor	SEQ ID NOS: 2933-2938
CKMT1A	Creatine kinase, mitochondrial 1A	SEQ ID NOS: 2939-2944
CKMT1B	Creatine kinase, mitochondrial 1B	SEQ ID NOS: 2945-2954
CLCA1	Chloride channel accessory 1	SEQ ID NOS: 2955-2956
CLCF1	Cardiotrophin-like cytokine factor 1	SEQ ID NOS: 2957-2958
CLDN15	Claudin 15	SEQ ID NOS: 2959-2964
CLDN7	Claudin 7	SEQ ID NOS: 2,965-2971
CLDND1	Claudin domain containing 1	SEQ ID NOS: 2972-2997
CLEC11A	C-type lectin domain family 11, member A	SEQ ID NOS: 2998-3000
CLEC16A	C-type lectin domain family 16, member A	SEQ ID NOS: 3001-3006
CLEC18A	C-type lectin domain family 18, member A	SEQ ID NOS: 3007-3012
CLEC18B	C-type lectin domain family 18, member B	SEQ ID NOS: 3013-3016
CLEC18C	C-type lectin domain family 18, member C	SEQ ID NOS: 3017-3023
CLEC19A	C-type lectin domain family 19, member A	SEQ ID NOS: 3024-3027
CLEC2B	C-type lectin domain family 2, member B	SEQ ID NOS: 3028-3029
CLEC3A	C-type lectin domain family 3, member A	SEQ ID NOS: 3030-3031
CLEC3B	C-type lectin domain family 3, member B	SEQ ID NOS: 3032-3033
CLGN	Calmodulin	SEQ ID NOS: 3034-3036
CLN5	Ceroid-lipofuscinosis, neuronal 5	SEQ ID NOS: 3037-3048
CLPS	Colipase, pancreatic	SEQ ID NOS: 3049-3051
CLPSL1	Colipase-like 1	SEQ ID NOS: 3052-3053
CLPSL2	Colipase-like 2	SEQ ID NOS: 3054-3055
CLPX	Caseinolytic mitochondrial matrix peptidase chaperone subunit	SEQ ID NOS: 3056-3058
CLSTN3	Calsyntenin 3	SEQ ID NOS: 3059-3065
CLU	Clusterin	SEQ ID NOS: 3066-3079
CLUL1	Clusterin-like 1 (retinal)	SEQ ID NOS: 3080-3087
CMA1	Chymase 1, mast cell	SEQ ID NOS: 3088-3089
CMPK1	Cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	SEQ ID NOS: 3090-3093
CNBD1	Cyclic nucleotide binding domain containing 1	SEQ ID NOS: 3094-3097
CNDP1	Carnosine dipeptidase 1 (metallopeptidase M20 family)	SEQ ID NOS: 3098-3100
RQCD1	RCD1 required for cell differentiation1 homolog (<i>S. pombe</i>)	SEQ ID NOS: 3101-3107

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CNPY2	Canopy FGF signaling regulator 2	SEQ ID NOS: 3108-3112
CNPY3	Canopy FGF signaling regulator 3	SEQ ID NOS: 3113-3114
CNPY4	Canopy FGF signaling regulator 4	SEQ ID NOS: 3115-3117
CNTFR	Ciliary neurotrophic factor receptor	SEQ ID NOS: 3118-3121
CNTN1	Contactin 1	SEQ ID NOS: 3122-3131
CNTN2	Contactin 2 (axonal)	SEQ ID NOS: 3132-3143
CNTN3	Contactin 3 (plasmacytoma associated)	SEQ ID NO: 3144
CNTN4	Contactin 4	SEQ ID NOS: 3145-3153
CNTN5	Contactin 5	SEQ ID NOS: 3154-3159
CNTNAP2	Contactin associated protein-like 2	SEQ ID NOS: 3160-3163
CNTNAP3	Contactin associated protein-like 3	SEQ ID NOS: 3164-3168
CNTNAP3B	Contactin associated protein-like 3B	SEQ ID NOS: 3169-3177
COASY	CoA synthase	SEQ ID NOS: 3178-3187
COCH	Cochlin	SEQ ID NOS: 3188-3199
COG3	Component of oligomeric golgi complex 3	SEQ ID NOS: 3200-3203
COL10A1	Collagen, type X, alpha 1	SEQ ID NOS: 3204-3207
COL11A1	Collagen, type XI, alpha 1	SEQ ID NOS: 3208-3218
COL11A2	Collagen, type XI, alpha 2	SEQ ID NOS: 3219-3223
COL12A1	Collagen, type XII, alpha 1	SEQ ID NOS: 3224-3231
COL14A1	Collagen, type XIV, alpha 1	SEQ ID NOS: 3232-3239
COL15A1	Collagen, type XV, alpha 1	SEQ ID NOS: 3240-3241
COL16A1	Collagen, type XVI, alpha 1	SEQ ID NOS: 3242-3246
COL18A1	Collagen, type XVIII, alpha 1	SEQ ID NOS: 3247-3251
COL19A1	Collagen, type XIX, alpha 1	SEQ ID NOS: 3252-3254
COL1A1	Collagen, type I, alpha 1	SEQ ID NOS: 3255-3256
COL1A2	Collagen, type I, alpha 2	SEQ ID NOS: 3257-3258
COL20A1	Collagen, type XX, alpha 1	SEQ ID NOS: 3259-3262
COL21A1	Collagen, type XXI, alpha 1	SEQ ID NOS: 3263-3268
COL22A1	Collagen, type XXII, alpha 1	SEQ ID NOS: 3269-3271
COL24A1	Collagen, type XXIV, alpha 1	SEQ ID NOS: 3272-3275
COL26A1	Collagen, type XXVI, alpha 1	SEQ ID NOS: 3276-3277
COL27A1	Collagen, type XXVII, alpha 1	SEQ ID NOS: 3278-3280
COL28A1	Collagen, type XXVIII, alpha 1	SEQ ID NOS: 3281-3285
COL2A1	Collagen, type II, alpha 1	SEQ ID NOS: 3286-3287
COL3A1	Collagen, type III, alpha 1	SEQ ID NOS: 3288-3290
COL4A1	Collagen, type IV, alpha 1	SEQ ID NOS: 3291-3293
COL4A2	Collagen, type IV, alpha 2	SEQ ID NOS: 3294-3296
COL4A3	Collagen, type IV, alpha 3 (Goodpasture antigen)	SEQ ID NOS: 3297-3300
COL4A4	Collagen, type IV, alpha 4	SEQ ID NOS: 3301-3302
COL4A5	Collagen, type IV, alpha 5	SEQ ID NOS: 3303-3309
COL4A6	Collagen, type IV, alpha 6	SEQ ID NOS: 3310-3315
COL5A1	Collagen, type V, alpha 1	SEQ ID NOS: 3316-3318
COL5A2	Collagen, type V, alpha 2	SEQ ID NOS: 3319-3320
COL5A3	Collagen, type V, alpha 3	SEQ ID NO: 3321
COL6A1	Collagen, type VI, alpha 1	SEQ ID NOS: 3322-3323
COL6A2	Collagen, type VI, alpha 2	SEQ ID NOS: 3324-3329
COL6A3	Collagen, type VI, alpha 3	SEQ ID NOS: 3330-3338
COL6A5	Collagen, type VI, alpha 5	SEQ ID NOS: 3339-3343
COL6A6	Collagen, type VI, alpha 6	SEQ ID NOS: 3344-3346
COL7A1	Collagen, type VII, alpha 1	SEQ ID NOS: 3347-3348
COL8A1	Collagen, type VIII, alpha 1	SEQ ID NOS: 3349-3352
COL8A2	Collagen, type VIII, alpha 2	SEQ ID NOS: 3353-3355
COL9A1	Collagen, type IX, alpha 1	SEQ ID NOS: 3356-3359
COL9A2	Collagen, type IX, alpha 2	SEQ ID NOS: 3360-3363
COL9A3	Collagen, type IX, alpha 3	SEQ ID NOS: 3364-3365
COLEC10	Collectin sub-family member 10 (C-type lectin)	SEQ ID NO: 3366
COLEC11	Collectin sub-family member 11	SEQ ID NOS: 3367-3376
COLGALT1	Collagen beta(1-O)galactosyltransferase 1	SEQ ID NOS: 3377-3379
COLGALT2	Collagen beta(1-O)galactosyltransferase 2	SEQ ID NOS: 3380-3382
COLQ	Collagen-like tail subunit (single strand of homotrimer) or asymmetric acetylcholinesterase	SEQ ID NOS: 3383-3387
COMP	Cartilage oligomeric matrix protein	SEQ ID NOS: 3388-3390
COPS6	COP9 signalosome subunit 6	SEQ ID NOS: 3391-3394
COQ6	Coenzyme Q6 monooxygenase	SEQ ID NOS: 3395-3402
CORT	Cortistatin	SEQ ID NO: 3403
CP	Ceruloplasmin (ferroxidase)	SEQ ID NOS: 3404-3408
CPA1	Carboxypeptidase A1 (pancreatic)	SEQ ID NOS: 3409-3413
CPA2	Carboxy peptidase A2 (pancreatic)	SEQ ID NOS: 3414-3415
CPA3	Carboxypeptidase A3 (mast cell)	SEQ ID NO: 3416
CPA4	Carboxypeptidase A4	SEQ ID NOS: 3417-3422
CPA6	Carboxypeptidase A6	SEQ ID NOS: 3423-3425
CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	SEQ ID NOS: 3426-3431
CPB1	Carboxypeptidase B1 (tissue)	SEQ ID NOS: 3432-3436

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CPB2	Carboxypeptidase B2 (plasma)	SEQ ID NOS: 3437-3439
CPE	Carboxypeptidase E	SEQ ID NOS: 3440-3444
CPM	Carboxypeptidase M	SEQ ID NOS: 3445-3454
CPN1	Carboxypeptidase N, polypeptide 1	SEQ ID NOS: 3455-3456
CPN2	Carboxypeptidase N, polypeptide 2	SEQ ID NOS: 3457-3458
CPO	Carboxypeptidase O	SEQ ID NO: 3459
CPQ	Carboxypeptidase Q	SEQ ID NOS: 3460-3465
CPVL	Carboxypeptidase, vitellogenin-like	SEQ ID NOS: 3466-3476
CPXM1	Carboxypeptidase X (M14 family), member 1	SEQ ID NO: 3477
CPXM2	Carboxypeptidase X (M14 family), member 2	SEQ ID NOS: 3478-3479
CPZ	Carboxypeptidase Z	SEQ ID NOS: 3480-3483
CRIL	Complement component (3b/4b) receptor 1-like	SEQ ID NOS: 3484-3485
CRB2	Crumbs family member 2	SEQ ID NOS: 3486-3488
CREG1	Cellular repressor of E1A-stimulated genes 1	SEQ ID NO: 3489
CREG2	Cellular repressor of E1A-stimulated genes 2	SEQ ID NO: 3490
CRELD1	Cysteine-rich with EGF-like domains 1	SEQ ID NOS: 3491-3496
CRELD2	Cysteine-rich with EGF-like domains 2	SEQ ID NOS: 3497-3501
CRH	Corticotropin releasing hormone	SEQ ID NO: 3502
CRHBP	Corticotropin releasing hormone binding protein	SEQ ID NOS: 3503-3504
CRHR1	Corticotropin releasing hormone receptor 1	SEQ ID NOS: 3505-3516
CRHR2	Corticotropin releasing hormone receptor 2	SEQ ID NOS: 3517-3523
CRISP1	Cysteine-rich secretory protein 1	SEQ ID NOS: 3524-3527
CRISP2	Cysteine-rich secretory protein 2	SEQ ID NOS: 3528-3530
CRISP3	Cysteine-rich secretory protein 3	SEQ ID NOS: 3531-3534
CRISPLD2	Cysteine-rich secretory protein LCCL domain containing 2	SEQ ID NOS: 3535-3542
CRLF1	Cytokine receptor-like factor 1	SEQ ID NOS: 3543-3544
CRP	C-reactive protein, pentraxin-related	SEQ ID NOS: 3545-3549
CRTAC1	Cartilage acidic protein 1	SEQ ID NOS: 3550-3554
CRTAP	Cartilage associated protein	SEQ ID NOS: 3555-3556
CRY2	Cryptochromes circadian clock 2	SEQ ID NOS: 3557-3560
CSAD	Cysteine sulfenic acid decarboxylase	SEQ ID NOS: 3561-3573
CSF1	Colony stimulating factor 1 (macrophage)	SEQ ID NOS: 3574-3581
CSF1R	Colony stimulating factor 1 receptor	SEQ ID NOS: 3582-3586
CSF2	Colony stimulating factor 2 (granulocyte-macrophage)	SEQ ID NO: 3587
CSF2RA	Colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	SEQ ID NOS: 3588-3599
CSF3	Colony stimulating factor 3 (granulocyte)	SEQ ID NOS: 3600-3606
CSGALNACT1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	SEQ ID NOS: 3607-3615
CSH1	Chorionic somatomammotropin hormone 1 (placental lactogen)	SEQ ID NOS: 3616-3619
CSH2	Chorionic somatomammotropin hormone 2.	SEQ ID NOS: 3620-3624
CSHL1	Chorionic somatomammotropin hormone-like 1	SEQ ID NOS: 3625-3631
CSN1S1	Casein alpha s1	SEQ ID NOS: 3632-3637
CSN2	Casein beta	SEQ ID NO: 3638
CSN3	Casein kappa	SEQ ID NO: 3639
CST1	Cystatin SN	SEQ ID NOS: 3640-3641
CST11	Cystatin 11	SEQ ID NOS: 3642-3643
CST2	Cystatin SA	SEQ ID NO: 3644
CST3	Cystatin C	SEQ ID NOS: 3645-3647
CST4	Cystatin S	SEQ ID NO: 3648
CST5	Cystatin D	SEQ ID NO: 3649
CST6	Cystatin E/M	SEQ ID NO: 3650
CST7	Cystatin F (leukocystatin)	SEQ ID NO: 3651
CST8	Cystatin 8 (cystatin-related epididymal specific)	SEQ ID NOS: 3652-3653
CST9	Cystatin 9 (testatin)	SEQ ID NO: 3654
CST9L	Cystatin 9-like	SEQ ID NO: 3655
CSTL1	Cystatin-like 1	SEQ ID NOS: 3656-3658
CT55	Cancer/testis antigen 55	SEQ ID NOS: 3659-3660
CTBS	Chitobiase, di-N-acetyl-	SEQ ID NOS: 3661-3663
CTGF	Connective tissue growth factor	SEQ ID NO: 3664
CTHRC1	Collagen triple helix repeat containing 1	SEQ ID NOS: 3665-3668
CTLA4	Cytotoxic T-lymphocyte-associated protein 4	SEQ ID NOS: 3669-3672
CTNS	Cystinosin, lysosomal cystine transporter	SEQ ID NOS: 3673-3680
CTRBI	Chymotrypsinogen B1	SEQ ID NOS: 3681-3683
CTRBI2	Chymotrypsinogen B2	SEQ ID NOS: 3684-3687
CTRC	Chymotrypsin C (caldecrin)	SEQ ID NOS: 3688-3689
CTRL	Chymotrypsin-like	SEQ ID NOS: 3690-3692
CTSA	Cathepsin A	SEQ ID NOS: 3693-3701
CTSB	Cathepsin B	SEQ ID NOS: 3702-3726
CTSC	Cathepsin C	SEQ ID NOS: 3727-3731
CTSD	Cathepsin D	SEQ ID NOS: 3732-3742

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
CTSE	Cathepsin E	SEQ ID NOS: 3743-3744
CTSF	Cathepsin F	SEQ ID NOS: 3745-3748
CTSG	Cathepsin G	SEQ ID NO: 3749
CTSH	Cathepsin H	SEQ ID NOS: 3750-3755
CTSK	Cathepsin K	SEQ ID NOS: 3756-3757
CTSL	Cathepsin L	SEQ ID NOS: 3758-3760
CTSO	Cathepsin O	SEQ ID NO: 3761
CTSS	Cathepsin S	SEQ ID NOS: 3762-3766
CTSV	Cathepsin V	SEQ ID NOS: 3767-3768
CTSW	Cathepsin W	SEQ ID NOS: 3769-3771
CTSZ	Cathepsin Z	SEQ ID NO: 3772
CUBN	Cubilin (intrinsic factor-cobalamin receptor)	SEQ ID NOS: 3773-3776
CUTA	CutA divalent cation tolerance homolog (<i>E. coli</i>)	SEQ ID NOS: 3777-3786
CX3CL1	Chemokine (C-X3-C motif) ligand 1	SEQ ID NOS: 3787-3790
CXADR	Coxsackie virus and adenovirus receptor	SEQ ID NOS: 3791-3795
CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	SEQ ID NO: 3796
CXCL10	Chemokine (C-X-C motif) ligand 10	SEQ ID NO: 3797
CXCL11	Chemokine (C-X-C motif) ligand 11	SEQ ID NOS: 3798-3799
CXCL12	Chemokine (C-X-C motif) ligand 12	SEQ ID NOS: 3800-3805
CXCL13	Chemokine (C-X-C motif) ligand 13	SEQ ID NO: 3806
CXCL14	Chemokine (C-X-C motif) ligand 14	SEQ ID NOS: 3807-3808
CXCL17	Chemokine (C-X-C motif) ligand 17	SEQ ID NOS: 3809-3810
CXCL2	Chemokine (C-X-C motif) ligand 2	SEQ ID NO: 3811
CXCL3	Chemokine (C-X-C motif) ligand 3	SEQ ID NO: 3812
CXCL5	Chemokine (C-X-C motif) ligand 5	SEQ ID NO: 3813
CXCL6	Chemokine (C-X-C motif) ligand 6	SEQ ID NOS: 3814-3815
CXCL8	Chemokine (C-X-C motif) ligand 8	SEQ ID NOS: 3816-3817
CXCL9	Chemokine (C-X-C motif) ligand 9	SEQ ID NO: 3818
CXorf36	Chromosome X open reading frame 36	SEQ ID NOS: 3819-3820
CYB5D2	Cytochrome b5 domain containing 2	SEQ ID NOS: 3821-3824
CYHR1	Cysteine/histidine-rich 1	SEQ ID NOS: 3825-3832
CYP17A1	Cytochrome P450, family 17, subfamily A, polypeptide 1	SEQ ID NOS: 3833-3837
CYP20A1	Cytochrome P450, family 20, subfamily A, polypeptide 1	SEQ ID NOS: 3838-3844
CYP21A2	Cytochrome P450, family 21, subfamily A, polypeptide 2	SEQ ID NOS: 3845-3852
CYP26B1	Cytochrome P450, family 26, subfamily B, polypeptide 1	SEQ ID NOS: 3853-3857
CYP2A6	Cytochrome P450, family 2, subfamily A, polypeptide 6	SEQ ID NOS: 3858-3859
CYP2A7	Cytochrome P450, family 2, subfamily A, polypeptide 7	SEQ ID NOS: 3860-3862
CYP2B6	Cytochrome P450, family 2, subfamily B, polypeptide 6	SEQ ID NOS: 3863-3866
CYP2C18	Cytochrome P450, family 2, subfamily C, polypeptide 18	SEQ ID NOS: 3867-3868
CYP2C19	Cytochrome P450, family 2, subfamily C, polypeptide 19	SEQ ID NOS: 3869-3870
CYP2C8	Cytochrome P450, family 2, subfamily C, polypeptide 8	SEQ ID NOS: 3871-3878
CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	SEQ ID NOS: 3879-3881
CYP2E1	Cytochrome P450, family 2, subfamily E, polypeptide 1	SEQ ID NOS: 3882-3887
CYP2F1	Cytochrome P450, family 2, subfamily F, polypeptide 1	SEQ ID NOS: 3888-3891
CYP2J2	Cytochrome P450, family 2, subfamily J, polypeptide 2	SEQ ID NO: 3892
CYP2R1	Cytochrome P450, family 2, subfamily R, polypeptide 1	SEQ ID NOS: 3893-3898
CYP2S1	Cytochrome P450, family 2, subfamily S, polypeptide 1	SEQ ID NOS: 3899-3904
CYP2W1	Cytochrome P450, family 2, subfamily W, polypeptide 1	SEQ ID NOS: 3905-3907
CYP46A1	Cytochrome P450, family 46, subfamily A, polypeptide 1	SEQ ID NOS: 3908-3912
CYP4F11	Cytochrome P450, family 4, subfamily F, polypeptide 11	SEQID NOS: 3913-3917
CYP4F2	Cytochrome P450, family 4, subfamily F, polypeptide 2	SEQ ID NOS: 3918-3922
CYR61	Cysteine-rich, angiogenic inducer, 61	SEQ ID NO: 3923
CYTL1	Cytokine-like 1	SEQ ID NOS: 3924-3926

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
D2HGDH	D-2-hydroxyglutarate dehydrogenase	SEQ ID NOS: 3927-3935
DAG1	Dystroglycan 1 (dystrophin-associated glycoprotein 1)	SEQ ID NOS: 3936-3950
DAND5	DAN domain family member 5, BMP antagonist	SEQ ID NOS: 3951-3952
DAO	D-amino-acid oxidase	SEQ ID NOS: 3953-3958
DAZAP2	DAZ associated protein 2	SEQ ID NOS: 3959-3967
DBH	Dopamine beta-hydroxylase (dopamine beta-monooxygenase)	SEQ ID NOS: 3968-3969
DBNL	Drebrin-like	SEQ ID NOS: 3970-3987
DCD	Dermcidin	SEQ ID NOS: 3988-3990
DCN	Decorin	SEQ ID NOS: 3991-4009
DD1AS	DNA damage-induced apoptosis suppressor	SEQ ID NOS: 4010-4019
DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit (non-catalytic)	SEQ ID NOS: 4020-4023
DDR1	Discoidin domain receptor tyrosine kinase 1	SEQ ID NOS: 4024-4069
DDR2	Discoidin domain receptor tyrosine kinase 2	SEQ ID NOS: 4070-4075
DDT	D-dopachrome tautomerase	SEQ ID NOS: 4076-4081
DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17	SEQ ID NOS: 4082-4086
DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	SEQ ID NOS: 4087-4089
DDX25	DEAD (Asp-Glu-Ala-Asp) box helicase 25	SEQ ID NOS: 4090-4096
DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	SEQ ID NO: 4097
DEAE1	DEAF1 transcription factor	SEQ ID NOS: 4098-4100
DEF8	Differentially expressed in FDCP 8 homolog (mouse)	SEQ ID NOS: 4101-4120
DEFA1	Defensin, alpha 1	SEQ ID NOS: 4121-4122
DEFA1B	Defensin, alpha 1B	SEQ ID NO: 4123
DEFA3	Defensin, alpha 3, neutrophil-specific	SEQ ID NO: 4124
DEFA4	Defensin, alpha 4, cortistatin	SEQ ID NO: 4125
DEFA5	Defensin, alpha 5, Paneth cell-specific	SEQ ID NO: 4126
DEFA6	Defensin, alpha 6, Paneth cell-specific	SEQ ID NO: 4127
DEFB1	Defensin, beta 1	SEQ ID NO: 4128
DEFB103A	Defensin, beta 103A	SEQ ID NO: 4129
DEFB103B	Defensin, beta 103B	SEQ ID NO: 4130
DEFB104A	Defensin, beta 104A	SEQ ID NO: 4131
DEFB104B	Defensin, beta 104B	SEQ ID NO: 4132
DEFB105A	Defensin, beta 105A	SEQ ID NO: 4133
DEFB105B	Defensin, beta 105B	SEQ ID NO: 4134
DEFB106A	Defensin, beta 106A	SEQ ID NO: 4135
DEFB106B	Defensin, beta 106B	SEQ ID NO: 4136
DEFB107A	Defensin, beta 107A	SEQ ID NO: 4137
DEFB107B	Defensin, beta 107B	SEQ ID NO: 4138
DEFB108B	Defensin, beta 108B	SEQ ID NO: 4139
DEFB110	Defensin, beta 110	SEQ ID NOS: 4140-4141
DEFB113	Defensin, beta 113	SEQ ID NO: 4142
DEFB114	Defensin, beta 114	SEQ ID NO: 4143
DEFB115	Defensin, beta 115	SEQ ID NO: 4144
DEFB116	Defensin, beta 116	SEQ ID NO: 4145
DEFB118	Defensin, beta 118	SEQ ID NO: 4146
DEFB119	Defensin, beta 119	SEQ ID NOS: 4147-4149
DEFB121	Defensin, beta 121	SEQ ID NO: 4150
DEEB123	Defensin, beta 123	SEQ ID NO: 4151
DEFB124	Defensin, beta 124	SEQ ID NO: 4152
DEFB125	Defensin, beta 125	SEQ ID NO: 4153
DEFB126	Defensin, beta 126	SEQ ID NO: 4154
DEFB127	Defensin, beta 127	SEQ ID NO: 4155
DEEB128	Defensin, beta 128	SEQ ID NO: 4156
DEFB129	Defensin, beta 129	SEQ ID NO: 4157
DEFB130	Defensin, beta 130	SEQ ID NO: 4158
RP11-1236K1.1		SEQ ID NO: 4159
DEFB131	Defensin, beta 131	SEQ ID NO: 4160
CTD-2313N18.7		SEQ ID NO: 4161
DEFB132	Defensin, beta 132	SEQ ID NO: 4162
DEFB133	Defensin, beta 133	SEQ ID NO: 4163
DEFB134	Defensin, beta 134	SEQ ID NOS: 4164-4165
DEFB135	Defensin, beta 135	SEQ ID NO: 4166
DEEB136	Defensin, beta 136	SEQ ID NO: 4167
DEFB4A	Defensin, beta 4A	SEQ ID NO: 4168
DEFB4B	Defensin, beta 4B	SEQ ID NO: 4169
C10orf10	Chromosome 10 open reading frame 10	SEQ ID NOS: 4170-4171
DGCR2	DiGeorge syndrome critical region gene 2	SEQ ID NOS: 4172-4175
DHH	Desert hedgehog	SEQ ID NO: 4176
DHRS4	Dehydrogenase/reductase (SDR family) member 4	SEQ ID NOS: 4177-4184

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
DHRS4L2	Dehydrogenase/reductase (SDR family) member 4 like 2	SEQ ID NOS: 4185-4194
DHRS7	Dehydrogenase/reductase (SDR family) member 7	SEQ ID NOS: 4195-4202
DHRS7C	Dehydrogenase/reductase (SDR family) member 7C	SEQ ID NOS: 4203-4205
DHRS9	Dehydrogenase/reductase (SDR family) member 9	SEQ ID NOS: 4206-4213
DHRSX	Dehydrogenase/reductase (SDR family) X-linked	SEQ ID NOS: 4214-4218
DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	SEQ ID NOS: 4219-4221
DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30	SEQ ID NOS: 4222-4229
DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	SEQ ID NOS: 4230-4234
DIO2	Deiodinase, iodothyronine, type II	SEQ ID NOS: 4235-4244
DIXDC1	DIX domain containing 1	SEQ ID NOS: 4245-4248
DKK1	Dickkopf WNT signaling pathway inhibitor 1	SEQ ID NO: 4249
DKK2	Dickkopf WNT signaling pathway inhibitor 2	SEQ ID NOS: 4250-4252
DKK3	Dickkopf WNT signaling pathway inhibitor 3	SEQ ID NOS: 4253-4258
DKK4	Dickkopf WNT signaling pathway inhibitor 4	SEQ ID NO: 4259
DKKL1	Dickkopf-like 1	SEQ ID NOS: 4260-4265
DLG4	Discs, large homolog 4 (<i>Drosophila</i>)	SEQ ID NOS: 4266-4274
DLK1	Delta-like 1 homolog (<i>Drosophila</i>)	SEQ ID NOS: 4275-4278
DLL1	Delta-like 1 (<i>Drosophila</i>)	SEQ ID NOS: 4279-4280
DLL3	Delta-like 3 (<i>Drosophila</i>)	SEQ ID NOS: 4281-4283
DMBT1	Deleted in malignant brain tumors 1	SEQ ID NOS: 4284-4290
DMKN	Dermokine	SEQ ID NOS: 4291-4337
DMP1	Dentin matrix acidic phosphoprotein 1	SEQ ID NOS: 4338-4339
DMRTA2	DMRT-like family A2	SEQ ID NOS: 4340-4341
DNAAF5	Dynein, axonemal, assembly factor 5	SEQ ID NOS: 4342-4345
DNAH14	Dynein, axonemal, heavy chain 14	SEQ ID NOS: 4346-4360
DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	SEQ ID NOS: 4361-4362
DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	SEQ ID NO: 4363
DNAJC25-GNG10	DNAJC25-GNG10 readthrough	SEQ ID NO: 4364
DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	SEQ ID NOS: 4365-4366
DNASE1	Deoxyribonuclease I	SEQ ID NOS: 4367-4377
DNASE1L1	Deoxyribonuclease I-like 1	SEQ ID NOS: 4378-4388
DNASE1L2	Deoxyribonuclease I-like 2	SEQ ID NOS: 4389-4394
DNASE1L3	Deoxyribonuclease I-like 3	SEQ ID NOS: 4395-4400
DNASE2	Deoxyribonuclease II, lysosomal	SEQ ID NOS: 4401-4402
DNASE2B	Deoxyribonuclease II beta	SEQ ID NOS: 4403-4404
DPEP1	Dipeptidase 1 (renal)	SEQ ID NOS: 4405-4409
DPEP2	Dipeptidase 2	SEQ ID NOS: 4410-4416
DPEP3	Dipeptidase 3	SEQ ID NO: 4417
DPF3	D4, zinc and double PHD fingers, family 3	SEQ ID NOS: 4418-4424
DPP4	Dipeptidyl-peptidase 4	SEQ ID NOS: 4425-4429
DPP7	Dipeptidyl-peptidase 7	SEQ ID NOS: 4430-4435
DPT	Dermatopontin	SEQ ID NO: 4436
DRAXIN	Dorsal inhibitory axon guidance protein	SEQ ID NO: 4437
DSE	Dermatan sulfate epimerase	SEQ ID NOS: 4438-4446
DSG2	Desmoglein 2	SEQ ID NOS: 4447-4448
DSPP	Dentin sialophosphoprotein	SEQ ID NOS: 4449-4450
DST	Dystonin	SEQ ID NOS: 4451-4469
DUOX1	Dual oxidase 1	SEQ ID NOS: 4470-4474
DYNLT3	Dynein, light chain, Tctex-type 3	SEQ ID NOS: 4475-4477
E2F5	E2F transcription factor 5, p130-binding	SEQ ID NOS: 4478-4484
EBAG9	Estrogen receptor binding site associated, antigen, 9	SEQ ID NOS: 4485-4493
EBI3	Epstein-Barr virus induced 3	SEQ ID NO: 4494
ECHDC1	Ethylmalonyl-CoA decarboxylase 1	SEQ ID NOS: 4495-4513
ECM1	Extracellular matrix protein 1	SEQ ID NOS: 4514-4516
ECM2	Extracellular matrix protein 2, female organ and adipocyte specific	SEQ ID NOS: 4517-4520
ECSIT	ECSIT signalling integrator	SEQ ID NOS: 4521-4532
EDDM3A	Epididymal protein 3A	SEQ ID NO: 4533
EDDM3B	Epididymal protein 3B	SEQ ID NO: 4534
EDEM2	ER degradation enhancer, mannosidase alpha-like 2	SEQ ID NOS: 4535-4536
EDEM3	ER degradation enhancer, mannosidase alpha-like 3	SEQ ID NOS: 4537-4539
EDIL3	EGF-like repeats and discoidin I-like domains 3	SEQ ID NOS: 4540-4541
EDN1	Endothelin 1	SEQ ID NO: 4542
EDN2	Endothelin 2	SEQ ID NO: 4543
EDN3	Endothelin 3	SEQ ID NOS: 4544-4549
EDNRB	Endothelin receptor type B	SEQ ID NOS: 4550-4558
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	SEQ ID NOS: 4559-4569

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	SEQ ID NOS: 4570-4581
EFNA1	Ephrin-A1	SEQ ID NOS: 4582-4583
EFNA2	Ephrin-A2	SEQ ID NO: 4584
EFNA4	Ephrin-A4	SEQ ID NOS: 4585-4587
EGFL6	EGF-like-domain, multiple 6	SEQ ID NOS: 4588-4589
EGFL7	EGF-like-domain, multiple 7	SEQ ID NOS: 4590-4594
EGFL8	EGF-like-domain, multiple 8	SEQ ID NOS: 4595-4597
EGFLAM	EGF-like, fibronectin type III and laminin G domains	SEQ ID NOS: 4598-4606
EGFR	Epidermal growth factor receptor	SEQ ID NOS: 4607-4614
EHBP1	EH domain binding protein 1	SEQ ID NOS: 4615-4626
EHF	Ets homologous factor	SEQ ID NOS: 4627-4636
EHMT1	Euchromatic histone-lysine N-methyltransferase 1	SEQ ID NOS: 4637-4662
EHMT2	Euchromatic histone-lysine N-methyltransferase 2	SEQ ID NOS: 4663-4667
EIF2AK1	Eukaryotic translation initiation factor 2-alpha kinase 1	SEQ ID NOS: 4668-4671
ELANE	Elastase, neutrophil expressed	SEQ ID NOS: 4672-4673
ELN	Elastin	SEQ ID NOS: 4674-4696
ELP2	Elongator acetyltransferase complex subunit 2	SEQ ID NOS: 4697-4709
ELSPBP1	Epididymal sperm binding protein 1	SEQ ID NOS: 4710-4715
EMC1	ER membrane protein complex subunit 1	SEQ ID NOS: 4716-4722
EMC10	ER membrane protein complex subunit 10	SEQ ID NOS: 4723-4729
EMC9	ER membrane protein complex subunit 9	SEQ ID NOS: 4730-4733
EMCN	Endomucin	SEQ ID NOS: 4734-4738
EMID1	EMI domain containing 1	SEQ ID NOS: 4739-4745
EMILIN1	Elastin microfibril interfacer 1	SEQ ID NOS: 4746-4747
EMILIN2	Elastin microfibril interfacer 2	SEQ ID NO: 4748
EMILIN3	Elastin microfibril interfacer 3	SEQ ID NO: 4749
ENAM	Enamelin	SEQ ID NO: 4750
ENDOG	Endonuclease G	SEQ ID NO: 4751
ENDOU	Endonuclease, polyU-specific	SEQ ID NOS: 4752-4754
ENHO	Energy homeostasis associated	SEQ ID NO: 4755
ENO4	Enolase family member 4	SEQ ID NOS: 4756-4760
ENPP6	Ectonucleotide pyrophosphatase/phosphodiesterase 6	SEQ ID NOS: 4761-4762
ENPP7	Ectonucleotide pyrophosphatase/phosphodiesterase 7	SEQ ID NOS: 4763-4764
ENTPD5	Ectonucleoside triphosphate diphosphohydrolase 5	SEQ ID NOS: 4765-4769
ENTPD8	Ectonucleoside triphosphate diphosphohydrolase 8	SEQ ID NOS: 4770-4773
EOGT	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	SEQ ID NOS: 4774-4781
EPCAM	Epithelial cell adhesion molecule	SEQ ID NOS: 4782-4785
EPDR1	Ependymin related 1	SEQ ID NOS: 4786-4789
EPGN	Epithelial mitogen	SEQ ID NOS: 4790-4798
EPHA10	EPH receptor A10	SEQ ID NOS: 4799-4806
EPHA3	EPH receptor A3	SEQ ID NOS: 4807-4809
EPHA4	EPH receptor A4	SEQ ID NOS: 4810-4819
EPHA7	EPH receptor A7	SEQ ID NOS: 4820-4821
EPHA8	EPH receptor A8	SEQ ID NOS: 4822-4823
EPHB2	EPH receptor B2	SEQ ID NOS: 4824-4828
EPHB4	EPH receptor B4	SEQ ID NOS: 4829-4831
EPHX3	Epoxide hydrolase 3	SEQ ID NOS: 4832-4835
EPO	Erythropoietin	SEQ ID NO: 4836
EPPIN	Epididymal peptidase inhibitor	SEQ ID NOS: 4837-4839
EPPIN-WFDC6	EPPIN-WFDC6 readthrough	SEQ ID NO: 4840
WFDC6		
EPS15	Epidermal growth factor receptor pathway substrate 15	SEQ ID NOS: 4841-4843
EPS8L1	EPS8-like 1	SEQ ID NOS: 4844-4849
EPX	Eosinophil peroxidase	SEQ ID NO: 4850
EPYC	Epiphykan	SEQ ID NOS: 4851-4852
EQTN	Equatorin, sperm acrosome associated	SEQ ID NOS: 4853-4855
ERAP1	Endoplasmic reticulum aminopeptidase 1	SEQ ID NOS: 4856-4861
ERAP2	Endoplasmic reticulum aminopeptidase 2	SEQ ID NOS: 4862-4869
ERBB3	Erb-b2 receptor tyrosine kinase 3	SEQ ID NOS: 4870-4883
FAM132B	Family with sequence similarity 132, member B	SEQ ID NOS: 4884-4886
ERLIN1	ER lipid raft associated 1	SEQ ID NOS: 4887-4889
ERLIN2	ER lipid raft associated 2	SEQ ID NOS: 4890-4898
ERN1	Endoplasmic reticulum to nucleus signaling 1	SEQ ID NOS: 4899-4900
ERN2	Endoplasmic reticulum to nucleus signaling 2	SEQ ID NOS: 4901-4905
ERO1A	Endoplasmic reticulum oxidoreductase alpha	SEQ ID NOS: 4906-4912
ERO1B	Endoplasmic reticulum oxidoreductase beta	SEQ ID NOS: 4913-4915
ERP27	Endoplasmic reticulum protein 27	SEQ ID NOS: 4916-4917

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ERP29	Endoplasmic reticulum protein 29	SEQ ID NOS: 4918-4921
ERP44	Endoplasmic reticulum protein 44	SEQ ID NO: 4922
ERV3-1	Endogenous retrovirus group 3, member 1	SEQ ID NO: 4923
ESM1	Endothelial cell-specific molecule 1	SEQ ID NOS: 4924-4926
ESRP1	Epithelial splicing regulatory protein 1	SEQ ID NOS: 4927-4935
EXOGL	Endo/exonuclease (5'-3'), endonuclease G-like	SEQ ID NOS: 4936-4949
EXTL1	Exostosin-like glycosyltransferase 1	SEQ ID NO: 4950
EXTL2	Exostosin-like glycosyltransferase 2	SEQ ID NOS: 4951-4955
F10	Coagulation factor X	SEQ ID NOS: 4956-4959
F11	Coagulation factor XI	SEQ ID NOS: 4960-4964
F12	Coagulation factor XII (Hageman factor)	SEQ ID NO: 4965
F13B	Coagulation factor XIII, B polypeptide	SEQ ID NO: 4966
F2	Coagulation factor II (thrombin)	SEQ ID NOS: 4967-4969
F2R	Coagulation factor II (thrombin) receptor	SEQ ID NOS: 4970-4971
F2RL3	Coagulation factor II (thrombin) receptor-like 3	SEQ ID NOS: 4972-4973
F5	Coagulation factor V (proaccelerin, labile factor)	SEQ ID NOS: 4974-4975
F7	Coagulation factor VII (serum prothrombin conversion accelerator)	SEQ ID NOS: 4976-4979
F8	Coagulation factor VIII, procoagulant component	SEQ ID NOS: 4980-4985
F9	Coagulation factor IX	SEQ ID NOS: 4986-4987
FABP6	Fatty acid binding protein 6, ileal	SEQ ID NOS: 4988-4990
FAM107B	Family with sequence similarity 107, member B	SEQ ID NOS: 4991-5012
FAM131A	Family with sequence similarity 131, member A	SEQ ID NOS: 5013-5021
FAM171A1	Family with sequence similarity 171, member A1	SEQ ID NOS: 5022-5023
FAM171B	Family with sequence similarity 171, member B	SEQ ID NOS: 5024-5025
FAM172A	Family with sequence similarity 172, member A	SEQ ID NOS: 5026-5030
FAM177A1	Family with sequence similarity 177, member A1	SEQ ID NOS: 5031-5040
FAM180A	Family with sequence similarity 180, member A	SEQ ID NOS: 5041-5043
FAM189A1	Family with sequence similarity 189, member A1	SEQ ID NOS: 5044-5045
FAM198A	Family with sequence similarity 198, member A	SEQ ID NOS: 5046-5048
FAM19A1	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	SEQ ID NOS: 5049-5051
FAM19A2	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	SEQ ID NOS: 5052-5059
FAM19A3	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A3	SEQ ID NOS: 5060-5061
FAM19A4	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	SEQ ID NOS: 5062-5064
FAM19A5	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	SEQ ID NOS: 5065-5068
FAM20A	Family with sequence similarity 20, member A	SEQ ID NOS: 5069-5072
FAM20C	Family with sequence similarity 20, member C	SEQ ID NO: 5073
FAM213A	Family with sequence similarity 213, member A	SEQ ID NOS: 5074-5079
FAM46B	Family with sequence similarity 46, member B	SEQ ID NO: 5080
FAM57A	Family with sequence similarity 57, member A	SEQ ID NOS: 5081-5086
FAM78A	Family with sequence similarity 78, member A	SEQ ID NOS: 5087-5089
FAM96A	Family with sequence similarity 96, member A	SEQ ID NOS: 5090-5094
FAM9B	Family with sequence similarity 9, member B	SEQ ID NOS: 5095-5098
FAP	Fibroblast activation protein, alpha	SEQ ID NOS: 5099-5105
FAS	Fas cell surface death receptor	SEQ ID NOS: 5106-5115
FAT1	FAT atypical cadherin 1	SEQ ID NOS: 5116-5122
FBLN1	Fibulin 1	SEQ ID NOS: 5123-5135
FBLN2	Fibulin 2	SEQ ID NOS: 5136-5141
FBLN5	Fibulin 5	SEQ ID NOS: 5142-5147
FBLN7	Fibulin 7	SEQ ID NOS: 5148-5153
FBN1	Fibrillin 1	SEQ ID NOS: 5154-5157
FBN2	Fibrillin 2	SEQ ID NOS: 5158-5163
FBN3	Fibrillin 3	SEQ ID NOS: 5164-5168
FBXW7	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	SEQ ID NOS: 5169-5179
FCAR	Fc fragment of IgA receptor	SEQ ID NOS: 5180-5189
FCGBP	Fc fragment of IgG binding protein	SEQ ID NOS: 5190-5192
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	SEQ ID NOS: 5193-5198
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	SEQ ID NOS: 5199-5205
FCGRT	Fc fragment of IgG, receptor, transporter, alpha	SEQ ID NOS: 5206-5216
FCMR	Fc fragment of IgM receptor	SEQ ID NOS: 5217-5223
FCN1	Ficolin (collagen/fibrinogen domain containing) 1	SEQ ID NOS: 5224-5225
FCN2	Ficolin (collagen/fibrinogen domain containing lectin) 2	SEQ ID NOS: 5226-5227
FCN3	Ficolin (collagen/fibrinogen domain containing) 3	SEQ ID NOS: 5228-5229
FCRL1	Fc receptor-like 1	SEQ ID NOS: 5230-5232
FCRL3	Fc receptor-like 3	SEQ ID NOS: 5233-5238

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
FCRL5	Fc receptor-like 5	SEQ ID NOS: 5239-5241
FCRLA	Fc receptor-like A	SEQ ID NOS: 5242-5253
FCRLB	Fc receptor-like B	SEQ ID NOS: 5254-5258
FDCSP	Follicular dendritic cell secreted protein	SEQ ID NO: 5259
FETUB	Fetuin B	SEQ ID NOS: 5260-5266
FGA	Fibrinogen alpha chain	SEQ ID NOS: 5267-5269
FGB	Fibrinogen beta chain	SEQ ID NOS: 5270-5272
FGF10	Fibroblast growth factor 10	SEQ ID NOS: 5273-5274
FGF17	Fibroblast growth factor 17	SEQ ID NOS: 5275-5276
FGF18	Fibroblast growth factor 18	SEQ ID NO: 5277
FGF19	Fibroblast growth factor 19	SEQ ID NO: 5278
FGF21	Fibroblast growth factor 21	SEQ ID NOS: 5279-5280
FGF22	Fibroblast growth factor 22	SEQ ID NOS: 5281-5282
FGF23	Fibroblast growth factor 23	SEQ ID NO: 5283
FGF3	Fibroblast growth factor 3	SEQ ID NO: 5284
FGF4	Fibroblast growth factor 4	SEQ ID NO: 5285
FGF5	Fibroblast growth factor 5	SEQ ID NOS: 5286-5288
FGF7	Fibroblast growth factor 7	SEQ ID NOS: 5289-5293
FGF8	Fibroblast growth factor 8 (androgen-induced)	SEQ ID NOS: 5294-5299
FGFBP1	Fibroblast growth factor binding protein 1	SEQ ID NO: 5300
FGFBP2	Fibroblast growth factor binding protein 2	SEQ ID NO: 5301
FGFBP3	Fibroblast growth factor binding protein 3	SEQ ID NO: 5302
FGFR1	Fibroblast growth factor receptor 1	SEQ ID NOS: 5303-5325
FGFR2	Fibroblast growth factor receptor 2	SEQ ID NOS: 5326-5347
FGFR3	Fibroblast growth factor receptor 3	SEQ ID NOS: 5348-5355
FGFR4	Fibroblast growth factor receptor 4	SEQ ID NOS: 5356-5365
FGFRL1	Fibroblast growth factor receptor-like 1	SEQ ID NOS: 5366-5371
FGG	Fibrinogen gamma chain	SEQ ID NOS: 5372-5377
FGL1	Fibrinogen-like 1	SEQ ID NOS: 5378-5384
FGL2	Fibrinogen-like 2	SEQ ID NOS: 5385-5386
FHL1	Four and a half LIM domains 1	SEQ ID NOS: 5387-5414
FHOD3	Formin homology 2 domain containing 3	SEQ ID NOS: 5415-5421
FIBIN	Fin bud initiation factor homolog (zebrafish)	SEQ ID NO: 5422
FICD	FIC domain containing	SEQ ID NOS: 5423-5426
FJX1	Four jointed box 1	SEQ ID NO: 5427
FKBP10	FK506 binding protein 10, 65 kDa	SEQ ID NOS: 5428-5433
FKBP11	FK506 binding protein 11, 19 kDa	SEQ ID NOS: 5434-5440
FKBP14	FK506 binding protein 14, 22 kDa	SEQ ID NOS: 5441-5443
FKBP2	FK506 binding protein 2, 13 kDa	SEQ ID NOS: 5444-5447
FKBP7	FK506 binding protein 7	SEQ ID NOS: 5448-5453
FKBP9	FK506 binding protein 9, 63 kDa	SEQ ID NOS: 5454-5457
FLT1	Fms-related tyrosine kinase 1	SEQ ID NOS: 5458-5466
FLT4	Fms-related tyrosine kinase 4	SEQ ID NOS: 5467-5471
FMO1	Flavin containing monooxygenase 1	SEQ ID NOS: 5472-5476
FMO2	Flavin containing monooxygenase 2 (non-functional)	SEQ ID NOS: 5477-5479
FMO3	Flavin containing monooxygenase 3	SEQ ID NOS: 5480-5482
FMO5	Flavin containing monooxygenase 5	SEQ ID NOS: 5483-5489
FMOD	Fibromodulin	SEQ ID NO: 5490
FN1	Fibronectin 1	SEQ ID NOS: 5491-5503
FNDC1	Fibronectin type III domain containing 1	SEQ ID NOS: 5504-5505
FNDC7	Fibronectin type III domain containing 7	SEQ ID NOS: 5506-5507
FOCAD	Focadhesin	SEQ ID NOS: 5508-5514
FOLR2	Folate receptor 2 (fetal)	SEQ ID NOS: 5515-5524
FOLR3	Folate receptor 3 (gamma)	SEQ ID NOS: 5525-5529
FOXRED2	FAD-dependent oxidoreductase domain containing 2	SEQ ID NOS: 5530-5533
FP325331.1	Uncharacterized protein UNQ6126/PRO20091	SEQ ID NO: 5534
CH507-9B2.3		SEQ ID NOS: 5535-5541
FPGS	Folylpolyglutamate synthase	SEQ ID NOS: 5542-5548
FRAS1	Fraser extracellular matrix complex subunit 1	SEQ ID NOS: 5549-5554
FREM1	FRAS1 related extracellular matrix 1	SEQ ID NOS: 5555-5559
FREM3	FRAS1 related extracellular matrix 3	SEQ ID NO: 5560
FRMPD2	FERM and PDZ domain containing 2	SEQ ID NOS: 5561-5564
FRZB	Frizzled-related protein	SEQ ID NO: 5565
FSHB	Follicle stimulating hormone, beta polypeptide	SEQ ID NOS: 5566-5568
FSHR	Follicle stimulating hormone receptor	SEQ ID NOS: 5569-5572
FST	Follistatin	SEQ ID NOS: 5573-5576
FSTL1	Follistatin-like 1	SEQ ID NOS: 5577-5580
FSTL3	Follistatin-like 3 (secreted glycoprotein)	SEQ ID NOS: 5581-5586

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
FSTL4	Follistatin-like 4	SEQ ID NOS: 5587-5589
FSTL5	Follistatin-like 5	SEQ ID NOS: 5590-5592
FTCDNL1	Formiminotransferase cyclodeaminase N-terminal like	SEQ ID NOS: 5593-5596
FUCA1	Fucosidase, alpha-L-1, tissue	SEQ ID NO: 5597
FUCA2	Fucosidase, alpha-L-2, plasma	SEQ ID NOS: 5598-5599
FURIN	Furin (paired basic amino acid cleaving enzyme)	SEQ ID NOS: 5600-5606
FUT10	Fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	SEQ ID NOS: 5607-5609
FUT11	Fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	SEQ ID NOS: 5610-5611
FXN	Frataxin	SEQ ID NOS: 5612-5619
FXR1	Fragile X mental retardation, autosomal homolog 1	SEQ ID NOS: 5620-5632
FXYD3	FXYD domain containing ion transport regulator 3	SEQ ID NOS: 5633-5645
GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1	SEQ ID NOS: 5646-5657
GABRA1	Gamma-aminobutyric acid (GABA) A receptor, alpha 1	SEQ ID NOS: 5658-5673
GABRA2	Gamma-aminobutyric acid (GABA) A receptor, alpha 2	SEQ ID NOS: 5674-5688
GABRA5	Gamma-aminobutyric acid (GABA) A receptor, alpha 5	SEQ ID NOS: 5689-5697
GABRG3	Gamma-aminobutyric acid (GABA) A receptor, gamma 3	SEQ ID NOS: 5698-5703
GABRP	Gamma-aminobutyric acid (GABA) A receptor, pi	SEQ ID NOS: 5704-5712
GAL	Galanin/GMAP prepropeptide	SEQ ID NO: 5713
GAL3ST1	Galactose-3-O-sulfotransferase 1	SEQ ID NOS: 5714-5735
GAL3ST2	Galactose-3-O-sulfotransferase 2	SEQ ID NO: 5736
GAL3ST3	Galactose-3-O-sulfotransferase 3	SEQ ID NOS: 5737-5738
GALC	Galactosylceramidase	SEQ ID NOS: 5739-5748
GALNS	Galactosamine (N-acetyl)-6-sulfatase	SEQ ID NOS: 5749-5754
GALNT10	Polypeptide N-acetylgalactosaminyltransferase 10	SEQ ID NOS: 5755-5758
GALNT12	Polypeptide N-acetylgalactosaminyltransferase 12	SEQ ID NOS: 5759-5760
GALNT15	Polypeptide N-acetylgalactosaminyltransferase 15	SEQ ID NOS: 5761-5764
GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	SEQ ID NO: 5765
GALNT6	Polypeptide N-acetylgalactosaminyltransferase 6	SEQ ID NOS: 5766-5777
GALNT8	Polypeptide N-acetylgalactosaminyltransferase 8	SEQ ID NOS: 5778-5781
GALNTL6	Polypeptide N-acetylgalactosaminyltransferase-like 6	SEQ ID NOS: 5782-5785
GALP	Galanin-like peptide	SEQ ID NOS: 5786-5788
GANAB	Glucosidase, alpha; neutral AB	SEQ ID NOS: 5789-5797
GARS	Glycyl-tRNA synthetase	SEQ ID NOS: 5798-5801
GAS1	Growth arrest-specific 1	SEQ ID NO: 5802
GAS6	Growth arrest-specific 6	SEQ ID NO: 5803
GAST	Gastrin	SEQ ID NO: 5804
PDDC1	Parkinson disease 7 domain containing 1	SEQ ID NOS: 5805-5813
GBA	Glucosidase, beta, acid	SEQ ID NOS: 5814-5817
GBGT1	Globoside alpha-1,3-N-acetylgalactosaminyltransferase	SEQ ID NOS: 5818-5826
GC	Group-specific component (vitamin D binding protein)	SEQ ID NOS: 5827-5831
GCG	Glucagon	SEQ ID NOS: 5832-5833
GCGR	Glucagon receptor	SEQ ID NOS: 5834-5836
GCNT7	Glucosaminyl (N-acetyl) transferase family member 7	SEQ ID NOS: 5837-5838
GCSH	Glycine cleavage system protein H (aminomethyl carrier)	SEQ ID NOS: 5839-5847
GDF1	Growth differentiation factor 1	SEQ ID NO: 5848
GDF10	Growth differentiation factor 10	SEQ ID NO: 5849
GDF11	Growth differentiation factor 11	SEQ ID NOS: 5850-5851
GDF15	Growth differentiation factor 15	SEQ ID NOS: 5852-5854
GDF2	Growth differentiation factor 2	SEQ ID NO: 5855
GDF3	Growth differentiation factor 3	SEQ ID NO: 5856
GDF5	Growth differentiation factor 5	SEQ ID NOS: 5857-5858
GDF6	Growth differentiation factor 6	SEQ ID NOS: 5859-5861
GDF7	Growth differentiation factor 7	SEQ ID NO: 5862
GDF9	Growth differentiation factor 9	SEQ ID NOS: 5863-5867
GDNF	Glial cell derived neurotrophic factor	SEQ ID NOS: 5868-5875
GFOD2	Glucose-fructose oxidoreductase domain containing 2	SEQ ID NOS: 5876-5881
GFPT2	Glutamine-fructose-6-phosphate transaminase 2	SEQ ID NOS: 5882-5884
GFRA2	GDNF family receptor alpha 2	SEQ ID NOS: 5885-5891
GFRA4	GDNF family receptor alpha 4	SEQ ID NOS: 5892-5894
GGA2	Golgi-associated, gamma adaptin ear containing, ARF binding protein 2	SEQ ID NOS: 5895-5903

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
GGH	Gamma-glutamyl hydrolase (conjugase, folicpolygammaglutamyl hydrolase)	SEQ ID NO: 5904
GGT1	Gamma-glutamyltransferase 1	SEQ ID NOS: 5905-5927
GGT5	Gamma-glutamyltransferase 5	SEQ ID NOS: 5928-5932
GH1	Growth hormone 1	SEQ ID NOS: 5933-5937
GH2	Growth hormone 2	SEQ ID NOS: 5938-5942
GHDC	GH3 domain containing	SEQ ID NOS: 5943-5950
GHRH	Growth hormone releasing hormone	SEQ ID NOS: 5951-5953
GHRHR	Growth hormone releasing hormone receptor	SEQ ID NOS: 5954-5959
GHLR	Ghrelin/obestatin prepropeptide	SEQ ID NOS: 5960-5970
GIF	Gastric intrinsic factor (vitamin B synthesis)	SEQ ID NOS: 5971-5972
GIP	Gastric inhibitory polypeptide	SEQ ID NO: 5973
GKN1	Gastrokine 1	SEQ ID NO: 5974
GKN2	Gastrokine 2	SEQ ID NOS: 5975-5976
GLA	Galactosidase, alpha	SEQ ID NOS: 5977-5978
GLB1	Galactosidase, beta 1	SEQ ID NOS: 5979-5987
GLB1L	Galactosidase, beta 1-like	SEQ ID NOS: 5988-5995
GLB1L2	Galactosidase, beta 1-like 2	SEQ ID NOS: 5996-5997
GLCE	Glucuronic acid epimerase	SEQ ID NOS: 5998-5999
GLG1	Golgi glycoprotein 1	SEQ ID NOS: 6000-6007
GLIPR1	GLI pathogenesis-related 1	SEQ ID NOS: 6008-6011
GLIPR1L1	GLI pathogenesis-related 1 like 1	SEQ ID NOS: 6012-6015
GLIS3	GLIS family zinc finger 3	SEQ ID NOS: 6016-6024
GLMP	Glycosylated lysosomal membrane protein	SEQ ID NOS: 6025-6033
GLRB	Glycine receptor, beta	SEQ ID NOS: 6034-6039
GLS	Glutaminase	SEQ ID NOS: 6040-6047
GLT6D1	Glycosyltransferase 6 domain containing 1	SEQ ID NOS: 6048-6049
GLTPD2	Glycolipid transfer protein domain containing 2	SEQ ID NO: 6050
GLUD1	Glutamate dehydrogenase 1	SEQ ID NO: 6051
GM2A	GM2 ganglioside activator	SEQ ID NOS: 6052-6054
GML	Glycosylphosphatidylinositol anchored molecule like	SEQ ID NOS: 6055-6056
GNAS	GNAS complex locus	SEQ ID NOS: 6057-6078
GNLY	Granulysin	SEQ ID NOS: 6079-6082
GNPTG	N-acetylglucosamine-1-phosphate transferase, gamma subunit	SEQ ID NOS: 6083-6087
GNRH1	Gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	SEQ ID NOS: 6088-6089
GNRH2	Gonadotropin-releasing hormone 2	SEQ ID NOS: 6090-6093
GNS	Glucosamine (N-acetyl)-6-sulfatase	SEQ ID NOS: 6094-6099
GOLM1	Golgi membrane protein 1	SEQ ID NOS: 6100-6104
GORAB	Golgin, RAB6-interacting	SEQ ID NOS: 6105-6107
GOT2	Glutamic-oxaloacetic transaminase 2, mitochondrial	SEQ ID NOS: 6108-6110
GP2	Glycoprotein 2 (zymogen granule membrane)	SEQ ID NOS: 6111-6119
GP6	Glycoprotein VI (platelet)	SEQ ID NOS: 6120-6123
GPC2	Glypican 2	SEQ ID NOS: 6124-6125
GPC5	Glypican 5	SEQ ID NOS: 6126-6128
GPC6	Glypican 6	SEQ ID NOS: 6129-6130
GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	SEQ ID NOS: 6131-6139
GPER1	G protein-coupled estrogen receptor 1	SEQ ID NOS: 6140-6146
GPHA2	Glycoprotein hormone alpha 2	SEQ ID NOS: 6147-6149
GPHB5	Glycoprotein hormone beta 5	SEQ ID NOS: 6150-6151
GPIHBP1	Glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	SEQ ID NO: 6152
GPLD1	Glycosylphosphatidylinositol specific phospholipase D1	SEQ ID NO: 6153
GPNMB	Glycoprotein (transmembrane) nmb	SEQ ID NOS: 6154-6156
GPR162	G protein-coupled receptor 162	SEQ ID NOS: 6157-6160
GPX3	Glutathione peroxidase 3	SEQ ID NOS: 6161-6168
GPX4	Glutathione peroxidase 4	SEQ ID NOS: 6169-6179
GPX5	Glutathione peroxidase 5	SEQ ID NOS: 6180-6181
GPX6	Glutathione peroxidase 6	SEQ ID NOS: 6182-6184
GPX7	Glutathione peroxidase 7	SEQ ID NO: 6185
GREM1	Gremlin 1, DAN family BMP antagonist	SEQ ID NOS: 6186-6188
GREM2	Gremlin 2, DAN family BMP antagonist	SEQ ID NO: 6189
GRHL3	Grainyhead-like transcription factor 3	SEQ ID NOS: 6190-6195
GRIA2	Glutamate receptor, ionotropic, AMPA 2	SEQ ID NOS: 6196-6207
GRIA3	Glutamate receptor, ionotropic, AMPA 3	SEQ ID NOS: 6208-6213
GRIA4	Glutamate receptor, ionotropic, AMPA 4	SEQ ID NOS: 6214-6225
GRIK2	Glutamate receptor, ionotropic, kainate 2	SEQ ID NOS: 6226-6234
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	SEQ ID NOS: 6235-6238

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
GRM2	Glutamate receptor, metabotropic 2	SEQ ID NOS: 6239-6242
GRM3	Glutamate receptor, metabotropic 3	SEQ ID NOS: 6243-6247
GRM5	Glutamate receptor, metabotropic 5	SEQ ID NOS: 6248-6252
GRN	Granulin	SEQ ID NOS: 6253-6268
GRP	Gastrin-releasing peptide	SEQ ID NOS: 6269-6273
DFNA5	Deafness, autosomal dominant 5	SEQ ID NOS: 6274-6282
GSG1	Germ cell associated 1	SEQ ID NOS: 6283-6291
GSN	Gelsolin	SEQ ID NOS: 6292-6300
GTDC1	Glycosyltransferase-like domain containing 1	SEQ ID NOS: 6301-6314
GTPBP10	GTP-binding protein 10 (putative)	SEQ ID NOS: 6315-6323
GUCA2A	Guanylate cyclase activator 2A (guanylin)	SEQ ID NO: 6324
GUCA2B	Guanylate cyclase activator 2B (uroguanylin)	SEQ ID NO: 6325
GUSB	Glucuronidase, beta	SEQ ID NOS: 6326-6330
GVQW1	GVQW motif containing 1	SEQ ID NO: 6331
GXYLT1	Glucoside xylosyltransferase 1	SEQ ID NOS: 6332-6333
GXYLT2	Glucoside xylosyltransferase 2	SEQ ID NOS: 6334-6336
GYPB	Glycoporphin B (MNS blood group)	SEQ ID NOS: 6337-6345
GZMA	Granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	SEQ ID NO: 6346
GZMB	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	SEQ ID NOS: 6347-6355
GZMH	Granzyme H (cathepsin G-like 2, protein h-CCPX)	SEQ ID NOS: 6356-6358
GZMK	Granzyme K (granzyme 3; tryptase II)	SEQ ID NO: 6359
GZMM	Granzyme M (lymphocyte met-ase 1)	SEQ ID NOS: 6360-6361
H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	SEQ ID NOS: 6362-6363
HABP2	Hyaluronan binding protein 2	SEQ ID NOS: 6364-6365
HADHB	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	SEQ ID NOS: 6366-6372
HAMP	Hepcidin antimicrobial peptide	SEQ ID NOS: 6373-6374
HAPLN1	Hyaluronan and proteoglycan link protein 1	SEQ ID NOS: 6375-6381
HAPLN2	Hyaluronan and proteoglycan link protein 2	SEQ ID NOS: 6382-6383
HAPLN3	Hyaluronan and proteoglycan link protein 3	SEQ ID NOS: 6384-6387
HAPLN4	Hyaluronan and proteoglycan link protein 4	SEQ ID NO: 6388
HARS2	Histidyl-tRNA synthetase 2, mitochondrial	SEQ ID NOS: 6389-6404
HAVCR1	Hepatitis A virus cellular receptor 1	SEQ ID NOS: 6405-6409
HCCS	Holocytchrome c synthase	SEQ ID NOS: 6410-6412
HCRT	Hypocretin (orexin) neuropeptide precursor	SEQ ID NO: 6413
CECR5	Cat eye syndrome chromosome region, candidate 5	SEQ ID NOS: 6414-6416
HEATR5A	HEAT repeat containing 5A	SEQ ID NOS: 6417-6423
HEPH	Hephaestin	SEQ ID NOS: 6424-6431
HEXA	Hexosaminidase A (alpha polypeptide)	SEQ ID NOS: 6432-6441
HEXB	Hexosaminidase B (beta polypeptide)	SEQ ID NOS: 6442-6447
HFE2	Hemochromatosis type 2 (juvenile)	SEQ ID NOS: 6448-6454
HGF	Hepatocyte growth factor (hepatopoietin A; scatter factor)	SEQ ID NOS: 6455-6465
HGFAC	HGF activator	SEQ ID NOS: 6466-6467
HHIP	Hedgehog interacting protein	SEQ ID NOS: 6468-6469
HHIPL1	HHIP-like 1	SEQ ID NOS: 6470-6471
HHIPL2	HHIP-like 2	SEQ ID NO: 6472
HHLA1	HERV-H LTR-associating 1	SEQ ID NOS: 6473-6474
HHLA2	HERV-H LTR-associating 2	SEQ ID NOS: 6475-6485
HIBADH	3-hydroxyisobutyrate dehydrogenase	SEQ ID NOS: 6486-6488
HINT2	Histidine triad nucleotide binding protein 2	SEQ ID NO: 6489
HLA-A	Major histocompatibility complex, class I, A	SEQ ID NOS: 6490-6494
HLA-C	Major histocompatibility complex, class I, C	SEQ ID NOS: 6495-6499
HLA-D	Major histocompatibility complex, class II, DO	SEQ ID NOS: 6500-6501
HLA-D	alpha	
DPA1	Major histocompatibility complex, class II, DP	SEQ ID NOS: 6502-6505
HLA-D	alpha 1	
DQA1	Major histocompatibility complex, class II, DQ	SEQ ID NOS: 6506-6511
HLA-D	alpha 1	
DQB1	Major histocompatibility complex, class II, DQ	SEQ ID NOS: 6512-6517
HLA-D	beta 1	
DQB2	Major histocompatibility complex, class II, DQ	SEQ ID NOS: 6518-6521
HMGN1	Hemicentin 1	SEQ ID NOS: 6522-6523
HMGN2	Hemicentin 2	SEQ ID NOS: 6524-6527
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	SEQ ID NOS: 6528-6531
HMSD	Histocompatibility (minor) serpin domain containing	SEQ ID NOS: 6532-6533
HP	Haptoglobin	SEQ ID NOS: 6534-6547
HPR	Haptoglobin-related protein	SEQ ID NOS: 6548-6550

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
HPSE	Heparanase	SEQ ID NOS: 6551-6557
HPSE2	Heparanase 2 (inactive)	SEQ ID NOS: 6558-6563
HPX	Hemopexin	SEQ ID NOS: 6564-6565
HRC	Histidine rich calcium binding protein	SEQ ID NOS: 6566-6568
HRG	Histidine-rich glycoprotein	SEQ ID NO: 6569
HS2ST1	Heparan sulfate 2-O-sulfotransferase 1	SEQ ID NOS: 6570-6572
HS3ST1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	SEQ ID NOS: 6573-6575
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	SEQ ID NO: 6576
HS6ST3	Heparan sulfate 6-O-sulfotransferase 3	SEQ ID NOS: 6577-6578
HSD11B1L	Hydroxysteroid (11-beta) dehydrogenase 1-like	SEQ ID NOS: 6579-6597
HSD17B11	Hydroxysteroid (17-beta) dehydrogenase 11	SEQ ID NOS: 6598-6599
HSD17B7	Hydroxysteroid (17-beta) dehydrogenase 7	SEQ ID NOS: 6600-6604
HSP90B1	Heat shock protein 90 kDa beta (Grp94), member 1	SEQ ID NOS: 6605-6610
HSPA13	Heat shock protein 70 kDa family, member 13	SEQ ID NO: 6611
HSPA5	Heat shock 70 kDa protein 5 (glucose-regulated protein, 78 kDa)	SEQ ID NO: 6612
HSPG2	Heparan sulfate proteoglycan 2	SEQ ID NOS: 6613-6617
HTATIP2	HIV-1 Tat interactive protein 2, 30 kDa	SEQ ID NOS: 6618-6625
HTN1	Histatin 1	SEQ ID NOS: 6626-6628
HTN3	Histatin 3	SEQ ID NOS: 6629-6631
HTRA1	HtrA serine peptidase 1	SEQ ID NOS: 6632-6633
HTRA3	HtrA serine peptidase 3	SEQ ID NOS: 6634-6635
HTRA4	HtrA serine peptidase 4	SEQ ID NO: 6636
HYAL1	Hyaluronoglucosaminidase 1	SEQ ID NOS: 6637-6645
IYAL2	Hyaluronoglucosaminidase 2	SEQ ID NOS: 6646-6654
HYAL3	Hyaluronoglucosaminidase 3	SEQ ID NOS: 6655-6661
HYOU1	Hypoxia up-regulated 1	SEQ ID NOS: 6662-6676
IAPP	Islet amyloid polypeptide	SEQ ID NOS: 6677-6681
IBSP	Integrin-binding sialoprotein	SEQ ID NO: 6682
ICAM1	Intercellular adhesion molecule 1	SEQ ID NOS: 6683-6685
ICAM2	Intercellular adhesion molecule 2	SEQ ID NOS: 6686-6696
ICAM4	Intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	SEQ ID NOS: 6697-6699
ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	SEQ ID NOS: 6700-6701
IDE	Insulin-degrading enzyme	SEQ ID NOS: 6702-6705
IDNK	IdnK, gluconokinase homolog (<i>E. coli</i>)	SEQ ID NOS: 6706-6711
IDS	Iduronate 2-sulfatase	SEQ ID NOS: 6712-6717
IDUA	Iduronidase, alpha-L	SEQ ID NOS: 6718-6723
IFI27L2	Interferon, alpha-inducible protein 27-like 2	SEQ ID NOS: 6724-6725
IFI30	Interferon, gamma-inducible protein 30	SEQ ID NOS: 6726-6727
IFNA1	Interferon, alpha 1	SEQ ID NO: 6728
IFNA10	Interferon, alpha 10	SEQ ID NO: 6729
IFNA13	Interferon, alpha 13	SEQ ID NOS: 6730-6731
IFNA14	Interferon, alpha 14	SEQ ID NO: 6732
IFNA16	Interferon, alpha 16	SEQ ID NO: 6733
IFNA17	Interferon, alpha 17	SEQ ID NO: 6734
IFNA2	Interferon, alpha 2	SEQ ID NO: 6735
IFNA21	Interferon, alpha 21	SEQ ID NO: 6736
IFNA4	Interferon, alpha 4	SEQ ID NO: 6737
IFNA5	Interferon, alpha 5	SEQ ID NO: 6738
IFNA6	Interferon, alpha 6	SEQ ID NOS: 6739-6740
IFNA7	Interferon, alpha 7	SEQ ID NO: 6741
IFNA8	Interferon, alpha 8	SEQ ID NO: 6742
IFNAR1	Interferon (alpha, beta and omega) receptor 1	SEQ ID NOS: 6743-6744
IFNB1	Interferon, beta 1, fibroblast	SEQ ID NO: 6745
IFNE	Interferon, epsilon	SEQ ID NO: 6746
IFXG	Interferon, gamma	SEQ ID NO: 6747
IFNGR1	Interferon gamma receptor 1	SEQ ID NOS: 6748-6758
IFNL1	Interferon, lambda 1	SEQ ID NO: 6759
IFNL2	Interferon, lambda 2	SEQ ID NO: 6760
IFNL3	Interferon, lambda 3	SEQ ID NOS: 6761-6762
IFNLR1	Interferon, lambda receptor 1	SEQ ID NOS: 6763-6767
IFNW1	Interferon, omega 1	SEQ ID NO: 6768
IGF1	Insulin-like growth factor I (somatomedin C)	SEQ ID NOS: 6769-6774
IGF2	Insulin-like growth factor 2	SEQ ID NOS: 6775-6782
IGFALS	Insulin-like growth factor binding protein, acid labile subunit	SEQ ID NOS: 6783-6785
IGFBP1	Insulin-like growth factor binding protein 1	SEQ ID NOS: 6786-6788
IGFBP2	Insulin-like growth factor binding protein 2, 36 kDa	SEQ ID NOS: 6789-6792
IGFBP3	Insulin-like growth factor binding protein 3	SEQ ID NOS: 6793-6800
IGFBP4	Insulin-like growth factor binding protein 4	SEQ ID NO: 6801
IGFBP5	Insulin-like growth factor binding protein 5	SEQ ID NOS: 6802-6803

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
IGFBP6	Insulin-like growth factor binding protein 6	SEQ ID NOS: 6804-6806
IGFBP7	Insulin-like growth factor binding protein 7	SEQ ID NOS: 6807-6808
IGFBPL1	Insulin-like growth factor binding protein-like 1	SEQ ID NO: 6809
IGFL1	IGF-like family member 1	SEQ ID NO: 6810
IGFL2	IGF-like family member 2	SEQ ID NOS: 6811-6813
IGFL3	IGF-like family member 3	SEQ ID NO: 6814
IGFLR1	IGF-like family receptor 1	SEQ ID NOS: 6815-6823
IGIP	IgA-inducing protein	SEQ ID NO: 6824
IGLON5	IgLON family member 5	SEQ ID NO: 6825
IGSF1	Immunoglobulin superfamily, member 1	SEQ ID NOS: 6826-6831
IGSF10	Immunoglobulin superfamily, member 10	SEQ ID NOS: 6832-6833
IGSF11	Immunoglobulin superfamily, member 11	SEQ ID NOS: 6834-6841
IGSF21	Immunoglobulin superfamily, member 21	SEQ ID NO: 6842
IGSF8	Immunoglobulin superfamily, member 8	SEQ ID NOS: 6843-6846
IGSF9	Immunoglobulin superfamily, member 9	SEQ ID NOS: 6847-6849
IHH	Indian hedgehog	SEQ ID NO: 6850
IL10	Interleukin 10	SEQ ID NOS: 6851-6852
IL11	Interleukin 11	SEQ ID NOS: 6853-6856
IL11RA	Interleukin 11 receptor, alpha	SEQ ID NOS: 6857-6867
IL12B	Interleukin 12B	SEQ ID NO: 6868
IL12RB1	Interleukin 12 receptor, beta 1	SEQ ID NOS: 6869-6874
IL12RB2	Interleukin 12 receptor, beta 2	SEQ ID NOS: 6875-6879
IL13	Interleukin 13	SEQ ID NOS: 6880-6881
IL13RA1	Interleukin 13 receptor, alpha 1	SEQ ID NOS: 6882-6883
IL15RA	Interleukin 15 receptor, alpha	SEQ ID NOS: 6884-6901
IL17A	Interleukin 17A	SEQ ID NO: 6902
IL17B	Interleukin 17B	SEQ ID NO: 6903
IL17C	Interleukin 17C	SEQ ID NO: 6904
IL17D	Interleukin 17D	SEQ ID NOS: 6905-6907
IL17F	Interleukin 17F	SEQ ID NO: 6908
IL17RA	Interleukin 17 receptor A	SEQ ID NOS: 6909-6910
IL17RC	Interleukin 17 receptor C	SEQ ID NOS: 6911-6926
IL17RE	Interleukin 17 receptor E	SEQ ID NOS: 6927-6933
IL18BP	Interleukin 18 binding protein	SEQ ID NOS: 6934-6944
IL18R1	Interleukin 18 receptor 1	SEQ ID NOS: 6945-6948
IL18RAP	Interleukin 18 receptor accessory protein	SEQ ID NOS: 6949-6951
IL19	Interleukin 19	SEQ ID NOS: 6952-6954
IL1R1	Interleukin 1 receptor, type I	SEQ ID NOS: 6955-6967
IL1R2	Interleukin 1 receptor, type II	SEQ ID NOS: 6968-6971
IL1RAP	Interleukin 1 receptor accessory protein	SEQ ID NOS: 6972-6985
IL1RL1	Interleukin 1 receptor-like 1	SEQ ID NOS: 6986-6991
IL1RL2	Interleukin 1 receptor-like 2	SEQ ID NOS: 6992-6994
IL1RN	Interleukin 1 receptor antagonist	SEQ ID NOS: 6995-6999
IL2	Interleukin 2	SEQ ID NO: 7000
IL20	Interleukin 20	SEQ ID NOS: 7001-7003
IL20RA	Interleukin 20 receptor, alpha	SEQ ID NOS: 7004-7010
IL21	Interleukin 21	SEQ ID NOS: 7011-7012
IL22	Interleukin 22	SEQ ID NOS: 7013-7014
IL22RA2	Interleukin 22 receptor, alpha 2	SEQ ID NOS: 7015-7017
IL23A	Interleukin 23, alpha subunit p19	SEQ ID NO: 7018
IL24	Interleukin 24	SEQ ID NOS: 7019-7024
IL25	Interleukin 25	SEQ ID NOS: 7025-7026
IL26	Interleukin 26	SEQ ID NO: 7027
IL27	Interleukin 27	SEQ ID NOS: 7028-7029
IL2RB	Interleukin 2 receptor, beta	SEQ ID NOS: 7030-7034
IL3	Interleukin 3	SEQ ID NO: 7035
IL31	Interleukin 31	SEQ ID NO: 7036
IL31RA	Interleukin 31 receptor A	SEQ ID NOS: 7037-7044
IL32	Interleukin 32	SEQ ID NOS: 7045-7074
IL34	Interleukin 34	SEQ ID NOS: 7075-7078
IL3RA	Interleukin 3 receptor, alpha (low affinity)	SEQ ID NOS: 7079-7081
IL4	Interleukin 4	SEQ ID NOS: 7082-7084
IL4I1	Interleukin 4 induced 1	SEQ ID NOS: 7085-7092
IL4R	Interleukin 4 receptor	SEQ ID NOS: 7093-7106
IL5	Interleukin 5	SEQ ID NOS: 7107-7108
IL5RA	Interleukin 5 receptor, alpha	SEQ ID NOS: 7109-7118
IL6	Interleukin 6	SEQ ID NOS: 7119-7125
IL6R	Interleukin 6 receptor	SEQ ID NOS: 7126-7131
IL6ST	Interleukin 6 signal transducer	SEQ ID NOS: 7132-7141
IL7	Interleukin 7	SEQ ID NOS: 7142-7149
IL7R	Interleukin 7 receptor	SEQ ID NOS: 7150-7156
IL9	Interleukin 9	SEQ ID NO: 7157
ILDR1	Immunoglobulin-like domain containing receptor 1	SEQ ID NOS: 7158-7162
ILDR2	Immunoglobulin-like domain containing receptor 2	SEQ ID NOS: 7163-7169

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
IMP4	IMP4, U3 small nucleolar ribonucleoprotein	SEQ ID NOS: 7170-7175
IMPG1	Interphotoreceptor matrix proteoglycan 1	SEQ ID NOS: 7176-7179
INHA	Inhibin, alpha	SEQ ID NO: 7180
INHBA	Inhibin, beta A	SEQ ID NOS: 7181-7183
INHBB	Inhibin, beta B	SEQ ID NO: 7184
INHBC	Inhibin, beta C	SEQ ID NO: 7185
INHBE	Inhibin, beta E	SEQ ID NOS: 7186-7187
INPP5A	Inositol polyphosphate-5-phosphatase A	SEQ ID NOS: 7188-7192
INS	Insulin	SEQ ID NOS: 7193-7197
INS-	INS-IGF2 readthrough	SEQ ID NOS: 7198-7199
IGF2		
INSL3	Insulin-like 3 (Leydig cell)	SEQ ID NOS: 7200-7202
INSL4	Insulin-like 4 (placenta)	SEQ ID NO: 7203
INSL5	Insulin-like 5	SEQ ID NO: 7204
INSL6	Insulin-like 6	SEQ ID NO: 7205
INTS3	Integrator complex subunit 3	SEQ ID NOS: 7206-7211
IPO11	Importin 11	SEQ ID NOS: 7212-7220
IPO9	Importin 9	SEQ ID NOS: 7221-7222
IQCF6	IQ motif containing F6	SEQ ID NOS: 7223-7224
IRAK3	Interleukin-1 receptor-associated kinase 3	SEQ ID NOS: 7225-7227
IRS4	Insulin receptor substrate 4	SEQ ID NO: 7228
ISLR	Immunoglobulin superfamily containing leucine-rich repeat	SEQ ID NOS: 7229-7232
ISLR2	Immunoglobulin superfamily containing leucine-rich repeat 2	SEQ ID NOS: 7233-7242
ISM1	Isthmin 1, angiogenesis inhibitor	SEQ ID NO: 7243
ISM2	Isthmin 2	SEQ ID NOS: 7244-7249
ITGA4	Integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	SEQ ID NOS: 7250-7252
ITGA9	Integrin, alpha 9	SEQ ID NOS: 7253-7255
ITGAL	Integrity alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	SEQ ID NOS: 7256-7265
ITGAX	Integrin, alpha X (complement component 3 receptor 4 subunit)	SEQ ID NOS: 7266-7268
ITGB1	Integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	SEQ ID NOS: 7269-7284
ITGB2	Integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	SEQ ID NOS: 7285-7301
ITGB3	Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	SEQ ID NOS: 7302-7304
ITGB7	Integrin, beta 7	SEQ ID NOS: 7305-7312
ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	SEQ ID NOS: 7313-7318
ITIH1	Inter-alpha-trypsin inhibitor heavy chain 1	SEQ ID NOS: 7319-7324
ITIH2	Inter-alpha-trypsin inhibitor heavy chain 2	SEQ ID NOS: 7325-7327
ITIH3	Inter-alpha-trypsin inhibitor heavy chain 3	SEQ ID NOS: 7328-7330
ITIH4	Inter-alpha-trypsin inhibitor heavy chain family, member 4	SEQ ID NOS: 7331-7334
ITIH5	Inter-alpha-trypsin inhibitor heavy chain family, member 5	SEQ ID NOS: 7335-7338
ITIH6	Inter-alpha-trypsin inhibitor heavy chain family, member 6	SEQ ID NO: 7339
ITLN1	Intelectin 1 (galactofuranose binding)	SEQ ID NO: 7340
ITLN2	Intelectin 2	SEQ ID NO: 7341
IZUMO1R	IZUMO1 receptor, JUNO	SEQ ID NOS: 7342-7343
IZUMO4	IZUMO family member 4	SEQ ID NOS: 7344-7350
AMICA1	Adhesion molecule, interacts with CXADR antigen 1	SEQ ID NOS: 7351-7359
JCHAIN	Joining chain of multimeric IgA and IgM	SEQ ID NOS: 7360-7365
JMD8	Junonji domain containing 8	SEQ ID NOS: 7366-7370
JSRP1	Junctional sarcoplasmic reticulum protein 1	SEQ ID NO: 7371
KANSL2	KAT8 regulatory NSL complex subunit 2	SEQ ID NOS: 7372-7382
KAZALD1	Kazal-type serine peptidase inhibitor domain 1	SEQ ID NO: 7383
KCNIP3	Kv channel interacting protein 3, calsenilin	SEQ ID NOS: 7384-7386
KCNK7	Potassium channel, two pore domain subfamily K, member 7	SEQ ID NOS: 7387-7392
KCNN4	Potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 4	SEQ ID NOS: 7393-7398
KCNU1	Potassium channel, subfamily U, member 1	SEQ ID NOS: 7399-7403
KCP	Kielin/chordin-like protein	SEQ ID NOS: 7404-7407
KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	SEQ ID NO: 7408

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	SEQ ID NOS: 7409-7412
KDM1A	Lysine (K)-specific demethylase 1A	SEQ ID NOS: 7413-7416
KDM3B	Lysine (K)-specific demethylase 3B	SEQ ID NOS: 7417-7420
KDM6A	Lysine (K)-specific demethylase 6A	SEQ ID NOS: 7421-7430
KDM7A	Lysine (K)-specific demethylase 7A	SEQ ID NOS: 7431-7432
KDSR	3-ketodihydrophosphingosine reductase	SEQ ID NOS: 7433-7439
KERA	Keratocan	SEQ ID NO: 7440
KIAA0100	KIAA0100	SEQ ID NOS: 7441-7446
KIAA0319	KIAA0319	SEQ ID NOS: 7447-7452
KIAA1324	KIAA1324	SEQ ID NOS: 7453-7461
KIFC2	Kinesin family member C2	SEQ ID NOS: 7462-7464
KIR2DL4	Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	SEQ ID NOS: 7465-7471
KIR3DX1	Killer cell immunoglobulin-like receptor, three domains, X1	SEQ ID NOS: 7472-7476
KIRREL2	Kin of IRRE like 2 (<i>Drosophila</i>)	SEQ ID NOS: 7477-7481
KISS1	KiSS-1 metastasis-suppressor	SEQ ID NOS: 7482-7483
KLHL11	Kelch-like family member 11	SEQ ID NO: 7484
KLHL22	Kelch-like family member 22	SEQ ID NOS: 7485-7491
KLK1	Kallikrein 1	SEQ ID NOS: 7492-7493
KLK10	Kallikrein-related peptidase 10	SEQ ID NOS: 7494-7498
KLK11	Kallikrein-related peptidase 11	SEQ ID NOS: 7499-7507
KLK12	Kallikrein-related peptidase 12	SEQ ID NOS: 7508-7514
KLK13	Kallikrein-related peptidase 13	SEQ ID NOS: 7515-7523
KLK14	Kallikrein-related peptidase 14	SEQ ID NOS: 7524-7525
KLK15	Kallikrein-related peptidase 15	SEQ ID NOS: 7526-7530
KLK2	Kallikrein-related peptidase 2	SEQ ID NOS: 7531-7543
KLK3	Kallikrein-related peptidase 3	SEQ ID NOS: 7544-7555
KLK4	Kallikrein-related peptidase 4	SEQ ID NOS: 7556-7560
KLK5	Kallikrein-related peptidase 5	SEQ ID NOS: 7561-7564
KLK6	Kallikrein-related peptidase 6	SEQ ID NOS: 7565-7571
KLK7	Kallikrein-related peptidase 7	SEQ ID NOS: 7572-7576
KLK8	Kallikrein-related peptidase 8	SEQ ID NOS: 7577-7584
KLK9	Kallikrein-related peptidase 9	SEQ ID NOS: 7585-7586
KLKB1	Kallikrein B, plasma (Fletcher factor) 1	SEQ ID NOS: 7587-7591
SETD8	SET domain containing (lysine methyltransferase) 8	SEQ ID NOS: 7592-7595
KNDC1	Kinase non-catalytic C-lobe domain (KIND) containing 1	SEQ ID NOS: 7596-7597
KNG1	Kininogen 1	SEQ ID NOS: 7598-7602
KRBA2	KRAB-A domain containing 2	SEQ ID NOS: 7603-7606
KREMEN2	Kringle containing transmembrane protein 2	SEQ ID NOS: 7607-7612
KRTDAP	Keratinocyte differentiation-associated protein	SEQ ID NOS: 7613-7614
L1CAM	L1 cell adhesion molecule	SEQ ID NOS: 7615-7624
L3MBTL2	L(3)mbt-like 2 (<i>Drosophila</i>)	SEQ ID NOS: 7625-7629
LACRT	Lacritin	SEQ ID NOS: 7630-7632
LACTB	Lactamase, beta	SEQ ID NOS: 7633-7635
LAG3	Lymphocyte-activation gene 3	SEQ ID NOS: 7636-7637
LAIR2	Leukocyte-associated immunoglobulin-like receptor 2	SEQ ID NOS: 7638-7641
LALBA	Lactalbumin, alpha-	SEQ ID NOS: 7642-7643
LAMA1	Laminin, alpha 1	SEQ ID NOS: 7644-7645
LAMA2	Laminin, alpha 2	SEQ ID NOS: 7646-7649
LAMA3	Laminin, alpha 3	SEQ ID NOS: 7650-7659
LAMA4	Laminin, alpha 4	SEQ ID NOS: 7660-7674
LAMA5	Laminin, alpha 5	SEQ ID NOS: 7675-7677
LAMB1	Laminin, beta 1	SEQ ID NOS: 7678-7682
LAMB2	Laminin, beta 2 (laminin S)	SEQ ID NOS: 7683-7685
LAMB3	Laminin, beta 3	SEQ ID NOS: 7686-7690
LAMB4	Laminin, beta 4	SEQ ID NOS: 7691-7694
LAMC1	Laminin, gamma 1 (formerly LAMB2)	SEQ ID NOS: 7695-7696
LAMC2	Laminin, gamma 2	SEQ ID NOS: 7697-7698
LAMC3	Laminin, gamma 3	SEQ ID NOS: 7699-7700
LAMP3	Lysosomal-associated membrane protein 3	SEQ ID NOS: 7701-7704
GYLTL1B	Glycosyltransferase-like 1B	SEQ ID NOS: 7705-7710
LAT	Linker for activation of T cells	SEQ ID NOS: 7711-7720
LAT2	Linker for activation of T cells family, member 2	SEQ ID NOS: 7721-7729
LBP	Lipopolsaccharide binding protein	SEQ ID NO: 7730
LCAT	Lecithin-cholesterol acyltransferase	SEQ ID NOS: 7733-7737
LCN1	Lipocalin 1	SEQ ID NOS: 7738-7739
LCN10	Lipocalin 10	SEQ ID NOS: 7740-7745
LCN12	Lipocalin 12	SEQ ID NOS: 7746-7748
LCN15	Lipocalin 15	SEQ ID NO: 7749
LCN2	Lipocalin 2	SEQ ID NOS: 7750-7752

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
LCN6	Lipocalin 6	SEQ ID NOS: 7753-7754
LCN8	Lipocalin 8	SEQ ID NOS: 7755-7756
LCN9	Lipocalin 9	SEQ ID NOS: 7757-7758
LCORL	Ligand dependent nuclear receptor corepressor-like	SEQ ID NOS: 7759-7764
LDLR	Low density lipoprotein receptor	SEQ ID NOS: 7765-7773
LDLRAD2	Low density lipoprotein receptor class A domain containing 2	SEQ ID NOS: 7774-7775
LEAP2	Liver expressed antimicrobial peptide 2	SEQ ID NO: 7776
LECT2	Leukocyte cell-derived chemotaxin 2	SEQ ID NOS: 7777-7780
LEFTY1	Left-right determination factor 1	SEQ ID NOS: 7781-7782
LEFTY2	Left-right determination factor 2	SEQ ID NOS: 7783-7784
LEP	Leptin	SEQ ID NO: 7785
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 7786-7791
LGALS3BP	Lectin, galactoside-binding, soluble, 3 binding protein	SEQ ID NOS: 7792-7806
LG11	Leucine-rich, glioma inactivated 1	SEQ ID NOS: 7807-7825
LG12	Leucine-rich repeat LGI family, member 2	SEQ ID NOS: 7826-7827
LG13	Leucine-rich repeat LGI family, member 3	SEQ ID NOS: 7828-7831
LG14	Leucine-rich repeat LGI family, member 4	SEQ ID NOS: 7832-7835
LGMN	Legumain	SEQ ID NOS: 7836-7849
LGR4	Leucine-rich repeat containing G protein-coupled receptor 4	SEQ ID NOS: 7850-7852
LHB	Luteinizing hormone beta polypeptide	SEQ ID NO: 7853
LHCGR	Luteinizing hormone/choriogonadotropin receptor	SEQ ID NOS: 7854-7858
LIF	Leukemia inhibitory factor	SEQ ID NOS: 7859-7860
LIFR	Leukemia inhibitory factor receptor alpha	SEQ ID NOS: 7861-7865
LILRA1	Leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	SEQ ID NOS: 7866-7867
LILRA2	Leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	SEQ ID NOS: 7868-7874
LILRB3	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	SEQ ID NOS: 7875-7879
LIME1	Lck interacting transmembrane adaptor 1	SEQ ID NOS: 7880-7885
LINGO1	Leucine rich repeat and Ig domain containing 1	SEQ ID NOS: 7886-7896
LIPA	Lipase A, lysosomal acid, cholesterol esterase	SEQ ID NOS: 7897-7901
LIPC	Lipase, hepatic	SEQ ID NOS: 7902-7905
LIPF	Lipase, gastric	SEQ ID NOS: 7906-7909
LIPG	Lipase, endothelial	SEQ ID NOS: 7910-7915
LIPH	Lipase, member H	SEQ ID NOS: 7916-7920
LIPK	Lipase, family member K	SEQ ID NO: 7921
LIPM	Lipase, family member M	SEQ ID NOS: 7922-7923
LIPN	Lipase, family member N	SEQ ID NO: 7924
LMAN2	Lectin, mannose-binding 2	SEQ ID NOS: 7925-7929
LMNTD1	Lamin tail domain containing 1	SEQ ID NOS: 7930-7940
LNX1	Ligand of numb-protein X 1, E3 ubiquitin protein ligase	SEQ ID NOS: 7941-7947
LOX	Lysyl oxidase	SEQ ID NOS: 7948-7950
LOXL1	Lysyl oxidase-like 1	SEQ ID NOS: 7951-7952
LOXL2	Lysyl oxidase-like 2	SEQ ID NOS: 7953-7961
LOXL3	Lysyl oxidase-like 3	SEQ ID NOS: 7962-7968
LOXL4	Lysyl oxidase-like 4	SEQ ID NO: 7969
LPA	Lipoprotein, Lp(a)	SEQ ID NOS: 7970-7972
LPL	Lipoprotein lipase	SEQ ID NOS: 7973-7977
LPO	Lactoperoxidase	SEQ ID NOS: 7978-7984
LRAT	Lecithin retinol acyltransferase (phosphatidylcholine-retinol O-acyltransferase)	SEQ ID NOS: 7985-7987
LRCH3	Leucine-rich repeats and calponin homology (CH) domain containing 3	SEQ ID NOS: 7988-7996
LRCOL1	Leucine rich colipase-like 1	SEQ ID NOS: 7997-8000
LRFN4	Leucine rich repeat and fibronectin type III domain containing 4	SEQ ID NOS: 8001-8002
LRFN5	Leucine rich repeat and fibronectin type III domain containing 5	SEQ ID NOS: 8003-8005
LRG1	Leucine-rich alpha-2-glycoprotein 1	SEQ ID NO: 8006
LRP1	Low density lipoprotein receptor-related protein 1	SEQ ID NOS: 8007-8012
LRP11	Low density lipoprotein receptor-related protein 11	SEQ ID NOS: 8013-8014
LRP1B	Low density lipoprotein receptor-related protein 1B	SEQ ID NOS: 8015-8018
LRP2	Low density lipoprotein receptor-related protein 2	SEQ ID NOS: 8019-8020
LRP4	Low density lipoprotein receptor-related protein 4	SEQ ID NOS: 8021-8022
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1	SEQ ID NOS: 8023-8024

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
RRRC17	Leucine rich repeat containing 17	SEQ ID NOS: 8025-8027
RRRC32	Leucine rich repeat containing 32	SEQ ID NOS: 8028-8031
RRRC3B	Leucine rich repeat containing 3B	SEQ ID NOS: 8032-8036
RRRC4B	Leucine rich repeat containing 4B	SEQ ID NOS: 8037-8039
RRRC70	Leucine rich repeat containing 70	SEQ ID NOS: 8040-8041
RRRN3	Leucine rich repeat neuronal 3	SEQ ID NOS: 8042-8045
RRRTM1	Leucine rich repeat transmembrane neuronal 1	SEQ ID NOS: 8046-8052
RRRTM2	Leucine rich repeat transmembrane neuronal 2	SEQ ID NOS: 8053-8055
RRRTM4	Leucine rich repeat transmembrane neuronal 4	SEQ ID NOS: 8056-8061
LRTM2	Leucine-rich repeats and transmembrane domains 2	SEQ ID NOS: 8062-8066
LSR	Lipolysis stimulated lipoprotein receptor	SEQ ID NOS: 8067-8077
LST1	Leukocyte specific transcript 1	SEQ ID NOS: 8078-8095
LTA	Lymphotoxin alpha	SEQ ID NOS: 8096-8097
LTBP1	Latent transforming growth factor beta binding protein 1	SEQ ID NOS: 8098-8107
LTBP2	Latent transforming growth factor beta binding protein 2	SEQ ID NOS: 8108-8111
LTBP3	Latent transforming growth factor beta binding protein 3	SEQ ID NOS: 8112-8124
LTBP4	Latent transforming growth factor beta binding protein 4	SEQ ID NOS: 8125-8140
LTBR	Lymphotoxin beta receptor (TNFR superfamily, member 3)	SEQ ID NOS: 8141-8146
LTF	Lactotransferrin	SEQ ID NOS: 8147-8151
LTK	Leukocyte receptor tyrosine kinase	SEQ ID NOS: 8152-8155
LUM	Lumican	SEQ ID NO: 8156
LUZP2	Leucine zipper protein 2	SEQ ID NOS: 8157-8160
LVRN	Laeverin	SEQ ID NOS: 8161-8166
LY6E	Lymphocyte antigen 6 complex, locus E	SEQ ID NOS: 8167-8180
LY6G5B	Lymphocyte antigen 6 complex, locus G5B	SEQ ID NOS: 8181-8182
LY6G6D	Lymphocyte antigen 6 complex, locus G6D	SEQ ID NOS: 8183-8184
LY6G6E	Lymphocyte antigen 6 complex, locus G6E (pseudogene)	SEQ ID NOS: 8185-8188
LY6H	Lymphocyte antigen 6 complex, locus H	SEQ ID NOS: 8189-8192
LY6K	lymphocyte antigen 6 complex, locus K	SEQ ID NOS: 8193-8196
RP11-520P18.5		SEQ ID NO: 8197
LY86	Lymphocyte antigen 86	SEQ ID NOS: 8198-8199
LY96	Lymphocyte antigen 96	SEQ ID NOS: 8200-8201
LYG1	Lysozyme G-like 1	SEQ ID NOS: 8202-8203
LYG2	Lysozyme G-like 2	SEQ ID NOS: 8204-8209
LYNX1	Ly6/neurotoxin 1	SEQ ID NOS: 8210-8214
LYPD1	LY6/PLAUR domain containing 1	SEQ ID NOS: 8215-8217
LYPD2	LY6/PLAUR domain containing 2	SEQ ID NO: 8218
LYPD4	LY6/PLAUR domain containing 4	SEQ ID NOS: 8219-8221
LYPD6	LY6/PLAUR domain containing 6	SEQ ID NOS: 8222-8226
LYPD6B	LY6/PLAUR domain containing 6B	SEQ ID NOS: 8227-8233
LYPD8	LY6/PLAUR domain containing 8	SEQ ID NOS: 8234-8235
LYZ	Lysozyme	SEQ ID NOS: 8236-8238
LYZL4	Lysozyme-like 4	SEQ ID NOS: 8239-8240
LYZL6	Lysozyme-like 6	SEQ ID NOS: 8241-8243
M6PR	Mannose-6-phosphate receptor (cation dependent)	SEQ ID NOS: 8244-8254
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	SEQ ID NOS: 8255-8267
MAG	Myelin associated glycoprotein	SEQ ID NOS: 8268-8273
MAGT1	Magnesium transporter 1	SEQ ID NOS: 8274-8277
MALSU1	Mitochondrial assembly of ribosomal large subunit 1	SEQ ID NO: 8278
MAMDC2	MAM domain containing 2	SEQ ID NO: 8279
MAN2B1	Mannosidase, alpha, class 2B, member 1	SEQ ID NOS: 8280-8285
MAN2B2	Mannosidase, alpha, class 2B, member 2	SEQ ID NOS: 8286-8288
MANBA	Mannosidase, beta A, lysosomal	SEQ ID NOS: 8289-8302
MANEAL	Mannosidase, endo-alpha-like	SEQ ID NOS: 8303-8307
MANF	Mesencephalic astrocyte-derived neurotrophic factor	SEQ ID NOS: 8308-8309
MANSC1	MANSC domain containing 1	SEQ ID NOS: 8310-8313
MAP3K9	Mitogen-activated protein kinase 9	SEQ ID NOS: 8314-8319
MASP1	Mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	SEQ ID NOS: 8320-8327
MASP2	Mannan-binding lectin serine peptidase 2	SEQ ID NOS: 8328-8329
MATN1	Matrilin 1, cartilage matrix protein	SEQ ID NO: 8330
MATN2	Matrilin 2	SEQ ID NOS: 8331-8343
MATN3	Matrilin 3	SEQ ID NOS: 8344-8345
MATN4	Matrilin 4	SEQ ID NOS: 8346-8350

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
MATR3	Matrin 3	SEQ ID NOS: 8351-8378
MAU2	MAU2 sister chromatid cohesion factor	SEQ ID NOS: 8379-8381
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	SEQ ID NOS: 8382-8396
MBD6	Methyl-CpG binding domain protein 6	SEQ ID NOS: 8397-8408
MBL2	Mannose-binding lectin (protein C) 2, soluble	SEQ ID NO: 8409
MBNL1	Muscleblind-like splicing regulator 1	SEQ ID NOS: 8410-8428
MCCCC1	Methylcrotonoyl-CoA carboxylase 1 (alpha)	SEQ ID NOS: 8429-8440
MCCCD1	Mitochondrial coiled-coil domain 1	SEQ ID NO: 8441
MCEE	Methylmalonyl CoA epimerase	SEQ ID NOS: 8442-8445
MCF2L	MCF.2 cell line derived transforming sequence-like	SEQ ID NOS: 8446-8467
MCFD2	Multiple coagulation factor deficiency 2	SEQ ID NOS: 8468-8479
MDFIC	MyoD family inhibitor domain containing	SEQ ID NOS: 8480-8487
MDGA1	MAM domain containing	SEQ ID NOS: 8488-8493
	glycosylphosphatidylinositol anchor 1	
MDK	Midkine (neutrite growth-promoting factor 2)	SEQ ID NOS: 8494-8503
MED20	Mediator complex subunit 20	SEQ ID NOS: 8504-8508
MEGF10	Multiple EGF-like-domains 10	SEQ ID NOS: 8509-8512
MEGF6	Multiple EGF-like-domains 6	SEQ ID NOS: 8513-8516
MEI1	Meiotic double-stranded break formation protein 1	SEQ ID NOS: 8517-8520
MEI4	Meiotic double-stranded break formation protein 4	SEQ ID NO: 8521
MEIS1	Meis homeobox 1	SEQ ID NOS: 8522-8527
MEIS3	Meis homeobox 3	SEQ ID NOS: 8528-8537
MFL2	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	SEQ ID NOS: 8538-8540
MEPE	Matrix extracellular phosphoglycoprotein	SEQ ID NOS: 8541-8547
MESDC2	Mesoderm development candidate 2	SEQ ID NOS: 8548-8552
MEST	Mesoderm specific transcript	SEQ ID NOS: 8553-8566
MET	MET proto-oncogene, receptor tyrosine kinase	SEQ ID NOS: 8567-8572
METRN	Meteorin, glial cell differentiation regulator	SEQ ID NOS: 8573-8577
METRNL	Meteorin, glial cell differentiation regulator-like	SEQ ID NOS: 8578-8581
METTL17	Methyltransferase like 17	SEQ ID NOS: 8582-8592
METTL24	Methyltransferase like 24	SEQ ID NO: 8593
METTL7B	Methyltransferase like 7B	SEQ ID NOS: 8594-8595
METTL9	Methyltransferase like 9	SEQ ID NOS: 8596-8604
MEX3C	Mex-3 RNA binding family member C	SEQ ID NOS: 8605-8607
MFAP2	Microfibrillar-associated protein 2	SEQ ID NOS: 8608-8609
MFAP3	Microfibrillar-associated protein 3	SEQ ID NOS: 8610-8614
MFAP3L	Microfibrillar-associated protein 3-like	SEQ ID NOS: 8615-8624
MFAP4	Microfibrillar-associated protein 4	SEQ ID NOS: 8625-8627
MFAP5	Microfibrillar associated protein 5	SEQ ID NOS: 8628-8638
MFGE8	Milk fat globule-EGF factor 8 protein	SEQ ID NOS: 8639-8645
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 8646-8653
MGA	MGA, MAX dimerization protein	SEQ ID NOS: 8654-8662
MGAT2	Mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	SEQ ID NO: 8663
MGAT3	Mannosyl (beta-1,4)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	SEQ ID NOS: 8664-8666
MGAT4A	Mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	SEQ ID NOS: 8667-8671
MGAT4B	Mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	SEQ ID NOS: 8672-8682
MGAT4D	MGAT4 family, member D	SEQ ID NOS: 8683-8688
MGLL	Monoglyceride lipase	SEQ ID NOS: 8689-8698
MGP	Matrix Gla protein	SEQ ID NOS: 8699-8701
MGST2	Microsomal glutathione S-transferase 2	SEQ ID NOS: 8702-8705
MIA	Melanoma inhibitory activity	SEQ ID NOS: 8706-8711
MIA2	Melanoma inhibitory activity 2	SEQ ID NO: 8712
MIA3	Melanoma inhibitory activity family, member 3	SEQ ID NOS: 8713-8717
MICU1	Mitochondrial calcium uptake 1	SEQ ID NOS: 8718-8727
M1ER1	Mesoderm induction early response 1, transcriptional regulator	SEQ ID NOS: 8728-8736
MINOS1-NBL1	MINOS1-NBL1 readthrough	SEQ ID NOS: 8737-8739
MINPP1	Multiple inositol-polyphosphate phosphatase 1	SEQ ID NOS: 8740-8742
MLEC	Malectin	SEQ ID NOS: 8743-8746
MLN	Motilin	SEQ ID NOS: 8747-8749
MLXIP	MLX interacting protein	SEQ ID NOS: 8750-8755
MLXIPL	MLX interacting protein-like	SEQ ID NOS: 8756-8763
MMP1	Matrix metallopeptidase 1	SEQ ID NO: 8764
MMP10	Matrix metallopeptidase 10	SEQ ID NOS: 8765-8766
MMP11	Matrix metallopeptidase 11	SEQ ID NOS: 8767-8770

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
MMP12	Matrix metallopeptidase 12	SEQ ID NO: 8771
MMP13	Matrix metallopeptidase 13	SEQ ID NOS: 8772-8774
MMP14	Matrix metallopeptidase 14 (membrane-inserted)	SEQ ID NOS: 8775-8777
MMP17	Matrix metallopeptidase 17 (membrane-inserted)	SEQ ID NOS: 8778-8785
MMP19	Matrix metallopeptidase 19	SEQ ID NOS: 8786-8791
MMP2	Matrix metallopeptidase 2	SEQ ID NOS: 8792-8799
MMP20	Matrix metallopeptidase 20	SEQ ID NO: 8800
MMP21	Matrix metallopeptidase 21	SEQ ID NO: 8801
MMP25	Matrix metallopeptidase 25	SEQ ID NOS: 8802-8803
MMP26	Matrix metallopeptidase 26	SEQ ID NOS: 8804-8805
MMP27	Matrix metallopeptidase 27	SEQ ID NO: 8806
MMP28	Matrix metallopeptidase 28	SEQ ID NOS: 8807-8812
MMP3	Matrix metallopeptidase 3	SEQ ID NOS: 8813-8815
MMP7	Matrix metallopeptidase 7	SEQ ID NO: 8816
MMP8	Matrix metallopeptidase 8	SEQ ID NOS: 8817-8822
MMP9	Matrix metallopeptidase 9	SEQ ID NO: 8823
MMRN1	Multiimerin 1	SEQ ID NOS: 8824-8826
MMRN2	Multiimerin 2	SEQ ID NOS: 8827-8831
MOXD1	Monooxygenase, DBH-like 1	SEQ ID NOS: 8832-8834
C6orf25	Chromosome 6 open reading frame 25	SEQ ID NOS: 8835-8842
MPO	Myeloperoxidase	SEQ ID NOS: 8843-8844
MPPED1	Metallophosphoesterase domain containing 1	SEQ ID NOS: 8845-8848
MPZL1	Myelin protein zero-like 1	SEQ ID NOS: 8849-8853
MR1	Major histocompatibility complex, class I-related	SEQ ID NOS: 8854-8859
MRPL2	Mitochondrial ribosomal protein L2	SEQ ID NOS: 8860-8864
MRPL21	Mitochondrial ribosomal protein L21	SEQ ID NOS: 8865-8871
MRPL22	Mitochondrial ribosomal protein L22	SEQ ID NOS: 8872-8876
MRPL24	Mitochondrial ribosomal protein L24	SEQ ID NOS: 8877-8881
MRPL27	Mitochondrial ribosomal protein L27	SEQ ID NOS: 8882-8887
MRPL32	Mitochondrial ribosomal protein L32	SEQ ID NOS: 8888-8890
MRPL34	Mitochondrial ribosomal protein L34	SEQ ID NOS: 8891-8895
MRPL35	Mitochondrial ribosomal protein L35	SEQ ID NOS: 8896-8899
MRPL52	Mitochondrial ribosomal protein L52	SEQ ID NOS: 8900-8910
MRPL55	Mitochondrial ribosomal protein L55	SEQ ID NOS: 8911-8936
MRPS14	Mitochondrial ribosomal protein S14	SEQ ID NOS: 8937-8938
MRPS22	Mitochondrial ribosomal protein S22	SEQ ID NOS: 8939-8947
MRPS28	Mitochondrial ribosomal protein S28	SEQ ID NOS: 8948-8955
MS4A14	Membrane-spanning 4-domains, subfamily A, member 14	SEQ ID NOS: 8956-8966
MS4A3	Membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	SEQ ID NOS: 8967-8971
MSH3	MutS homolog 3	SEQ ID NO: 8972
MSH5	MutS homolog 5	SEQ ID NOS: 8973-8984
MSLN	Mesothelin	SEQ ID NOS: 8985-8992
MSMB	Microseminoprotein, beta-	SEQ ID NOS: 8993-8994
MSRA	Methionine sulfoxide reductase A	SEQ ID NOS: 8995-9002
MSRB2	Methionine sulfoxide reductase B2	SEQ ID NOS: 9003-9004
MSRB3	Methionine sulfoxide reductase B3	SEQ ID NOS: 9005-9018
MST1	Macrophage stimulating 1	SEQ ID NOS: 9019-9020
MSTN	Myostatin	SEQ ID NO: 9021
MT1G	Metallothionein 1G	SEQ ID NOS: 9022-9025
MTHFD2	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	SEQ ID NOS: 9026-9030
MTMR14	Myotubularin related protein 14	SEQ ID NOS: 9031-9041
MTRNR2L11	MT-RNR2-like 11 (pseudogene)	SEQ ID NO: 9042
MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	SEQ ID NOS: 9043-9055
MTTP	Microsomal triglyceride transfer protein	SEQ ID NOS: 9056-9066
MTX2	Metaxin 2	SEQ ID NOS: 9067-9071
MUC1	Mucin 1, cell surface associated	SEQ ID NOS: 9072-9097
MUC13	Mucin 13, cell surface associated	SEQ ID NOS: 9098-9099
MUC20	Mucin 20, cell surface associated	SEQ ID NOS: 9100-9104
MUC3A	Mucin 3A, cell surface associated	SEQ ID NOS: 9105-9107
MUC5AC	Mucin 5AC, oligomeric mucus/gel-forming	SEQ ID NO: 9108
MUC5B	Mucin 5B, oligomeric mucus/gel-forming	SEQ ID NOS: 9109-9110
MUC6	Mucin 6, oligomeric mucus/gel-forming	SEQ ID NOS: 9111-9114
MUC7	Mucin 7, secreted	SEQ ID NOS: 9115-9118
MUCL1	Mucin-like 1	SEQ ID NOS: 9119-9121
MXRA5	Matrix-remodelling associated 5	SEQ ID NO: 9122
MXRA7	Matrix-remodelling associated 7	SEQ ID NOS: 9123-9129
MYDGF	Myeloid-derived growth factor	SEQ ID NOS: 9130-9132

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
MYL1	Myosin, light chain 1, alkali; skeletal, fast	SEQ ID NOS: 9133-9134
MYOC	Myocilin, trabecular meshwork inducible glucocorticoid response	SEQ ID NOS: 9135-9136
MYRFL	Myclin regulatory factor-like	SEQ ID NOS: 9137-9141
MZB1	Marginal zone B and B1 cell-specific protein	SEQ ID NOS: 9142-9146
N4BP2L2	NEDD4 binding protein 2-like 2	SEQ ID NOS: 9147-9152
NAA38	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	SEQ ID NOS: 9153-9158
NAAA	N-acylethanolamine acid amidase	SEQ ID NOS: 9159-9164
NAGA	N-acetylgalactosaminidase, alpha-	SEQ ID NOS: 9165-9167
NAGLU	N-acetylglucosaminidase, alpha	SEQ ID NOS: 9168-9172
NAGS	N-acetylglutamate synthase	SEQ ID NOS: 9173-9174
NAPSA	Napsin A aspartic peptidase	SEQ ID NOS: 9175-9177
CARKD	Carbohydrate kinase domain containing	SEQ ID NOS: 9178-9179
APOA1BP	Apolipoprotein A-I binding protein	SEQ ID NOS: 9180-9182
NBL1	Neuroblastoma 1, DAN family BMP antagonist	SEQ ID NOS: 9183-9196
NCAM1	Neural cell adhesion molecule 1	SEQ ID NOS: 9197-9216
NCAN	Neuropican	SEQ ID NOS: 9217-9218
NCBP2-AS2	NCBP2 antisense RNA 2 (head to head)	SEQ ID NO: 9219
NCSTN	Nicastrin	SEQ ID NOS: 9220-9229
NDNF	Neuron-derived neurotrophic factor	SEQ ID NOS: 9230-9232
NDP	Norrie disease (pseudoglioma)	SEQ ID NOS: 9233-9235
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42 kDa	SEQ ID NOS: 9236-9245
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16 kDa	SEQ ID NOS: 9246-9254
NDUFS8	NADH dehydrogenase (ubiquinone) Fe—S protein 8, 23 kDa (NADH-coenzyme Q reductase)	SEQ ID NOS: 9255-9264
NDUFW1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51 kDa	SEQ ID NOS: 9265-9278
NECAB3	N-terminal EF-hand calcium binding protein 3	SEQ ID NOS: 9279-9288
PVRL1	Poliovirus receptor-related 1 (herpesvirus entry mediator C)	SEQ ID NOS: 9289-92.91
NELL1	Neural EGFL like 1	SEQ ID NOS: 9292-9295
NELL2	Neural EGFL like 2	SEQ ID NOS: 9296-9310
NENF	Neudesin neurotrophic factor	SEQ ID NO: 9311
NETO1	Neuropilin (NRP) and tollloid (TLL)-like 1	SEQ ID NOS: 9312-9316
NFASC	Neurofascin	SEQ ID NOS: 9317-9331
NFE2L1	Nuclear factor, erythroid 2-like 1	SEQ ID NOS: 9332-9350
NFE2L3	Nuclear factor, erythroid 2-like 3	SEQ ID NOS: 9351-9352
NGEF	Neuronal guanine nucleotide exchange factor	SEQ ID NOS: 9353-9358
NGF	Nerve growth factor (beta polypeptide)	SEQ ID NO: 9359
NGLY1	N-glycanase 1	SEQ ID NOS: 9360-9366
NGRN	Neugrin, neurite outgrowth associated	SEQ ID NOS: 9367-9368
NHLRC3	NHL repeat containing 3	SEQ ID NOS: 9369-9371
NID1	Nidogen 1	SEQ ID NOS: 9372-9373
NID2	Nidogen 2 (osteonidogen)	SEQ ID NOS: 9374-9376
NKG7	Natural killer cell granule protein 7	SEQ ID NOS: 9377-9381
NLGN3	Neuroligin 3	SEQ ID NOS: 9382-9386
NLGN4Y	Neuroligin 4, Y-linked	SEQ ID NOS: 9387-9393
NLRP5	NLR family, pyrin domain containing 5	SEQ ID NOS: 9394-9396
NMB	Neuromedin B	SEQ ID NOS: 9397-9398
NME1	NME/NM23 nucleoside diphosphate kinase 1	SEQ ID NOS: 9399-9405
NME1-	NME1-NME2 readthrough	SEQ ID NOS: 9406-9408
NME2		
NME3	NME/NM23 nucleoside diphosphate kinase 3	SEQ ID NOS: 9409-9413
NMS	Neuromedin S	SEQ ID NO: 9414
NMU	Neuromedin U	SEQ ID NOS: 9415-9418
NOA1	Nitric oxide associated 1	SEQ ID NO: 9419
NODAL	Nodal growth differentiation factor	SEQ ID NOS: 9420-9421
NOG	Noggin	SEQ ID NO: 9422
NOMO3	NODAL modulator 3	SEQ ID NOS: 9423-9429
NOS1AP	Nitric oxide synthase 1 (neuronal) adaptor protein	SEQ ID NOS: 9430-9434
NOTCH3	Notch 3	SEQ ID NOS: 9435-9438
NOTUM	Notum pectinacetyl esterase homolog (<i>Drosophila</i>)	SEQ ID NOS: 9439-9441
NOV	Nephroblastoma overexpressed	SEQ ID NO: 9442
NPB	Neuropeptide B	SEQ ID NOS: 9443-9444
NPC2	Niemann-Pick disease, type C2	SEQ ID NOS: 9445-9453
NPFF	Neuropeptide FF-amide peptide precursor	SEQ ID NO: 9454
NPFFR2	Neuropeptide FF receptor 2	SEQ ID NOS: 9455-9458
NPHS1	Nephrosis I, congenital, Finnish type (nephrin)	SEQ ID NOS: 9459-9460
NPNT	Nephronectin	SEQ ID NOS: 9461-9471
NPPA	Natriuretic peptide A	SEQ ID NOS: 9472-9474
NPPB	Natriuretic peptide B	SEQ ID NO: 9475

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
NPPC	Natriuretic peptide C	SEQ ID NOS: 9476-9477
NPS	Neuropeptide S	SEQ ID NO: 9478
NPTX1	Neuronal pentraxin I	SEQ ID NO: 9479
NPTX2	Neuronal pentraxin II	SEQ ID NO: 9480
NPTXR	Neuronal pentraxin receptor	SEQ ID NOS: 9481-9482
NPVF	Neuropeptide VF precursor	SEQ ID NO: 9483
NPW	Neuropeptide W	SEQ ID NOS: 9484-9486
NPY	Neuropeptide Y	SEQ ID NOS: 9487-9489
NQO2	NAD(P)H dehydrogenase, quinone 2	SEQ ID NOS: 9490-9498
NRCAM	Neuronal cell adhesion molecule	SEQ ID NOS: 9499-9511
NRG1	Neuregulin 1	SEQ ID NOS: 9512-9529
NRN1L	Neuritin 1-like	SEQ ID NOS: 9530-9532
NRP1	Neuropilin 1	SEQ ID NOS: 9533-9546
NRP2	Neuropilin 2	SEQ ID NOS: 9547-9553
NRTN	Neurturin	SEQ ID NO: 9554
NRXN1	Neurexin 1	SEQ ID NOS: 9555-9585
NRXN2	Neurexin 2	SEQ ID NOS: 9586-9594
NTSC3A	5'-nucleotidase, cytosolic IIIA	SEQ ID NOS: 9595-9605
NT5DC3	5'-nucleotidase domain containing 3	SEQ ID NOS: 9606-9608
NTSE	5'-nucleotidase, ecto (CD73)	SEQ ID NOS: 9609-9613
NTF3	Neurotrophin 3	SEQ ID NOS: 9614-9615
NTF4	Neurotrophin 4	SEQ ID NOS: 9616-9617
NTM	Neurotrumin	SEQ ID NOS: 9618-9627
NTN1	Netrin 1	SEQ ID NOS: 9628-9629
NTN3	Netrin 3	SEQ ID NO: 9630
NTN4	Netrin 4	SEQ ID NOS: 9631-9635
NTN5	Netrin 5	SEQ ID NOS: 9636-9637
NTNG1	Netrin G1	SEQ ID NOS: 9638-9644
NTNG2	Netrin G2	SEQ ID NOS: 9645-9646
NTS	Neurotensin	SEQ ID NOS: 9647-9648
NUBPL	Nucleotide binding protein-like	SEQ ID NOS: 9649-9655
NUCB1	Nucleobindin 1	SEQ ID NOS: 9656-9662
NUCB2	Nucleobindin 2	SEQ ID NOS: 9663-9678
NUDT19	Nudix (nucleoside diphosphate linked moiety X)-type motif 19	SEQ ID NO: 9679
NUDT9	Nudix (nucleoside diphosphate linked moiety X)-type motif 9	SEQ ID NOS: 9680-9684
NUP155	Nucleoporin 155 kDa	SEQ ID NOS: 9685-9688
NUP214	Nucleoporin 214 kDa	SEQ ID NOS: 9689-9700
NUP85	Nucleoporin 85 kDa	SEQ ID NOS: 9701-9715
NXPE3	Neurexophilin and PC-esterase domain family, member 3	SEQ ID NOS: 9716-9721
NXPE4	Neurexophilin and PC-esterase domain family, member 4	SEQ ID NOS: 9722-9723
NXPH1	Neurexophilin 1	SEQ ID NOS: 9724-9727
NXPH2	Neurexophilin 2	SEQ ID NO: 9728
NXPH3	Neurexophilin 3	SEQ ID NOS: 9729-9730
NXPH4	Neurexophilin 4	SEQ ID NOS: 9731-9732
NYX	Nyctalopin	SEQ ID NOS: 9733-9734
OAF	Out at first homolog	SEQ ID NOS: 9735-9736
OBP2A	Odorant binding protein 2A	SEQ ID NOS: 9737-9743
OBP2B	Odorant binding protein 2B	SEQ ID NOS: 9744-9747
OC90	Otoconin 90	SEQ ID NO: 9748
OCLN	Occludin	SEQ ID NOS: 9749-9751
ODAM	Odontogenic, ameloblast assosciated	SEQ ID NOS: 9752-9755
C4orf26	Chromosome 4 open reading frame 26	SEQ ID NOS: 9756-9759
OGG1	8-oxoguanine DMA glycosylase	SEQ ID NOS: 9760-9773
OGN	Osteoglycin	SEQ ID NOS: 9774-9776
OIT3	Oncoprotein induced transcript 3	SEQ ID NOS: 9777-9778
OLFM1	Olfactomedin 1	SEQ ID NOS: 9779-9789
OLFM2	Olfactomedin 2	SEQ ID NOS: 9790-9793
OLFM3	Olfactomedin 3	SEQ ID NOS: 9794-9796
OLFM4	Olfactomedin 4	SEQ ID NO: 9797
OLFML1	Olfactomedin-like 1	SEQ ID NOS: 9798-9801
OLFML2A	Olfactomedin-like 2A	SEQ ID NOS: 9802-9804
OLFML2B	Olfactomedin-like 2B	SEQ ID NOS: 9805-9809
OLFML3	Olfactomedin-like 3	SEQ ID NOS: 9810-9812
OMD	Osteomodulin	SEQ ID NO: 9813
OMG	Oligodendrocyte myelin glycoprotein	SEQ ID NO: 9814
OOSP2	Oocyte secreted protein 2	SEQ ID NOS: 9815-9816
OPCML	Opioid binding protein/cell adhesion molecule-like	SEQ ID NOS: 9817-9821

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
PROL1	Proline rich, lacrimal 1	SEQ ID NO: 9822
OPTC	Opticin	SEQ ID NOS: 9823-9824
ORAI1	ORAI calcium release-activated calcium modulator 1	SEQ ID NO: 9825
ORM1	Orosomucoid 1	SEQ ID NO: 9826
ORM2	Orosomucoid 2	SEQ ID NO: 9827
ORMDL2	ORMDL sphingolipid biosynthesis regulator 2	SEQ ID NOS: 9828-9831
OS9	Osteosarcoma amplified 9, endoplasmic reticulum lectin	SEQ ID NOS: 9832-9846
OSCAR	Osteoclast associated, immunoglobulin-like receptor	SEQ ID NOS: 9847-9857
OSM	Oncostatin M	SEQ ID NOS: 9858-9860
OSMR	Oncostatin M receptor	SEQ ID NOS: 9861-9865
OSTN	Osteocrin	SEQ ID NOS: 9866-9867
OTOA	Otoancorin	SEQ ID NOS: 9868-9873
OTOG	Otogelin	SEQ ID NOS: 9874-9876
OTOGGL	Otogelin-like	SEQ ID NOS: 9877-9883
OTOL1	Otolin 1	SEQ ID NO: 9884
OTOR	Otoraplin	SEQ ID NO: 9885
OTOS	Otospiralin	SEQ ID NOS: 9886-9887
OVCH1	Ovochymase 1	SEQ ID NOS: 9888-9890
OVCH2	Ovochymase 2 (gene/pseudogene)	SEQ ID NOS: 9891-9892
OVGP1	Oviductal glycoprotein 1, 120 kDa	SEQ ID NO: 9893
OXCT1	3-oxoacid CoA transferase 1	SEQ ID NOS: 9894-9897
OXCT2	3-oxoacid CoA transferase 2	SEQ ID NO: 9898
OXNAD1	Oxidoreductase NAD-binding domain containing 1	SEQ ID NOS: 9899-9905
OXT	Oxytocin/neurophysin I prepropeptide	SEQ ID NO: 9906
P3H1	Prolyl 3-hydroxylase 1	SEQ ID NOS: 9907-9911
P3H2	Prolyl 3-hydroxylase 2	SEQ ID NOS: 9912-9915
P3H3	Prolyl 3-hydroxylase 3	SEQ ID NO: 9916
P3H4	Prolyl 3-hydroxylase family member 4 (non-enzymatic)	SEQ ID NOS: 9917-9921
P4HA1	Prolyl 4-hydroxylase, alpha polypeptide I	SEQ ID NOS: 9922-9926
P4HA2	Prolyl 4-hydroxylase, alpha polypeptide II	SEQ ID NOS: 9927-9941
P4HA3	Prolyl 4-hydroxylase, alpha polypeptide III	SEQ ID NOS: 9942-9946
P4HB	Prolyl 4-hydroxylase, beta polypeptide	SEQ ID NOS: 9947-9958
PAEP	Progesterone-associated endometrial protein	SEQ ID NOS: 9959-9967
PAM	Peplidylglycine alpha-amidating monooxygenase	SEQ ID NOS: 9968-9981
PAMR1	Peptidase domain containing associated with muscle regeneration 1	SEQ ID NOS: 9982-9988
PAPLN	Papilin, proteoglycan-like sulfated glycoprotein	SEQ ID NOS: 9989-9996
PAPPA	Pregnancy-associated plasma protein A, pappalysin 1	SEQ ID NO: 9997
PAPPA2	Pappalysin 2	SEQ ID NOS: 9998-9999
PARP15	Poly (ADP-ribose) polymerase family, member 15	SEQ ID NOS: 10000-10003
PARVB	Parvin, beta	SEQ ID NOS: 10004-10008
PATE1	Prostate and testis expressed 1	SEQ ID NOS: 10009-10010
PATE2	Prostate and testis expressed 2	SEQ ID NOS: 10011-10012
PATE3	Prostate and testis expressed 3	SEQ ID NO: 10013
PATE4	Prostate and testis expressed 4	SEQ ID NOS: 10014-10015
PATL2	Protein associated with topoisomerase II homolog 2 (yeast)	SEQ ID NOS: 10016-10021
PAX2	Paired box 2	SEQ ID NOS: 10022-10027
PAX4	Paired box 4	SEQ ID NOS: 10028-10034
PCCB	Propionyl CoA carboxylase, beta polypeptide	SEQ ID NOS: 10035-10049
PCDH1	Protocadherin 1	SEQ ID NOS: 10050-10055
PCDH12	Protocadherin 12	SEQ ID NOS: 10056-10057
PCDH15	Protocadherin-related 15	SEQ ID NOS: 10058-10091
PCDHA1	Protocadherin alpha 1	SEQ ID NOS: 10092-10094
PCDHA10	Protocadherin alpha 10	SEQ ID NOS: 10095-10097
PCDHA11	Protocadherin alpha 11	SEQ ID NOS: 10098-10100
PCDHA6	Protocadherin alpha 6	SEQ ID NOS: 10101-10103
PCDHB12	Protocadherin beta 12	SEQ ID NOS: 10104-10106
PCDHGA11	Protocadherin gamma subfamily A, 11	SEQ ID NOS: 10107-10109
PCF11	PCF11 cleavage and polyadenylation factor subunit	SEQ ID NOS: 10110-10114
PCOLCE	Procollagen C-endopeptidase enhancer	SEQ ID NO: 10115
PCOLCE2	Procollagen C-endopeptidase enhancer 2	SEQ ID NOS: 10116-10119
PCSK1	Proprotein convertase subtilisin/kexin type 1	SEQ ID NOS: 10120-10122
PCSK1N	Proprotein convertase subtilisin/kexin type 1 inhibitor	SEQ ID NO: 10123
PCSK2	Proprotein convertase subtilisin/kexin type 2	SEQ ID NOS: 10124-10126
PCSK4	Proprotein convertase subtilisin/kexin type 4	SEQ ID NOS: 10127-10129
PCSK5	Proprotein convertase subtilisin/kexin type 5	SEQ ID NOS: 10130-10134

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
PCSK9	Proprotein convertase subtilisin/kexin type 9	SEQ ID NO: 10135
PCYOX1	Prenylcysteine oxidase 1	SEQ ID NOS: 10136-10140
PCYOX1L	Prenylcysteine oxidase 1 like	SEQ ID NOS: 10141-10145
PDE11A	Phosphodiesterase 11A	SEQ ID NOS: 10146-10151
PDE2A	Phosphodiesterase 2A, cGMP-stimulated	SEQ ID NOS: 10152-10173
PDE7A	Phosphodiesterase 7A	SEQ ID NOS: 10174-10177
PDF	Peptide deformylase (mitochondrial)	SEQ ID NO: 10178
PDGFA	Platelet-derived growth factor alpha polypeptide	SEQ ID NOS: 10179-10182
PDGFB	Platelet-derived growth factor beta polypeptide	SEQ ID NOS: 10183-10186
PDGFC	Platelet derived growth factor C	SEQ ID NOS: 10187-10190
PDGFD	Platelet derived growth factor D	SEQ ID NOS: 10191-10193
PDGFRA	Platelet-derived growth factor receptor, alpha polypeptide	SEQ ID NOS: 10194-10200
PDGFRB	Platelet-derived growth factor receptor, beta polypeptide	SEQ ID NOS: 10201-10204
PDGFRL	Platelet-derived growth factor receptor-like	SEQ ID NOS: 10205-10206
PDHA1	Pyruvate dehydrogenase (lipoamide) alpha 1	SEQ ID NOS: 10207-10215
PDIA2	Protein disulfide isomerase family A, member 2	SEQ ID NOS: 10216-10219
PDIA3	Protein disulfide isomerase family A, member 3	SEQ ID NOS: 10220-10223
PDIA4	Protein disulfide isomerase family A, member 4	SEQ ID NOS: 10224-10225
PDIA5	Protein disulfide isomerase family A, member 5	SEQ ID NOS: 10226-10229
PDIA6	Protein disulfide isomerase family A, member 6	SEQ ID NOS: 10230-10236
PDILT	Protein disulfide isomerase-like, testis expressed	SEQ ID NOS: 10237-10238
PDYN	Prodynorphin	SEQ ID NOS: 10239-10241
PDZD8	PDZ domain containing 8	SEQ ID NO: 10242
PDZRN4	PDZ domain containing ring finger 4	SEQ ID NOS: 10243-10245
PEAR1	Platelet endothelial aggregation receptor 1	SEQ ID NOS: 10246-10249
PEBP4	Phosphatidylethanolamine-binding protein 4	SEQ ID NOS: 10250-10251
PECAM1	Platelet/endothelial cell adhesion molecule 1	SEQ ID NOS: 10252-10255
PENK	Proenkephalin	SEQ ID NOS: 10256-10261
PET117	PET117 homolog	SEQ ID NO: 10262
PF4	Platelet factor 4	SEQ ID NO: 10263
PF4V1	Platelet factor 4 variant 1	SEQ ID NO: 10264
PFKP	Phosphofructokinase, platelet	SEQ ID NOS: 10265-10273
PIN1	Profilin 1	SEQ ID NOS: 10274-10276
PGA3	Pepsinogen 3, group I (pepsinogen A)	SEQ ID NOS: 10277-10280
PGA4	Pepsinogen 4, group I (pepsinogen A)	SEQ ID NOS: 10281-10283
PGA5	Pepsinogen 5, group I (pepsinogen A)	SEQ ID NOS: 10284-10286
PGAM5	PGAM family member 5, serine/threonine protein phosphatase, mitochondrial	SEQ ID NOS: 10287-10290
PGAP3	Post-GPI attachment to proteins 3	SEQ ID NOS: 10291-10298
PGC	Progastriicsin (pepsinogen C)	SEQ ID NOS: 10299-10302
PGF	Placental growth factor	SEQ ID NOS: 10303-10306
PGLYRP1	Peptidoglycan recognition protein 1	SEQ ID NO: 10307
PGLYRP2	Peptidoglycan recognition protein 2	SEQ ID NOS: 10308-10311
PGLYRP3	Peptidoglycan recognition protein 3	SEQ ID NO: 10312
PGLYRP4	Peptidoglycan recognition protein 4	SEQ ID NOS: 10313-10314
PHACTR1	Phosphatase and actin regulator 1	SEQ ID NOS: 10315-10321
PHB	Prohibitin	SEQ ID NOS: 10322-10330
PI15	Peptidase inhibitor 15	SEQ ID NOS: 10331-10332
PI3	Peptidase inhibitor 3, skin-derived	SEQ ID NO: 10333
PIANP	PILR alpha associated neural protein	SEQ ID NOS: 10334-10339
PICK	Phosphatidylinositol glycan anchor biosynthesis, class K	SEQ ID NOS: 10340-10343
PIGL	Phosphatidylinositol glycan anchor biosynthesis, class L	SEQ ID NOS: 10344-10351
PIGT	Phosphatidylinositol glycan anchor biosynthesis, class T	SEQ ID NOS: 10352-10406
PIGZ	Phosphatidylinositol glycan anchor biosynthesis, class Z	SEQ ID NOS: 10407-10409
PIK3AP1	Phosphoinositide-3-kinase adaptor protein 1	SEQ ID NOS: 10410-10412
PIK3IP1	Phosphoinositide-3-kinase interacting protein 1	SEQ ID NOS: 10413-10416
PILRA	Paired immunoglobulin-like type 2 receptor alpha	SEQ ID NOS: 10417-10421
PILRB	Paired immunoglobulin-like type 2 receptor beta	SEQ ID NOS: 10422-10433
PINLYP	Phospholipase A2 inhibitor and LY6/PLAUR domain containing	SEQ ID NOS: 10434-10438
PIP	Prolactin-induced protein	SEQ ID NO: 10439
PIWIL4	Piwi-like RNA-mediated gene silencing 4	SEQ ID NOS: 10440-10444
PKDCC	Protein kinase domain containing, cytoplasmic	SEQ ID NOS: 10445-10446
PKHD1	Polycystic kidney and hepatic disease 1 (autosomal recessive)	SEQ ID NOS: 10447-10448
PLA1A	Phospholipase A1 member A	SEQ ID NOS: 10449-10453
PLA2G10	Phospholipase A2, group X	SEQ ID NOS: 10454-10455
PLA2G12A	Phospholipase A2, group XIIA	SEQ ID NOS: 10456-10458

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
PLA2G12B	Phospholipase A2, group XIIIB	SEQ ID NO: 10459
PLA2G15	Phospholipase A2, group XV	SEQ ID NOS: 10460-10467
PLA2G1B	Phospholipase A2, group IB (pancreas)	SEQ ID NOS: 10468-10470
PLA2G2A	Phospholipase A2, group IIA (platelets, synovial fluid)	SEQ ID NOS: 10471-10472
PLA2G2C	Phospholipase A2, group IIC	SEQ ID NOS: 10473-10474
PLA2G2D	Phospholipase A2, group IID	SEQ ID NOS: 10475-10476
PLA2G2E	Phospholipase A2, group IIE	SEQ ID NO: 10477
PLA2G3	Phospholipase A2, group III	SEQ ID NO: 10478
PLA2G5	Phospholipase A2, group V	SEQ ID NO: 10479
PLA2G7	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	SEQ ID NOS: 10480-10481
PLA2R1	Phospholipase A2 receptor 1, 180 kDa	SEQ ID NOS: 10482-10483
PLAC1	Placenta-specific 1	SEQ ID NO: 10484
PLAC9	Placenta-specific 9	SEQ ID NOS: 10485-10487
PLAT	Plasminogen activator, tissue	SEQ ID NOS: 10488-10496
PLAU	Plasminogen activator, urokinase	SEQ ID NOS: 10497-10499
PLAUR	Plasminogen activator, urokinase receptor	SEQ ID NOS: 10500-10511
PLBD1	Phospholipase B domain containing 1	SEQ ID NOS: 10512-10514
PLBD2	Phospholipase B domain containing 2	SEQ ID NOS: 10515-10517
PLG	Plasminogen	SEQ ID NOS: 10518-10520
PLGLB1	Plasminogen-like B1	SEQ ID NOS: 10521-10524
PLGLB2	Plasminogen-like B2	SEQ ID NOS: 10525-10526
PLOD1	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	SEQ ID NOS: 10527-10529
PLOD2	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	SEQ ID NOS: 10530-10535
PLOD3	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	SEQ ID NOS: 10536-10542
PLTP	Phospholipid transfer protein	SEQ ID NOS: 10543-10547
PLXNA4	Plexin A4	SEQ ID NOS: 10548-10551
PLXNB2	Plexin B2	SEQ ID NOS: 10552-10560
PM20D1	Peptidase M20 domain containing 1	SEQ ID NO: 10561
PMCH	Pro-melanin-concentrating hormone	SEQ ID NO: 10562
PMEL	Premelanosome protein	SEQ ID NOS: 10563-10574
PMEPA1	Prostate transmembrane protein, androgen induced 1	SEQ ID NOS: 10575-10581
PNLIP	Pancreatic lipase	SEQ ID NO: 10582
PNLIPRP1	Pancreatic lipase-related protein 1	SEQ ID NOS: 10583-10591
PNLIPRP3	Pancreatic lipase-related protein 3	SEQ ID NO: 10592
FNOC	Prepronociceptin	SEQ ID NOS: 10593-10595
PNP	Purine nucleoside phosphorylase	SEQ ID NOS: 10596-10599
PNPLA4	Patatin-like phospholipase domain containing 4	SEQ ID NOS: 10600-10603
PODNL1	Podocan-like 1	SEQ ID NOS: 10604-10615
POFUT1	Protein O-fucosyltransferase 1	SEQ ID NOS: 10616-10617
POFUT2	Protein O-fucosyltransferase 2	SEQ ID NOS: 10618-10623
POGLUT1	Protein O-glucosyltransferase 1	SEQ ID NOS: 10624-10628
POLL	Polymerase (DNA directed), lambda	SEQ ID NOS: 10629-10641
POMC	Proopiomelanocortin	SEQ ED NOS: 10642-10646
POMGNT2	Protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	SEQ ID NOS: 10647-10648
PON1	Paraoxonase 1	SEQ ID NOS: 10649-10650
PON2	Paraoxonase 2	SEQ ID NOS: 10651-10663
PON3	Paraoxonase 3	SEQ ID NOS: 10664-10669
POSTN	Periostin, osteoblast specific factor	SEQ ID NOS: 10670-10675
PPBP	Pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	SEQ ID NO: 10676
PIIB	Peptidylprolyl isomerase B (cyclophilin B)	SEQ ID NO: 10677
PPIC	Peptidylprolyl isomerase C (cyclophilin C)	SEQ ID NO: 10678
PPOX	Protoporphyrinogen oxidase	SEQ ID NOS: 10679-10689
PPP1CA	Protein phosphatase 1, catalytic subunit, alpha isozyme	SEQ ID NOS: 10690-10695
PPT1	Palmitoyl-protein thioesterase 1	SEQ ID NOS: 10696-10712
PPT2	Palmitoyl-protein thioesterase 2	SEQ ID NOS: 10713-10720
PPY	Pancreatic polypeptide	SEQ ID NOS: 10721-10725
PRAC2	Prostate cancer susceptibility candidate 2	SEQ ID NOS: 10726-10727
PRADC1	Protease-associated domain containing 1	SEQ ID NO: 10728
PRAP1	Proline-rich acidic protein 1	SEQ ID NOS: 10729-10730
PRB1	Proline-rich protein BstNI subfamily 1	SEQ ID NOS: 10731-10734
PRB2	Proline-rich protein BstNI subfamily 2	SEQ ID NOS: 10735-10736
PRB3	Proline-rich protein BstNI subfamily 3	SEQ ID NOS: 10737-10738
PRB4	Proline-rich protein BstNI subfamily 4	SEQ ID NOS: 10739-10742
PRCD	Progressive rod-cone degeneration	SEQ ID NOS: 10743-10744

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
PRCP	Prolylcarboxypeptidase (angiotensinase C)	SEQ ID NOS: 10745-10756
PRDM12	PR domain containing 12	SEQ ID NO: 10757
PRDX4	Peroxiredoxin 4	SEQ ID NOS: 10758-10761
PRELP	Proline/arginine-rich end leucine-rich repeat protein	SEQ ID NO: 10762
PRF1	Perforin 1 (pore forming protein)	SEQ ID NOS: 10763-10765
PRG2	Proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	SEQ ID NOS: 10766-10768
PRG3	Proteoglycan 3	SEQ ID NO: 10769
PRG4	Proteoglycan 4	SEQ ID NOS: 10770-10775
PRH1	Proline-rich protein HacIII subfamily 1	SEQ ID NOS: 10776-10778
PRH2	Proline-rich protein HacIII subfamily 2	SEQ ID NOS: 10779-10780
PRKAG1	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	SEQ ID NOS: 10781-10795
PRKCSH	Protein kinase C substrate 80K-H	SEQ ID NOS: 10796-10805
PRKD1	Protein kinase D1	SEQ ID NOS: 10806-10811
PRL	Prolactin	SEQ ID NOS: 10812-10814
PRLH	Prolactin releasing hormone	SEQ ID NO: 10815
PRLR	Prolactin receptor	SEQ ID NOS: 10816-10834
PRNP	Prion protein	SEQ ID NOS: 10835-10838
PRNT	Prion protein (testis specific)	SEQ ID NO: 10839
PROC	Protein C (inactivator of coagulation factors Va and VIIa)	SEQ ID NOS: 10840-10847
PROK1	Prokineticin 1	SEQ ID NO: 10848
PROK2	Prokineticin 2	SEQ ID NOS: 10849-10850
PROM1	Prominin 1	SEQ ID NOS: 10851-10862
PROS1	Protein S (alpha)	SEQ ID NOS: 10863-10866
PROZ	Protein Z, vitamin K-dependent plasma glycoprotein	SEQ ID NOS: 10867-10868
PRR27	Proline rich 27	SEQ ID NOS: 10869-10872
PRR4	Proline rich 4 (lacrimal)	SEQ ID NOS: 10873-10875
PRRG2	Proline rich Gla (G-carboxyglutamic acid) 2	SEQ ID NOS: 10876-10878
PRRT3	Proline-rich transmembrane protein 3	SEQ ID NOS: 10879-10881
PRRT4	Proline-rich transmembrane protein 4	SEQ ID NOS: 10882-10888
PRSS1	Protease, serine, 1 (trypsin 1)	SEQ ID NOS: 10889-10892
PRSS12	Protease, serine, 12 (neurotrypsin, motopsin)	SEQ ID NO: 10893
PRSS16	Protease, serine, 16 (thymus)	SEQ ID NOS: 10894-10901
PRSS2	Protease, serine, 2 (trypsin 2)	SEQ ID NOS: 10902-10905
PRSS21	Protease, serine, 21 (testisin)	SEQ ID NOS: 10906-10911
PRSS22	Protease, serine, 22	SEQ ID NOS: 10912-10914
PRSS23	Protease, serine, 23	SEQ ID NOS: 10915-10918
PRSS27	Protease, serine 27	SEQ ID NOS: 10919-10921
PRSS3	Protease, serine, 3	SEQ ID NOS: 10922-10926
PRSS33	Protease, serine, 33	SEQ ID NOS: 10927-10930
PRSS35	Protease, serine, 35	SEQ ID NO: 10931
PRSS36	Protease, serine, 36	SEQ ID NOS: 10932-10935
PRSS37	Protease, serine, 37	SEQ ID NOS: 10936-10939
PRSS38	Protease, serine, 38	SEQ ID NO: 10940
PRSS42	Protease, serine, 42	SEQ ID NOS: 10941-10942
PRSS48	Protease, serine, 48	SEQ ID NOS: 10943-10944
PRSS50	Protease, serine, 50	SEQ ID NO: 10945
PRSS53	Protease, serine, 53	SEQ ID NO: 10946
PRSS54	Protease, serine, 54	SEQ ID NOS: 10947-10951
PRSS55	Protease, serine, 55	SEQ ID NOS: 10952-10954
PRSS56	Protease, serine, 56	SEQ ID NOS: 10955-10956
PRSS57	Protease, serine, 57	SEQ ID NOS: 10957-10958
PRSS58	Protease, serine, 58	SEQ ID NOS: 10959-10960
PRSS8	Protease, serine, 8	SEQ ID NOS: 10961-10964
PRTG	Protoporphyrinogen oxidase	SEQ ID NOS: 10965-10968
PTRN3	Proteinase 3	SEQ ID NOS: 10969-10970
PSAP	Prosaposin	SEQ ID NOS: 10971-10974
PSAPL1	Prosaposin-like 1 (gene/pseudogene)	SEQ ID NO: 10975
PSG1	Pregnancy specific beta-1-glycoprotein 1	SEQ ID NOS: 10976-10983
PSG11	Pregnancy specific beta-1-glycoprotein 11	SEQ ID NOS: 10984-10988
PSG2	Pregnancy specific beta-1-glycoprotein 2	SEQ ID NOS: 10989-10990
PSG3	Pregnancy specific beta-1-glycoprotein 3	SEQ ID NOS: 10991-10994
PSG4	Pregnancy specific beta-1-glycoprotein 4	SEQ ID NOS: 10995-11006
PSG5	Pregnancy specific beta-1-glycoprotein 5	SEQ ID NOS: 11007-11012
PSG6	Pregnancy specific beta-1-glycoprotein 6	SEQ ID NOS: 11013-11018
PSG7	Pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	SEQ ID NOS: 11019-11021
PSG8	Pregnancy specific beta-1-glycoprotein 8	SEQ ID NOS: 11022-11026
PSG9	Pregnancy specific beta-1-glycoprotein 9	SEQ ID NOS: 11027-11034
PSMD1	Proteasome 26S subunit, non-ATPase 1	SEQ ID NOS: 11035-11042

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
PSORS1C2	Psoriasis susceptibility 1 candidate 2	SEQ ID NO: 11043
PSPN	Persephin	SEQ ID NOS: 11044-11045
PTGDS	Prostaglandin D2 synthase 21 kDa (brain)	SEQ ID NOS: 11046-11050
PTGIR	Prostaglandin I2 (prostacyclin) receptor (IP)	SEQ ID NOS: 11051-11055
PTGS1	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	SEQ ID NOS: 11056-11064
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	SEQ ID NOS: 11065-11066
PTH	Parathyroid hormone	SEQ ID NOS: 11067-11068
PTH2	Parathyroid hormone 2	SEQ ID NO: 11069
PTHLH	Parathyroid hormone-like hormone	SEQ ID NOS: 11070-11078
PTK7	Protein tyrosine kinase 7 (inactive)	SEQ ID NOS: 11079-11094
PTN	Pleiotrophin	SEQ ID NOS: 11095-11096
PTPRA	Protein tyrosine phosphatase, receptor type, A	SEQ ID NOS: 11097-11104
PTPRB	Protein tyrosine phosphatase, receptor type, B	SEQ ID NOS: 11105-11112
PTPRC	Protein tyrosine phosphatase, receptor type, C	SEQ ID NOS: 11113-11123
PTPRCAP	Protein tyrosine phosphatase, receptor type, C-associated protein	SEQ ID NO: 11124
PTPRD	Protein tyrosine phosphatase, receptor type, D	SEQ ID NOS: 11125-11136
PTPRF	Protein tyrosine phosphatase, receptor type, F	SEQ ID NOS: 11137-11144
PTPRJ	Protein tyrosine phosphatase, receptor type, J	SEQ ID NOS: 11145-11150
PTPRO	Protein tyrosine phosphatase, receptor type, O	SEQ ID NOS: 11151-11159
PTPRS	Protein tyrosine phosphatase, receptor type, S	SEQ ID NOS: 11160-11167
PTTG1IP	Pituitary tumor-transforming 1 interacting protein	SEQ ID NOS: 11168-11171
PTX3	Pentraxin 3, long	SEQ ID NO: 11172
PTX4	Pentraxin 4, long	SEQ ID NOS: 11173-11175
PVR	Poliovirus receptor	SEQ ID NOS: 11176-11181
PXDNL	Peroxidasin	SEQ ID NOS: 11182-11186
PXDNL	Peroxidasin-like	SEQ ID NOS: 11187-11189
PXYLP1	2-phosphoxylose phosphatase 1	SEQ ID NOS: 11190-11202
PYY	Peptide YY	SEQ ID NOS: 11203-11204
PZP	Pregnancy-zone protein	SEQ ID NOS: 11205-11206
QPCT	Glutaminyl-peptide cyclotransferase	SEQ ID NOS: 11207-11209
QPRT	Quinolinate phosphoribosyltransferase	SEQ ID NOS: 11210-11211
QRFP	Pyroglutamylated RFamide peptide	SEQ ID NOS: 11212-11213
QSOX1	Quiescin Q6 sulphydryl oxidase 1	SEQ ID NOS: 11214-11217
R3HDML	R3H domain containing-like	SEQ ID NO: 11218
RAB26	RAB26, member RAS oncogene family	SEQ ID NOS: 11219-11222
RAB36	RAB36, member RAS oncogene family	SEQ ID NOS: 11223-11225
RAB9B	RAB9B, member RAS oncogene family	SEQ ID NO: 11226
RAET1E	Retinoic acid early transcript 1E	SEQ ID NOS: 11227-11232
RAET1G	Retinoic acid early transcript 1G	SEQ ID NOS: 11233-11235
RAMP2	Receptor (G protein-coupled) activity modifying protein 2	SEQ ID NOS: 11236-11240
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	SEQ ID NOS: 11241-11247
RARRES1	Retinoic acid receptor responder (tazarotene induced) 1	SEQ ID NOS: 11248-11249
RARRES2	Retinoic acid receptor responder (tazarotene induced) 2	SEQ ID NOS: 11250-11253
RASA2	RAS p21 protein activator 2	SEQ ID NOS: 11254-11256
RBM3	RNA binding motif (RNP1, RRM) protein 3	SEQ ID NOS: 11257-11259
RBP3	Retinol binding protein 3, interstitial	SEQ ID NO: 11260
RBP4	Retinol binding protein 4, plasma	SEQ ID NOS: 11261-11264
RCN1	Reticulocalbin 1, EF-hand calcium binding domain	SEQ ID NOS: 11265-11268
RCN2	Reticulocalbin 2, EF-hand calcium binding domain	SEQ ID NOS: 11269-11272
RCN3	Reticulocalbin 3, EF-hand calcium binding domain	SEQ ID NOS: 11273-11276
RCOR1	REST corepressor 1	SEQ ID NOS: 11277-11278
RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	SEQ ID NOS: 11279-11286
RDH12	Retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	SEQ ID NOS: 11287-11288
RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	SEQ ID NOS: 11289-11297
RDH5	Retinol dehydrogenase 5 (11-cis/9-cis)	SEQ ID NOS: 11298-11302
RDH8	Retinol dehydrogenase 8 (all-trans)	SEQ ID NOS: 11303-11304
REGIA	Regenerating islet-derived 1 alpha	SEQ ID NO: 11305
REG1B	Regenerating islet-derived 1 beta	SEQ ID NOS: 11306-11307
REG3A	Regenerating islet-derived 3 alpha	SEQ ID NOS: 11308-11310
REG3G	Regenerating islet-derived 3 gamma	SEQ ID NOS: 11311-11313
REG4	Regenerating islet-derived family, member 4	SEQ ID NOS: 11314-11317
RELN	Reelin	SEQ ID NOS: 11318-11321
RELT	RELT tumor necrosis factor receptor	SEQ ID NOS: 11322-11325
REN	Renin	SEQ ID NOS: 11326-11327
REPIN1	Replication initiator 1	SEQ ID NOS: 11328-11341
REPS2	RALBP1 associated Eps domain containing 2	SEQ ID NOS: 11342-11343
RET	Ret proto-oncogene	SEQ ID NOS: 11344-11349
RETN	Resistin	SEQ ID NOS: 11350-11352

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
RETNLB	Resistin like beta	SEQ ID NO: 11353
RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)	SEQ ID NOS: 11354-11358
RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 11359-11361
RGCC	Regulator of cell cycle	SEQ ID NO: 11362
RGL4	Ral guanine nucleotide dissociation stimulator-like 4	SEQ ID NOS: 11363-11369
RGMA	Repulsive guidance molecule family member a	SEQ ID NOS: 11370-11379
RGMB	Repulsive guidance molecule family member b	SEQ ID NOS: 11380-11381
RHOQ	Ras homolog family member Q	SEQ ID NOS: 11382-11386
RIC3	RIC3 acetylcholine receptor chaperone	SEQ ID NOS: 11387-11394
HRSP12	Heat-responsive protein 12	SEQ ID NOS: 11395-11398
RIMS1	Regulating synaptic membrane exocytosis 1	SEQ ID NOS: 11399-11414
RIPPLY1	Ripply transcriptional repressor 1	SEQ ID NOS: 11415-11416
RLN1	Relaxin 1	SEQ ID NO: 11417
RLN2	Relaxin 2	SEQ ID NOS: 11418-11419
RLN3	Relaxin 3	SEQ ID NOS: 11420-11421
RMDN1	Regulator of microtubule dynamics 1	SEQ ID NOS: 11422-11435
RNASE1	Ribonuclease, RNase A family, 1 (pancreatic)	SEQ ID NOS: 11436-11440
RNASE10	Ribonuclease, RNase A family, 10 (non-active)	SEQ ID NOS: 11441-11442
RNASE11	Ribonuclease, RNase A family, 11 (non-active)	SEQ ID NOS: 11443-11453
RNASE12	Ribonuclease, RNase A family, 12 (non-active)	SEQ ID NO: 11454
RNASE13	Ribonuclease, RNase A family, 13 (non-active)	SEQ ID NO: 11455
RNASE2	Ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	SEQ ID NO: 11456
RNASE3	Ribonuclease, RNase A family, 3	SEQ ID NO: 11457
RNASE4	Ribonuclease, RNase A family, 4	SEQ ID NOS: 11458-11460
RNASE6	Ribonuclease, RNase A family, k6	SEQ ID NO: 11461
RNASE7	Ribonuclease, RNase A family, 7	SEQ ID NOS: 11462-11463
RNASE8	Ribonuclease, RNase A family, 8	SEQ ID NO: 11464
RNASE9	Ribonuclease, RNase A family, 9 (non-active)	SEQ ID NOS: 11465-11475
RNASEH1	Ribonuclease H1	SEQ ID NOS: 11476-11478
RNASET2	Ribonuclease T2	SEQ ID NOS: 11479-11486
RNF146	Ring finger protein 146	SEQ ID NOS: 11487-11498
RNF148	Ring finger protein 148	SEQ ID NOS: 11499-11500
RNF150	Ring finger protein 150	SEQ ID NOS: 11501-11505
RNF167	Ring finger protein 167	SEQ ID NOS: 11506-11516
RNF220	Ring finger protein 220	SEQ ID NOS: 11517-11523
RNF34	Ring finger protein 34, E3 ubiquitin protein ligase	SEQ ID NOS: 11524-11531
RNLS	Renalase, FAD-dependent amine oxidase	SEQ ID NOS: 11532-11534
RNPEP	Arginyl aminopeptidase (aminopeptidase B)	SEQ ID NOS: 11535-11540
ROR1	Receptor tyrosine kinase-like orphan receptor 1	SEQ ID NOS: 11541-11543
RPL3	Ribosomal protein L3	SEQ ID NOS: 11544-11549
RPLP2	Ribosomal protein, large, P2	SEQ ID NOS: 11550-11552
RPN2	Ribophorin II	SEQ ID NOS: 11553-11559
RPS27L	Ribosomal protein S27-like	SEQ ID NOS: 11560-11565
RS1	Retinoschisin 1	SEQ ID NO: 11566
RSF1	Remodeling and spacing factor 1	SEQ ID NOS: 11567-11573
RSPO1	R-spondin 1	SEQ ID NOS: 11574-11577
RSPO2	R-spondin 2	SEQ ID NOS: 11578-11585
RSPO3	R-spondin 3	SEQ ID NOS: 11586-11587
RSPO4	R-spondin 4	SEQ ID NOS: 11588-11589
RSPRY1	Ring finger and SPRY domain containing 1	SEQ ID NOS: 11590-11596
RTBDN	Retbindin	SEQ ID NOS: 11597-11609
RTN4RL1	Reticulon 4 receptor-like 1	SEQ ID NO: 11610
RTN4RL2	Reticulon 4 receptor-like 2	SEQ ID NOS: 11611-11613
SAA1	Seram amyloid A1	SEQ ID NOS: 11614-11616
SAA2	Seram amyloid A2	SEQ ID NOS: 11617-11622
SAA4	Serum amyloid A4, constitutive	SEQ ID NO: 11623
SAP30	Sin3A-associated protein, 30 kDa	SEQ ID NO: 11624
SARIA	Secretion associated, Ras related GTPase 1A	SEQ ID NOS: 11625-11631
SARAF	Store-operated calcium entry-associated regulatory factor	SEQ ID NOS: 11632-11642
SARM1	Sterile alpha and TIR motif containing 1	SEQ ID NOS: 11643-11646
SATB1	SATB homeobox 1	SEQ ID NOS: 11647-11659
SAXO2	Stabilizer of axonemal microtubules 2	SEQ ID NOS: 11660-11664
SBSN	Suprabasin	SEQ ID NOS: 11665-11667
SBSPON	Somatomedin B and thrombospondin, type 1 domain containing	SEQ ID NO: 11668
SCARF1	Scavenger receptor class F, member 1	SEQ ID NOS: 11669-11673
SCG2	Secretogranin II	SEQ ID NOS: 11674-11676
SCG3	Secretogranin III	SEQ ID NOS: 11677-11679
SCG5	Secretogranin V	SEQ ID NOS: 11680-11684
SCGB1A1	Secretoglobin, family 1A, member 1 (uteroglobin)	SEQ ID NOS: 11685-11686

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
SCGB1C1	Secretoglobin, family 1C, member 1	SEQ ID NO: 11687
SCGB1C2	Secretoglobin, family 1C, member 2	SEQ ID NO: 11688
SCGB1D1	Secretoglobin, family 1D, member 1	SEQ ID NO: 11689
SCGB1D2	Secretoglobin, family 1D, member 2	SEQ ID NO: 11690
SCGB1D4	Secretoglobin, family 1D, member 4	SEQ ID NO: 11691
SCGB2A1	Secretoglobin, family 2A, member 1	SEQ ID NO: 11692
SCGB2A2	Secretoglobin, family 2A, member 2	SEQ ID NOS: 11693-11694
SCGB2B2	Secretoglobin, family 2B, member 2	SEQ ID NOS: 11695-11696
SCGB3A1	Secretoglobin, family 3A, member 1	SEQ ID NO: 11697
SCGB3A2	Secretoglobin, family 3A, member 2	SEQ ID NOS: 11698-11699
SCN1B	Sodium channel, voltage gated, type I beta subunit	SEQ ID NOS: 11700-11705
SCN3B	Sodium channel, voltage gated, type III beta subunit	SEQ ID NOS: 11706-11710
SCPEP1	Serine carboxypeptidase 1	SEQ ID NOS: 11711-11718
SCRG1	Stimulator of chondrogenesis 1	SEQ ID NOS: 11719-11720
SCT	Secretin	SEQ ID NO: 11721
SCUBE1	Signal peptide, CUB domain, EGF-like 1	SEQ ID NOS: 11722-11725
SCUBE2	Signal peptide, CUB domain, EGF-like 2	SEQ ID NOS: 11726-11732
SCUBE3	Signal peptide, CUB domain, EGF-like 3	SEQ ID NO: 11733
SDC1	Syndecan 1	SEQ ID NOS: 11734-11738
SDF2	Stromal cell-derived factor 2	SEQ ID NOS: 11739-11741
SDF2L1	Stromal cell-derived factor 2-like 1	SEQ ID NO: 11742
SDF4	Stromal cell derived factor 4	SEQ ID NOS: 11743-11746
SDHAF2	Succinate dehydrogenase complex assembly factor 2	SEQ ID NOS: 11747-11754
SDHAF4	Succinate dehydrogenase complex assembly factor 4	SEQ ID NO: 11755
SDHB	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	SEQ ID NOS: 11756-11758
SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein	SEQ ID NOS: 11759-11768
SEC14L3	SEC14-like lipid binding 3	SEQ ID NOS: 11769-11775
SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	SEQ ID NOS: 11776-11782
SEC16B	SEC16 homolog B, endoplasmic reticulum export factor	SEQ ID NOS: 11783-11786
SEC22C	SEC22 homolog C, vesicle trafficking protein	SEQ ID NOS: 11787-11799
SEC31A	SEC31 homolog A, COP11 coat complex component	SEQ ID NOS: 11800-11829
SECISBP2	SECIS binding protein 2	SEQ ID NOS: 11830-11834
SECTM1	Secreted and transmembrane 1	SEQ ID NOS: 11835-11842
SEL1L	Sel-1 suppressor of lin-12-like (<i>C. elegans</i>)	SEQ ID NOS: 11843-11845
SEPT15	15 kDa selenoprotein	SEQ ID NOS: 11846-11852
SELM	Selenoprotein M	SEQ ID NOS: 11853-11855
SEPN1	Selenoprotein N, 1	SEQ ID NOS: 11856-11859
SELO	Selenoprotein O	SEQ ID NOS: 11860-11861
SEPP1	Selenoprotein P, plasma, 1	SEQ ID NOS: 11862-11867
SEMA3A	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	SEQ ID NOS: 11868-11872
SEMA3B	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	SEQ ID NOS: 11873-11879
SEMA3C	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEQ ID NOS: 11880-11884
SEMA3E	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	SEQ ID NOS: 11885-11889
SEMA3F	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEQ ID NOS: 11890-11896
SEMA3G	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	SEQ ID NOS: 11897-11899
SEMA4A	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	SEQ ID NOS: 11900-11908
SEMA4B	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	SEQ ID NOS: 11909-11919
SEMA4C	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	SEQ ID NOS: 11920-11922
SEMA4D	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	SEQ ID NOS: 11923-11936
SEMA4F	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	SEQ ID NOS: 11937-11945

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
SEMA4G	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	SEQ ID NOS: 11946-11953
SEMA5A	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	SEQ ID NOS: 11954-11955
SEMA6A	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	SEQ ID NOS: 11956-11963
SEMA6C	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	SEQ ID NOS: 11964-11969
SEMA6D	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	SEQ ID NOS: 11970-11983
SEMG1	Semenogelin I	SEQ ID NO: 11984
SEMG2	Semenogelin II	SEQ ID NO: 11985
SEPT9	Septin 9	SEQ ID NOS: 11986-12022
SERPINA1	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SEQ ID NOS: 12023-12039
SERPINA10	Serpin peptidase inhibitor, clade A (alpha-1 antiprotecinase, antitrypsin), member 10	SEQ ID NOS: 12040-12043
SERPINA11	Serpin peptidase inhibitor, clade A (alpha-1 anti proteinase, antitrypsin), member 11	SEQ ID NO: 12044
SERPINA12	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	SEQ ID NOS: 12045-12046
SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	SEQ ID NOS: 12047-12053
SERPINA4	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4	SEQ ID NOS: 12054-12056
SERPINA5	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	SEQ ID NOS: 12057-12068
SERPINA6	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	SEQ ID NOS: 12069-12071
SERPINA7	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7	SEQ ID NOS: 12072-12073
SERPINA9	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	SEQ ID NOS: 12074-12080
SERPINB2	Serpin peptidase inhibitor, clade B (ovalbumin), member 2	SEQ ID NOS: 12081-12085
SERPINC1	Serpin peptidase inhibitor, clade C (antithrombin), member 1	SEQ ID NOS: 12086-12087
SERPIND1	Serpin peptidase inhibitor, clade D (heparin cofactor), member 1	SEQ ID NOS: 12088-12089
SERPINE1	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SEQ ID NO: 12090
SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	SEQ ID NOS: 12091-12097
SERPINE3	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3	SEQ ID NOS: 12098-12101
SERPINF1	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	SEQ ID NOS: 12102-12110
SERPINF2	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	SEQ ID NOS: 12111-12115
SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	SEQ ID NOS: 12116-12126
SERPINH1	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	SEQ ID NOS: 12127-12141
SERPINI1	Serpin peptidase inhibitor, clade I (neuroserpin), member 1	SEQ ID NOS: 12142-12146
SERPINI2	Serpin peptidase inhibitor, clade I (panepin), member 2	SEQ ID NOS: 12147-12153
SEZ6L2	Seizure related 6 homolog (mouse)-like 2	SEQ ID NOS: 12154-12160
SFRP1	Secreted frizzled-related protein 1	SEQ ID NOS: 12161-12162
SFRP2	Secreted frizzled-related protein 2	SEQ ID NO: 12163
SFRP4	Secreted frizzled-related protein 4	SEQ ID NOS: 12164-12165
SFRP5	Secreted frizzled-related protein 5	SEQ ID NO: 12166
SFTA2	Surfactant associated 2	SEQ ID NOS: 12167-12168
SFTPA1	Surfactant protein A1	SEQ ID NOS: 12169-12173
SFTPA2	Surfactant protein A2	SEQ ID NOS: 12174-12178
SFTPB	Surfactant protein B	SEQ ID NOS: 12179-12183
SFTPD	Surfactant protein D	SEQ ID NOS: 12184-12185
SFXN5	Sideroflexin 5	SEQ ID NOS: 12186-12190
SGCA	Sarcoglycan, alpha (50 kDa dystrophin-associated glycoprotein)	SEQ ID NOS: 12191-12198

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
SGSH	N-sulfoglucosamine sulfohydrolase	SEQ ID NOS: 12199-12207
SH3RF3	SH3 domain containing ring finger 3	SEQ ID NO: 12208
SHBG	Sex hormone-binding globulin	SEQ ID NOS: 12209-12227
SHE	Src homology 2 domain containing E	SEQ ID NOS: 12228-12230
SHH	Sonic hedgehog	SEQ ID NOS: 12231-12234
SH3KBP1	SH3KBP1 binding protein 1	SEQ ID NOS: 12235-12250
SIAE	Sialic acid acetyl esterase	SEQ ID NOS: 12251-12253
SIDT2	SID1 transmembrane family, member 2	SEQ ID NOS: 12254-12263
SIGLEC10	Sialic acid binding Ig-like lectin 10	SEQ ID NOS: 12264-12272
SIGLEC6	Sialic acid binding Ig-like lectin 6	SEQ ID NOS: 12273-12278
SIGLEC7	Sialic acid binding Ig-like lectin 7	SEQ ID NOS: 12279-12283
SIGLECL1	SIGLEC family like 1	SEQ ID NOS: 12284-12289
SIGMAR1	Sigma non-opioid intracellular receptor 1	SEQ ID NOS: 12290-12293
SIL1	SIL1 nucleotide exchange factor	SEQ ID NOS: 12294-12302
SIRPB1	Signal-regulatory protein beta 1	SEQ ID NOS: 12303-12315
SIRPD	Signal-regulatory protein delta	SEQ ID NOS: 12316-12318
SLAMF1	Signaling lymphocytic activation molecule family member 1	SEQ ID NOS: 12319-12321
SLAMF7	SLAM family member 7	SEQ ID NOS: 12322-12330
SLC10A3	Solute carrier family 10, member 3	SEQ ID NOS: 12331-12335
SLC15A3	Solute carrier family 15 (oligopeptide transporter), member 3	SEQ ID NOS: 12336-12341
SLC25A14	Solute carrier family 25 (mitochondrial carrier, brain), member 14	SEQ ID NOS: 12342-12348
SLC25A25	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	SEQ ID NOS: 12349-12355
SLC2A5	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SEQ ID NOS: 12356-12364
SLC35E3	Solute carrier family 35, member E3	SEQ ID NOS: 12365-12366
SLC39A10	Solute carrier family 39 (zinc transporter), member 10	SEQ ID NOS: 12367-12373
SLC39A14	Solute carrier family 39 (zinc transporter), member 14	SEQ ID NOS: 12374-12384
SLC39A4	Solute carrier family 39 (zinc transporter), member 4	SEQ ID NOS: 12385-12387
SLC39A5	Solute carrier family 39 (zinc transporter), member 5	SEQ ID NOS: 12388-12394
SLC3A1	Solute carrier family 3 (amino acid transporter heavy chain), member 1	SEQ ID NOS: 12395-12404
SLC51A	Solute carrier family 51, alpha subunit	SEQ ID NOS: 12405-12409
SLC52A2	Solute carrier family 52 (riboflavin transporter), member 2	SEQ ID NOS: 12410-12420
SLC5A6	Solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6	SEQ ID NOS: 12421-12431
SLC6A9	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9	SEQ ID NOS: 12432-12439
SLC8A1	Solute carrier family 8 (sodium/calcium exchanger), member 1	SEQ ID NOS: 12440-12451
SLC8B1	Solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	SEQ ID NOS: 12452-12462
SLC9A6	Solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6	SEQ ID NOS: 12463-12474
SLCO1A2	Solute carrier organic anion transporter family, member 1A2	SEQ ID NOS: 12475-12488
SLIT1	Slit guidance ligand 1	SEQ ID NOS: 12489-12492
SLIT2	Slit guidance ligand 2	SEQ ID NOS: 12493-12501
SLIT3	Slit guidance ligand 3	SEQ ID NOS: 12502-12504
SLTRK3	SLIT and NTRK-like family, member 3	SEQ ID NOS: 12505-12507
SLPI	Secretory leukocyte peptidase inhibitor	SEQ ID NO: 12508
SLTM	SAFB-like, transcription modulator	SEQ ID NOS: 12509-12522
SLURP1	Secreted LY6/PLAUR domain containing 1	SEQ ID NO: 12523
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID NOS: 12524-12571
SMG6	SMG6 nonsense mediated mRNA decay factor	SEQ ID NOS: 12572-12583
SMM7	Small integral membrane protein 7	SEQ ID NOS: 12584-12600
SMOC1	SPARC related modular calcium binding 1	SEQ ID NOS: 12601-12602
SMOC2	SPARC related modular calcium binding 2	SEQ ID NOS: 12603-12607
SMPDL3A	Sphingomyelin phosphodiesterase, acid-like 3A	SEQ ID NOS: 12608-12609
SMPDL3B	Sphingomyelin phosphodiesterase, acid-like 3B	SEQ ID NOS: 12610-12614
SMR3A	Submaxillary gland androgen regulated protein 3A	SEQ ID NO: 12615

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
SMR3B	Submaxillary gland androgen regulated protein 3B	SEQ ID NOS: 12616-12618
SNED1	Sushi, nidogen and EGF-like domains 1	SEQ ID NOS: 12619-12625
SNTB1	Syntrophin, beta 1 (dystrophin-associated protein A1, 59 kDa, basic component 1)	SEQ ID NOS: 12626-12628
SNTB2	Syntrophin, beta 2 (dystrophin-associated protein A1, 59 kDa, basic component 2)	SEQ ID NOS: 12629-12633
SNX14	Sorting nexin 14	SEQ ID NOS: 12634-12645
SOD3	Superoxide dismutase 3, extracellular	SEQ ID NOS: 12646-12647
SOST	Sclerostin	SEQ ID NO: 12648
SOSTDC1	Sclerostin domain containing 1	SEQ ID NOS: 12649-12650
SOWAHA	Sosondowah ankyrin repeat domain family member A	SEQ ID NO: 12651
SPACA3	Sperm acrosome associated 3	SEQ ID NOS: 12652-12654
SPACA4	Sperm acrosome associated 4	SEQ ID NO: 12655
SPACA5	Sperm acrosome associated 5	SEQ ID NOS: 12656-12657
SPACA5B	Sperm acrosome associated 5B	SEQ ID NO: 12658
SPACA7	Sperm acrosome associated 7	SEQ ID NOS: 12659-12662
SPAG11A	Sperm associated antigen 11A	SEQ ID NOS: 12663-12671
SPAG11B	Sperm associated antigen 11B	SEQ ID NOS: 12672-12680
SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)	SEQ ID NOS: 12681-12685
SPARCL1	SPARC-like 1 (hevin)	SEQ ID NOS: 12686-12695
SPATA20	Spermatogenesis associated 20	SEQ ID NOS: 12696-12709
SPESP1	Sperm equatorial segment protein 1	SEQ ID NO: 12710
SPINK1	Serine peptidase inhibitor, Kazal type 1	SEQ ID NOS: 12711-12712
SPINK13	Serine peptidase inhibitor, Kazal type 13 (putative)	SEQ ID NOS: 12713-12715
SPINK14	Serine peptidase inhibitor, Kazal type 14 (putative)	SEQ ID NOS: 12716-12717
SPINK2	Serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	SEQ ID NOS: 12718-12723
SPINK4	Serine peptidase inhibitor, Kazal type 4	SEQ ID NOS: 12724-12725
SPINK5	Serine peptidase inhibitor, Kazal type 5	SEQ ID NOS: 12726-12731
SPINK6	Serine peptidase inhibitor, Kazal type 6	SEQ ID NOS: 12732-12734
SPINK7	Serine peptidase inhibitor, Kazal type 7 (putative)	SEQ ID NOS: 12735-12736
SPINK8	Serine peptidase inhibitor, Kazal type 8 (putative)	SEQ ID NO: 12737
SPINK9	Serine peptidase inhibitor, Kazal type 9	SEQ ID NOS: 12738-12739
SPINT1	Serine peptidase inhibitor, Kunitz type 1	SEQ ID NOS: 12740-12747
SPINT2	Serine peptidase inhibitor, Kunitz type, 2	SEQ ID NOS: 12748-12755
SPINT3	Serine peptidase inhibitor, Kunitz type, 3	SEQ ID NO: 12756
SPINT4	Serine peptidase inhibitor, Kunitz type 4	SEQ ID NO: 12757
SPOCK1	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	SEQ ID NOS: 12758-12761
SPOCK2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SEQ ID NOS: 12762-12765
SPOCK3	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	SEQ ID NOS: 12766-12791
SPON1	Spondin 1, extracellular matrix protein	SEQ ID NO: 12792
SPON2	Spondin 2, extracellular matrix protein	SEQ ID NOS: 12793-12802
SPP1	Secreted phosphoprotein 1	SEQ ID NOS: 12803-12807
SPP2	Secreted phosphoprotein 2, 24 kDa	SEQ ID NOS: 12808-12810
SPRN	Shadow of prion protein homolog (zebrafish)	SEQ ID NO: 12811
SPRYD3	SPRY domain containing 3	SEQ ID NOS: 12812-12815
SPRYD4	SPRY domain containing 4	SEQ ID NO: 12816
SPTY2D1-AS1	SPTY2D1 antisense RNA 1	SEQ ID NOS: 12817-12822
SPX	Spexin hormone	SEQ ID NOS: 12823-12824
SRGN	Serglycin	SEQ ID NO: 12825
SRL	Sarcalumenin	SEQ ID NOS: 12826-12828
SRP14	Signal recognition particle 14 kDa (homologous Alu RNA binding protein)	SEQ ID NOS: 12829-12832
SRPX	Sushi-repeat containing protein, X-linked	SEQ ID NOS: 12833-12836
SRPX2	Sushi-repeat containing protein, X-linked 2	SEQ ID NOS: 12837-12840
SSC4D	Scavenger receptor cysteine rich family, 4 domains	SEQ ID NO: 12841
SSC5D	Scavenger receptor cysteine rich family, 5 domains	SEQ ID NOS: 12842-12845
SSPO	SCO-spondin	SEQ ID NO: 12846
SSR2	Signal sequence receptor, beta (translocon-associated protein beta)	SEQ ID NOS: 12847-12856
SST	Somatostatin	SEQ ID NO: 12857
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	SEQ ID NOS: 12858-12865
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	SEQ ID NOS: 12866-12881
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	SEQ ID NOS: 12882-12897
ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	SEQ ID NOS: 12898-12902

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	SEQ ID NOS: 12903-12904
ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	SEQ ID NOS: 12905-12912
ST8SIA2	ST8 alpha-N-acetyl-neuraminiide alpha-2,8-sialyltransferase 2	SEQ ID NOS: 12913-12915
ST8SIA4	ST8 alpha-N-acetyl-neuraminiide alpha-2,8-sialyltransferase 4	SEQ ID NOS: 12916-12918
ST8SIA6	ST8 alpha-N-acetyl-neuraminiide alpha-2,8-sialyltransferase 6	SEQ ID NOS: 12919-12920
STARD7	StAR-related lipid transfer (START) domain containing 7	SEQ ID NOS: 12921-12922
STATH	Statherin	SEQ ID NOS: 12923-12925
STC1	Stanniocalcin 1	SEQ ID NOS: 12926-12927
STC2	Stanniocalcin 2	SEQ ID NOS: 12928-12930
STMND1	Stathmin domain containing 1	SEQ ID NOS: 12931-12932
C7orf73	Chromosome 7 open reading frame 73	SEQ ID NOS: 12933-12934
STOML2	Stomatin (EPB72)-like 2	SEQ ID NOS: 12935-12938
STOX1	Storkhead box 1	SEQ ID NOS: 12939-12943
STRC	Stereocilin	SEQ ID NOS: 12944-12949
SUCLG1	Succinate-CoA ligase, alpha subunit	SEQ ID NOS: 12950-12951
SUDS3	SDS3 homolog, SIN3A corepressor complex component	SEQ ID NO: 12952
SULF1	Sulfatase 1	SEQ ID NOS: 12953-12963
SULF2	Sulfatase 2	SEQ ID NOS: 12964-12968
SUMF1	Sulfatase modifying factor 1	SEQ ID NOS: 12969-12973
SUMF2	Sulfatase modifying factor 2	SEQ ID NOS: 12974-12987
SUSD1	Sushi domain containing 1	SEQ ID NOS: 12988-12993
SUSD5	Sushi domain containing 5	SEQ ID NOS: 12994-12995
SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	SEQ ID NOS: 12996-12998
SWSAP1	SWIM-type zinc finger 7 associated protein 1	SEQ ID NO: 12999
SYAP1	Synapse associated protein 1	SEQ ID NO: 13000
SYCN	Syncoilin	SEQ ID NO: 13001
TAC1	Tachykinin, precursor 1	SEQ ID NOS: 13002-13004
TAC3	Tachykinin 3	SEQ ID NOS: 13005-13014
TAC4	Tachykinin 4 (hemokinin)	SEQ ID NOS: 13015-13020
TAGLN2	Transgelin 2	SEQ ID NOS: 13021-13024
TAPBP	TAP binding protein (tapasin)	SEQ ID NOS: 13025-13030
TAPBPL	TAP binding protein-like	SEQ ID NOS: 13031-13032
TBL2	Transducin (beta)-like 2	SEQ ID NOS: 13033-13045
TBX10	T-box 10	SEQ ID NO: 13046
TCF12	Transcription factor 12	SEQ ID NOS: 13047-13060
TCN1	Transcobalamin I (vitamin B12, binding protein, R binder family)	SEQ ID NO: 13061
TCN2	Transcobalamin II	SEQ ID NOS: 13062-13065
TCTN1	Tectonic family member 1	SEQ ID NOS: 13066-13084
TCTN3	Tectonic family member 3	SEQ ID NOS: 13085-13089
TDP2	Tyrosyl-DNA phosphodiesterase 2	SEQ ID NOS: 13090-13091
C14orf80	Chromosome 14 open reading frame 80	SEQ ID NOS: 13092-13105
TEK	TEK tyrosine kinase, endothelial	SEQ ID NOS: 13106-13110
TEPP	Testis, prostate and placenta expressed	SEQ ID NOS: 13111-13112
TEX101	Testis expressed 101	SEQ ID NOS: 13113-13114
TEX264	Testis expressed 264	SEQ ID NOS: 13115-13126
C1orf234	Chromosome 1 open reading frame 234	SEQ ID NOS: 13127-13129
TF	Transferrin	SEQ ID NOS: 13130-13136
TFAM	Transcription factor A, mitochondrial	SEQ ID NOS: 13137-13139
TFF1	Trefoil factor 1	SEQ ID NO: 13140
TFF2	Trefoil factor 2	SEQ ID NO: 13141
TFF3	Trefoil factor 3 (intestinal)	SEQ ID NOS: 13142-13144
TFPI	Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	SEQ ID NOS: 13145-13154
TFPI2	Tissue factor pathway inhibitor 2	SEQ ID NOS: 13155-13156
TG	Thyroglobulin	SEQ ID NOS: 13157-13166
TGFB1	Transforming growth factor, beta 1	SEQ ID NOS: 13167-13168
TGFB2	Transforming growth factor, beta 2	SEQ ID NOS: 13169-13170
TGFB3	Transforming growth factor, beta 3	SEQ ID NOS: 13171-13172
TGFB1	Transforming growth factor, beta-induced, 68 kDa	SEQ ID NOS: 13173-13180
TGFRB1	Transforming growth factor, beta receptor III	SEQ ID NOS: 13181-13190
TGFRB3	Transforming growth factor, beta receptor III	SEQ ID NOS: 13191-13197
THBS1	Thrombospondin 1	SEQ ED NOS: 13198-13199
THBS2	Thrombospondin 2	SEQ ID NOS: 13200-13202

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
THBS3	Thrombospondin 3	SEQ ID NOS: 13203-13207
THBS4	Thrombospondin 4	SEQ ID NOS: 13208-13209
THOC3	THO complex 3	SEQ ID NOS: 13210-13219
THPO	Thrombopoietin	SEQ ID NOS: 13220-13225
THSD4	Thrombospondin, type I, domain containing 4	SEQ ID NOS: 13226-13229
THY1	Thy-1 cell surface antigen	SEQ ID NOS: 13230-13235
TIE1	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1	SEQ ID NOS: 13236-13237
TIMMDC1	Translocase of inner mitochondrial membrane domain containing 1	SEQ ID NOS: 13238-13245
TIMP1	TIMP metallopeptidase inhibitor 1	SEQ ID NOS: 13246-13250
TIMP2	TIMP metallopeptidase inhibitor 2	SEQ ID NOS: 13251-13255
TIMP3	TIMP metallopeptidase inhibitor 3	SEQ ID NO: 13256
TIMP4	TIMP metallopeptidase inhibitor 4	SEQ ID NO: 13257
TINAGL1	Tubulointerstitial nephritis antigen-like 1	SEQ ID NOS: 13258-13260
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	SEQ ID NOS: 13261-13270
TLL2	Tolloid-like 2	SEQ ID NO: 13271
TLR1	Toll-like receptor 1	SEQ ID NOS: 13272-13277
TLR3	Toll-like receptor 3	SEQ ID NOS: 13278-13280
TM2D2	TM2 domain containing 2	SEQ ID NOS: 13281-13286
TM2D3	TM2 domain containing 3	SEQ ID NOS: 13287-13294
TM7SF3	Transmembrane 7 superfamily member 3	SEQ ID NOS: 13295-13309
TM9SF1	Transmembrane 9 superfamily member 1	SEQ ID NOS: 13310-13320
TMCO6	Transmembrane and coiled-coil domains 6	SEQ ID NOS: 13321-13328
TMED1	Transmembrane p24 trafficking protein 1	SEQ ID NOS: 13329-13335
TMED2	Transmembrane p24 trafficking protein 2	SEQ ID NOS: 13336-13338
TMED3	Transmembrane p24 trafficking protein 3	SEQ ID NOS: 13339-13342
TMED4	Transmembrane p24 trafficking protein 4	SEQ ID NOS: 13343-13345
TMED5	Transmembrane p24 trafficking protein 5	SEQ ID NOS: 13346-13349
TMED7	Transmembrane p24 trafficking protein 7	SEQ ID NOS: 13350-13351
TMED7-	TMED7-TICAM2 readthrough	SEQ ID NOS: 13352-13353
TICAM2		
TMEM108	Transmembrane protein 108	SEQ ID NOS: 13354-13362
TMEM116	Transmembrane protein 116	SEQ ID NOS: 13363-13374
TMEM119	Transmembrane protein 119	SEQ ID NOS: 13375-13378
TMEM155	Transmembrane protein 155	SEQ ID NOS: 13379-13382
TMEM168	Transmembrane protein 168	SEQ ID NOS: 13383-13388
TMEM178A	Transmembrane protein 178A	SEQ ID NOS: 13389-13390
TMEM179	Transmembrane protein 179	SEQ ID NOS: 13391-13396
TMEM196	Transmembrane protein 196	SEQ ID NOS: 13397-13401
TMEM199	Transmembrane protein 199	SEQ ID NOS: 13402-13405
TMEM205	Transmembrane protein 205	SEQ ID NOS: 13406-13419
TMEM213	Transmembrane protein 213	SEQ ID NOS: 13420-13423
TMEM25	Transmembrane protein 25	SEQ ID NOS: 13424-13440
TMEM30C	Transmembrane protein 30C	SEQ ID NO: 13441
TMEM38B	Transmembrane protein 38B	SEQ ID NOS: 13442-13446
TMEM44	Transmembrane protein 44	SEQ ID NOS: 13447-13456
TMEM52	Transmembrane protein 52	SEQ ID NOS: 13457-13461
TMEM52B	Transmembrane protein 52B	SEQ ID NOS: 13462-13464
TMEM59	Transmembrane protein 59	SEQ ID NOS: 13465-13472
TMEM67	Transmembrane protein 67	SEQ ID NOS: 13473-13484
TMEM70	Transmembrane protein 70	SEQ ID NOS: 13485-13487
TMEM87A	Transmembrane protein 87A	SEQ ID NOS: 13488-13497
TMEM94	Transmembrane protein 94	SEQ ID NOS: 13498-13513
TMEM95	Transmembrane protein 95	SEQ ID NOS: 13514-13516
TMIGD1	Transmembrane and immunoglobulin domain containing 1	SEQ ID NOS: 13517-13518
TMPRSS12	Transmembrane (C-terminal) protease, serine 12	SEQ ID NOS: 13519-13520
TMPRSS5	Transmembrane protease, serine 5	SEQ ID NOS: 13521-13532
TMUB1	Transmembrane and ubiquitin-like domain containing 1	SEQ ID NOS: 13533-13539
TMX2	Thioredoxin-related transmembrane protein 2	SEQ ID NOS: 13540-13547
TMX3	Thioredoxin-related transmembrane protein 3	SEQ ID NOS: 13548-13555
TNC	Tenascin C	SEQ ID NOS: 13556-13564
TNFAIP6	Tumor necrosis factor, alpha-induced protein 6	SEQ ID NO: 13565
TNFRSF11A	Tumor necrosis factor receptor superfamily, member 11a, NFKB activator	SEQ ID NOS: 13566-13570
TNFRSF11B	Tumor necrosis factor receptor superfamily, member 11b	SEQ ID NOS: 13571-13572
TNFRSF12A	Tumor necrosis factor receptor superfamily, member 12A	SEQ ID NOS: 13573-13578

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
TNFRSF14	Tumor necrosis factor receptor superfamily, member 14	SEQ ID NOS: 13579-13585
TNFRSF18	Tumor necrosis factor receptor superfamily, member 18	SEQ ID NOS: 13586-13589
TNFRSF1A	Tumor necrosis factor receptor superfamily, member 1A	SEQ ID NOS: 13590-13598
TNFRSF1B	Tumor necrosis factor receptor superfamily, member 1B	SEQ ID NOS: 13599-13600
TNFRSF25	Tumor necrosis factor receptor superfamily, member 25	SEQ ID NOS: 13601-13612
TNFRSF6B	Tumor necrosis factor receptor superfamily, member 6b, decoy	SEQ ID NO: 13613
TNFSF11	Tumor necrosis factor (ligand) superfamily, member 11	SEQ ID NOS: 13614-13618
TNFSF12	Tumor necrosis factor (ligand) superfamily, member 12,	SEQ ID NOS: 13619-13620
TNFSF12-TNFSF13	TNFSF12-TNFSF13 readthrough	SEQ ID NO: 13621
TNFSF15	Tumor necrosis factor (ligand) superfamily, member 15	SEQ ID NOS: 13622-13623
TNN	Tenascin N	SEQ ID NOS: 13624-13626
TNR	Tenascin R	SEQ ID NOS: 13627-13629
TNXB	Tenascin XB	SEQ ID NOS: 13630-13636
FAM179B	Family with sequence similarity 179, member B	SEQ ID NOS: 13637-13642
TOMM7	Translocase of outer mitochondrial membrane 7 homolog (yeast)	SEQ ID NOS: 13643-13646
TOP1MT	Topoisomerase (DMA) I, mitochondrial	SEQ ID NOS: 13647-13661
TOR1A	Torsin family 1, member A (torsin A)	SEQ ID NO: 13662
TOR1B	Torsin family 1, member B (torsin B)	SEQ ID NOS: 13663-13664
TOR2A	Torsin family 2, member A	SEQ ID NOS: 13665-13671
TOR3A	Torsin family 3, member A	SEQ ID NOS: 13672-13676
TPD52	Tumor protein D52	SEQ ID NOS: 13677-13689
TPO	Thyroid peroxidase	SEQ ID NOS: 13690-13700
TPP1	Tripeptidyl peptidase I	SEQ ID NOS: 13701-13718
TPSAB1	Tryptase alpha/beta 1	SEQ ID NOS: 13719-13721
TPSB2	Tryptase beta 2 (gene/pseudogene)	SEQ ID NOS: 13722-13724
TPSD1	Tryptase delta 1	SEQ ID NOS: 13725-13726
TPST1	Tyrosylprotein sulfotransferase 1	SEQ ID NOS: 13727-13729
TPST2	Tyrosylprotein sulfotransferase 2	SEQ ID NOS: 13730-13738
TRABD2A	TraB domain containing 2A	SEQ ID NOS: 13739-13741
TRABD2B	TraB domain containing 2B	SEQ ID NO: 13742
TREH	Trehalase (brush-border membrane glycoprotein)	SEQ ID NOS: 13743-13745
TREM1	Triggering receptor expressed on myeloid cells 1	SEQ ID NOS: 13746-13749
TREM2	Triggering receptor expressed on myeloid cells 2	SEQ ID NOS: 13750-13752
TRH	Thyrotropin-releasing hormone	SEQ ID NOS: 13753-13754
TRIM24	Tripartite motif containing 24	SEQ ID NOS: 13755-13756
TRIM28	Tripartite motif containing 28	SEQ ID NOS: 13757-13762
TRIO	Trio Rho guanine nucleotide exchange factor	SEQ ID NOS: 13763-13769
TRNP1	TMF1-regulated nuclear protein 1	SEQ ID NOS: 13770-13771
TSC22D4	TSC22 domain family, member 4	SEQ ID NOS: 13772-13775
TSHB	Thyroid stimulating hormone, beta	SEQ ID NOS: 13776-13777
TSHR	Thyroid stimulating hormone receptor	SEQ ID NOS: 13778-13785
TSKU	Tsukushi, small leucine rich proteoglycan	SEQ ID NOS: 13786-13790
TSLP	Thymic stromal lymphopoietin	SEQ ID NOS: 13791-13793
TSPAN3	Tetraspanin 3	SEQ ID NOS: 13794-13799
TSPAN31	Tetraspanin 31	SEQ ID NOS: 13800-13806
TSPEAR	Thrombospondin-type laminin G domain and EAR repeats	SEQ ID NOS: 13807-13810
TTC13	Tetratricopeptide repeat domain 13	SEQ ID NOS: 13811-13817
TTC19	Tetratricopeptide repeat domain 19	SEQ ID NOS: 13818-13823
TTC9B	Tetratricopeptide repeat domain 9B	SEQ ID NO: 13824
TTL11	Tubulin tyrosine ligase-like family member 11	SEQ ID NOS: 13825-13829
TTR	Transthyretin	SEQ ID NOS: 13830-13832
TWSG1	Twisted gastrulation BMP signaling modulator 1	SEQ ID NOS: 13833-13835
TXND12	Thioredoxin domain containing 12 (endoplasmic reticulum)	SEQ ID NOS: 13836-13838
TXND15	Thioredoxin domain containing 15	SEQ ID NOS: 13839-13845
TXND5	Thioredoxin domain containing 5 (endoplasmic reticulum)	SEQ ID NOS: 13846-13847
TXNRD2	Thioredoxin reductase 2	SEQ ID NOS: 13848-13860
TYRP1	Tyrosinase-related protein 1	SEQ ID NOS: 13861-13863
UBAC2	UBA domain containing 2	SEQ ID NOS: 13864-13868
UBALD1	UBA-like domain containing 1	SEQ ID NOS: 13869-13877
UBAP2	Ubiquitin associated protein 2	SEQ ID NOS: 13878-13884

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
UBXN8	UBX domain protein 8	SEQ ID NOS: 13885-13891
UCMA	Upper zone of growth plate and cartilage matrix associated	SEQ ID NOS: 13892-13893
UCN	Urocortin	SEQ ID NO: 13894
UCN2	Urocortin 2	SEQ ID NO: 13895
UCN3	Urocortin 3	SEQ ID NO: 13896
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	SEQ ID NOS: 13897-13902
UGT1A10	UDP glucuronosyltransferase 1 family, polypeptide A10	SEQ ID NOS: 13903-13904
UGT2A1	UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus	SEQ ID NOS: 13905-13909
UGT2B11	UDP glucuronosyltransferase 2 family, polypeptide B11	SEQ ID NO: 13910
UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	SEQ ID NOS: 13911-13912
UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	SEQ ID NOS: 13913-13916
UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	SEQ ID NOS: 13917-13920
UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1	SEQ ID NOS: 13921-13926
UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	SEQ ID NOS: 13927-13930
UGT8	UDP glycosyltransferase 8	SEQ ID NOS: 13931-13933
ULBP3	UL16 binding protein 3	SEQ ID NOS: 13934-13935
UMOD	Uromodulin	SEQ ID NOS: 13936-13947
UNCSC	Unc-5 netrin receptor C	SEQ ID NOS: 13948-13952
UPK3B	Uroplakin 3B	SEQ ID NOS: 13953-13955
USP11	Ubiquitin specific peptidase 11	SEQ ID NOS: 13956-13959
USP14	Ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	SEQ ID NOS: 13960-13966
USP3	Ubiquitin specific peptidase 3	SEQ ID NOS: 13967-13982
CIRH1A	Cirrhosis, autosomal recessive 1A (cirhin)	SEQ ID NOS: 13983-13992
UTS2	Urotensin 2	SEQ ID NOS: 13993-13995
UTS2B	Urotensin 2B	SEQ ID NOS: 13996-14001
UTY	Ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	SEQ ID NOS: 14002-14014
UXS1	UDP-glucuronate decarboxylase 1	SEQ ID NOS: 14015-14022
VASH1	Vasohibin 1	SEQ ID NOS: 14023-14025
VCAN	Versican	SEQ ID NOS: 14026-14032
VEGFA	Vascular endothelial growth factor A	SEQ ID NOS: 14033-14058
VEGFB	Vascular endothelial growth factor B	SEQ ID NOS: 14059-14061
VEGFC	Vascular endothelial growth factor C	SEQ ID NO: 14062
FIGF	C-fos induced growth factor (vascular endothelial growth factor D)	SEQ ID NO: 14063
VGF	VGF nerve growth factor inducible	SEQ ID NOS: 14064-14066
VIP	Vasoactive intestinal peptide	SEQ ID NOS: 14067-14069
VIPR2	Vasoactive intestinal peptide receptor 2	SEQ ID NOS: 14070-14073
VIT	Vitrin	SEQ ID NOS: 14074-14081
VKORC1	Vitamin K epoxide reductase complex, subunit 1	SEQ ID NOS: 14082-14089
VLDLR	Very low density lipoprotein receptor	SEQ ID NOS: 14090-14092
VMO1	Vitelline membrane outer layer 1 homolog (chicken)	SEQ ID NOS: 14093-14096
VNN1	Vanin 1	SEQ ID NO: 14097
VNN2	Vanin 2	SEQ ID NOS: 14098-14111
VNN3	Vanin 3	SEQ ID NOS: 14112-14123
VOPP1	Vesicular, overexpressed in cancer, prosurvival protein 1	SEQ ID NOS: 14124-14136
VPREB1	Pre-B lymphocyte 1	SEQ ID NOS: 14137-14138
VPREB3	Pre-B lymphocyte 3	SEQ ID NOS: 14139-14140
VPS37B	Vacuolar protein sorting 37 homolog B (<i>S. cerevisiae</i>)	SEQ ID NOS: 14141-14143
VPS51	Vacuolar protein sorting 51 homolog (<i>S. cerevisiae</i>)	SEQ ID NOS: 14144-14155
VSIG1	V-set and immunoglobulin domain containing 1	SEQ ID NOS: 14156-14158
VSIG10	V-set and immunoglobulin domain containing 10	SEQ ID NOS: 14159-14160
VSTM1	V-set and transmembrane domain containing 1	SEQ ID NOS: 14161-14167
VSTM2A	V-set and transmembrane domain containing 2A	SEQ ID NOS: 14168-14171
VSTM2B	V-set and transmembrane domain containing 2B	SEQ ID NO: 14172
VSTM2L	V-set and transmembrane domain containing 2 like	SEQ ID NOS: 14173-14175
VSTM4	V-set and transmembrane domain containing 4	SEQ ID NOS: 14176-14177
VTN	Vitronectin	SEQ ID NOS: 14178-14179
VWA1	Von Willebrand factor A domain containing 1	SEQ ID NOS: 14180-14183
VWA2	Von Willebrand factor A domain containing 2	SEQ ID NOS: 14184-14185
VWA5B2	Von Willebrand factor A domain containing 5B2	SEQ ID NOS: 14186-14187
VWA7	Von Willebrand factor A domain containing 7	SEQ ID NO: 14188

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
VWC2	Von Willebrand factor C domain containing 2	SEQ ED NO: 14189
VWC2L	Von Willebrand factor C domain containing protein 2-like	SEQ ID NOS: 14190-14191
VWCE	Von Willebrand factor C and EGF domains	SEQ ID NOS: 14192-14196
VWDDE	Von Willebrand factor D and EGF domains	SEQ ID NOS: 14197-14202
VWF	Von Willebrand factor	SEQ ID NOS: 14203-14205
WDR25	WD repeat domain 25	SEQ ID NOS: 14206-14212
WDR81	WD repeat domain 81	SEQ ID NOS: 14213-14222
WDR90	WD repeat domain 90	SEQ ID NOS: 14223-14230
WFDC1	WAP four-disulfide core domain 1	SEQ ID NOS: 14231-14233
WFDC10A	WAP four-disulfide core domain 10A	SEQ ID NO: 14234
WFDC10B	WAP four-disulfide core domain 10B	SEQ ID NOS: 14235-14236
WFDC11	WAP four-disulfide core domain 11	SEQ ID NOS: 14237-14239
WFDC12	WAP four-disulfide core domain 12	SEQ ID NO: 14240
WFDC13	WAP four-disulfide core domain 13	SEQ ID NO: 14241
WFDC2	WAP four-disulfide core domain 2	SEQ ID NOS: 14242-14246
WFDC3	WAP four-disulfide core domain 3	SEQ ID NOS: 14247-14250
WFDC5	WAP four-disulfide core domain 5	SEQ ID NOS: 14251-14252
WFDC6	WAP four-disulfide core domain 6	SEQ ID NOS: 14253-14254
WFDC8	WAP four-disulfide core domain 8	SEQ ID NOS: 14255-14256
WFIKKN1	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	SEQ ID NO: 14257
WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	SEQ ID NOS: 14258-14259
DFNB31	Deafness, autosomal recessive 31	SEQ ID NOS: 14260-14263
WIF1	WNT inhibitory factor 1	SEQ ID NOS: 14264-14266
WISP1	WNT1 inducible signaling pathway protein 1	SEQ ID NOS: 14267-14271
WISP2	WNT1 inducible signaling pathway protein 2	SEQ ID NOS: 14272-14274
WISP3	WNT1 inducible signaling pathway protein 3	SEQ ID NOS: 14275-14282
WNK1	WNK lysine deficient protein kinase 1	SEQ ID NOS: 14283-14296
WNT1	Wingless-type MMTV integration site family, member 1	SEQ ID NOS: 14297-14298
WNT10B	Wingless-type MMTV integration site family, member 10B	SEQ ID NOS: 14299-14303
WNT11	Wingless-type MMTV integration site family, member 11	SEQ ID NOS: 14304-14306
WNT16	Wingless-type MMTV integration site family, member 16	SEQ ID NOS: 14307-14308
WNT2	Wingless-type MMTV integration site family, member 2	SEQ ID NOS: 14309-14311
WNT3	Wingless-type MMTV integration site family, member 3	SEQ ID NO: 14312
WNT3A	Wingless-type MMTV integration site family, member 3A	SEQ ID NO: 14313
WNT5A	Wingless-type MMTV integration site family, member 5A	SEQ ID NOS: 14314-14317
WNT5B	Wingless-type MMTV integration site family, member 5B	SEQ ID NOS: 14318-14324
WNT6	Wingless-type MMTV integration site family, member 6	SEQ ID NO: 14325
WNT7A	Wingless-type MMTV integration site family, member 7A	SEQ ID NO: 14326
WNT7B	Wingless-type MMTV integration site family, member 7B	SEQ ID NOS: 14327-14331
WNT8A	Wingless-type MMTV integration site family, member 8A	SEQ ID NOS: 14332-14335
WNT8B	Wingless-type MMTV integration site family, member 8B	SEQ ID NO: 14336
WNT9A	Wingless-type MMTV integration site family, member 9A	SEQ ID NO: 14337
WNT9B	Wingless-type MMTV integration site family, member 9B	SEQ ID NOS: 14338-14340
WSB1	WD repeat and SOCS box containing 1	SEQ ID NOS: 14341-14350
WSCD1	WSC domain containing 1	SEQ ID NOS: 14351-14360
WSCD2	WSC domain containing 2	SEQ ID NOS: 14361-14364
XCL1	Chemokine (C motif) ligand 1	SEQ ID NO: 14365
XCL2	Chemokine (C motif) ligand 2	SEQ ID NO: 14366
XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	SEQ ID NOS: 14367-14368
XXYLT1	Xyloside xylosyltransferase I	SEQ ID NOS: 14369-14374
XYLT1	Xylosyltransferase I	SEQ ID NO: 14375
XYLT2	Xylosyltransferase II	SEQ ID NOS: 14376-14381
ZFYVE21	Zinc finger, FYVE domain containing 21	SEQ ID NOS: 14382-14386
ZG16	Zymogen granule protein 16	SEQ ID NO: 14387

TABLE 1-continued

Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy). Compositions of the disclosure may comprise a promoter of one or more of the proteins of Table 1 driving expression of any sequence of the disclosure.

Gene Name	Gene Description	Protein SEQ ID NO
ZG16B	Zymogen granule protein 16B	SEQ ID NOS: 14388-14391
ZIC4	Zic family member 4	SEQ ID NOS: 14392-14400
ZNF207	Zinc finger protein 207	SEQ ID NOS: 14401-14411
ZNF26	Zinc finger protein 26	SEQ ID NOS: 14412-14415
ZNF34	Zinc finger protein 34	SEQ ID NOS: 14416-14419
ZNF419	Zinc finger protein 419	SEQ ID NOS: 14420-14434
ZNF433	Zinc finger protein 433	SEQ ID NOS: 14435-14444
ZNF449	Zinc finger protein 449	SEQ ID NOS: 14445-14446
ZNF488	Zinc finger protein 488	SEQ ID NOS: 14447-14448
ZNF511	Zinc finger protein 511	SEQ ID NOS: 14449-14450
ZNF570	Zinc finger protein 570	SEQ ID NOS: 14451-14456
ZNF691	Zinc finger protein 691	SEQ ID NOS: 14457-14464
ZNF98	Zinc finger protein 98	SEQ ID NOS: 14465-14468
ZPBP	Zona pellucida binding protein	SEQ ID NOS: 14469-14472
ZPBP2	Zona pellucida binding protein 2	SEQ ID NOS: 14473-14476
ZSCAN29	Zinc finger and SCAN domain containing 29	SEQ ID NOS: 14477-14483

Expression of Cell Markers

In certain embodiments of the disclosure, T cells are modified to express detectable markers or indicators. In some embodiments, these detectable markers include, but are not limited to, fluorescent proteins. Non-limiting examples of fluorescent proteins include TagBFP, mTagBFP2, Azurite, EBFP2, mKalamal1, Sirius, Sapphire, T-Sapphire, ECFP, Cerulean, SCFP3A, mTurquoise, mTurquoise2, monomeric Midorishi-Cyan, TagCFP, mTFP1, EGFP, Emerald, Superfolder GFP, monomeric Azami Green, mUKG, mWasabi, Clover, mNeonGreen, EYFP, Citrine, Venus, SYFP2, TagYFP, monomeric Kusabira Orange, mKok, mKO2, mOrange, mOrange2, mRaspberry, mCherr, mStrawberry, mTangerine, tdTomato, TagRFP, TagFRP-T, mApple, mRuby, mRuby2, mPlum, HcRed-Tandem, mKate2, mNeptune, NiRFP, TagRFP657, iFP1.4, mRFP, mKeima Red, LSS-mKate1, LSS-mKate2, mBeRFP and spectrally shifted variants thereof. In some embodiments of the disclosure, the detectable marker or indicator comprises luciferase. In some embodiments, the detectable marker or indicator is codon optimized for expression in humans. In some embodiments, the detectable marker or indicator is an intracellular marker or indicator. In some embodiments, the detectable marker or indicator is a cytoplasmic marker or indicator. In some embodiments, the detectable marker or indicator is a nuclear marker or indicator. In some embodiments, the detectable marker or indicator is a mitochondrial marker or indicator. In some embodiments, the detectable marker or indicator is a cell surface marker. In some embodiments, particularly those embodiments where the markers or indicators are cell surface markers, the marker or indicator may be tethered to the membrane of the cell. Cells modified to express markers with the compositions and methods of the disclosure can be used as indicator cells *in vivo*, *ex vivo*, *in vitro* and *in situ*. In certain embodiments of the disclosure, a marker or indicator is under the control of an inducible promoter of the disclosure such that when the inducible promoter is targeted, the promoter induces expression of the marker or indicator.

Inducible Promoters

In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an NF κ B promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) com-

prises a sequence encoding an interferon (IFN) promoter or a sequence encoding an interleukin-2 promoter. In certain embodiments, the interferon (IFN) promoter is an IFN γ promoter. In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a cytokine or a chemokine. In certain embodiments, the cytokine or chemokine comprises IL2, IL3, IL4, IL5, IL6, IL10, IL12, IL13, IL17A/F, IL21, IL22, 1L23, transforming growth factor beta (TGF β), colony stimulating factor 2 (GM-CSF), interferon gamma (IFN γ), Tumor necrosis factor (TNF α), LT α , perforin, Granzyme C (Gzmc), Granzyme B (Gzmb), C-C motif chemokine ligand 5 (CCL5), C-C motif chemokine ligand 4 (Ccl4), C-C motif chemokine ligand 3 (Ccl3), X-C motif chemokine ligand 1 (Xcl1) and LIF interleukin 6 family cytokine (Lif).

In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene comprising a surface protein involved in cell differentiation, activation, exhaustion and function. In certain embodiments, the gene comprises CD69, CD71, CTLA4, PD-1, TIGIT, LAG3, TIM-3, GITR, MHCII, COX-2, FASL and 4-1BB.

In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene involved in CD metabolism and differentiation. In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of Nr4a1, Nr4a3, Tnfrsf9 (4-1BB), Sema7a, Zfp3612, Gadd45b, Dusp5, Dusp6 and Neto2.

Nucleic Acid Molecules

Nucleic acid molecules of the disclosure encoding protein scaffolds can be in the form of RNA, such as mRNA, hnRNA, tRNA or any other form, or in the form of DNA, including, but not limited to, cDNA and genomic DNA obtained by cloning or produced synthetically, or any combinations thereof. The DNA can be triple-stranded, double-stranded or single-stranded, or any combination thereof. Any portion of at least one strand of the DNA or RNA can be the coding strand, also known as the sense strand, or it can be the non-coding strand, also referred to as the anti-sense strand.

Isolated nucleic acid molecules of the disclosure can include nucleic acid molecules comprising an open reading frame (ORF), optionally, with one or more introns, e.g., but

not limited to, at least one specified portion of at least one protein scaffold; nucleic acid molecules comprising the coding sequence for a protein scaffold or loop region that binds to the target protein; and nucleic acid molecules which comprise a nucleotide sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode the protein scaffold as described herein and/or as known in the art. Of course, the genetic code is well known in the art. Thus, it would be routine for one skilled in the art to generate such degenerate nucleic acid variants that code for specific protein scaffolds of the present invention. See, e.g., Ausubel, et al., *supra*, and such nucleic acid variants are included in the present invention.

As indicated herein, nucleic acid molecules of the disclosure which comprise a nucleic acid encoding a protein scaffold can include, but are not limited to, those encoding the amino acid sequence of a protein scaffold fragment, by itself; the coding sequence for the entire protein scaffold or a portion thereof; the coding sequence for a protein scaffold, fragment or portion, as well as additional sequences, such as the coding sequence of at least one signal leader or fusion peptide, with or without the aforementioned additional coding sequences, such as at least one intron, together with additional, non-coding sequences, including but not limited to, non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences that play a role in transcription, mRNA processing, including splicing and polyadenylation signals (for example, ribosome binding and stability of mRNA); an additional coding sequence that codes for additional amino acids, such as those that provide additional functionalities. Thus, the sequence encoding a protein scaffold can be fused to a marker sequence, such as a sequence encoding a peptide that facilitates purification of the fused protein scaffold comprising a protein scaffold fragment or portion.

Polynucleotides Selectively Hybridizing to a Polynucleotide as Described Herein

The disclosure provides isolated nucleic acids that hybridize under selective hybridization conditions to a polynucleotide disclosed herein. Thus, the polynucleotides of this embodiment can be used for isolating, detecting, and/or quantifying nucleic acids comprising such polynucleotides. For example, polynucleotides of the present invention can be used to identify, isolate, or amplify partial or full-length clones in a deposited library. In some embodiments, the polynucleotides are genomic or cDNA sequences isolated, or otherwise complementary to, a cDNA from a human or mammalian nucleic acid library.

Preferably, the cDNA library comprises at least 80% full-length sequences, preferably, at least 85% or 90% full-length sequences, and, more preferably, at least 95% full-length sequences. The cDNA libraries can be normalized to increase the representation of rare sequences. Low or moderate stringency hybridization conditions are typically, but not exclusively, employed with sequences having a reduced sequence identity relative to complementary sequences. Moderate and high stringency conditions can optionally be employed for sequences of greater identity. Low stringency conditions allow selective hybridization of sequences having about 70% sequence identity and can be employed to identify orthologous or paralogous sequences.

Optionally, polynucleotides of this invention will encode at least a portion of a protein scaffold encoded by the polynucleotides described herein. The polynucleotides of this invention embrace nucleic acid sequences that can be employed for selective hybridization to a polynucleotide

encoding a protein scaffold of the present invention. See, e.g., Ausubel, *supra*; Colligan, *supra*, each entirely incorporated herein by reference.

Construction of Nucleic Acids

5 The isolated nucleic acids of the disclosure can be made using (a) recombinant methods, (b) synthetic techniques, (c) purification techniques, and/or (d) combinations thereof, as well-known in the art.

10 The nucleic acids can conveniently comprise sequences in addition to a polynucleotide of the present invention. For example, a multi-cloning site comprising one or more endonuclease restriction sites can be inserted into the nucleic acid to aid in isolation of the polynucleotide. Also, translatable sequences can be inserted to aid in the isolation of the translated polynucleotide of the disclosure. For example, a hexa-histidine marker sequence provides a convenient means to purify the proteins of the disclosure. The nucleic acid of the disclosure, excluding the coding sequence, is 15 optionally a vector, adapter, or linker for cloning and/or expression of a polynucleotide of the disclosure.

15 Additional sequences can be added to such cloning and/or expression sequences to optimize their function in cloning and/or expression, to aid in isolation of the polynucleotide, 20 or to improve the introduction of the polynucleotide into a cell. Use of cloning vectors, expression vectors, adapters, and linkers is well known in the art. (See, e.g., Ausubel, *supra*; or Sambrook, *supra*).

Recombinant Methods for Constructing Nucleic Acids

25 The isolated nucleic acid compositions of this disclosure, such as RNA, cDNA, genomic DNA, or any combination thereof, can be obtained from biological sources using any number of cloning methodologies known to those of skill in the art. In some embodiments, oligonucleotide probes that selectively hybridize, under stringent conditions, to the polynucleotides of the present invention are used to identify the desired sequence in a cDNA or genomic DNA library. The isolation of RNA, and construction of cDNA and 30 genomic libraries are well known to those of ordinary skill in the art. (See, e.g., Ausubel, *supra*; or Sambrook, *supra*).

Nucleic Acid Screening and Isolation Methods

35 A cDNA or genomic library can be screened using a probe based upon the sequence of a polynucleotide of the disclosure. Probes can be used to hybridize with genomic DNA or cDNA sequences to isolate homologous genes in the same or different organisms. Those of skill in the art will appreciate that various degrees of stringency of hybridization can be employed in the assay; and either the hybridization or the wash medium can be stringent. As the conditions for hybridization become more stringent, there must be a greater degree of complementarity between the probe and the target for duplex formation to occur. The degree of stringency can be controlled by one or more of temperature, 40 ionic strength, pH and the presence of a partially denaturing solvent, such as formamide. For example, the stringency of hybridization is conveniently varied by changing the polarity of the reactant solution through, for example, manipulation of the concentration of formamide within the range of 0% to 50%. The degree of complementarity (sequence identity) required for detectable binding will vary in accordance with the stringency of the hybridization medium and/or wash medium. The degree of complementarity will optimally be 45 100%, or 70-100%, or any range or value therein. However, it should be understood that minor sequence variations in the probes and primers can be compensated for by reducing the stringency of the hybridization and/or wash medium.

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Methods of amplification of RNA or DNA are well known in the art and can be used according to the disclosure without undue experimentation, based on the teaching and guidance presented herein.

Known methods of DNA or RNA amplification include, but are not limited to, polymerase chain reaction (PCR) and related amplification processes (see, e.g., U.S. Pat. Nos. 4,683,195, 4,683,202, 4,800,159, 4,965,188, to Mullis, et al.; U.S. Pat. No. 4,795,699 and 4,921,794 to Tabor, et al; U.S. Pat. No. 5,142,033 to Innis; U.S. Pat. No. 5,122,464 to Wilson, et al.; U.S. Pat. No. 5,091,310 to Innis; U.S. Pat. No. 5,066,584 to Gyllensten, et al; U.S. Pat. No. 4,889,818 to Gelfand, et al; U.S. Pat. No. 4,994,370 to Silver, et al; U.S. Pat. No. 4,766,067 to Biswas; U.S. Pat. No. 4,656,134 to Ringold) and RNA mediated amplification that uses anti-sense RNA to the target sequence as a template for double-stranded DNA synthesis (U.S. Pat. No. 5,130,238 to Malek, et al, with the tradename NASBA), the entire contents of which references are incorporated herein by reference. (See, e.g., Ausubel, supra; or Sambrook, supra.)

For instance, polymerase chain reaction (PCR) technology can be used to amplify the sequences of polynucleotides of the disclosure and related genes directly from genomic DNA or cDNA libraries. PCR and other in vitro amplification methods can also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes. Examples of techniques sufficient to direct persons of skill through in vitro amplification methods are found in Berger, *supra*, Sambrook, *supra*, and Ausubel, *supra*, as well as Mullis, et al., U.S. Pat. No. 4,683,202 (1987); and Innis, et al., PCR Protocols A Guide to Methods and Applications, Eds., Academic Press Inc., San Diego, Calif. (1990). Commercially available kits for genomic PCR amplification are known in the art. See, e.g., Advantage-GC Genomic PCR Kit (Clontech). Additionally, e.g., the T4 gene 32 protein (Boehringer Mannheim) can be used to improve yield of long PCR products.

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Synthetic Methods for Constructing Nucleic Acids

The isolated nucleic acids of the disclosure can also be prepared by direct chemical synthesis by known methods (see, e.g., Ausubel, et al., *supra*). Chemical synthesis generally produces a single-stranded oligonucleotide, which can be converted into double-stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template. One of skill in the art will recognize that while chemical synthesis of DNA can be limited to sequences of about 100 or more bases, longer sequences can be obtained by the ligation of shorter sequences.

Recombinant Expression Cassettes

The disclosure further provides recombinant expression cassettes comprising a nucleic acid of the disclosure. A nucleic acid sequence of the disclosure, for example, a cDNA or a genomic sequence encoding a protein scaffold of the disclosure, can be used to construct a recombinant expression cassette that can be introduced into at least one desired host cell. A recombinant expression cassette will typically comprise a polynucleotide of the disclosure operably linked to transcriptional initiation regulatory sequences that will direct the transcription of the polynucleotide in the intended host cell. Both heterologous and non-heterologous (i.e., endogenous) promoters can be employed to direct expression of the nucleic acids of the disclosure.

In some embodiments, isolated nucleic acids that serve as promoter, enhancer, or other elements can be introduced in the appropriate position (upstream, downstream or in the intron) of a non-heterologous form of a polynucleotide of the disclosure so as to up or down regulate expression of a polynucleotide of the disclosure. For example, endogenous promoters can be altered in vivo or in vitro by mutation, deletion and/or substitution.

Vectors and Host Cells

The disclosure also relates to vectors that include isolated nucleic acid molecules of the disclosure, host cells that are genetically engineered with the recombinant vectors, and the production of at least one protein scaffold by recombinant techniques, as is well known in the art. See, e.g., Sambrook, et al., *supra*; Ausubel, et al., *supra*, each entirely incorporated herein by reference.

For example, the PB-EF1a vector may be used. The vector comprises the following nucleotide sequence:

(SEQ ID NO. 17073)

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tgtacatagattaaccctagaaagataatcatattgtgacgtacgttaagataatcatgcgtaaaattgacgcatgttttat
cggtctgtatatcgagggttatttattaaatttgaatagatattaaatgtttttatattacacttacataataataattca
acaacaatttatattatgtttatttattttataaaaaaaacaaaaactcaaaatttcttctataaagtaacaaaactttatcg
aatacatgcagccggggatgcagaggacagcccccccccaagccccccagggatgttaatcgtccctcccgctagggg
cagcagcgagccgggggtccgtccggcgtcccccgcattcccgatcccgccgatcccgatcccgatcccgatcccgatcccg
cgggaaaggtggcacgggatcgcttcgtctttgcgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc
agtgtactgtgccttcgatcgaaccatggacagtttagcttgcataagatggataaagttaaacagagaggaatcttgcac
taatggaccttctaggcttgcataaggagtgggattggctccggctcgatggcagagccatcgccacatcgccacatcgcc
agaagttgggggggggtcgcaatttgcacccgtgcctagagaaggtggcgccggtaaactggaaagtgtcgactgtact
gctccgcctttcccgagggtggggagaaccgtatataagtgcgtatgcgcgtgaacgttttcgcacccgggttgc
gccagaacacaggtaagtgcgtgtggttcccgccggctggcctttacgggttatggccctgcgtgccttgcattactt
ccacctggctgcgtacgtgatcttgcgtcccgatcccgatcccgatcccgatcccgatcccgatcccgatcccgatcccg
cccttcgcctgtgcgtggatggcctggcctggcgctggggccggccgcgtgcgaatctggcggcaccctcgccgtctc
gctgtttcgataagtcttagccattaaatttgtatgcacccgtctgcgtcccgatcccgatcccgatcccgatcccgatcc

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tcggtcttgcacaaaagaaccggggccctgcgctgacagccggAACACGGCGGcatcagAGCAGCCatTTCTGTGTC
agtcatagccgaatacgctctccacccaagcgccggagaacctgcgtcaatccatTTGTCAATCATATAATTATTAAGCA
tttatcagggttcgttcgtccggctccatccaatgcgtcaatattGCCATTAGCCATTATTCATTGGTTATAGCA
taaatcaatattggctattggcattgcatacgtttatctatatcataata.

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The polynucleotides can optionally be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid or nanoplasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it can be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The DNA insert should be operatively linked to an appropriate promoter. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating at the beginning and a termination codon (e.g., UAA, UGA or UAG) appropriately positioned at the end of the mRNA to be translated, with UAA and UAG preferred for mammalian or eukaryotic cell expression.

Expression vectors will preferably but optionally include at least one selectable marker. Such markers include, e.g., but are not limited to, ampicillin, zeocin (sh bla gene), puromycin (pac gene), hygromycin B (hygB gene), G418/Geneticin (neo gene), mycophenolic acid, or glutamine synthetase (GS, U.S. Pat. Nos. 5,122,464; 5,770,359; 5,827,739), blasticidin (bsd gene), resistance genes for eukaryotic cell culture as well as ampicillin, zeocin (Sh bla gene), puromycin (pac gene), hygromycin B (hvgB gene), G418/Geneticin (neo gene), kanamycin, spectinomycin, streptomycin, carbenicillin, bleomycin, erythromycin, polymyxin B, or tetracycline resistance genes for culturing in *E. coli* and other bacteria or prokaryotics (the above patents are entirely incorporated hereby by reference). Appropriate culture mediums and conditions for the above-described host cells are known in the art. Suitable vectors will be readily apparent to the skilled artisan. Introduction of a vector construct into a host cell can be effected by calcium phosphate transfection. DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other known methods. Such methods are described in the art, such as Sambrook, supra, Chapters 1-4 and 16-18; Ausubel, supra, Chapters 1, 9, 13, 15, 16.

Expression vectors will preferably but optionally include at least one selectable cell surface marker for isolation of cells modified by the compositions and methods of the disclosure. Selectable cell surface markers of the disclosure comprise surface proteins, glycoproteins, or group of proteins that distinguish a cell or subset of cells from another defined subset of cells. Preferably the selectable cell surface marker distinguishes those cells modified by a composition or method of the disclosure from those cells that are not modified by a composition or method of the disclosure. Such cell surface markers include, e.g., but are not limited to, "cluster of designation" or "classification determinant" proteins (often abbreviated as "CD") such as a truncated or full length form of CD19, CD271, CD34, CD22, CD20, CD33, CD52, or any combination thereof. Cell surface markers further include the suicide gene marker RQR8 (Philip B et al. Blood. 2014 Aug. 21; 124(8):1277-87).

10 Expression vectors will preferably but optionally include at least one selectable drug resistance marker for isolation of cells modified by the compositions and methods of the disclosure. Selectable drug resistance markers of the disclosure may comprise wild-type or mutant Neo, DHFR, TYMS, FRANCF, RAD51C, GCS, MDR1, ALDH1, NKX2.2, or any combination thereof.

15 At least one protein scaffold of the disclosure can be expressed in a modified form, such as a fusion protein, and can include not only secretion signals, but also additional heterologous functional regions. For instance, a region of 20 additional amino acids, particularly charged amino acids, can be added to the N-terminus of a protein scaffold to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. 25 Also, peptide moieties can be added to a protein scaffold of the disclosure to facilitate purification. Such regions can be removed prior to final preparation of a protein scaffold or at least one fragment thereof. Such methods are described in many standard laboratory manuals, such as Sambrook, 30 supra, Chapters 17.29-17.42 and 18.1-18.74; Ausubel, supra. Chapters 16, 17 and 18.

35 Those of ordinary skill in the art are knowledgeable in the numerous expression systems available for expression of a nucleic acid encoding a protein of the disclosure. Alternatively, nucleic acids of the disclosure can be expressed in a host cell by turning on (by manipulation) in a host cell that contains endogenous DNA encoding a protein scaffold of the disclosure. Such methods are well known in the art, e.g., as described in U.S. Pat. Nos. 5,580,734, 5,641,670, 5,733,746, 40 and 5,733,761, entirely incorporated herein by reference.

45 Illustrative of cell cultures useful for the production of the protein scaffolds, specified portions or variants thereof, are bacterial, yeast, and mammalian cells as known in the art. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions or bioreactors can also be used. A number of suitable host cell lines capable of expressing intact glycosylated proteins have been developed in the art, and include the COS-1 (e.g., ATCC CRL 1650), COS-7 (e.g., ATCC CRL-1651), 50 HEK293, BHK21 (e.g., ATCC CRL-10), CHO (e.g., ATCC CRL 1610) and BSC-1 (e.g., ATCC CRL-26) cell lines, Cos-7 cells, CHO cells, hep G2 cells, P3X63Ag8.653, SP2/0-Ag14, 293 cells, HeLa cells and the like, which are readily available from, for example, American Type Culture 55 Collection, Manassas, Va. (www.atcc.org). Preferred host cells include cells of lymphoid origin, such as myeloma and lymphoma cells. Particularly preferred host cells are P3X63Ag8.653 cells (ATCC Accession Number CRL-1580) and SP2/0-Ag14 cells (ATCC Accession Number CRL-1851). In a particularly preferred embodiment, the recombinant cell is a P3X63Ab8.653 or an SP2/0-Ag14 cell.

60 Expression vectors for these cells can include one or more of the following expression control sequences, such as, but not limited to, an origin of replication; a promoter (e.g., late or early SV40 promoters, the CMV promoter (U.S. Pat. Nos. 5,168,062; 5,385,839), an HSV tk promoter, a pgk (phosphoglycerate kinase) promoter, an EF-1 alpha promoter

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(U.S. Pat. No. 5,266,491), at least one human promoter; an enhancer, and/or processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. See, e.g., Ausubel et al., *supra*; Sambrook, et al., *supra*. Other cells useful for production of nucleic acids or proteins of the present invention are known and/or available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (www.atcc.org) or other known or commercial sources.

When eukaryotic host cells are employed, polyadenylation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript can also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, et al., *J. Virol.* 45:773-781 (1983)). Additionally, gene sequences to control replication in the host cell can be incorporated into the vector, as known in the art.

Amino Acid Codes

The amino acids that make up protein scaffolds of the disclosure are often abbreviated. The amino acid designations can be indicated by designating the amino acid by its single letter code, its three letter code, name, or three nucleotide codon(s) as is well understood in the art (see Alberts, B., et al., *Molecular Biology of The Cell*, Third Ed., Garland Publishing, Inc., New York, 1994). A protein scaffold of the disclosure can include one or more amino acid substitutions, deletions or additions, either from natural mutations or human manipulation, as specified herein. Amino acids in a protein scaffold of the disclosure that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (e.g., Ausubel, *supra*, Chapters 8, 15; Cunningham and Wells, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity, such as, but not limited to, at least one neutralizing activity. Sites that are critical for protein scaffold binding can also be identified by structural analysis, such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith, et al., *J. Mol. Biol.* 224:899-904 (1992) and de Vos, et al., *Science* 255: 306-312 (1992)).

As those of skill will appreciate, the invention includes at least one biologically active protein scaffold of the disclosure. Biologically active protein scaffolds have a specific activity at least 20%, 30%, or 40%, and, preferably, at least 50%, 60%, or 70%, and, most preferably, at least 80%, 90%, or 95%-99% or more of the specific activity of the native (non-synthetic), endogenous or related and known protein scaffold. Methods of assaying and quantifying measures of enzymatic activity and substrate specificity are well known to those of skill in the art.

In another aspect, the disclosure relates to protein scaffolds and fragments, as described herein, which are modified by the covalent attachment of an organic moiety. Such modification can produce a protein scaffold fragment with improved pharmacokinetic properties (e.g., increased *in vivo* serum half-life). The organic moiety can be a linear or branched hydrophilic polymeric group, fatty acid group, or fatty acid ester group. In particular embodiments, the hydrophilic polymeric group can have a molecular weight of about 800 to about 120,000 Daltons and can be a polyalkane glycol (e.g., polyethylene glycol (PEG), polypropylene glycol

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(PPG)), carbohydrate polymer, amino acid polymer or polyvinyl pyrrolidone, and the fatty acid or fatty acid ester group can comprise from about eight to about forty carbon atoms. T Cell Isolation From a Leukapheresis Product

5 A leukapheresis product or blood may be collected from a subject at clinical site using a closed system and standard methods (e.g., a COBE Spectra Apheresis System) Preferably, the product is collected according to standard hospital or institutional Leukapheresis procedures in standard Leukapheresis collection bags. For example, in preferred embodiments of the methods of the disclosure, no additional anticoagulants or blood additives (heparin, etc.) are included beyond those normally used during leukapheresis.

Alternatively, white blood cells (WBC)/Peripheral Blood 10 Mononuclear Cells (PBMC) (using Biosafe Sepax 2 (Closed/Automated)) or T cells (using ClinIMACS® Prodigy (Closed/Automated)) may be isolated directly from whole blood. However, in certain subjects (e.g. those diagnosed and/or treated for cancer), the WBC/PBMC yield may 15 be significantly lower when isolated from whole blood than when isolated by leukapheresis.

Either the leukapheresis procedure and/or the direct cell isolation procedure may be used for any subject of the disclosure.

20 The leukapheresis product, blood. WBC/PBMC composition and/or T-cell composition should be packed in insulated containers and should be kept at controlled room temperature (+19° C. to +25° C.) according to standard hospital or institutional blood collection procedures approved for use with the clinical protocol. The leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should not be refrigerated.

25 The cell concentration leukapheresis product, blood. WBC/PBMC composition and/or T-cell composition should not exceed 0.2×10^9 cells per mL during transportation. Intense mixing of the leukapheresis product, blood. WBC/PBMC composition and/or T-cell composition should be avoided.

30 If the leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition has to be stored, e.g. overnight, it should be kept at controlled room temperature (same as above). During storage, the concentration of the leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should never exceed 0.2×10^9 cell 35 per mL.

40 Preferably, cells of the leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should be stored in autologous plasma. In certain embodiments, if the cell concentration of the leukapheresis product, blood. WBC/PBMC composition and/or T-cell composition is higher than 0.2×10^9 cell per mL, the product should be 45 diluted with autologous plasma.

45 Preferably, the leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should not be older than 24 hours when starting the labeling and separation procedure. The leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition may be processed and/or prepared for cell labeling using a closed and/or automated system (e.g., ClinIMACS Prodigy).

50 An automated system may perform additional buffy coat isolation, possibly by ficolation, and/or washing of the cellular product (e.g., the leukapheresis product, blood. WBC/PBMC composition and/or T cell composition).

55 A closed and/or automated system may be used to prepare and label cells for T-Cell isolation (from, for example, the leukapheresis product, blood, WBC/PBMC composition and/or T cell composition).

Although WBC/PBMCs may be nucleofected directly (which is easier and saves additional steps), the methods of the disclosure may include first isolating T cells prior to nucleofection. The easier strategy of directly nucleofecting PBMC requires selective expansion of CAR+ cells that is mediated via CAR signaling, which by itself is proving to be an inferior expansion method that directly reduces the in vivo efficiency of the product by rendering T cells functionally exhausted. The product may be a heterogeneous composition of CAR+ cells including T cells, NK cells, NKT cells, monocytes, or any combination thereof, which increases the variability in product from patient to patient and makes dosing and CRS management more difficult. Since T cells are thought to be the primary effectors in tumor suppression and killing, T cell isolation for the manufacture of an autologous product may result in significant benefits over the other more heterogeneous composition.

T cells may be isolated directly, by enrichment of labeled cells or depletion of labeled cells in a one-way labeling procedure or, indirectly, in a two-step labeling procedure. According to certain enrichment strategies of the disclosure, T cells may be collected in a Cell Collection Bag and the non-labeled cells (non-target cells) in a Negative Fraction Bag. In contrast to an enrichment strategy of the disclosure, the non-labeled cells (target cells) are collected in a Cell Collection Bag and the labeled cells (non-target cells) are collected in a Negative Fraction Bag or in the Non-Target Cell Bag, respectively. Selection reagents may include, but are not limited to, antibody-coated beads. Antibody-coated beads may either be removed prior to a modification and/or an expansion step, or, retained on the cells prior to a modification and/or an expansion step. One or more of the following non-limiting examples of cellular markers may be used to isolate T-cells: CD3, CD4, CD8, CD25, anti-biotin, CD1c, CD3/CD19, CD3/CD56, CD14, CD19, CD34, CD45RA, CD56, CD62L, CD133, CD137, CD271, CD304, IFN-gamma, TCR alpha/beta, and/or any combination thereof. Methods for the isolation of T-cells may include one or more reagents that specifically bind and/or detectably-label one or more of the following non-limiting examples of cellular markers may be used to isolate T-cells. CD3, CD4, CD8, CD25, anti-biotin, CD1c, CD3/CD19, CD3/CD56, CD14, CD19, CD34, CD45RA, CD56, CD62L, CD133, CD137, CD271, CD304, IFN-gamma, TCR alpha/beta, and/or any combination thereof. These reagents may or may not be "Good Manufacturing Practices" ("GMP") grade. Reagents may include, but are not limited to, Thermo DynaBeads and Miltenyi CliniMACS products. Methods of isolating T-cells of the disclosure may include multiple iterations of labeling and/or isolation steps. At any point in the methods of isolating T-cells of the disclosure, unwanted cells and/or unwanted cell types may be depleted from a T cell product composition of the disclosure by positively or negatively selecting for the unwanted cells and/or unwanted cell types. A T cell product composition of the disclosure may contain additional cell types that may express CD4, CD8, and/or another T cell marker(s).

Methods of the disclosure for nucleofection of T cells may eliminate the step of T cell isolation by, for example, a process for nucleofection of T cells in a population or composition of WBC/PBMCs that, following nucleofection, includes an isolation step or a selective expansion step via TCR signaling.

Certain cell populations may be depleted by positive or negative selection before or after T cell enrichment and/or sorting. Examples of cell compositions that may be depleted from a cell product composition may include myeloid cells,

CD25+ regulatory T cells (T Regs), dendritic cells, macrophages, red blood cells, mast cells, gamma-delta T cells, natural killer (NK) cells, a Natural Killer (NK)-like cell (e.g. a Cytokine Induced Killer (CIK) cell), induced natural killer (iNK) T cells, NK T cells, B cells, or any combination thereof.

T cell product compositions of the disclosure may include CD4+ and CD8+ T-Cells. CD4+ and CD8+ T-Cells may be isolated into separate collection bags during an isolation or 10 selection procedure. CD4+ T cells and CD8+ T cells may be further treated separately, or treated after reconstitution (combination into the same composition) at a particular ratio.

The particular ratio at which CD4+ T cells and CD8+ T 15 cells may be reconstituted may depend upon the type and efficacy of expansion technology used, cell medium, and/or growth conditions utilized for expansion of T-cell product compositions. Examples of possible CD4+: CD8+ ratios include, but are not limited to, 50%:50%, 60%:40%, 40%: 20 60% 75%:25% and 25%:75%.

CD8+ T cells exhibit a potent capacity for tumor cell killing, while CD4+ T cells provide many of the cytokines required to support CD8+ T cell proliferative capacity and function. Because T cells isolated from normal donors are 25 predominantly CD4+, the T-cell product compositions are artificially adjusted in vitro with respect to the CD4+:CD8+ ratio to improve upon the ratio of CD4+ T cells to CD8+ T cells that would otherwise be present in vivo. An optimized ratio may also be used for the ex vivo expansion of the 30 autologous T-cell product composition. In view of the artificially adjusted CD4+:CD8+ ratio of the T-cell product composition, it is important to note that the product compositions of the disclosure may be significantly different and provide significantly greater advantage than any endogenously-occurring population of T-cells.

Preferred methods for T cell isolation may include a negative selection strategy for yielding untouched pan T cell, meaning that the resultant T-cell composition includes T-cells that have not been manipulated and that contain an endogenously-occurring variety/ratio of T-cells.

Reagents that may be used for positive or negative selection include, but are not limited to, magnetic cell separation beads. Magnetic cell separation beads may or 45 may not be removed or depleted from selected populations of CD4+ T cells, CD8+ T cells, or a mixed population of both CD4+ and CD8+ T cells before performing the next step in a T-cell isolation method of the disclosure.

T cell compositions and T cell product compositions may be prepared for cryopreservation, storage in standard T Cell 50 Culture Medium, and/or genetic modification.

T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof may be cryopreserved using a standard cryopreservation method optimized for storing and 55 recovering human cells with high recovery, viability, phenotype, and/or functional capacity. Commercially-available cryopreservation media and/or protocols may be used. Cryopreservation methods of the disclosure may include a DMSO free cryopreservant (e.g. CryoSOfree™ DMSO-free 60 Cryopreservation Medium) reduce freezing-related toxicity.

T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof may be stored in a culture medium. T cell culture media of the disclosure may be 65 optimized for cell storage, cell genetic modification, cell phenotype and/or cell expansion. T cell culture media of the disclosure may include one or more antibiotics. Because the

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inclusion of an antibiotic within a cell culture media may decrease transfection efficiency and/or cell yield following genetic modification via nucleofection, the specific antibiotics (or combinations thereof) and their respective concentration(s) may be altered for optimal transfection efficiency and/or cell yield following genetic modification via nucleofection.

T cell culture media of the disclosure may include serum, and, moreover, the serum composition and concentration may be altered for optimal cell outcomes. Human AB serum is preferred over FBS/FCS for culture of T cells because, although contemplated for use in T cell culture media of the disclosure, FBS/FCS may introduce xeno-proteins. Serum may be isolated from the blood of the subject for whom the T-cell composition in culture is intended for administration, thus, a T cell culture medium of the disclosure may comprise autologous serum. Serum-free media or serum-substitute may also be used in T-cell culture media of the disclosure. In certain embodiments of the T-cell culture media and methods of the disclosure, serum-free media or serum-substitute may provide advantages over supplementing the medium with xeno-serum, including, but not limited to, healthier cells that have greater viability, nucleofect with higher efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies.

T cell culture media may include a commercially-available cell growth media. Exemplary commercially-available cell growth media include, but are not limited to, PBS, HBSS, OptiMEM, DMEM, RPMI 1640, AIM-V, X-VIVO 15, CellGro DC Medium, CTS OpTimer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium, ImmunoCult-XF T Cell Expansion Medium, or any combination thereof.

T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof may be prepared for genetic modification. Preparation of T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof for genetic modification may include cell washing and/or resuspension in a desired nucleofection buffer. Cryopreserved T-cell compositions may be thawed and prepared for genetic modification by nucleofection. Cryopreserved cells may be thawed according to standard or known protocols. Thawing and preparation of cryopreserved cells may be optimized to yield cells that have greater viability, nucleofect with higher efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. For example, Grifols Albutein (25% human albumin) may be used in the thawing and/or preparation process.

Genetic Modification of an Autologous T Cell Product Composition

T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof may be genetically modified using, for example, a nucleofection strategy such as electroporation. The total number of cells to be nucleofected, the total volume of the nucleofection reaction, and the precise timing of the preparation of the sample may be optimized to yield cells that have greater viability, nucleofect with higher efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies.

Nucleofection and/or electroporation may be accomplished using, for example, Lonza Amaxa, MaxCyte Pul-

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seAgile, Harvard Apparatus BTX, and/or Invitrogen Neon. Non-metal electrode systems, including, but not limited to, plastic polymer electrodes, may be preferred for nucleofection.

- 5 Prior to genetic modification by nucleofection, T cell compositions, T cell product compositions, unstimulated T cell compositions, resting T cell compositions or any portion thereof may be resuspended in a nucleofection buffer. Nucleofection buffers of the disclosure include commercially-available nucleofection buffers. Nucleofection buffers of the disclosure may be optimized to yield cells that have greater viability, nucleofect with higher efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. Nucleofection buffers of the disclosure may include, but are not limited to, PBS, HBSS, OptiMEM, BTXpress, Amaxa Nucleofector, Human T cell nucleofection buffer and any combination thereof. Nucleofection buffers of the disclosure may comprise one or more supplemental factors to yield cells that have greater viability, nucleofect with higher efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. Exemplary supplemental factors include, but are not limited to, recombinant human cytokines, chemokines, interleukins and any combination thereof. Exemplary cytokines, chemokines, and interleukins include, but are not limited to, IL2, IL7, IL12, IL15, IL21, IL1, IL3, IL4, IL5, IL6, IL8, CXCL8, IL9, IL10, IL11, IL13, IL14, IL16, IL17, IL18, IL19, IL20, IL22, IL23, IL25, IL26, IL27, IL28, IL29, IL30, IL31, IL32, IL33, IL35, IL36, GM-CSF, IFN-gamma, IL-1 alpha/IL-1F1, IL-1 beta/IL-1F2, IL-12 p70, IL-12/IL-35 p35, IL-13, IL-17/IL-17A, IL-17A/F Heterodimer, IL-17F, IL-18/IL-1F4, IL-23, IL-24, IL-32, IL-32 beta, IL-32 gamma, IL-33, LAP (TGF-beta 1), Lymphotoxin-alpha/TNF-beta, TGF-beta, TNF-alpha, TRANCE/TNFSF11/RANK L and any combination thereof. Exemplary supplemental factors include, but are not limited to, salts, minerals, metabolites or any combination thereof.
- 10 Exemplary salts, minerals, and metabolites include, but are not limited to, HEPES, Nicotinamide, Heparin, Sodium Pyruvate, L-Glutamine, MEM Non-Essential Amino Acid Solution, Ascorbic Acid, Nucleosides, FBS/FCS, Human serum, serum-substitute, anti-biotics, pH adjusters, Earle's Salts, 2-Mercaptoethanol, Human transferrin, Recombinant human insulin, Human serum albumin, Nucleofector PLUS Supplement, KCL, MgCl2, Na2HPO4, NaH2PO4, Sodium lactobionate, Manitol, Sodium succinate, Sodium Chloride, C1Na, Glucose, Ca(NO3)2, Tris/HC, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer407, Poly-vinylpyrrolidone, Pop313, Crown-5, and any combination thereof. Exemplary supplemental factors include, but are not limited to, media such as PBS, HBSS, OptiMEM, DMEM, RPMI 1640, AIM-V, X-VIVO 15, CellGro DC Medium, CTS OpTimer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium and any combination thereof. Exemplary supplemental factors include, but are not limited to, inhibitors of cellular DNA sensing, metabolism, differentiation, signal transduction, the apoptotic pathway and combinations thereof. Exemplary inhibitors include, but are not limited to, inhibitors of TLR9, MyD88, IRAK, TRAF6, TRAF3, IRF-7, NF-KB, Type 1 Interferons, pro-inflammatory cytokines, cGAS, STING, Sec5, TBK1, IRF-3, RNA pol III, RIG-1, IPS-1, FADD, RIP1, TRAF3, AIM2, ASC, Caspase1, Pro-L1B, PI3K, Akt, Wnt3A, inhibitors of glycogen synthase
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kinase-30 (GSK-3 β) (e.g. TWS119), Bafilomycin, Chloroquine, Quinacrine, AC-YVAD-CMK, Z-VAD-FMK, Z-ETD-FMK and any combination thereof. Exemplary supplemental factors include, but are not limited to, reagents that modify or stabilize one or more nucleic acids in a way to enhance cellular delivery, enhance nuclear delivery or transport, enhance the facilitated transport of nucleic acid into the nucleus, enhance degradation of epi-chromosomal nucleic acid, and/or decrease DNA-mediated toxicity. Exemplary reagents that modify or stabilize one or more nucleic acids include, but are not limited to, pH modifiers, DNA-binding proteins, lipids, phospholipids, CaPO₄, net neutral charge DNA binding peptides with or without NLS sequences, TREX1 enzyme, and any combination thereof.

Transposition reagents, including a transposon and a transposase, may be added to a nucleofection reaction of the disclosure prior to, simultaneously with, or after an addition of cells to a nucleofection buffer (optionally, contained within a nucleofection reaction vial or cuvette). Transposons of the disclosure may comprise plasmid DNA, nanoplasmid, linearized plasmid DNA, a PCR product, DOGGYBONE™ DNA, an mRNA template, a single or double-stranded DNA, a protein-nucleic acid combination or any combination thereof. Transposons of the disclosure may comprise one or more sequences that encode one or more TTAA site(s), one or more inverted terminal repeat(s) (ITRs), one or more long terminal repeat(s) (LTRs), one or more insulator(s), one or more promotor(s), one or more full-length or truncated gene(s), one or more polyA signal(s), one or more self-cleaving 2A peptide cleavage site(s), one or more internal ribosome entry site(s) (IRES), one or more enhancer(s), one or more regulator(s), one or more replication origin(s), and any combination thereof.

Transposons of the disclosure may comprise one or more sequences that encode one or more full-length or truncated gene(s). Full-length and/or truncated gene(s) introduced by transposons of the disclosure may encode one or more of a signal peptide, a Centyrin, a single chain variable fragment (scFv), a hinge, a transmembrane domain, a costimulatory domain, a chimeric antigen receptor (CAR), a chimeric T-cell receptor (CAR-T), a CARTyrin (a CAR-T comprising a Centyrin), a receptor, a ligand, a cytokine, a drug resistance gene, a tumor antigen, an allo or auto antigen, an enzyme, a protein, a peptide, a poly-peptide, a fluorescent protein, a muttein or any combination thereof.

Transposons of the disclosure may be prepared in water, TAE, TBE, PBS, HBSS, media, a supplemental factor of the disclosure or any combination thereof.

Transposons of the disclosure may be designed to optimize clinical safety and/or improve manufacturability. As a non-limiting example, transposons of the disclosure may be designed to optimize clinical safety and/or improve manufacturability by eliminating unnecessary sequences or regions and/or including a non-antibiotic selection marker. Transposons of the disclosure may or may not be GMP grade.

Transposase enzymes of the disclosure may be encoded by one or more sequences of plasmid DNA, nanoplasmid DNA, mRNA, protein, protein-nucleic acid combination or any combination thereof.

Transposase enzymes of the disclosure may be prepared in water, TAE, TBE, PBS, HBSS, media, a supplemental factor of the disclosure or any combination thereof. Transposase enzymes of the disclosure or the sequences/constructs encoding or delivering them may or may not be GMP grade.

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Transposons and transposase enzymes of the disclosure may be delivered to a cell by am means.

Although compositions and methods of the disclosure include delivery of a transposon and/or transposase of the disclosure to a cell by plasmid DNA (pDNA) or nanoplasmid DNA, the use of a plasmid or a nanoplasmid for delivery may allow the transposon and/or transposase to be integrated into the chromosomal DNA of the cell, which may lead to continued transposase expression. Accordingly, transposon and/or transposase enzymes of the disclosure may be delivered to a cell as either mRNA or protein to remove any possibility for chromosomal integration.

Transposons and transposases of the disclosure may be pre-incubated alone or in combination with one another prior to the introduction of the transposon and/or transposase into a nucleofection reaction. The absolute amounts of each of the transposon and the transposase, as well as the relative amounts, e.g., a ratio of transposon to transposase may be optimized.

Following preparation of nucleofection reaction, optionally, in a vial or cuvette, the reaction may be loaded into a nucleofector apparatus and activated for delivery of an electric pulse according to the manufacturer's protocol. Electric pulse conditions used for delivery of a transposon and/or a transposase of the disclosure (or a sequence encoding a transposon and/or a transposase of the disclosure) to a cell may be optimized for yielding cells with enhanced viability, higher nucleofection efficiency, greater viability post-nucleofection, desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. When using Amaxa nucleofector technology, each of the various nucleofection programs for the Amaxa 2B or 4D nucleofector are contemplated.

Following a nucleofection reaction of the disclosure, cells may be gently added to a cell medium. For example, when T cells undergo the nucleofection reaction, the T cells may be added to a T cell medium. Post-nucleofection cell media of the disclosure may comprise any one or more commercially-available media. Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may be optimized to yield cells with greater viability, higher nucleofection efficiency, exhibit greater viability post-nucleofection, display a more desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may comprise PBS, HBSS, OptiMEM, DMEM, RPMI 1640, AIM-V, X-VIVO 15, CellGro DC Medium, CTS OpTimizer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium, Immunocult-XF T Cell Expansion Medium and any combination thereof. Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may comprise one or more supplemental factors of the disclosure to enhance viability, nucleofection efficiency, viability post-nucleofection, cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. Exemplary supplemental factors include, but are not limited to, recombinant human cytokines, chemokines, interleukins and any combination thereof. Exemplary cytokines, chemokines, and interleukins include, but are not limited to, IL2, IL7, IL12, IL15, IL21, IL1, IL3, IL4, IL5, IL6, IL8, CXCL8, IL9, IL10, IL11, IL13, IL14, IL16, IL17, IL18, IL19, IL20, IL22, IL23, IL25, IL26, IL27, IL28, IL29, IL30, IL31, IL32, IL33, IL35, IL36, GM-CSF, IFN-gamma, IL-1 alpha/IL-1F1, IL-1 beta IL-1F2, IL-12 p70, IL-12/IL-35 p35, IL-13, IL-17, IL-17A, IL-17A/F Heterodimer, IL-17F, IL-18/IL-

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1F4, IL-23, IL-24, IL-32, IL-32 beta, IL-32 gamma, IL-33, LAP (TGF-beta 1), Lymphotoxin-alpha-TNF-beta, TGF-beta, TNF-alpha, TRANCE/TNFSF11/RANK L and any combination thereof. Exemplary supplemental factors include, but are not limited to, salts, minerals, metabolites or any combination thereof. Exemplary salts, minerals, and metabolites include, but are not limited to, HEPES, Nicotinamide, Heparin, Sodium Pyruvate, L-Glutamine, MEM Non-Essential Amino Acid Solution, Ascorbic Acid, Nucleosides, FBS/FCS, Human serum, serum-substitute, anti-biotics, pH adjusters, Earle's Salts, 2-Mercaptoethanol, Human transferrin, Recombinant human insulin, Human serum albumin, Nucleofector PLUS Supplement, KCL, MgCl₂, Na₂HPO₄, NaH₂PO₄, Sodium lactobionate, Mannitol, Sodium succinate, Sodium Chloride, ClNa, Glucose, Ca(NO₃)₂, Tris/HCl, K₂HPO₄, KH₂PO₄, Polyethyleneimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, Pop313, Crown-5, and any combination thereof. Exemplary supplemental factors include, but are not limited to, media such as PBS, HBSS, OptiMEM, DMEM, RPMI 1640, AIM-V, X-VIVO 15, CellGro DC Medium, CTS OpTimizer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium, ImmunoCult-XF T Cell Expansion Medium and any combination thereof. Exemplary supplemental factors include, but are not limited to, inhibitors of cellular DNA sensing, metabolism, differentiation, signal transduction, the apoptotic pathway and combinations thereof. Exemplary inhibitors include, but are not limited to, inhibitors of TLR9, MyD88, IRAK, TRAF6, TRAF3, IRF-7, NF-KB, Type 1 Interferons, pro-inflammatory cytokines, cGAS, STING, Sec5, TBK1, IRF-3, RNA pol III, RIG-1, IPS-1, FADD, RIP1, TRAF3, AIM2, ASC, Caspase1, Pro-IL1B, PI3K, Akt, Wnt3A, inhibitors of glycogen synthase kinase-3β(GSK-3 β) (e.g. TWS119), Bafilomycin, Chloroquine, Quinacrine, AC-YVAD-CMK, Z-VAD-FMK, Z-IETD-FMK and any combination thereof. Exemplary supplemental factors include, but are not limited to, reagents that modify or stabilize one or more nucleic acids in a way to enhance cellular delivery, enhance nuclear delivery or transport, enhance the facilitated transport of nucleic acid into the nucleus, enhance degradation of epi-chromosomal nucleic acid, and/or decrease DNA-mediated toxicity. Exemplary reagents that modify or stabilize one or more nucleic acids include, but are not limited to, pH modifiers, DNA-binding proteins, lipids, phospholipids, CaPO₄, net neutral charge DNA binding peptides with or without NLS sequences, TREX1 enzyme, and any combination thereof.

Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may be used at room temperature or pre-warmed to, for example to between 32° C. to 37° C., inclusive of the endpoints. Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may be pre-warmed to any temperature that maintains or enhances cell viability and/or expression of a transposon or portion thereof of the disclosure.

Post-nucleofection cell media of the disclosure (including post-nucleofection T cell media of the disclosure) may be contained in tissue culture flasks or dishes, G-Rex flasks, Bioreactor or cell culture bags, or any other standard receptacle. Post-nucleofection cell cultures of the disclosure (including post-nucleofection T cell cultures of the disclosure) may be kept still, or, alternatively, they may be perturbed (e.g. rocked, swirled, or shaken).

Post-nucleofection cell cultures may comprise genetically-modified cells. Post-nucleofection T cell cultures may

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comprise genetically-modified T cells. Genetically modified cells of the disclosure may be either rested for a defined period of time or stimulated for expansion by, for example, the addition of a T Cell Expander technology. In certain embodiments, genetically modified cells of the disclosure may be either rested for a defined period of time or immediately stimulated for expansion by, for example, the addition of a T Cell Expander technology. Genetically modified cells of the disclosure may be rested to allow them sufficient time to acclimate, time for transposition to occur, and/or time for positive or negative selection, resulting in cells with enhanced viability, higher nucleofection efficiency, greater viability post-nucleofection, desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies. Genetically modified cells of the disclosure may be rested, for example, for 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 hours. In certain embodiments, genetically modified cells of the disclosure may be rested, for example, for an overnight. In certain aspects, an overnight is about 12 hours. Genetically modified cells of the disclosure may be rested, for example, for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or more days.

Genetically modified cells of the disclosure may be selected following a nucleofection reaction and prior to addition of an expander technology. For optimal selection of genetically-modified cells, the cells may be allowed to rest in a post-nucleofection cell medium for at least 2-14 days to facilitate identification of modified cells (e.g., differentiation of modified from non-modified cells).

As early as 24-hours post-nucleofection, expression of a CAR/CARTyrin and selection marker of the disclosure may be detectable in modified T cells upon successful nucleofection of a transposon of the disclosure. Due to epi-chromosomal expression of the transposon, expression of a selection marker alone may not differentiate modified T cells (those cells in which the transposon has been successfully integrated) from unmodified T cells (those cells in which the transposon was not successfully integrated). When epi-chromosomal expression of the transposon obscures the detection of modified cells by the selection marker, the nucleofected cells (both modified and unmodified cells) may be rested for a period of time (e.g. 2-14 days) to allow the cells to cease expression or lose all epi-chromosomal transposon expression. Following this extended resting period, only modified T cells should remain positive for expression of selection marker. The length of this extended resting period may be optimized for each nucleofection reaction and selection process. When epi-chromosomal expression of the transposon obscures the detection of modified cells by the selection marker, selection may be performed without this extended resting period, however, an additional selection step may be included at a later time point (e.g. either during or after the expansion stage).

Selection of genetically modified cells of the disclosure may be performed by any means. In certain embodiments of the methods of the disclosure, selection of genetically modified cells of the disclosure may be performed by isolating cells expressing a specific selection marker. Selection markers of the disclosure may be encoded by one or more sequences in the transposon. Selection markers of the disclosure may be expressed by the modified cell as a result of successful transposition (i.e., not encoded by one or more sequences in the transposon). In certain embodiments, genetically modified cells of the disclosure contain a selection marker that confers resistance to a deleterious compound of the post-nucleofection cell medium. The deleterious compound may comprise, for example, an antibiotic or

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a drug that, absent the resistance conferred by the selection marker to the modified cells, would result in cell death. Exemplary selection markers include, but are not limited to, wild type (WT) or mutant forms of one or more of the following genes: neo, DHFR, TYMS, ALDH, MDR1, MGMT, FANCF, RAD51C, GCS, and NKX2.2. Exemplary selection markers include, but are not limited to, a surface-expressed selection marker or surface-expressed tag may be targeted by Ab-coated magnetic bead technology or column selection, respectively. A cleavable tag such as those used in protein purification may be added to a selection marker of the disclosure for efficient column selection, washing, and elution. In certain embodiments, selection markers of the disclosure are not expressed by the modified cells (including modified T cells) endogenously and, therefore, may be useful in the physical isolation of modified cells (by, for example, cell sorting techniques). Exemplary selection markers of the disclosure are not expressed by the modified cells (including modified T cells) endogenously include, but are not limited to, full-length, mutated, or truncated forms of CD271, CD19, CD52, CD34, RQR8, CD22, CD20, CD33 and any combination thereof.

Genetically modified cells of the disclosure may be selectively expanded following a nucleofection reaction. In certain embodiments, modified T cells comprising a CAR/CARTyin may be selectively expanded by CAR/CARTyin stimulation. Modified T cells comprising a CAR/CARTyin may be stimulated by contact with a target-covered reagent (e.g. a tumor line or a normal cell line expressing a target or expander beads covered in a target). Alternatively, modified T cells comprising a CAR/CARTyin may be stimulated by contact with an irradiated tumor cell, an irradiated allogeneic normal cell, an irradiated autologous PBMC. To minimize contamination of cell product compositions of the disclosure with a target-expressing cell used for stimulation, for example, when the cell product composition may be administered directly to a subject, the stimulation may be performed using expander beads coated with CAR/CARTyin target protein. Selective expansion of modified T cells comprising a CAR/CARTyin by CAR/CARTyin stimulation may be optimized to avoid functionally-exhausting the modified T-cells.

Selected genetically-modified cells of the disclosure may be cryopreserved, rested for a defined period of time, or stimulated for expansion by the addition of a Cell Expander technology. Selected genetically-modified cells of the disclosure may be cryopreserved, rested for a defined period of time, or immediately stimulated for expansion by the addition of a Cell Expander technology. When the selected genetically-modified cells are T cells, the T cells may be stimulated for expansion by the addition of a T-Cell Expander technology. Selected genetically modified cells of the disclosure may be rested, for example, for 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 hours. In certain embodiments, selected genetically modified cells of the disclosure may be rested, for example, for an overnight. In certain aspects, an overnight is about 12 hours. Selected genetically modified cells of the disclosure may be rested, for example, for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or more days. Selected genetically modified cells of the disclosure may be rested for any period of time resulting in cells with enhanced viability, higher nucleofection efficiency, greater viability post-nucleofection, desirable cell phenotype, and/or greater/faster expansion upon addition of expansion technologies.

Selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may be cryo-

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preserved using any standard cryopreservation method, which may be optimized for storing and/or recovering human cells with high recovery, viability, phenotype, and/or functional capacity. Cryopreservation methods of the disclosure may include commercially-available cryopreservation media and/or protocols.

A transposition efficiency of selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may be assessed by any means. For example, prior to the application of an expander technology, expression of the transposon by selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may be measured by fluorescence-activated cell sorting (FACS). Determination of a transposition efficiency of selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may include determining a percentage of selected cells expressing the transposon (e.g. a CAR). Alternatively, or in addition, a purity of T cells, a Mean Fluorescence Intensity (MFI) of the transposon expression (e.g. CAR expression), an ability of a CAR (delivered in the transposon) to mediate degranulation and/or killing of a target cell expressing the CAR ligand, and/or a phenotype of selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may be assessed by any means.

Cell product compositions of the disclosure may be released for administration to a subject upon meeting certain release criteria. Exemplary release criteria may include, but are not limited to, a particular percentage of modified, selected and/or expanded T cells expressing detectable levels of a CAR on the cell surface.

Genetic Modification of an Autologous T Cell Product Composition

Genetically-modified cells (including genetically-modified T cells) of the disclosure may be expanded using an expander technology. Expander technologies of the disclosure may comprise a commercially-available expander technology. Exemplary expander technologies of the disclosure include stimulation a genetically-modified T cell of the disclosure via the TCR. While all means for stimulation of a genetically-modified T cell of the disclosure are contemplated, stimulation a genetically-modified T cell of the disclosure via the TCR is a preferred method, yielding a product with a superior level of killing capacity.

To stimulate a genetically-modified T cell of the disclosure via the TCR, Thermo Expander DynaBeads may be used at a 3:1 bead to T cell ratio. If the expander beads are not biodegradable, the beads may be removed from the expander composition. For example, the beads may be removed from the expander composition after about 5 days. To stimulate a genetically-modified T cell of the disclosure via the TCR, a Miltenyi T Cell Activation/Expansion Reagent may be used. To stimulate a genetically-modified T cell of the disclosure via the TCR, StemCell Technologies' ImmunoCult Human CD3/CD28 or CD3/CD28/CD2 T Cell Activator Reagent may be used. This technology may be preferred since the soluble tetrameric antibody complexes would degrade after a period and would not require removal from the process.

Artificial antigen presenting cells (APCs) may be engineered to co-express the target antigen and may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure. Artificial APCs may comprise or may be derived from a tumor cell line (including, for example, the immortalized myelogenous leukemia line K562) and may be engineered to co-express multiple costimulatory molecules or technologies (such as CD28,

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4-1BBL, CD64, mbIL-21, mbIL-15, CAR target molecule, etc.). When artificial APCs of the disclosure are combined with costimulatory molecules, conditions may be optimized to prevent the development or emergence of an undesirable phenotype and functional capacity, namely terminally-differentiated effector T cells.

Irradiated PBMCs (auto or allo) may express some target antigens, such as CD19, and may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure. Alternatively, or in addition, irradiated tumor cells may express some target antigens and may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure.

Plate-bound and/or soluble anti-CD3, anti-CD2 and/or anti-CD28 stimulate may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure.

Antigen-coated beads may display target protein and may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure. Alternatively, or in addition, expander beads coated with a CAR/CARTylin target protein may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CAR of the disclosure.

Expansion methods drawn to stimulation of a cell or T-cell of the disclosure through the TCR or CAR/CARTylin and via surface-expressed CD2, CD3, CD28, 4-1BB, and/or other markers on genetically-modified T cells.

An expansion technology may be applied to a cell of the disclosure immediately post-nucleofection until approximately 24 hours post-nucleofection. While various cell media may be used during an expansion procedure, a desirable T Cell Expansion Media of the disclosure may yield cells with, for example, greater viability, cell phenotype, total expansion, or greater capacity for in vivo persistence, engraftment, and/or CAR-mediated killing. Cell media of the disclosure may be optimized to improve/enhance expansion, phenotype, and function of genetically-modified cells of the disclosure. A preferred phenotype of expanded T cells may include a mixture of T stem cell memory, T central, and T effector memory cells. Expander Dynabeads may yield mainly central memory T cells which may lead to superior performance in the clinic.

Exemplary T cell expansion media of the disclosure may include, in part or in total, PBS, HBSS, OptiMEM, DMEM, RPMI 1640, AIM-V, X-VIVO 15, CellGro DC Medium, CTS OpTimizer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium, Immunocult-XF T Cell Expansion Medium, or any combination thereof. T cell expansion media of the disclosure may further include one or more supplemental factors. Supplemental factors that may be included in a T cell expansion media of the disclosure enhance viability, cell phenotype, total expansion, or increase capacity for in vivo persistence, engraftment, and/or CAR-mediated killing. Supplemental factors that may be included in a T cell expansion media of the disclosure include, but are not limited to, recombinant human cytokines, chemokines, and/or interleukins such as IL2, IL7, IL12, IL15, IL21, IL1, IL3, IL4, IL5, IL6, IL8, CXCL8, IL9, IL10, IL11, IL13, IL14, IL16, IL17, IL18, IL19, IL20, IL22, IL23, IL25, IL26, IL27, IL28, IL29, IL30, IL31, IL32, IL33, IL35, IL36, GM-CSF, IFN-gamma, IL-1 alpha/IL-1F1, IL-1 beta/IL-1F2, IL-12 p70, IL-12/IL-35 p35, IL-13, IL-17/IL-17A, IL-17A/F Heterodimer, IL-17F, IL-18/IL-1F4, IL-23, IL-24, IL-32, IL-32 beta, IL-32 gamma, IL-33, LAP (TGF-beta 1), Lymphotxin-alpha/TNF-beta, TGF-beta, TNF-alpha, TRANCE/TNFSF11/RANK L, or any combination thereof. Supplemental factors

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that may be included in a T cell expansion media of the disclosure include, but are not limited to, salts, minerals, and/or metabolites such as HEPES, Nicotinamide, Heparin, Sodium Pyruvate, L-Glutamine, MEM Non-Essential Amino Acid Solution, Ascorbic Acid, Nucleosides, FBS/FCS, Human serum, serum-substitute, anti-biotics, pH adjusters, Earle's Salts, 2-Mercaptoethanol, Human transferrin, Recombinant human insulin, Human serum albumin, Nucleofector PLUS Supplement, KCL, MgCl2, Na2HPO4, NAH2PO4, Sodium lactobionate, Manitol, Sodium succinate, Sodium Chloride, ClNa, Glucose, Ca(NO3)2, Tris/HC, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Polyvinylpyrrolidone, Pop313, Crown-5 or any combination thereof. Supplemental factors that may be included in a T cell expansion media of the disclosure include, but are not limited to, inhibitors of cellular DNA sensing, metabolism, differentiation, signal transduction, and/or the apoptotic pathway such as inhibitors of TLR9, MyD88, IRAK, TRAF6, TRAF3, IRF-7, NF-KB, Type 1 Interferons, pro-inflammatory cytokines, cGAS, STING, Sec5, TBK1, IRF-3, RNA pol III, RIG-1, IPS-1, FADD, RIP1, TRAF3, AIM2, ASC, Caspase1, Pro-IL1B, PI3K Akt, Wnt3A, inhibitors of glycogen synthase kinase-3β (GSK-3 β) (e.g. TWS119), Bafilomycin, Chloroquine, Quinacrine, AC-YVAD-CMK, Z-VAD-FMK, Z-IETD-FMK, or any combination thereof. Supplemental factors that may be included in a T cell expansion media of the disclosure include, but are not limited to, reagents that modify or stabilize nucleic acids in a way to enhance cellular delivery, enhance nuclear delivery or transport, enhance the facilitated transport of nucleic acid into the nucleus, enhance degradation of epi-chromosomal nucleic acid, and/or decrease DNA-mediated toxicity, such as pH modifiers, DNA-binding proteins, lipids, phospholipids, CaPO4, net neutral charge DNA binding peptides with or without NLS sequences, TREX1 enzyme, or any combination thereof. Genetically-modified cells of the disclosure may be selected during the expansion process by the use of selectable drugs or compounds. For example, in certain embodiments, when a transposon of the disclosure may encode a selection marker that confers to genetically-modified cells resistance to a drug added to the culture medium, selection may occur during the expansion process and may require approximately 1-14 days of culture for selection to occur. Examples of drug resistance genes that may be used as selection markers encoded by a transposon of the disclosure, include, but are not limited to, wild type (WT) or mutant forms of the genes neo, DHFR, TYMS, ALDH, MDR1, MGMT, FANCF, RAD51C, GCS, NKX2.2, or any combination thereof. Examples of corresponding drugs or compounds that may be added to the culture medium to which a selection marker may confer resistance include, but are not limited to, G418, Puromycin, Ampicillin, Kanamycin, Methotrexate, Mephalan, Temozolomide, Vincristine, Etoposide, Doxorubicin, Bendamustine, Fludarabine, Aredia (Pamidronate Disodium), Becenium (Carmustine), BiCNU (Carmustine), Bortezomib, Carfilzomib, Carmubris (Carmustine), Carmustine, Clafen (Cyclophosphamide), Cyclophosphamide, Cytoxan (Cyclophosphamide), Daratumumab, Darzalex (Daratumumab), Doxil (Doxorubicin Hydrochloride Liposome), Doxorubicin Hydrochloride Liposome, Dox-SL (Doxorubicin Hydrochloride Liposome), Elotuzumab, Empliciti (Elotuzumab), Evacet (Doxorubicin Hydrochloride Liposome), Farydak (Panobinostat), ixazomib Citrate, Kyprolis (Carfilzomib), Lenalidomide, LipoDox (Doxorubicin Hydrochloride Liposome), Mozobil

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(Plerixafor), Neosar (Cyclophosphamide), Ninlaro (Ixazomib Citrate), Pamidronate Disodium, Panobinostat, Plerixafor, Pomalidomide, Pomalyst (Pomalidomide), Revlimid (Lenalidomide), Synovir (Thalidomide), Thalidomide, Thalomid (Thalidomide), Velcade (Bortezomib), Zoledronic Acid, Zometa (Zoledronic Acid), or any combination thereof.

A T-Cell Expansion process of the disclosure may occur in a cell culture bag in a WAVE Bioreactor, a G-Rex flask, or in any other suitable container and/or reactor.

A cell or T-cell culture of the disclosure may be kept steady, rocked, swirled, or shaken.

A cell or T-cell expansion process of the disclosure may optimize certain conditions, including, but not limited to culture duration, cell concentration, schedule for T cell medium addition/removal, cell size, total cell number, cell phenotype, purity of cell population, percentage of genetically-modified cells in growing cell population, use and composition of supplements, the addition/removal of expander technologies, or any combination thereof.

A cell or T-cell expansion process of the disclosure may continue until a predefined endpoint prior to formulation of the resultant expanded cell population. For example, a cell or T-cell expansion process of the disclosure may continue for a predetermined amount of time: at least, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 hours; at least 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 days; at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 weeks; at least 1, 2, 3, 4, 5, 6, months, or at least 1 year. A cell or T-cell expansion process of the disclosure may continue until the resultant culture reaches a predetermined overall cell density: 1, 10, 100, 1000, 104, 105, 106, 107, 108, 109, 1010 cells per volume (μl , ml, L) or any density in between. A cell or T-cell expansion process of the disclosure may continue until the genetically-modified cells of a resultant culture demonstrate a predetermined level of expression of a transposon of the disclosure: 1%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% or any percentage in between of a threshold level of expression (a minimum, maximum or mean level of expression indicating the resultant genetically-modified cells are clinically-efficacious). A cell or T-cell expansion process of the disclosure may continue until the proportion of genetically-modified cells of a resultant culture to the proportion of unmodified cells reaches a predetermined threshold: at least 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1, 2:1, 2:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1 10:1 or any ratio in between.

Analysis of Genetically-Modified Autologous T Cells for Release

A percentage of genetically-modified cells may be assessed during or after an expansion process of the disclosure. Cellular expression of a transposon by a genetically-modified cell of the disclosure may be measured by fluorescence-activated cell sorting (FACS) For example, FACS may be used to determine a percentage of cells or T cells expressing a CAR of the disclosure. Alternatively, or in addition, a purity of genetically-modified cells or T cells, the Mean Fluorescence Intensity (MFI) of a CAR expressed by a genetically-modified cell or T cell of the disclosure, an ability of the CAR to mediate degranulation and/or killing of a target cell expressing the CAR ligand, and/or a phenotype of CAR+ T cells may be assessed.

Compositions of the disclosure intended for administration to a subject may be required to meet one or more “release criteria” that indicate that the composition is safe and efficacious for formulation as a pharmaceutical product and/or administration to a subject. Release criteria may

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include a requirement that a composition of the disclosure (e.g. a T-cell product of the disclosure) comprises a particular percentage of T cells expressing detectable levels of a CAR of the disclosure on their cell surface.

The expansion process should be continued until a specific criterion has been met (e.g. achieving a certain total number of cells, achieving a particular population of memory cells, achieving a population of a specific size).

Certain criterion signal a point at which the expansion process should end. For example, cells should be formulated, reactivated, or cryopreserved once they reach a cell size of 300 fL (otherwise, cells reaching a size above this threshold may start to die). Cryopreservation immediately once a population of cells reaches an average cell size of less than 300 fL may yield better cell recovery upon thawing and culture because the cells haven't yet reached a fully quiescent state prior to cryopreservation (a fully quiescent size is approximately 180 fL). Prior to expansion, T cells of the disclosure may have a cell size of about 180 fL, but may more than quadruple their cell size to approximately 900 fL at 3 days post-expansion. Over the next 6-12 days, the population of T-cells will slowly decrease cell size to full quiescence at 180 fL.

A process for preparing a cell population for formulation may include, but is not limited to the steps of, concentrating the cells of the cell population, washing the cells, and/or further selection of the cells via drug resistance or magnetic bead sorting against a particular surface-expressed marker.

A process for preparing a cell population for formulation may further include a sorting step to ensure the safety and purity of the final product. For example, if a tumor cell from a patient has been used to stimulate a genetically-modified T-cell of the disclosure or that have been genetically-modified in order to stimulate a genetically-modified T-cell of the disclosure that is being prepared for formulation, it is critical that no tumor cells from the patient are included in the final product.

Cell Product Infusion and/or Cryopreservation for Infusion

A pharmaceutical formulation of the disclosure may be distributed into bags for infusion, cryopreservation, and/or storage.

A pharmaceutical formulation of the disclosure may be cryopreserved using a standard protocol and, optionally, an infusible cryopreservation medium. For example, a DMSO free cryopreservant (e.g. CryoSOfree™, DMSO-free Cryopreservation Medium) may be used to reduce freezing-related toxicity. A cryopreserved pharmaceutical formulation of the disclosure may be stored for infusion to a patient at a later date. An effective treatment may require multiple administrations of a pharmaceutical formulation of the disclosure and, therefore, pharmaceutical formulations may be packaged in pre-aliquoted “doses” that may be stored frozen but separated for thawing of individual doses.

A pharmaceutical formulation of the disclosure may be stored at room temperature. An effective treatment may require multiple administrations of a pharmaceutical formulation of the disclosure and, therefore, pharmaceutical formulations may be packaged in pre-aliquoted “doses” that may be stored together but separated for administration of individual doses.

A pharmaceutical formulation of the disclosure may be archived for subsequent re-expansion and/or selection for generation of additional doses to the same patient in the case of an allogenic therapy who may need an administration at a future date following, for example, a remission and relapse of a condition.

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Formulations

As noted above, the disclosure provides for stable formulations, which preferably comprise a phosphate buffer with saline or a chosen salt, as well as preserved solutions and formulations containing a preservative as well as multi-use preserved formulations suitable for pharmaceutical or veterinary use, comprising at least one protein scaffold in a pharmaceutically acceptable formulation. Preserved formulations contain at least one known preservative or optionally selected from the group consisting of at least one phenol, m-cresol, p-cresol, o-cresol, chlorocresol, benzyl alcohol, phenylmercuric nitrite, phenoxyethanol, formaldehyde, chlorobutanol, magnesium chloride (e.g., hexahydrate), alkylparaben (methyl, ethyl, propyl, butyl and the like), benzalkonium chloride, benzethonium chloride, sodium dehydroacetate and thimerosal, polymers, or mixtures thereof in an aqueous diluent. Any suitable concentration or mixture can be used as known in the art, such as about 0.0015%, or any range, value, or fraction therein. Non-limiting examples include, no preservative, about 0.1-2% m-cresol (e.g., 0.2, 0.3, 0.4, 0.5, 0.9, 1.0%), about 0.1-3% benzyl alcohol (e.g., 0.5, 0.9, 1.1, 1.5, 1.9, 2.0, 2.5%), about 0.001-0.5% thimerosal (e.g., 0.005, 0.01), about 0.001-2.0% phenol (e.g., 0.05, 0.25, 0.28, 0.5, 0.9, 1.0%), 0.0005-1.0% alkylparaben(s) (e.g., 0.00075, 0.0009, 0.001, 0.002, 0.005, 0.0075, 0.009, 0.01, 0.02, 0.05, 0.075, 0.09, 0.1, 0.2, 0.3, 0.5, 0.75, 0.9, 1.0%), and the like.

As noted above, the invention provides an article of manufacture, comprising packaging material and at least one vial comprising a solution of at least one protein scaffold with the prescribed buffers and/or preservatives, optionally in an aqueous diluent, wherein said packaging material comprises a label that indicates that such solution can be held over a period of 1, 2, 3, 4, 5, 6, 9, 12, 18, 20, 24, 30, 36, 40, 48, 54, 60, 66, 72 hours or greater. The invention further comprises an article of manufacture, comprising packaging material, a first vial comprising lyophilized at least one protein scaffold, and a second vial comprising an aqueous diluent of prescribed buffer or preservative, wherein said packaging material comprises a label that instructs a patient to reconstitute the at least one protein scaffold in the aqueous diluent to form a solution that can be held over a period of twenty-four hours or greater.

The at least one protein scaffold used in accordance with the present invention can be produced by recombinant means, including from mammalian cell or transgenic preparations, or can be purified from other biological sources, as described herein or as known in the art.

The range of at least one protein scaffold in the product of the present invention includes amounts yielding upon reconstitution, if in a wet/dry system, concentrations from about 1.0 µg/ml to about 1000 mg/ml, although lower and higher concentrations are operable and are dependent on the intended delivery vehicle, e.g., solution formulations will differ from transdermal patch, pulmonary, transmucosal, or osmotic or micro pump methods.

Preferably, the aqueous diluent optionally further comprises a pharmaceutically acceptable preservative. Preferred preservatives include those selected from the group consisting of phenol, m-cresol, p-cresol, o-cresol, chlorocresol, benzyl alcohol, alkylparaben (methyl, ethyl, propyl, butyl and the like), benzalkonium chloride, benzethonium chloride, sodium dehydroacetate and thimerosal, or mixtures thereof. The concentration of preservative used in the formulation is a concentration sufficient to yield an anti-

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microbial effect. Such concentrations are dependent on the preservative selected and are readily determined by the skilled artisan.

Other excipients, e.g., isotonicity agents, buffers, antioxidants, and preservative enhancers, can be optionally and preferably added to the diluent. An isotonicity agent, such as glycerin, is commonly used at known concentrations. A physiologically tolerated buffer is preferably added to provide improved pH control. The formulations can cover a wide range of pHs, such as from about pH 4 to about pH 10, and preferred ranges from about pH 5 to about pH 9, and a most preferred range of about 6.0 to about 8.0. Preferably, the formulations of the present invention have a pH between about 6.8 and about 7.8. Preferred buffers include phosphate buffers, most preferably, sodium phosphate, particularly, phosphate buffered saline (PBS).

Other additives, such as a pharmaceutically acceptable solubilizers like Tween 20 (polyoxyethylene (20) sorbitan monolaurate), Tween 40 (polyoxyethylene (20) sorbitan monopalmitate), Tween 80 (polyoxyethylene (20) sorbitan monooleate), Pluronic F68 (polyoxyethylene polyoxypropylene block copolymers), and PEG (polyethylene glycol) or non-ionic surfactants, such as polysorbate 20 or 80 or poloxamer 184 or 188, Pluronic® polyols, other block copolymers, and chelators, such as EDTA and EGTA, can optionally be added to the formulations or compositions to reduce aggregation. These additives are particularly useful if a pump or plastic container is used to administer the formulation. The presence of pharmaceutically acceptable surfactant mitigates the propensity for the protein to aggregate.

The formulations of the present invention can be prepared by a process which comprises mixing at least one protein scaffold and a preservative selected from the group consisting of phenol, m-cresol, p-cresol, o-cresol, chlorocresol, benzyl alcohol, alkylparaben, (methyl, ethyl, propyl, butyl and the like), benzalkonium chloride, benzethonium chloride, sodium dehydroacetate and thimerosal or mixtures thereof in an aqueous diluent. Mixing the at least one protein scaffold and preservative in an aqueous diluent is carried out using conventional dissolution and mixing procedures. To prepare a suitable formulation, for example, a measured amount of at least one protein scaffold in buffered solution is combined with the desired preservative in a buffered solution in quantities sufficient to provide the protein and preservative at the desired concentrations. Variations of this process would be recognized by one of ordinary skill in the art. For example, the order the components are added, whether additional additives are used, the temperature and pH at which the formulation is prepared, are all factors that can be optimized for the concentration and means of administration used.

The claimed formulations can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized at least one protein scaffold that is reconstituted with a second vial containing water, a preservative and/or excipients, preferably, a phosphate buffer and/or saline and a chosen salt, in an aqueous diluent. Either a single solution vial or dual vial requiring reconstitution can be reused multiple times and can suffice for a single or multiple cycles of patient treatment and thus can provide a more convenient treatment regimen than currently available.

The present claimed articles of manufacture are useful for administration over a period ranging from immediate to twenty-four hours or greater. Accordingly, the presently claimed articles of manufacture offer significant advantages to the patient. Formulations of the invention can optionally be safely stored at temperatures of from about 2° C. to about

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40° C. and retain the biological activity of the protein for extended periods of time, thus allowing a package label indicating that the solution can be held and/or used over a period of 6, 12, 18, 24, 36, 48, 72, or 96 hours or greater. If preserved diluent is used, such label can include use up to 1-12 months, one-half, one and a half, and/or two years.

The solutions of at least one protein scaffold of the invention can be prepared by a process that comprises mixing at least one protein scaffold in an aqueous diluent. Mixing is carried out using conventional dissolution and mixing procedures. To prepare a suitable diluent, for example, a measured amount of at least one protein scaffold in water or buffer is combined in quantities sufficient to provide the protein and, optionally, a preservative or buffer at the desired concentrations. Variations of this process would be recognized by one of ordinary skill in the art. For example, the order the components are added, whether additional additives are used, the temperature and pH at which the formulation is prepared, are all factors that can be optimized for the concentration and means of administration used.

The claimed products can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized at least one protein scaffold that is reconstituted with a second vial containing the aqueous diluent. Either a single solution vial or dual vial requiring reconstitution can be reused multiple times and can suffice for a single or multiple cycles of patient treatment and thus provides a more convenient treatment regimen than currently available.

The claimed products can be provided indirectly to patients by providing to pharmacies, clinics, or other such institutions and facilities, clear solutions or dual vials comprising a vial of lyophilized at least one protein scaffold that is reconstituted with a second vial containing the aqueous diluent. The clear solution in this case can be up to one liter or even larger in size, providing a large reservoir from which smaller portions of the at least one protein scaffold solution can be retrieved one or multiple times for transfer into smaller vials and provided by the pharmacy or clinic to their customers and/or patients.

Recognized devices comprising single vial systems include pen-injector devices for delivery of a solution, such as BD Pens, BD Autojector®, Humaject®, NovoPen®, B-D® Pen, AutoPen®, and OptiPen®, GenotropinPen®, Genotronorm Pen®, Humatro Pen®, Reco-Pen®, Roferon Pen®, Biojector®, Iject®, J-tip Needle-Free Injector®, Intraject®, Medi-Ject®, e.g., as made or developed by Becton Dickinson (Franklin Lakes, N.J., www.bectondickinson.com), Disetronic (Burgdorf, Switzerland, www.disetronic.com, Bioject, Portland, Oreg. (www.bioject.com); National Medical Products, Weston Medical (Peterborough, UK, www.weston-medical.com), Medi-Ject Corp (Minneapolis, Minn., www.mediject.com), and similarly suitable devices. Recognized devices comprising a dual vial system include those pen-injector systems for reconstituting a lyophilized drug in a cartridge for delivery of the reconstituted solution, such as the HumatroPen®. Examples of other devices suitable include pre-filled syringes, auto-injectors, needle free injectors and needle free IV infusion sets.

The products presently claimed include packaging material. The packaging material provides, in addition to the information required by the regulatory agencies, the conditions under which the product can be used. The packaging material of the present invention provides instructions to the patient to reconstitute at least one protein scaffold in the aqueous diluent to form a solution and to use the solution over a period of 2-24 hours or greater for the two vial,

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wet/dry, product. For the single vial, solution product, the label indicates that such solution can be used over a period of 2-24 hours or greater. The presently claimed products are useful for human pharmaceutical product use.

5 The formulations of the present invention can be prepared by a process that comprises mixing at least one protein scaffold and a selected buffer, preferably, a phosphate buffer containing saline or a chosen salt. Mixing at least one protein scaffold and buffer in an aqueous diluent is carried 10 out using conventional dissolution and mixing procedures. To prepare a suitable formulation, for example, a measured amount of at least one protein scaffold in water or buffer is combined with the desired buffering agent in water in 15 quantities sufficient to provide the protein and buffer at the desired concentrations. Variations of this process would be recognized by one of ordinary skill in the art. For example, the order the components are added, whether additional additives are used, the temperature and pH at which the formulation is prepared, are all factors that can be optimized 20 for the concentration and means of administration used.

The claimed stable or preserved formulations can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized protein scaffold that is reconstituted with a second vial containing a preservative or 25 buffer and excipients in an aqueous diluent. Either a single solution vial or dual vial requiring reconstitution can be reused multiple times and can suffice for a single or multiple cycles of patient treatment and thus provides a more convenient treatment regimen than currently available.

30 Other formulations or methods of stabilizing the protein scaffold may result in other than a clear solution of lyophilized powder comprising the protein scaffold. Among non-clear solutions are formulations comprising particulate suspensions, said particulates being a composition containing the protein scaffold in a structure of variable dimension and known variously as a microsphere, microparticle, nanoparticle, nanosphere, or liposome. Such relatively homogeneous, essentially spherical, particulate formulations containing an active agent can be formed by contacting an 35 aqueous phase containing the active agent and a polymer and a nonaqueous phase followed by evaporation of the nonaqueous phase to cause the coalescence of particles from the aqueous phase as taught in U.S. Pat. No. 4,589,330. Porous microparticles can be prepared using a first phase 40 containing active agent and a polymer dispersed in a continuous solvent and removing said solvent from the suspension by freeze-drying or dilution-extraction-precipitation as taught in U.S. Pat. No. 4,818,542. Preferred polymers for such preparations are natural or synthetic copolymers or 45 polymers selected from the group consisting of gelatin agar, starch, arabinogalactan, albumin, collagen, polyglycolic acid, polylactic acid, glycolide-L(-) lactide poly(epsilon-caprolactone, poly(epsilon-caprolactone-CO-lactic acid), poly(epsilon-caprolactone-CO-gly colic acid), poly(β -hydroxy butyric acid), polyethylene oxide, polyethylene, poly(alkyl-2-cyanoacrylate), poly(hydroxyethyl methacrylate), 50 polyamides, poly(amino acids), poly(2-hydroxyethyl DL-aspartamide), poly(ester urea), poly(L-phenylalanine/ethylene glycol/1,6-diisocyanatohexane) and poly(methyl methacrylate). Particularly preferred polymers are polyesters, such as polyglycolic acid, polylactic acid, glycolide-L(-) lactide poly(epsilon-caprolactone, poly(epsilon-caprolactone-CO-lactic acid), and poly(epsilon-caprolactone-CO-glycolic acid). Solvents useful for dissolving the polymer 55 and/or the active include: water, hexafluoroisopropanol, methylenechloride, tetrahydrofuran, hexane, benzene, or hexafluoroacetone sesquihydrate. The process of dispersing 60 65

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the active containing phase with a second phase may include pressure forcing said first phase through an orifice in a nozzle to affect droplet formation.

Dry powder formulations may result from processes other than lyophilization, such as by spray drying or solvent extraction by evaporation or by precipitation of a crystalline composition followed by one or more steps to remove aqueous or nonaqueous solvent. Preparation of a spray-dried protein scaffold preparation is taught in U.S. Pat. No. 6,019,968. The protein scaffold-based dry powder compositions may be produced by spray drying solutions or slurries of the protein scaffold and, optionally, excipients, in a solvent wider conditions to provide a respirable dry powder. Solvents may include polar compounds, such as water and ethanol, which may be readily dried. Protein scaffold stability may be enhanced by performing the spray drying procedures in the absence of oxygen, such as under a nitrogen blanket or by using nitrogen as the drying gas. Another relatively dry formulation is a dispersion of a plurality of perforated microstructures dispersed in a suspension medium that typically comprises a hydrofluoroalkane propellant as taught in WO 9916419. The stabilized dispersions may be administered to the lung of a patient using a metered dose inhaler. Equipment useful in the commercial manufacture of spray dried medicaments are manufactured by Buchi Ltd. or Niro Corp.

At least one protein scaffold in either the stable or preserved formulations or solutions described herein, can be administered to a patient in accordance with the present invention via a variety of delivery methods including SC or IM injection; transdermal, pulmonary, transmucosal, implant, osmotic pump, cartridge, micro pump, or other means appreciated by the skilled artisan, as well-known in the art.

Therapeutic Applications

The present invention also provides a method for modulating or treating a disease, in a cell, tissue, organ, animal, or patient, as known in the art or as described herein, using at least one protein scaffold of the present invention. e.g., administering or contacting the cell, tissue, organ, animal, or patient with a therapeutic effective amount of protein scaffold. The present invention also provides a method for modulating or treating a disease, in a cell, tissue, organ, animal, or patient.

Any method of the present invention can comprise administering an effective amount of a composition or pharmaceutical composition comprising at least one protein scaffold to a cell, tissue, organ, animal or patient in need of such modulation, treatment or therapy. Such a method can optionally further comprise co-administration or combination therapy for treating such diseases or disorders, wherein the administering of said at least one protein scaffold, specified portion or variant thereof, further comprises administering, before concurrently, and/or after, at least one selected from at least one of an alkylating agent, an mitotic inhibitor, and a radiopharmaceutical. Suitable dosages are well known in the art. See, e.g., Wells et al., eds., *Pharmacotherapy Handbook*, 2nd Edition, Appleton and Lange, Stamford, Conn. (2000); PDR *Pharmacopoeia*, Tarascon Pocket Pharmacopoeia 2000, Deluxe Edition. Tarascon Publishing, Loma Linda, Calif. (2000); *Nursing 2001 Handbook of Drugs*, 21st edition, Springhouse Corp., Springhouse, Pa., 2001; *Health Professional's Drug Guide 2001*, ed., Shannon, Wilson, Stang, Prentice-Hall, Inc, Upper Saddle River, N.J., each of which references are entirely incorporated herein by reference.

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Preferred doses can optionally include about 0.1-99 and/or 100-500 mg/kg/administration, or any range, value or fraction thereof, or to achieve a serum concentration of about 0.1-5000 µg/ml serum concentration per single or multiple administration, or any range, value or fraction thereof. A preferred dosage range for the protein scaffold of the present invention is from about 1 mg/kg, up to about 3, about 6 or about 12 mg/kg of body weight of the patient.

Alternatively, the dosage administered can vary depending upon known factors, such as the pharmacodynamic characteristics of the particular agent, and its mode and route of administration, age, health, and weight of the recipient; nature and extent of symptoms, kind of concurrent treatment, frequency of treatment, and the effect desired. Usually a dosage of active ingredient can be about 0.1 to 100 milligrams per kilogram of body weight. Ordinarily 0.1 to 50, and preferably, 0.1 to 10 milligrams per kilogram per administration or in sustained release form is effective to obtain desired results.

As a non-limiting example, treatment of humans or animals can be provided as a one-time or periodic dosage of at least one protein scaffold of the present invention about 0.1 to 100 mg/kg or any range, value or fraction thereof per day, on at least one of day 1-40, or, alternatively or additionally, at least one of week 1-52, or, alternatively or additionally, at least one of 1-20 years, or any combination thereof, using single, infusion or repeated doses.

Dosage forms (composition) suitable for internal administration generally contain from about 0.001 milligram to about 500 milligrams of active ingredient per unit or container. In these pharmaceutical compositions the active ingredient will ordinarily be present in an amount of about 0.5-99.99% by weight based on the total weight of the composition.

For parenteral administration, the protein scaffold can be formulated as a solution, suspension, emulsion, particle, powder, or lyophilized powder in association, or separately provided, with a pharmaceutically acceptable parenteral vehicle. Examples of such vehicles are water, saline, Ringer's solution, dextrose solution, and about 1-10% human serum albumin. Liposomes and nonaqueous vehicles, such as fixed oils, can also be used. The vehicle or lyophilized powder can contain additives that maintain isotonicity (e.g., sodium chloride, mannitol) and chemical stability (e.g., buffers and preservatives). The formulation is sterilized by known or suitable techniques.

Suitable pharmaceutical carriers are described in the most recent edition of Remington's *Pharmaceutical Sciences*, A. Osol, a standard reference text in this field.

Alternative Administration

Many known and developed modes can be used according to the present invention for administering pharmaceutically effective amounts of at least one protein scaffold according to the present invention. While pulmonary administration is used in the following description, other modes of administration can be used according to the present invention with suitable results. Protein scaffolds of the present invention can be delivered in a carrier, as a solution, emulsion, colloid, or suspension, or as a dry powder, using any of a variety of devices and methods suitable for administration by inhalation or other modes described here within or known in the art.

Parenteral Formulations and Administration

Formulations for parenteral administration can contain as common excipients sterile water or saline, polyalkylene glycols, such as polyethylene glycol, oils of vegetable origin, hydrogenated naphthalenes and the like. Aqueous or

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oily suspensions for injection can be prepared by using an appropriate emulsifier or humidifier and a suspending agent, according to known methods. Agents for injection can be a non-toxic, non-orally administrable diluting agent, such as aqueous solution, a sterile injectable solution or suspension in a solvent. As the usable vehicle or solvent, water, Ringer's solution, isotonic saline, etc. are allowed; as an ordinary solvent or suspending solvent, sterile involatile oil can be used. For these purposes, any kind of involatile oil and fatty acid can be used, including natural or synthetic or semisynthetic fatty oils or fatty acids; natural or synthetic or semi-synthetic mono- or di- or tri-glycerides. Parental administration is known in the art and includes, but is not limited to, conventional means of injections, a gas pressured needleless injection device as described in U.S. Pat. No. 5,851,198, and a laser perforator device as described in U.S. Pat. No. 5,839,446 entirely incorporated herein by reference.

Alternative Delivery

The invention further relates to the administration of at least one protein scaffold by parenteral, subcutaneous, intramuscular, intravenous, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitory, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intraretinal, intrarenal, intrarectal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravesical, intralesional, bolus, vaginal, rectal, buccal, sublingual, intranasal, or transdermal means. At least one protein scaffold composition can be prepared for use for parenteral (subcutaneous, intramuscular or intravenous) or any other administration particularly in the form of liquid solutions or suspensions; for use in vaginal or rectal administration particularly in semisolid forms, such as, but not limited to, creams and suppositories; for buccal, or sublingual administration, such as, but not limited to, in the form of tablets or capsules; or intranasally, such as, but not limited to, the form of powders, nasal drops or aerosols or certain agents; or transdermally, such as not limited to a gel, ointment, lotion, suspension or patch delivery system with chemical enhancers such as dimethyl sulfoxide to either modify the skin structure or to increase the drug concentration in the transdermal patch (Junginger, et al. In "Drug Permeation Enhancement;" Hsieh, D. S., Eds., pp. 59-90 (Marcel Dekker, Inc. New York 1994, entirely incorporated herein by reference), or with oxidizing agents that enable the application of formulations containing proteins and peptides onto the skin (WO 98/53847), or applications of electric fields to create transient transport pathways, such as electroporation, or to increase the mobility of charged drugs through the skin, such as iontophoresis, or application of ultrasound, such as sonophoresis (U.S. Pat. Nos. 4,309,989 and 4,767,402) (the above publications and patents being entirely incorporated herein by reference).

Infusion of Modified Cells as Adoptive Cell Therapy

The disclosure provides modified cells that express one or more CARs and/or CARTyrrins of the disclosure that have been selected and/or expanded for administration to a subject in need thereof. Modified cells of the disclosure may be formulated for storage at any temperature including room temperature and body temperature. Modified cells of the disclosure may be formulated for cryopreservation and subsequent thawing. Modified cells of the disclosure may be formulated in a pharmaceutically acceptable carrier for direct administration to a subject from sterile packaging. Modified cells of the disclosure may be formulated in a pharmaceutically acceptable carrier with an indicator of cell

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viability and/or CAR/CARTyrrin expression level to ensure a minimal level of cell function and CAR/CARTyrrin expression. Modified cells of the disclosure may be formulated in a pharmaceutically acceptable carrier at a prescribed density with one or more reagents to inhibit further expansion and/or prevent cell death.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises between 2×10^5 and 5×10^8 cells per kg of body weight of the patient per administration, or any range, value or fraction thereof.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises between 0.2×10^6 to 20×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 0.2×10^6 cells per kg of body weight of the patient per administration, 2×10^6 cells per kg of body weight of the patient per administration, 20×10^6 cells per kg of body weight of the patient per administration, or any cells per kg of body weight of the patient per administration in between.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 1×10^6 cells or about 1×10^6 cells per kg of body weight of the patient per administration.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 3×10^6 cells or about 3×10^6 cells per kg of body weight of the patient per administration.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises between 0.7×10^6 to 6.7×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 0.7×10^6 cells per kg of body weight of the patient per administration, 6.7×10^6 cells per kg of body weight of the patient per administration or any cells per kg of body weight of the patient per administration in between.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises between 0.7×10^6 to 16×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 0.7×10^6 cells per kg of body

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weight of the patient per administration, 2×10^6 cells per kg of body weight of the patient per administration, 6×10^6 cells per kg of body weight of the patient per administration, 10.7×10^6 cells per kg of body weight of the patient per administration, 16×10^6 cells per kg of body weight of the patient per administration or any cells per kg of body weight of the patient per administration in between.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 1.2×10^6 to 7.1×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 1.2×10^6 cells per kg of body weight of the patient per administration, 7.1×10^6 cells per kg of body weight of the patient per administration or any number of cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises between 2×10^6 to 3×10^6 cells per kg of body weight of the patient per administration.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 1106×10^6 to 2106×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 1106×10^6 cells per kg of body weight of the patient per administration, 2106×10^6 cells per kg of body weight of the patient per administration or any number of cells per kg of body weight of the patient per administration in between. In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 0.7×10^6 to 1.3×10^6 cells per kg of body weight of the patient per administration. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises 0.7×10^6 cells per kg of body weight of the patient per administration, 1.3×10^6 cells per kg of body weight of the patient per administration or any number of cells per kg of body weight of the patient per administration in between.

In certain embodiments of the disclosure, modified cells of the disclosure are delivered to a patient via injection or intravenous infusion. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises a single or multiple doses. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises a split dose. In certain embodiments, a therapeutically effective dose of a composition of the disclosure or of compositions comprising modified cells of the disclosure comprises an initial dose and a maintenance dose.

In certain embodiments of the disclosure, the modified cells are T cells and the T cells may be sorted according to

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T cell markers prior to either in vitro expansion or formulation with a pharmaceutically acceptable carrier. In some embodiments, modified T cells may be sorted on using CD8+ and/or CD4+ markers.

5 Inducible Proapoptotic Polypeptides

Inducible proapoptotic polypeptides of the disclosure are superior to existing inducible polypeptides because the inducible proapoptotic polypeptides of the disclosure are far less immunogenic. While inducible proapoptotic polypeptides of the disclosure are recombinant polypeptides, and, therefore, non-naturally occurring, the sequences that are recombined to produce the inducible proapoptotic polypeptides of the disclosure do not comprise non-human sequences that the host human immune system could recognize as "non-self" and, consequently, induce an immune response in the subject receiving an inducible proapoptotic polypeptide of the disclosure, a cell comprising the inducible proapoptotic polypeptide or a composition comprising the inducible proapoptotic polypeptide or the cell comprising the inducible proapoptotic polypeptide.

The disclosure provides inducible proapoptotic polypeptides comprising a ligand binding region, a linker, and a proapoptotic peptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In 10 certain embodiments, the non-human sequence comprises a restriction site. In certain embodiments, the proapoptotic peptide is a caspase polypeptide. In certain embodiments, the caspase polypeptide is a caspase 9 polypeptide. In certain 15 embodiments, the caspase 9 polypeptide is a truncated caspase 9 polypeptide. Inducible proapoptotic polypeptides of the disclosure may be non-naturally occurring.

Caspase polypeptides of the disclosure include, but are not limited to, caspase 1, caspase 2, caspase 3, caspase 4, caspase 5, caspase 6, caspase 7, caspase 8, caspase 9, caspase 10, caspase 11, caspase 12, and caspase 14. Caspase 25 polypeptides of the disclosure include, but are not limited to, those caspase polypeptides associated with apoptosis including caspase 2, caspase 3, caspase 6, caspase 7, caspase 8, caspase 9, and caspase 10. Caspase polypeptides of the disclosure include, but are not limited to, those caspase polypeptides that initiate apoptosis, including caspase 2, caspase 8, caspase 9, and caspase 10. Caspase polypeptides of the disclosure include, but are not limited to, those caspase polypeptides that execute apoptosis, including caspase 3, caspase 6, and caspase 7.

Caspase polypeptides of the disclosure may be encoded by an amino acid or a nucleic acid sequence having one or more modifications compared to a wild type amino acid or a nucleic acid sequence. The nucleic acid sequence encoding 30 a caspase polypeptide of the disclosure may be codon optimized. The one or more modifications to an amino acid and/or nucleic acid sequence of a caspase polypeptide of the disclosure may increase an interaction, a cross-linking, a cross-activation, or an activation of the caspase polypeptide 35 of the disclosure compared to a wild type amino acid or a nucleic acid sequence. Alternatively, or in addition, the one or more modifications to an amino acid and/or nucleic acid sequence of a caspase polypeptide of the disclosure may decrease the immunogenicity of the caspase poly peptide of the disclosure compared to a wild type amino acid or a nucleic acid sequence.

Caspase polypeptides of the disclosure may be truncated compared to a wild type caspase polypeptide. For example, a caspase polypeptide may be truncated to eliminate a 40 sequence encoding a Caspase Activation and Recruitment Domain (CARD) to eliminate or minimize the possibility of activating a local inflammatory response in addition to 45

initiating apoptosis in the cell comprising an inducible caspase polypeptide of the disclosure. The nucleic acid sequence encoding a caspase polypeptide of the disclosure may be spliced to form a variant amino acid sequence of the caspase polypeptide of the disclosure compared to a wild type caspase polypeptide. Caspase polypeptides of the disclosure may be encoded by recombinant and/or chimeric sequences. Recombinant and/or chimeric caspase polypeptides of the disclosure may include sequences from one or more different caspase polypeptides. Alternatively, or in addition, recombinant and/or chimeric caspase poly peptides of the disclosure may include sequences from one or more species (e.g. a human sequence and a non-human sequence). Caspase polypeptides of the disclosure may be non-naturally occurring.

The ligand binding region of an inducible proapoptotic polypeptide of the disclosure may include any polypeptide sequence that facilitates or promotes the dimerization of a first inducible proapoptotic polypeptide of the disclosure with a second inducible proapoptotic polypeptide of the disclosure, the dimerization of which activates or induces cross-linking of the proapoptotic polypeptides and initiation of apoptosis in the cell.

The ligand-binding ("dimerization") region may comprise any polypeptide or functional domain thereof that will allow for induction using an endogenous or non-naturally occurring ligand (i.e., and induction agent), for example, a non-naturally occurring synthetic ligand. The ligand-binding region may be internal or external to the cellular membrane, depending upon the nature of the inducible proapoptotic polypeptide and the choice of ligand (i.e. induction agent). A wide variety of ligand-binding polypeptides and functional domains thereof, including receptors, are known. Ligand-binding regions of the disclosure may include one or more sequences from a receptor. Of particular interest are ligand-binding regions for which ligands (for example, small organic ligands) are known or may be readily produced. These ligand-binding regions or receptors may include, but are not limited to, the FKBP_s and cyclophilin receptors, the steroid receptors, the tetracycline receptor, and the like, as well as "non-naturally occurring" receptors, which can be obtained from antibodies, particularly the heavy or light chain subunit, mutated sequences thereof, random amino acid sequences obtained by stochastic procedures, combinatorial syntheses, and the like. In certain embodiments, the ligand-binding region is selected from the group consisting of a FKBP ligand-binding region, a cyclophilin receptor ligand-binding region, a steroid receptor ligand-binding region, a cyclophilin receptors ligand-binding region, and a tetracycline receptor ligand-binding region.

The ligand-binding regions comprising one or more receptor domain(s) may be at least about 50 amino acids, and fewer than about 350 amino acids, usually fewer than 200 amino acids, either as the endogenous domain or truncated active portion thereof. The binding region may, for example, be small (<25 kDa, to allow efficient transfection in viral vectors), monomeric, nonimmunogenic, have synthetically accessible, cell permeable, nontoxic ligands that can be configured for dimerization.

The ligand-binding regions comprising one or more receptor domain(s) may be intracellular or extracellular depending upon the design of the inducible proapoptotic polypeptide and the availability of an appropriate ligand (i.e. induction agent). For hydrophobic ligands, the binding region can be on either side of the membrane, but for hydrophilic ligands, particularly protein ligands, the binding region will usually be external to the cell membrane, unless

there is a transport system for internalizing the ligand in a form in which it is available for binding. For an intracellular receptor, the inducible proapoptotic polypeptide or a transposon or vector comprising the inducible proapoptotic polypeptide may encode a signal peptide and transmembrane domain 5' or 3' of the receptor domain sequence or may have a lipid attachment signal sequence 5' of the receptor domain sequence. Where the receptor domain is between the signal peptide and the transmembrane domain, the receptor domain will be extracellular.

Antibodies and antibody subunits, e.g., heavy or light chain, particularly fragments, more particularly all or part of the variable region, or fusions of heavy and light chain to create high-affinity binding, can be used as a ligand binding region of the disclosure. Antibodies that are contemplated include ones that are an ectopically expressed human product, such as an extracellular domain that would not trigger an immune response and generally not expressed in the periphery (i.e., outside the CNS/brain area). Such examples, 15 include, but are not limited to low affinity nerve growth factor receptor (LNGFR), and embryonic surface proteins (i.e., carcinoembryonic antigen). Yet further, antibodies can be prepared against haptene molecules, which are physiologically acceptable, and the individual antibody subunits 20 screened for binding affinity. The cDNA encoding the sub-units can be isolated and modified by deletion of the constant region, portions of the variable region, mutagenesis of the variable region, or the like, to obtain a binding protein domain that has the appropriate affinity for the ligand. In this 25 way, almost any physiologically acceptable haptene compound can be employed as the ligand or to provide an epitope for the ligand. Instead of antibody units, endogenous receptors can be employed, where the binding region or domain is known and there is a useful or known ligand for 30 binding.

For multimerizing the receptor, the ligand for the ligand-binding region/receptor domains of the inducible proapoptotic polypeptides may be multimeric in the sense that the ligand can have at least two binding sites, with each of the 40 binding sites capable of binding to a ligand receptor region (i.e. a ligand having a first binding site capable of binding the ligand-binding region of a first inducible proapoptotic polypeptide and a second binding site capable of binding the ligand-binding region of a second inducible proapoptotic 45 polypeptide, wherein the ligand-binding regions of the first and the second inducible proapoptotic polypeptides are either identical or distinct). Thus, as used herein, the term "multimeric ligand binding region" refers to a ligand-binding region of an inducible proapoptotic polypeptide of the disclosure that binds to a multimeric ligand. Multimeric ligands of the disclosure include dimeric ligands. A dimeric ligand of the disclosure may have two binding sites capable of binding to the ligand receptor domain. In certain embodiments, multimeric ligands of the disclosure are a dimer or higher order oligomer, usually not greater than about tetrameric, of small synthetic organic molecules, the individual molecules typically being at least about 150 Da and less than about 5 kDa, usually less than about 3 kDa. A variety of pairs of synthetic ligands and receptors can be employed. For 50 example, in embodiments involving endogenous receptors, dimeric FK506 can be used with an FKBP12 receptor, dimerized cyclosporin A can be used with the cyclophilin receptor, dimerized estrogen with an estrogen receptor, dimerized glucocorticoids with a glucocorticoid receptor, dimerized tetracycline with the tetracycline receptor, 55 dimerized vitamin D with the vitamin D receptor, and the like. Alternatively higher orders of the ligands, e.g., trimeric

can be used. For embodiments involving non-naturally occurring receptors, e.g., antibody subunits, modified antibody subunits, single chain antibodies comprised of heavy and light chain variable regions in tandem, separated by a flexible linker, or modified receptors, and mutated sequences thereof, and the like, any of a large variety of compounds can be used. A significant characteristic of the units comprising a multimeric ligand of the disclosure is that each binding site is able to bind the receptor with high affinity, and preferably, that they are able to be dimerized chemically. Also, methods are available to balance the hydrophobicity/hydrophilicity of the ligands so that they are able to dissolve in serum at functional levels, yet diffuse across plasma membranes for most applications.

Activation of inducible proapoptotic polypeptides of the disclosure may be accomplished through, for example, chemically induced dimerization (CID) mediated by an induction agent to produce a conditionally controlled protein or polypeptide. Proapoptotic polypeptides of the disclosure not only inducible, but the induction of these polypeptides is also reversible, due to the degradation of the labile dimerizing agent or administration of a monomeric competitive inhibitor.

In certain embodiments, the ligand binding region comprises a FK506 binding protein 12 (FKBP12) polypeptide. In certain embodiments, the ligand binding region comprises a FKBP12 poly peptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V). In certain embodiments, in which the ligand binding region comprises a FKBP12 polypeptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V), the induction agent may comprise AP1903, a synthetic drug (CAS Index Name: 2-Piperidinecarboxylic acid, 1-[*(2S)*-1-oxo-2-(3,4,5-trimethoxyphenyl)butyl]-, 1,2-ethanediylbis[imino(2-oxo-2,1-ethanediyl)oxy-3,1-phenylene]([1 R)-3-(3,4-dimethoxy-phenyl)propylidene]ester, [2*S*-(R*)₂*R**[S*[S*(1(R*), 2R*)]]]-)(9CI) CAS Registry Number 195514-63-7; Molecular Formula: C78H98N4O20; Molecular Weight: 1411.65)). In certain embodiments, in which the ligand binding region comprises a FKBP12 polypeptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V), the induction agent may comprise AP20187 (CAS Registry Number: 195514-80-8 and Molecular Formula: C82H107N5O20). In certain embodiments, the induction agent is an AP20187 analog, such as, for example, AP1510. As used herein, the induction agents AP20187, AP1903 and AP1510 may be used interchangeably.

AP1903 API is manufactured by Alphora Research Inc, and AP1903 Drug Product for Injection is made by Formatech Inc. It is formulated as a 5 mg/mL solution of AP1903 in a 25% solution of the non-ionic solubilizer Solutol HS 15 (250 mg/mL, BASF). At room temperature, this formulation is a clear, slightly yellow solution. Upon refrigeration, this formulation undergoes a reversible phase transition, resulting in a milky solution. This phase transition is reversed upon re-warming to room temperature. The fill is 2.33 mL in a 3 mL glass vial (approximately 10 mg AP1903 for Injection total per vial). Upon determining a need to administer AP1903, patients may be, for example, administered a single fixed dose of AP1903 for Injection (0.4 mg/kg) via IV infusion over 2 hours, using a non-DEHP, non-ethylene oxide sterilized infusion set. The dose of AP1903 is calculated individually for all patients, and is not be recalculated unless body weight fluctuates by ≥10%. The calculated dose is diluted in 100 mL in 0.9% normal saline before infusion. In a previous Phase I study of AP1903, 24 healthy volunteers were treated with single doses of AP1903 for Injection at

dose levels of 0.01, 0.05, 0.1, 0.5 and 1.0 mg/kg infused IV over 2 hours. AP1903 plasma levels were directly proportional to dose, with mean Cmax values ranging from approximately 10-1275 ng/mL over the 0.01-1.0 mg/kg dose range. Following the initial infusion period, blood concentrations demonstrated a rapid distribution phase, with plasma levels reduced to approximately 18, 7, and 1% of maximal concentration at 0.5, 2 and 10 hours post-dose, respectively. AP1903 for Injection was shown to be safe and well tolerated at all dose levels and demonstrated a favorable pharmacokinetic profile. Iuliucci J D, et al., *J Clin Pharmacol.* 41: 870-9, 2001.

The fixed dose of AP1903 for injection used, for example, may be 0.4 mg/kg intravenously infused over 2 hours. The amount of AP1903 needed in vitro for effective signaling of cells is 10-100 nM (1600 Da MW). This equates to 16-160 µg/L or ~0.016-1.6 µg/kg (1.6-160 µg/kg). Doses up to 1 mg/kg were well-tolerated in the Phase I study of AP1903 described above. Therefore, 0.4 mg/kg may be a safe and effective dose of AP1903 for this Phase I study in combination with the therapeutic cells.

The amino acid and/or nucleic acid sequence encoding ligand binding of the disclosure may contain sequence one or more modifications compared to a wild type amino acid or nucleic acid sequence. For example, the amino acid and/or nucleic acid sequence encoding ligand binding region of the disclosure may be a codon-optimized sequence. The one or more modifications may increase the binding affinity of a ligand (e.g. an induction agent) for the ligand binding region of the disclosure compared to a wild type polypeptide. Alternatively, or in addition, the one or more modifications may decrease the immunogenicity of the ligand binding region of the disclosure compared to a wild type polypeptide. Ligand binding regions of the disclosure and/or induction agents of the disclosure may be non-naturally occurring.

Inducible proapoptotic polypeptides of the disclosure comprise a ligand binding region, a linker and a proapoptotic peptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, the non-human sequence comprises a restriction site. The linker may comprise any organic or inorganic material that permits, upon dimerization of the ligand binding region, interaction, cross-linking, cross-activation, or activation of the proapoptotic polypeptides such that the interaction or activation of the proapoptotic polypeptides initiates apoptosis in the cell. In certain embodiments, the linker is a polypeptide. In certain embodiments, the linker is a polypeptide comprising a G/S rich amino acid sequence (a "GS" linker). In certain embodiments, the linker is a polypeptide comprising the amino acid sequence GGGGS (SEQ ID NO: 17014). In preferred embodiments, the linker is a polypeptide and the nucleic acid encoding the poly peptide does not contain a restriction site for a restriction endonuclease. Linkers of the disclosure may be non-naturally occurring.

Inducible proapoptotic polypeptides of the disclosure may be expressed in a cell under the transcriptional regulation of any promoter capable of initiating and/or regulating the expression of an inducible proapoptotic polypeptide of the disclosure in that cell. The term "promoter" as used herein refers to a promoter that acts as the initial binding site for RNA polymerase to transcribe a gene. For example, inducible proapoptotic polypeptides of the disclosure may be expressed in a mammalian cell under the transcriptional regulation of any promoter capable of initiating and/or regulating the expression of an inducible proapoptotic poly-

peptide of the disclosure in a mammalian cell, including, but not limited to native, endogenous, exogenous, and heterologous promoters. Preferred mammalian cells include human cells. Thus, inducible proapoptotic polypeptides of the disclosure may be expressed in a human cell under the transcriptional regulation of any promoter capable of initiating and/or regulating the expression of an inducible proapoptotic polypeptide of the disclosure in a human cell, including, but not limited to, a human promoter or a viral promoter. Exemplary promoters for expression in human cells include, but are not limited to, a human cytomegalovirus (CMV) immediate early gene promoter, a SV40 early promoter, a Rous sarcoma virus long terminal repeat, β -actin promoter, a rat insulin promoter and a glyceraldehyde-3-phosphate dehydrogenase promoter, each of which may be used to obtain high-level expression of an inducible proapoptotic polypeptide of the disclosure. The use of other viral or mammalian cellular or bacterial phage promoters which are well known in the art to achieve expression of an inducible proapoptotic polypeptide of the disclosure is contemplated as well, provided that the levels of expression are sufficient for initiating apoptosis in a cell. By employing a promoter with well-known properties, the level and pattern of expression of the protein of interest following transfection or transformation can be optimized.

Selection of a promoter that is regulated in response to specific physiologic or synthetic signals can permit inducible expression of the inducible proapoptotic polypeptide of the disclosure. The ecdysone system (Invitrogen, Carlsbad, Calif.) is one such system. This system is designed to allow regulated expression of a gene of interest in mammalian cells. It consists of a tightly regulated expression mechanism that allows virtually no basal level expression of a transgene, but over 200-fold inducibility. The system is based on the heterodimeric ecdysone receptor of *Drosophila*, and when ecdysone or an analog such as muristerone A binds to the receptor, the receptor activates a promoter to turn on expression of the downstream transgene high levels of mRNA transcripts are attained. In this system, both monomers of the heterodimeric receptor are constitutively expressed from one vector, whereas the ecdysone-responsive promoter, which drives expression of the gene of interest, is on another plasmid. Engineering of this type of system into a vector of interest may therefore be useful. Another inducible system that may be useful is the Tet-OffTM or Tet-OnTM system (Clontech, Palo Alto, Calif.) originally developed by Gossen and Bujard (Gossen and Bujard, Proc. Natl. Acad. Sci. USA, 89:5547-5551, 1992; Gossen et al., Science, 268:1766-1769, 1995). This system also allows high levels of gene expression to be regulated in response to tetracycline or tetracycline derivatives such as doxycycline. In the Tet-OnTM system, gene expression is turned on in the presence of doxycycline, whereas in the Tet-OffTM system, gene expression is turned on in the absence of doxycycline. These systems are based on two regulatory elements derived from the tetracycline resistance operon of *E. coli*: the tetracycline operator sequence (to which the tetracycline repressor binds) and the tetracycline repressor protein. The gene of interest is cloned into a plasmid behind a promoter that has tetracycline-responsive elements present in it. A second plasmid contains a regulatory element called the tetracycline-controlled transactivator, which is composed, in the Tet-OffTM system, of the VP16 domain from the herpes simplex virus and the wild-type tetracycline repressor. Thus in the absence of doxycycline, transcription is constitutively on. In the Tet-OnTM system, the tetracycline repressor is not wild type and in the presence of doxycycline activates transcription.

For gene therapy vector production, the Tet-OffTM system may be used so that the producer cells could be grown in the presence of tetracycline or doxycycline and prevent expression of a potentially toxic transgene, but when the vector is introduced to the patient, the gene expression would be constitutively on.

In some circumstances, it is desirable to regulate expression of a transgene in a gene therapy vector. For example, different viral promoters with varying strengths of activity are utilized depending on the level of expression desired. In mammalian cells, the CMV immediate early promoter is often used to provide strong transcriptional activation. The CMV promoter is reviewed in Donnelly, J. J., et al., 1997. Annu. Rev. Immunol. 15:617-48. Modified versions of the CMV promoter that are less potent have also been used when reduced levels of expression of the transgene are desired. When expression of a transgene in hematopoietic cells is desired, retroviral promoters such as the LTRs from MLV or MMTV are often used. Other viral promoters that are used depending on the desired effect include SV40, RSV LTR, HIV-1 and HIV-2 LTR, adenovirus promoters such as from the E1A, E2A, or MLP region, AAV LTR, HSV-TK, and avian sarcoma virus.

In other examples, promoters may be selected that are developmentally regulated and are active in particular differentiated cells. Thus, for example, a promoter may not be active in a pluripotent stem cell, but, for example, where the pluripotent stem cell differentiates into a more mature cell, the promoter may then be activated.

Similarly tissue specific promoters are used to effect transcription in specific tissues or cells so as to reduce potential toxicity or undesirable effects to non-targeted tissues. These promoters may result in reduced expression compared to a stronger promoter such as the CMV promoter, but may also result in more limited expression, and immunogenicity (Bojak, A., et al., 2002. Vaccine. 20:1975-79; Cazeaux, N., et al., 2002. Vaccine 20:3322-31). For example, tissue specific promoters such as the PSA associated promoter or prostate-specific glandular kallikrein, or the muscle creatine kinase gene may be used where appropriate.

Examples of tissue specific or differentiation specific promoters include, but are not limited to, the following: B29 (B cells); CD14 (monocytic cells); CD43 (leukocytes and platelets); CD45 (hematopoietic cells); CD68 (macrophages); desmin (muscle); elastase-1 (pancreatic acinar cells); endoglin (endothelial cells); fibronectin (differentiating cells, healing tissues); and Flt-1 (endothelial cells); GFAP (astrocytes).

In certain indications, it is desirable to activate transcription at specific times after administration of the gene therapy vector. This is done with such promoters as those that are hormone or cytokine regulatable Cytokine and inflammatory protein responsive promoters that can be used include K and T kininogen (Kageyama et al., (1987) J. Biol. Chem., 262, 2345-2351), c-fos, TNF-alpha, C-reactive protein (Arcone, et al., (1988) Nucl. Acids Res., 16(8), 3195-3207), haptoglobin (Oliviero et al., (1987) EMBO J., 6, 1905-1912), serum amyloid A2, C/EBP alpha, IL-1, IL-6 (Poli and Cortese. (1989) Proc. Nat'l Acad. Sci. USA, 86, 8202-8206), Complement C3 (Wilson et al., (1990) Mol. Cell. Biol., 6181-6191), IL-8, alpha-1 acid glycoprotein (Prowse and Baumann. (1988) Mol Cell Biol, 8, 42-51), alpha-1 antitrypsin, lipoprotein lipase (Zechner et al., Mol. Cell. Biol., 2394-2401, 1988), angiotensinogen (Ron, et al., (1991) Mol. Cell. Biol., 2887-2895), fibrinogen, c-jun (inducible by phorbol esters, TNF-alpha, UV radiation, retinoic acid, and

hydrogen peroxide), collagenase (induced by phorbol esters and retinoic acid), metallothionein (heavy metal and glucocorticoid inducible), Stromelysin (inducible by phorbol ester, interleukin-1 and EGF), alpha-2 macroglobulin and alpha-1 anti-chymotrypsin. Other promoters include, for example, SV40, MMTV, Human Immunodeficiency Virus (MV), Moloney virus, ALV, Epstein Barr virus, Rous Sarcoma virus, human actin, myosin, hemoglobin, and creatine.

It is envisioned that any of the above promoters alone or in combination with another can be useful depending on the action desired. Promoters, and other regulatory elements, are selected such that they are functional in the desired cells or tissue. In addition, this list of promoters should not be construed to be exhaustive or limiting; other promoters that are used in conjunction with the promoters and methods disclosed herein.

Armored T-Cells “Knock Down” Strategy

T-cells of the disclosure may be genetically modified to enhance their therapeutic potential. Alternatively, or in addition, T-cells of the disclosure may be modified to render them less sensitive to immunologic and/or metabolic checkpoints. Modifications of this type “armor” the T cells of the disclosure, which, following the modification, may be referred to here as “armored” T cells. Armored T cells of the disclosure may be produced by, for example, blocking and/or diluting specific endogenous checkpoint signals delivered to the T-cells (i.e. checkpoint inhibition) within the tumor immunosuppressive microenvironment, for example.

In some embodiments, an armored T-cell of the disclosure is derived from a T cell, a NK cell, a hematopoietic progenitor cell, a peripheral blood (PB) derived T cell (including a T cell isolated or derived from G-CSF-mobilized peripheral blood), or an umbilical cord blood (UCB) derived T cell. In some embodiments, an armored T-cell of the disclosure comprises one or more of a chimeric ligand receptor (CLR comprising a protein scaffold, an antibody, an ScFv, or an antibody mimetic)/chimeric antigen receptor (CAR comprising a protein scaffold, an antibody, an ScFv, or an antibody mimetic), a CARTyrrin (a CAR comprising a Centryrrin), and/or a VCAR (a CAR comprising a camelid VHH or a single domain VH) of the disclosure. In some embodiments, an armored T-cell of the disclosure comprises an inducible proapoptotic polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 poly peptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In

some embodiments, the non-human sequence is a restriction site. In some embodiments, the ligand binding region inducible caspase polypeptide comprises a FK506 binding protein 12 (FKBP12) polypeptide. In some embodiments, the amino acid sequence of the FK506 binding protein 12 (FKBP12) polypeptide comprises a modification at position 36 of the sequence. In some embodiments, the modification is a substitution of valine (V) for phenylalanine (F) at position 36 (F36V). In some embodiments, an armored T-cell of the disclosure comprises an exogenous sequence. In some embodiments, the exogenous sequence comprises a sequence encoding a therapeutic protein. Exemplary therapeutic proteins may be nuclear, cytoplasmic, intracellular, transmembrane, cell-surface bound, or secreted proteins. Exemplary therapeutic proteins expressed by the armored T cell may modify an activity of the armored T cell or may modify an activity of a second cell. In some embodiments, an armored T-cell of the disclosure comprises a selection gene or a selection marker. In some embodiments, an armored T-cell of the disclosure comprises a synthetic gene expression cassette (also referred to herein as an inducible transgene construct).

In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression one or more gene(s) encoding receptor(s) of inhibitory checkpoint signals to produce an armored T-cell of the disclosure. Examples of inhibitory checkpoint signals include, but are not limited to, a PD-L1 ligand binding to a PD-1 receptor on a CAR-T cell of the disclosure or a TGF β cytokine binding to a TGF β RII receptor on a CAR-T cell. Receptors of inhibitory checkpoint signals are expressed on the cell surface or within the cytoplasm of a T-cell. Silencing or reducing expressing of the gene encoding the receptor of the inhibitory checkpoint signal results a loss of protein expression of the inhibitory checkpoint receptors on the surface or within the cytoplasm of an armored T-cell of the disclosure. Thus, armored T cells of the disclosure having silenced or reduced expression of one or more genes encoding an inhibitory checkpoint receptor is resistant, non-receptive or insensitive to checkpoint signals. The armored T cell's resistance or decreased sensitivity to inhibitory checkpoint signals enhances the armored T cell's therapeutic potential in the presence of these inhibitory checkpoint signals. Inhibitory checkpoint signals include but are not limited to the examples listed in Table 2. Exemplary inhibitory checkpoint signals that may be silenced in an armored T cell of the disclosure include, but are not limited to, PD-1 and TGF β RII.

TABLE 2

Exemplary Inhibitory Checkpoint Signals (and proteins that induce immunosuppression).		
Full Name	Abbreviation	SEQ ID NO:
Programmed cell death protein 1	PD1	14643-14644
transforming growth factor β Receptor 1	TGF β R1	14645
transforming growth factor β Receptor 2	TGF β R2	14646
T-cell immunoglobulin and mucin-domain containing-3	TIM3	14647
Lymphocyte-activation gene 3	LAG3	14648
Cytotoxic T-lymphocyte protein 4	CTLA4	14649
B- and T-lymphocyte attenuator	BT LA	14650
Killer cell immunoglobulin-like receptor	KIR	14651
Alpha-2A adrenergic receptor	A2aR	14652
V-type immunoglobulin domain-containing suppressor of T-cell activation	VISTA	14653
T-cell immunoreceptor with Ig and ITIM domains	TIGIT	14654
Programmed cell death 1 ligand 1	B7H1 or PD-L1	14655
Programmed cell death 1 ligand 2	B7DC or PD-L2	14656

TABLE 2-continued

Exemplary Inhibitory Checkpoint Signals (and proteins that induce immunosuppression).		
Full Name	Abbreviation	SEQ ID NO:
T-lymphocyte activation antigen CD80	B7-1 or CD80	14657
T-lymphocyte activation antigen CD86	B7-2 or CD86	14658
CD160 antigen	CD160	14659
Leukocyte-associated immunoglobulin-like receptor 1	LAIR1	14660
T-cell immunoglobulin and mucin domain-containing protein 4	TIM4 or TIMD4	14661
Natural killer cell receptor 2B4	2B4 or CD244	14662
Major Histocompatibility Complex type I	MHC I	14663
Major Histocompatibility Complex type II	MHC II	
Putative 2-methylcitrate dehydratase receptor	PDH1R	
T-cell immunoglobulin and mucin domain 1 receptor	TIM1R	
T-cell immunoglobulin and mucin domain 4 receptor	TIM4R	
B7-H3 receptor	B7H3R or CD176 Receptor	
B7-H4 receptor	B7H4R	
Immunoglobulin-like transcript (ILT) 3 receptor	ILT3R	
phosphoinositide 3-kinase, subunit alpha	PI3K alpha	14664
phosphoinositide 3-kinase, subunit gamma	PI3K gamma	14665
Tyrosine-protein phosphatase non-receptor type 11	SHP2 or PTPN11	14666
Protein phosphatase 2, subunit gamma	PP2A gamma	14667
Protein phosphatase 2, subunit beta	PP2A beta	14668
Protein phosphatase 2, subunit delta	PP2A delta	14669
Protein phosphatase 2, subunit epsilon	PP2A epsilon	14670
Protein phosphatase 2, subunit alpha	PP2A alpha	14671
T-cell Receptor, subunit alpha	TCR alpha	14672
T-cell Receptor, subunit beta	TCR beta	14673
T-cell Receptor, subunit zeta	TCR zeta	14674
T-cell Receptor, subunit CD3 epsilon	TCR CD3 epsilon	14675
T-cell Receptor, subunit CD3 gamma	TCR CD3 gamma	14676
T-cell Receptor, subunit CD3 delta	TCR CD3 delta	14677
Cluster of Differentiation 28	CD28	14678
Galectins	Galectins	
Galectin 9	Galectin 9	14679
High Mobility Group Box 1	HMGB1	14680
Arginase 1	ARG1	14681
Prostaglandin-Endoperoxide Synthase 1	PTGS1	14682
Prostaglandin-Endoperoxide Synthase 2	PTGS2	14683
Mucin 1, Cell Surface Associated	MUC1	14684
Mucin 2, Oligomeric Mucus/Gel-Forming	MUC2	14685
Mucin 3A, Cell Surface Associated	MUC3A	14686
Mucin 3B, Cell Surface Associated	MUC3B	14687
Mucin 4, Cell Surface Associated	MUC4	14688
Mucin 5AC, Oligomeric Mucus/Gel-Forming	MUC5AC	14689
Mucin 5B, Oligomeric Mucus/Gel-Forming	MUC5B	14690
Mucin 6, Oligomeric Mucus/Gel-Forming	MUC6	14691
Mucin 7, Secreted	MUC7	14692
Mucin 8	MUC8	
Mucin 12, Cell Surface Associated	MUC12	14693
Mucin 13, Cell Surface Associated	MUC13	14694
Mucin 15, Cell Surface Associated	MUC15	14695
Mucin 16, Cell Surface Associated	MUC16	14696
Mucin 17, Cell Surface Associated	MUC17	14697
Mucin 19, Oligomeric	MUC19	14698
Mucin 20, Cell Surface Associated	MUC20	14699
Mucin 21, Cell Surface Associated	MUC21	14700
Mucin 22	MUC22	14701
Indoleamine 2,3-Dioxygenase 1	IDO1	14702
Indoleamine 2,3-Dioxygenase 2	IDO2	14703
Inducible T Cell Costimulator Ligand	ICOSLG	14704
ROS Proto-Oncogene 1, Receptor Tyrosine Kinase	ROS1	14705
Tumor Necrosis Factor Receptor Superfamily Member 9	4-1BB, CD137, ILA or TNFRSF9	14706
4-1BB Ligand	4-1BB-L	14707
Glucocorticoid-induced TNFR family related gene	GITR	14708
Glucocorticoid-induced TNFR family related gene ligand	GITRL	14709

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In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding intracellular proteins involved in checkpoint signaling to produce an armored T-cell of the disclosure. The activity of a T-cell of the disclosure may be enhanced by targeting any intracellular signaling protein involved in a

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checkpoint signaling pathway thereby achieving checkpoint inhibition or interference to one or more checkpoint pathways. Intracellular signaling proteins involved in checkpoint signaling include, but are not limited to, exemplary intracellular signaling proteins listed in Table 3.

TABLE 3

Exemplary Intracellular Signaling Proteins.		
Full Name	Abbreviation	SEQ ID NO:
phosphoinositide 3-kinase, subunit alpha	PI3K alpha	14710
phosphoinositide 3-kinase, subunit gamma	PI3K gamma	14711
Tyrosine-protein phosphatase non-receptor type 11	SHP2 or PTPN11	14712
Protein phosphatase 2, subunit gamma	PP2A gamma	14713
Protein phosphatase 2, subunit beta	PP2A beta	14714
Protein phosphatase 2, subunit delta	PP2A delta	14715
Protein phosphatase 2, subunit epsilon	PP2A epsilon	14716
Protein phosphatase 2, subunit alpha	PP2A alpha	14717
RAC-alpha serine/threonine-protein kinase	AKT or PKB	14718
Tyrosine-protein kinase ZAP-70	ZAP70	14719
Amino acid sequence (KIEELE)-containing domain protein	KIEELE-domain containing proteins	
BCL2 associated athanogene 6	Bat3, Bag6 or Scythe	14720
B-cell lymphoma-extra large	Bcl-xL	14721
Bcl-2-related protein A1	Bfl-1 or BCL2A1	14722

In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding a transcription factor that hinders the efficacy of a therapy to produce an armored T-cell of the disclosure. The activity of armored T-cells may be enhanced or modulated by silencing or reducing expression (or repressing a function) of a transcription factor that hinders the efficacy of therapy. Exemplary transcription factors that may be modified to silence or reduce expression or to repress a function thereof include, but are not limited to the exemplary transcription factors listed in Table 4. For example expression of a FOXP3 gene may be silenced or reduced in an armored T cell of the disclosure to prevent or reduce the formation of T regulatory CAR-T-cells (CAR-Treg cells), the expression or activity of which may reduce efficacy of a therapy.

TABLE 4

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
activity-dependent neuroprotector homeobox	ADNP	14723
ADNP homeobox 2	ADNP2	14724
AE binding protein 1	AEBP1	14725
AE binding protein 2	AEBP2	14726
AF4/FMR2 family member 1	AFF1	14727
AF4/FMR2 family member 2	AFF2	14728
AF4/FMR2 family member 3	AFF3	14729
AF4/FMR2 family member 4	AFF4	14730
AT-hook containing transcription factor 1	AHCTF1	14731
aryl hydrocarbon receptor	AHR	14732
aryl-hydrocarbon receptor repressor	AHRR	14733
autoimmune regulator	AIRE	14734
AT-hook transcription factor	AKNA	14735
ALX homeobox 1	ALX1	14736
ALX homeobox 3	ALX3	14737
ALX homeobox 4	ALX4	14738
ankyrin repeat and zinc finger domain containing 1	ANKZF1	14739
adaptor related protein complex 5 zeta 1 subunit	AP5Z1	14740
androgen receptor	AR	14741
arginine-fifty homeobox	ARGFX	14742
Rho GTPase activating protein 35	ARHGAP35	14743
AT-rich interaction domain 1A	ARID1A	14744
AT-rich interaction domain 1B	ARID1B	14745
AT-rich interaction domain 2	ARID2	14746

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
AT-rich interaction domain 3A	ARID3A	14747
AT-rich interaction domain 3B	ARID3B	14748
AT-rich interaction domain 3C	ARID3C	14749
AT-rich interaction domain 4A	ARID4A	14750
AT-rich interaction domain 4B	ARID4B	14751
AT-rich interaction domain 5A	ARID5A	14752
AT-rich interaction domain 5B	ARID5B	14753
aryl hydrocarbon receptor nuclear translocator	ARNT	14754
aryl hydrocarbon receptor nuclear translocator 2	ARNT2	14755
aryl hydrocarbon receptor nuclear translocator like	ARNTL	14756
aryl hydrocarbon receptor nuclear translocator like 2	ARNTL2	14757
aristaless related homeobox	ARX	14758
achaete-scute family bHLH transcription factor 1	ASCL1	14759
achaete-scute family bHLH transcription factor 2	ASCL2	14760
achaete-scute family bHLH transcription factor 3	ASCL3	14761
achaete-scute family bHLH transcription factor 4	ASCL4	14762
achaete-scute family bHLH transcription factor 5	ASCL5	14763
ash1 (absent, small, or homeotic)-like (<i>Drosophila</i>)	ASH1L	14764
ash2 (absent, small, or homeotic)-like (<i>Drosophila</i>)	ASH2L	14765
activating transcription factor 1	ATF1	14766
activating transcription factor 2	ATF2	14767
activating transcription factor 3	ATF3	14768
activating transcription factor 4	ATF4	14769
activating transcription factor 5	ATF5	14770
activating transcription factor 6	ATF6	14771
activating transcription factor 6 beta	ATF6B	14772
activating transcription factor 7	ATF7	14773
atonal bHLH transcription factor 1	ATOH1	14774
atonal bHLH transcription factor 7	ATOH7	14775
atonal bHLH transcription factor 8	ATOH8	14776
alpha thalassemia/mental retardation syndrome X-linked	ATRX	14777
ataxin 7	ATXN7	14778
BTB and CNC homology 1, basic leucine zipper transcription factor1	BACH1	14779-14780
BTB domain and CNC homolog 2	BACH2	14781
BarH like homeobox 1	BARHL1	14782
BarH like homeobox 2	BARHL2	14783
BARX homeobox 1	BARX1	14784
BARX homeobox 2	BARX2	14785
Basic Leucine Zipper ATF-Like Transcription Factor, basic leucine zipper transcription factor, ATF-like	Batf	14786
basic leucine zipper transcription factor, ATF-like 2	BATF	14786
basic leucine zipper transcription factor, ATF-like 2	BATF2	14787
basic leucine zipper transcription factor, ATF-like 3	BATF3	14788
bobby sox homolog (<i>Drosophila</i>)	BBX	14789
B-cell CLL/lymphoma 11A	BCL11A	14790
B-cell CLL/lymphoma 11B	BCL11B	14791
B-cell CLL/lymphoma 3	BCL3	14792
B-cell CLL/lymphoma 6	BCL6	14793
B-cell CLL/lymphoma 6, member B	BCL6B	14794
BCL2 associated transcription factor 1	BCLAF1	14795
basic helix-loop-helix family member a15	BHLHA15	14796
basic helix-loop-helix family member a9	BHLHA9	14797
basic helix-loop-helix domain containing, class B, 9	BHLHB9	14798
basic helix-loop-helix family member e22	BHLHE22	14799
basic helix-loop-helix family member e23	BHLHE23	14800
basic helix-loop-helix family member e40	BHLHE40	14801
basic helix-loop-helix family member e41	BHLHE41	14802
Beta-Interferon Gene Positive-Regulatory Domain I	Blimp-1	14803
Binding Factor		
bone morphogenetic protein 2	BMP2	14804
basonuclin 1	BNC1	14805
basonuclin 2	BNC2	14806
bolA family member 1	BOLA1	14807
bolA family member 2	BOLA2	14808
bolA family member 3	BOLA3	14809
bromodomain PHD finger transcription factor	BPTF	14810
breast cancer 1	BRCA1	14811
brain specific homeobox	BSX	14812
chromosome 20 open reading frame 194	C20orf194	14813
calmodulin binding transcription activator 1	CAMTA1	14814
calmodulin binding transcription activator 2	CAMTA2	14815
calcium regulated heat stable protein 1	CARHSP1	14816
castor zinc finger 1	CASZ1	14817
core-binding factor, beta subunit	CBFB	14818
coiled-coil domain containing 79	CCDC79	14819

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
cell division cycle 5 like	CDC5L	14820
caudal type homeobox 1	CDX1	14821
caudal type homeobox 2	CDX2	14822
caudal type homeobox 4	CDX4	14823
CCAAT/enhancer binding protein alpha	CEBPA	14824
CCAAT/enhancer binding protein beta	CEBPB	14825
CCAAT/enhancer binding protein delta	CEBD	14826
CCAAT/enhancer binding protein epsilon	CEBPE	14827
CCAAT/enhancer binding protein gamma	CEBPG	14828
CCAAT/enhancer binding protein zeta	CEBPZ	14829
centromere protein T	CENPT	14830
ceramide synthase 3	CERS3	14831
ceramide synthase 6	CERS6	14832
chromosome alignment maintaining phosphoprotein 1	CHAMP1	14833
capicua transcriptional repressor	CIC	14834
CDKN1A interacting zinc finger protein 1	CIZ1	14835
clock circadian regulator	CLOCK	14836
CCR4-NOT transcription complex subunit 4	CNOT4	14837
CPX chromosome region, candidate 1	CPXCR1	14838
cramped chromatin regulator homolog 1	CRAMP1	14839
cAMP responsive element binding protein 1	CREB1	14840
cAMP responsive element binding protein 3	CREB3	14841
cAMP responsive element binding protein 3-like 1	CREB3L1	14842
cAMP responsive element binding protein 3-like 2	CREB3L2	14843
cAMP responsive element binding protein 3-like 3	CREB3L3	14844
cAMP responsive element binding protein 3-like 4	CREB3L4	14845
cAMP responsive element binding protein 5	CREB5	14846
CREB binding protein	CREBBP	14847
cAMP responsive element binding protein-like 2	CREBL2	14848
CREB3 regulatory factor	CREBRF	14849
CREB/ATF bZIP transcription factor	CREBF	14850
cAMP responsive element modulator	CREM	14851
cone-rod homeobox	CRX	14852
cysteine-serine-rich nuclear protein 1	CSRNP1	14853
cysteine-serine-rich nuclear protein 2	CSRNP2	14854
cysteine-serine-rich nuclear protein 3	CSRNP3	14855
CCCTC-binding factor (zinc finger protein)	CTCF	14856
CCCTC-binding factor like	CTCFL	14857
cut-like homeobox 1	CUX1	14858-14859
cut-like homeobox 2	CUX2	14860
CXXC finger protein 1	CXXC1	14861
dachshund family transcription factor 1	DACH1	14862
dachshund family transcription factor 2	DACH2	14863
D site of albumin promoter (albumin D-box) binding protein	DBP	14864
developing brain homeobox 1	DBX1	14865
developing brain homeobox 2	DBX2	14866
damage specific DNA binding protein 2	DDD2	14867
DNA damage inducible transcript 3	DDIT3	14868
DEAF1, transcription factor	DEAF1	14869
distal-less homeobox 1	DLX1	14870
distal-less homeobox 2	DLX2	14871
distal-less homeobox 3	DLX3	14872
distal-less homeobox 4	DLX4	14873
distal-less homeobox 5	DLX5	14874
distal-less homeobox 6	DLX6	14875
DNA methyltransferase 1 associated protein 1	DMAP1	14876
diencephalon/mesencephalon homeobox 1	DMBX1	14877
doublesex and mab-3 related transcription factor 1	DMRT1	14878
doublesex and mab-3 related transcription factor 2	DMRT2	14879
doublesex and mab-3 related transcription factor 3	DMRT3	14880
DMRT like family A1	DMRTA1	14881
DMRT like family A2	DMRTA2	14882
DMRT like family B with proline rich C-terminal 1	DMRTB1	14883
DMRT like family C1	DMRTC1	14884
DMRT like family C1B	DMRTC1B	14884
DMRT like family C2	DMRTC2	14885
cyclin D binding myb like transcription factor 1	DMTF1	14886
DnaJ heat shock protein family (Hsp40) member C1	DNAJC1	14887
DnaJ heat shock protein family (Hsp40) member C2	DNAJC2	14888
DnaJ heat shock protein family (Hsp40) member C21	DNAJC21	14889
DNA (cytosine-5')-methyltransferase 1	DNMT1	14890
DNA (cytosine-5')-methyltransferase 3 alpha	DNMT3A	14891
DNA (cytosine-5')-methyltransferase 3 beta	DNMT3B	14892
DNA (cytosine-5')-methyltransferase 3-like	DNMT3L	14893
double PHD fingers 1	DPF1	14894

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
double PHD fingers 2	DPF2	14895
double PHD fingers 3	DPF3	14896
divergent-paired related homeobox	DPRX	14897
down-regulator of transcription 1	DR1	14898
DR1 associated protein 1	DRAP1	14899
dorsal root ganglia homeobox	DRGX	14900
double homeobox 4	DUX4	14901
double homeobox 4 like 9	DUX4L9	14902
double homeobox A	DUXA	14903
E2F transcription factor 1	E2F1	14904
E2F transcription factor 2	E2F2	14905
E2F transcription factor 3	E2F3	14906
E2F transcription factor 4	E2F4	14907
E2F transcription factor 5	E2F5	14908
E2F transcription factor 6	E2F6	14909
E2F transcription factor 7	E2F7	14910
E2F transcription factor 8	E2F8	14911
E4F transcription factor 1	E4F1	14912
early B-cell factor 1	EBF1	14913
early B-cell factor 2	EBF2	14914
early B-cell factor 3	EBF3	14915
early B-cell factor 4	EBF4	14916
early growth response 1	EGR1	14917
early growth response 2	EGR2	14918
early growth response 3	EGR3	14919
early growth response 4	EGR4	14920
ets homologous factor	EHF	14921
E74-like factor 1 (ets domain transcription factor)	ELF1	14922
E74-like factor 2 (ets domain transcription factor)	ELF2	14923
E74-like factor 3 (ets domain transcription factor, epithelial-specific)	ELF3	14924
E74-like factor 4 (ets domain transcription factor)	ELF4	14925
E74-like factor 5 (ets domain transcription factor)	ELF5	14926
ELK1, member of ETS oncogene family	ELK1	14927
ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	14928
ELK4, ETS-domain protein (SRF accessory protein 1)	ELKA	14929
ELM2 and Myb/SANT-like domain containing 1	ELMSAN1	14930
empty spiracles homeobox 1	EMX1	14931
empty spiracles homeobox 2	EMX2	14932
engrailed homeobox 1	EN1	14933
engrailed homeobox 2	EN2	14934
enolase 1, (alpha)	ENO1	14935
comesoderm	EOMES	14936
endothelial PAS domain protein 1	EPAS1	14937
Ets2 repressor factor	ERF	14938
v-ets avian erythroblastosis virus E26 oncogene homolog	ERG	14939-14940
estrogen receptor 1	ESR1	14941
estrogen receptor 2 (ER beta)	ESR2	14942
estrogen related receptor alpha	ESERRA	14943
estrogen related receptor beta	ESRRB	14944
estrogen related receptor gamma	ESRRG	14945
ESX homeobox 1	ESX1	14946
v-ets avian erythroblastosis virus E26 oncogene homolog 1	ETS1	14947
v-ets avian erythroblastosis virus E26 oncogene homolog 2	ETS2	14948
ets variant 1	ETV1	14949
ets variant 2	ETV2	14950
ets variant 3	ETV3	14951
ets variant 3-like	ETV3L	14952
ets variant 4	ETV4	14953
ets variant 5	ETV5	14954
ets variant 6	ETV6	14955
ets variant 7	ETV7	14956
even-skipped homeobox 1	EVX1	14957
even-skipped homeobox 2	EVX2	14958
enhancer of zeste 1 polycomb repressive complex 2 subunit	EZH1	14959
enhancer of zeste 2 polycomb repressive complex 2 subunit	EZH2	14960
family with sequence similarity 170 member A	FAM170A	14961
Fer3-like bHLH transcription factor	FERD3L	14962
FEV (ETS oncogene family)	FEV	14963
FEZ family zinc finger 1	FEZF1	14964
FEZ family zinc finger 2	FEZF2	14965

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
folliculogenesis specific bHLH transcription factor	FIGLA	14966
FLT3-interacting zinc finger 1	FIZ1	14967
Fli-1 proto-oncogene, ETS transcription factor	FLI1	14968
FBF murine osteosarcoma viral oncogene homolog	FOS	14969
FBF murine osteosarcoma viral oncogene homolog B	FOSB	14970
FOS like antigen 1	FOSL1	14971
FOS like antigen 2	FOSL2	14972
forkhead box A1	FOXA1	14973
forkhead box A2	FOXA2	14974
forkhead box A3	FOXA3	14975
forkhead box B1	FOXB1	14976
forkhead box B2	FOXB2	14977
forkhead box C1	FOXC1	14978
forkhead box C2	FOXC2	14979
forkhead box D1	FOXD1	14980
forkhead box D2	FOXD2	14981
forkhead box D3	FOXD3	14982
forkhead box D4	FOXD4	14983
forkhead box D4-like 1	FOXD4L1	14984
forkhead box D4-like 3	FOXD4L3	14985
forkhead box D4-like 4	FOXD4L4	14986
forkhead box D4-like 5	FOXD4L5	14987
forkhead box D4-like 6	FOXD4L6	14988
forkhead box E1	FOXE1	14989
forkhead box E3	FOXE3	14990
forkhead box F1	FOXF1	14991
forkhead box F2	FOXF2	14992
forkhead box G1	FOXG1	14993
forkhead box H1	FOXH1	14994
forkhead box I1	FOXI1	14995
forkhead box I2	FOXI2	14996
forkhead box I3	FOXI3	14997
forkhead box J1	FOXJ1	14998
forkhead box J2	FOXJ2	14999
forkhead box J3	FOXJ3	15000
forkhead box K1	FOXK1	15001
forkhead box K2	FOXK2	15002
forkhead box L1	FOXL1	15003
forkhead box L2	FOXL2	15004
forkhead box M1	FOXM1	15005
forkhead box N1	FOXN1	15006
forkhead box N2	FOXN2	15007
forkhead box N3	FOXN3	15008
forkhead box N4	FOXN4	15009
forkhead box O1	FOXO1	15010
forkhead box O3	FOXO3	15011
forkhead box O4	FOXO4	15012
forkhead box O6	FOXO6	15013
forkhead box P1	FOXP1	15014
forkhead box P2	FOXP3	15015
forkhead box P3	FOXP4	15016
forkhead box P4	FOXQ1	15017
forkhead box Q1	FOXR1	15018
forkhead box R1	FOXR2	15019
forkhead box R2	FOXS1	15020
forkhead box S1	FOXP3	15021
far upstream element binding protein 1	FUBP1	15022
far upstream element (FUSE) binding protein 3	FUBP3	15023
GA binding protein transcription factor alpha subunit	GABPA	15024
GA binding protein transcription factor, beta subunit 1	GABPB1	15025
GA binding protein transcription factor, beta subunit 2	GABPB2	15026
GATA binding protein 1 (globin transcription factor 1)	GATA1	15027
GATA binding protein 2	GATA2	15028
GATA binding protein 3	GATA3	15029
GATA binding protein 4	GATA4	15030
GATA binding protein 5	GATA5	15031
GATA binding protein 6	GATA6	15032
GATA zinc finger domain containing 1	GATAD1	15033
GATA zinc finger domain containing 2A	GATAD2A	15034
GATA zinc finger domain containing 2B	GATAD2B	15035
gastrulation brain homeobox 1	GBX1	15036
gastrulation brain homeobox 2	GBX2	15037
GC-rich sequence DNA-binding factor 2	GCFC2	15038
glial cells missing homolog 1	GCM1	15039
glial cells missing homolog 2	GCM2	15040
growth factor independent 1 transcription repressor	GFI1	15041

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
growth factor independent 1B transcription repressor	GFI1B	15042
GLI family zinc finger 1	GLI1	15043
GLI family zinc finger 2	GLI2	15044
GLI family zinc finger 3	GLI3	15045
GLI family zinc finger 4	GLI4	15046
GLIS family zinc finger 1	GLIS1	15047
GLIS family zinc finger 2	GLIS2	15048
GLIS family zinc finger 3	GLIS3	15049
glucocorticoid modulatory element binding protein 1	GMEB1	15050
glucocorticoid modulatory element binding protein 2	GMEB2	15051
gon-4-like (<i>C. elegans</i>)	GON4L	15052
grainyhead like transcription factor 1	GRHL1	15053
grainyhead like transcription factor 2	GRHL2	15054
grainyhead like transcription factor 3	GRHL3	15055
goosecoid homeobox	GSC	15056
goosecoid homeobox 2	GSC2	15057
GS homeobox 1	GSX1	15058
GS homeobox 2	GSX2	15059
general transcription factor IIIi	GTF2I	15060
general transcription factor IIIA	GTF3A	15061
GDNF inducible zinc finger protein 1	GZF1	15062
heart and neural crest derivatives expressed 1	HAND1	15063
heart and neural crest derivatives expressed 2	HAND2	15064
HMG-box transcription factor 1	HBP1	15065-15066
highly divergent homeobox	HDX	15067
helt bHLH transcription factor	HELT	15068
hes family bHLH transcription factor 1	HES1	15069-15070
hes family bHLH transcription factor 2	HES2	15071
hes family bHLH transcription factor 3	HES3	15072
hes family bHLH transcription factor 4	HES4	15073
hes family bHLH transcription factor 5	HES5	15074
hes family bHLH transcription factor 6	HES6	15075
hes family bHLH transcription factor 7	HES7	15076
HESX homeobox 1	HESX1	15077
hes-related family bHLH transcription factor with YRPW motif 1	HEY1	15078
hes-related family bHLH transcription factor with YRPW motif 2	HEY2	15079
hes-related family bHLH transcription factor with YRPW motif-like	HEYL	15080
hematopoietically expressed homeobox	HHEX	15081
hypermethylated in cancer 1	HIC1	15082
hypermethylated in cancer 2	HIC2	15083
hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A	15084
hypoxia inducible factor 3, alpha subunit	HIF3A	15085
histone H4 transcription factor	HINFP	15086
human immunodeficiency virus type I enhancer binding protein 1	HIVEP1	15087
human immunodeficiency virus type I enhancer binding protein 2	HIVEP2	15088
human immunodeficiency virus type I enhancer binding protein 3	HIVEP3	15089
HKR1, GLI-Kruppel zinc finger family member	HKR1	15090
hepatic leukemia factor	HLF	15091
helicase-like transcription factor	HTLF	15092
H2.0-like homeobox	HLX	15093
homeobox containing 1	HMBOX1	15094
high mobility group 20A	HMG20A	15095
high mobility group 20B	HMG20B	15096
high mobility group AT-hook 1	HMGAA1	15097
high mobility group AT-hook 2	HMGAA2	15098
HMG-box containing 3	HMGXB3	15099
HMG-box containing 4	HMGXB4	15100
H6 family homeobox 1	HMX1	15101
H6 family homeobox 2	HMX2	15102
H6 family homeobox 3	HMX3	15103-15104
HNF1 homeobox A	HNF1A	15105
HNF1 homeobox B	HNF1B	15106
hepatocyte nuclear factor 4 alpha	HNF4A	15107
hepatocyte nuclear factor 4 gamma	HNF4G	15108
heterogeneous nuclear ribonucleoprotein K	HNRNPK	15109
homeobox and leucine zipper encoding	HOMEZ	15110
HOP homeobox	HOPX	15111
homeobox A1	HOXA1	15112
homeobox A10	HOXA10	15113

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
homeobox A11	HOXA11	15114
homeobox A13	HOXA13	15115
homeobox A2	HOXA2	15116
homeobox A3	HOXA3	15117
homeobox A4	HOXA4	15118
homeobox A5	HOXA5	15119
homeobox A6	HOXA6	15120
homeobox A7	HOXA7	15121
homeobox A9	HOXA9	15122
homeobox B1	HOXB1	15123
homeobox B13	HOXB13	15124
homeobox B2	HOXB2	15125
homeobox B3	HOXB3	15126
homeobox B4	HOXB4	15127
homeobox B5	HOXB5	15128
homeobox B6	HOXB6	15129
homeobox B7	HOXB7	15130
homeobox B8	HOXB8	15131
homeobox B9	HOXB9	15132
homeobox C10	HOXC10	15133
homeobox C11	HOXC11	15134
homeobox C12	HOXC12	15135
homeobox C13	HOXC13	15136
homeobox C4	HOXC4	15137
homeobox C5	HOXC5	15138
homeobox C6	HOXC6	15139
homeobox C8	HOXC8	15140
homeobox C9	HOXC9	15141
homeobox D1	HOXD1	15142
homeobox D10	HOXD10	15143
homeobox D11	HOXD11	15144
homeobox D12	HOXD12	15145
homeobox D13	HOXD13	15146
homeobox D3	HOXD3	15147
homeobox D4	HOXD4	15148
homeobox D8	HOXD8	15149
homeobox D9	HOXD9	15150
heat shock transcription factor 1	HSF1	15151
heat shock transcription factor 2	HSF2	15152
heat shock transcription factor 4	HSF4	15153
heat shock transcription factor family member 5	HSF5	15154
heat shock transcription factor family, X-linked 1	HSFX1	15155
heat shock transcription factor, Y-linked 1	HSFY1	15156
heat shock transcription factor, Y-linked 2	HSFY2	15156
inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	ID1	15157
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2	15158
inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	ID3	15159
inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	ID4	15160
interferon, gamma-inducible protein 16	IFI16	15161
IKAROS family zinc finger 1	IKZF1	15162
IKAROS family zinc finger 2	IKZF2	15163
IKAROS family zinc finger 3	IKZF3	15164
IKAROS family zinc finger 4	IKZF4	15165
IKAROS family zinc finger 5	IKZF5	15166
insulinoma associated 1	INSM1	15167
insulinoma-associated 2	INSM2	15168
interferon regulatory factor 1	IRF1	15169
interferon regulatory factor 2	IRF2	15170
interferon regulatory factor 3	IRF3	15171
interferon regulatory factor 4	IRF4	15172
interferon regulatory factor 5	IRF5	15173
interferon regulatory factor 6	IRF6	15174
interferon regulatory factor 7	IRF7	15175
interferon regulatory factor 8	IRF8	15176
interferon regulatory factor 9	IRF9	15177
iroquois homeobox 1	IRX1	15178
iroquois homeobox 2	IRX2	15179
iroquois homeobox 3	IRX3	15180
iroquois homeobox 4	IRX4	15181
iroquois homeobox 5	IRX5	15182
iroquois homeobox 6	IRX6	15183
ISL LIM homeobox 1	ISL1	15184

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
ISL LIM homeobox 2	ISL2	15185
intestine specific homeobox	ISX	15186
jumonji and AT-rich interaction domain containing 2	JARID2	15187
JAZF zinc finger 1	JAZF1	15188
Jun dimerization protein 2	JDP2	15189
jun proto-oncogene	JUN	15190
jun B proto-oncogene	JUNB	15191
jun D proto-oncogene	JUND	15192
K(lysine) acetyltransferase 5	KATS	15193
lysine acetyltransferase 6A	KAT6A	15194
lysine acetyltransferase 6B	KAT6B	15195
lysine acetyltransferase 7	KAT7	15196
lysine acetyltransferase 8	KAT8	15197
potassium channel modulatory factor 1	KCMF1	15198
potassium voltage-gated channel interacting protein 3	KCNIP3	15199
lysine demethylase 2A	KDM2A	15200
lysine demethylase 5A	KDM5A	15201
lysine demethylase 5B	KDM5B	15202
lysine demethylase 5C	KDM5C	15203
lysine demethylase 5D	KDM5D	15204
KH-type splicing regulatory protein	KHSRP	15205
KIAA1549	KIAA1549	15206
Kruppel-like factor 1 (erythroid)	KLF1	15207
Kruppel-like factor 10	KLF10	15208
Kruppel-like factor 11	KLF11	15209
Kruppel-like factor 12	KLF12	15210
Kruppel-like factor 13	KLF13	15211
Kruppel-like factor 14	KLF14	15212
Kruppel-like factor 15	KLF15	15213
Kruppel-like factor 16	KLF16	15214
Kruppel-like factor 17	KLF17	15215
Kruppel-like factor 2	KLF2	15216
Kruppel-like factor 3 (basic)	KLF3	15217
Kruppel-like factor 4 (gut)	KLF4	15218
Kruppel-like factor 5 (intestinal)	KLF5	15219
Kruppel-like factor 6	KLF6	15220
Kruppel-like factor 7 (ubiquitous)	KLF7	15221
Kruppel-like factor 8	KLF8	15222
Kruppel-like factor 9	KLF9	15223
lysine methyltransferase 2A	KMT2A	15224
lysine methyltransferase 2B	KMT2B	15225
lysine methyltransferase 2C	KMT2C	15226
lysine methyltransferase 2E	KMT2E	15227
l(3)mbt-like 1 (<i>Drosophila</i>)	L3MBTL1	15228
l(3)mbt-like 2 (<i>Drosophila</i>)	L3MBTL2	15229
l(3)mbt-like 3 (<i>Drosophila</i>)	L3MBTL3	15230
l(3)mbt-like 4 (<i>Drosophila</i>)	L3MBTL4	15231
ladybird homeobox 1	LBX1	15232
ladybird homeobox 2	LBX2	15233
ligand dependent nuclear receptor corepressor	LCOR	15234
ligand dependent nuclear receptor corepressor like	LCORL	15235
lymphoid enhancer binding factor 1	LEF1	15236
leucine twenty homeobox	LEUTX	15237
LIM homeobox 1	LHX1	15238
LIM homeobox 2	LHX2	15239
LIM homeobox 3	LHX3	15240
LIM homeobox 4	LHX4	15241
LIM homeobox 5	LHX5	15242
LIM homeobox 6	LHX6	15243
LIM homeobox 8	LHX8	15244
LIM homeobox 9	LHX9	15245
LIM homeobox transcription factor 1, alpha	LMX1A	15246
LIM homeobox transcription factor 1, beta	LMX1B	15247
LOC730110	LOC730110	
leucine rich repeat (in FLII) interacting protein 1	LRRFIP1	15248
leucine rich repeat (in FLII) interacting protein 2	LRRFIP2	15249
Ly1 antibody reactive	LYAR	15250
lymphoblastic leukemia associated hematopoiesis regulator 1	LYL1	15251
maelstrom spermatogenic transposon silencer	MAEL	15252
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog	MAF	15253
MAF1 homolog, negative regulator of RNA polymerase III	MAF1	15254
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog A	MAFA	15255-15256

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B	MAFB	15257
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	MAFF	15258
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog G	MAFG	15259
v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K	MAFK	15260
matrix 3	MATR3	15261
MYC associated factor X	MAX	15262
MYC associated zinc finger protein	MAZ	15263
methyl-CpG binding domain protein 1	MBD1	15264
methyl-CpG binding domain protein 2	MBD2	15265
methyl-CpG binding domain protein 3	MBD3	15266
methyl-CpG binding domain protein 3-like 1	MBD3L1	15267
methyl-CpG binding domain protein 3-like 2	MBD3L2	15268
methyl-CpG binding domain 4 DNA glycosylase	MBD4	15269
methyl-CpG binding domain protein 5	MBD5	15270
methyl-CpG binding domain protein 6	MBD6	15271
muscleblind like splicing regulator 3	MBNL3	15272
MDS1 and EVII complex locus	MFCOM	15273
methyl-CpG binding protein 2	MECP2	15274
myocyte enhancer factor 2A	MEF2A	15275
myocyte enhancer factor 2B	MEF2B	15276
myocyte enhancer factor 2C	MEF2C	15277
myocyte enhancer factor 2D	MEF2D	15278
Meis homeobox 1	MEIS1	15279
Meis homeobox 2	MEIS2	15280
Meis homeobox 3	MEIS3	15281
Meis homeobox 3 pseudogene 1	MEIS3P1	15282
Meis homeobox 3 pseudogene 2	MEIS3P2	15283
mesenchyme homeobox 1	MEOX1	15284
mesenchyme homeobox 2	MEOX2	15285
mesoderm posterior bHLH transcription factor 1	MESP1	15286
mesoderm posterior bHLH transcription factor 2	MESP2	15287
MGA, MAX dimerization protein	MGA	15288-15289
MIER1 transcriptional regulator	MIER1	15290
MIER family member 2	MIER2	15291
MIER family member 3	MIER3	15292
MIS18 binding protein 1	MIS18BP1	15293
microphthalmia-associated transcription factor	MITF	15294
Mix paired-like homeobox	MIXL1	15295
mohawk homeobox	MXK	15296
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 1	MLLT1	15297
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 10	MLLT10	15298
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11	MLLT11	15299
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 3	MLLT3	15300
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 4	MLLT4	15301
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	MLLT6	15302
MLX, MAX dimerization protein	MLX	15303
MLX interacting protein	MLXIP	15304
MLX interacting protein-like	MLXIPL	15305
MAX network transcriptional repressor	MNT	15306
motor neuron and pancreas homeobox 1	MNX1	15307
musculin	MSC	15308
mesogenin 1	MSGN1	15309
msh homeobox 1	MSX1	15310
msh homeobox 2	MSX2	15311
metastasis associated 1	MTA1	15312
metastasis associated 1 family member 2	MTA2	15313
metastasis associated 1 family member 3	MTA3	15314
metal-regulatory transcription factor 1	MTF1	15315
metal response element binding transcription factor 2	MTF2	15316
MAX dimerization protein 1	MD1	15317
MAX dimerization protein 3	MD3	15318
MAX dimerization protein 4	MD4	15319
MAX interactor 1, dimerization protein	MXI1	15320
v-myb avian myeloblastosis viral oncogene homolog	MYB	15321
v-myb avian myeloblastosis viral oncogene homolog-like 1	MYBL1	15322

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
v-myb avian myeloblastosis viral oncogene homolog-like 2	MYBL2	15323
v-myc avian myelocytomatosis viral oncogene homolog	MYC	15324
v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	MYCL	15325
MYCL pseudogene 1	MYCLP1	15326
v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	MYCN	15327
myogenic factor 5	MYF5	15328
myogenic factor 6	MYF6	15329
myoneurin	MYNN	15330
myogenic differentiation 1	MYOD1	15331
myogenin (myogenic factor 4)	MYOG	15332
myelin regulatory factor	MYRF	15333
Myb-like, SWIRM and MPN domains 1	MYSM1	15334
myelin transcription factor 1	MYT1	15335-15336
myelin transcription factor 1 like	MYT1L	15337
myeloid zinc finger 1	MZF1	15338
Nanog homeobox	NANOG	15339
NANOG neighbor homeobox	NANOGNB	15340
Nanog homeobox pseudogene 1	NANOGP1	15341
Nanog homeobox pseudogene 8	NANOGP8	15342
nuclear receptor coactivator 1	NCOA1	15343
nuclear receptor coactivator 2	NCOA2	15344
nuclear receptor coactivator 3	NCOA3	15345
nuclear receptor coactivator 4	NCOA4	15346
nuclear receptor coactivator 5	NCOA5	15347
nuclear receptor coactivator 6	NCOA6	15348
nuclear receptor coactivator 7	NCOA7	15349
nuclear receptor corepressor 1	NCOR1	15350
nuclear receptor corepressor 2	NCOR2	15351
neuronal differentiation 1	NEUROD1	15352
neuronal differentiation 2	NEUROD2	15353
neuronal differentiation 4	NEUROD4	15354
neuronal differentiation 6	NEUROD6	15355
neuro genin 1	NEUROG1	15356
neuro genin 2	NEUROG2	15357
neuro genin 3	NEUROG3	15358
nuclear factor of activated T-cells 5, tonicity-responsive	NFAT5	15359
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	NFATC1	15360
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	NFATC2	15361
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NFATC3	15362
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	NFATC4	15363
nuclear factor, erythroid 2	NFE2	15364
nuclear factor, erythroid 2 like 1	NFE2L1	15365
nuclear factor, erythroid 2 like 2	NFE2L2	15366
nuclear factor, erythroid 2 like 3	NFE2L3	15367
nuclear factor I/A	NFIA	15368
nuclear factor I/B	NFIB	15369
nuclear factor I/C (CCAAT-binding transcription factor)	NFIC	15370
nuclear factor, interleukin 3 regulated	NFIL3	15371
nuclear factor I/X (CCAAT-binding transcription factor)	NFIX	15372
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	NFKB1	15373
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	15374
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	15375
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	NFKBIB	15376
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	NFKBID	15377
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NFKBIE	15378
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	NFKBIL1	15379
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	NFKBIZ	15380

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
nuclear factor related to kappaB binding protein	NFRKB	15381
nuclear transcription factor, X-box binding 1	NFX1	15382
nuclear transcription factor, X-box binding-like 1	NFXL1	15383
nuclear transcription factor Y subunit alpha	NFYA	15384
nuclear transcription factor Y subunit beta	NFYB	15385
nuclear transcription factor Y subunit gamma	NFYC	15386
nescient helix-loop-helix 1	NHLH1	15387
nescient helix-loop-helix 2	NHLH2	15388
NFKB repressing factor	NKRF	15389
NK1 homeobox 1	NKX1-1	15390
NK1 homeobox 2	NKX1-2	15391
NK2 homeobox 1	NKX2-1	15392
NK2 homeobox 2	NKX2-2	15393
NK2 homeobox 3	NKX2-3	15394
NK2 homeobox 4	NKX2-4	15395
NK2 homeobox 5	NKX2-5	15396
NK2 homeobox 6	NKX2-6	15397
NK2 homeobox 8	NKX2-8	15398
NK3 homeobox 1	NKX3-1	15399
NK3 homeobox 2	NKX3-2	15400
NK6 homeobox 1	NKX6-1	15401
NK6 homeobox 2	NKX6-2	15402
NK6 homeobox 3	NKX6-3	15403
NOBOX oogenesis homeobox	NOBOX	15404
NOC3 like DNA replication regulator	NOC3L	15405
nucleolar complex associated 4 homolog	NOC4L	15406
non-POU domain containing, octamer-binding	NONO	15407
notochord homeobox	NOTO	15408
neuronal PAS domain protein 1	NPAS1	15409
neuronal PAS domain protein 2	NPAS2	15410
neuronal PAS domain protein 3	NPAS3	15411
neuronal PAS domain protein 4	NPAS4	15412
nuclear receptor subfamily 0 group B member 1	NR0B1	15413
nuclear receptor subfamily 0 group B member 2	NR0B2	15414
nuclear receptor subfamily 1 group D member 1	NR1D1	15415
nuclear receptor subfamily 1 group D member 2	NR1D2	15416
nuclear receptor subfamily 1 group H member 2	NR1H2	15417
nuclear receptor subfamily 1 group H member 3	NR1H3	15418
nuclear receptor subfamily 1 group H member 4	NR1H4	15419
nuclear receptor subfamily 1 group I member 2	NR1I2	15420
nuclear receptor subfamily 1 group I member 3	NR1I3	15421
nuclear receptor subfamily 2 group C member 1	NR2C1	15422
nuclear receptor subfamily 2 group C member 2	NR2C2	15423
nuclear receptor subfamily 2 group E member 1	NR2E1	15424
nuclear receptor subfamily 2 group E member 3	NR2E3	15425
nuclear receptor subfamily 2 group F member 1	NR2F1	15426
nuclear receptor subfamily 2 group F member 2	NR2F2	15427
nuclear receptor subfamily 2 group F member 6	NR2F6	15428
nuclear receptor subfamily 3 group C member 1	NR3C1	15429
nuclear receptor subfamily 3 group C member 2	NR3C2	15430
nuclear receptor subfamily 4 group A member 1	NR4A1	15431
nuclear receptor subfamily 4 group A member 2	NR4A2	15432
nuclear receptor subfamily 4 group A member 3	NR4A3	15433
nuclear receptor subfamily 5 group A member 1	NR5A1	15434
nuclear receptor subfamily 5 group A member 2	NR5A2	15435
nuclear receptor subfamily 6 group A member 1	NR6A1	15436
nuclear respiratory factor 1	NRF1	15437-15438
neural retina leucine zipper	NRL	15439
oligodendrocyte transcription factor 1	OLIG1	15440
oligodendrocyte lineage transcription factor 2	OLIG2	15441
oligodendrocyte transcription factor 3	OLIG3	15442
one cut homeobox 1	ONECUT1	15443
one cut homeobox 2	ONECUT2	15444
one cut homeobox 3	ONECUT3	15445
odd-skipped related transcription factor 1	OSR1	15446
odd-skipped related transcription factor 2	OSR2	15447
orthopedic homeobox	OTP	15448
orthodenticle homeobox 1	OTX1	15449
orthodenticle homeobox 2	OTX2	15450
ovo like zinc finger 1	OVOL1	15451
ovo like zinc finger 2	OVOL2	15452
ovo like zinc finger 3	OVOL3	15453
poly(ADP-ribose) polymerase 1	PARP1	15454
poly(ADP-ribose) polymerase family member 12	PARP12	15455
POZ/BTB and AT hook containing zinc finger 1	PATZ1	15456
PRKC, apoptosis, WT1, regulator	PAWR	15457

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
paired box 1	PAX1	15458
paired box 2	PAX2	15459
paired box 3	PAX3	15460
paired box 4	PAX4	15461
paired box 5	PAX5	15462
paired box 6	PAX6	15463
paired box 7	PAX7	15464
paired box 8	PAX8	15465
paired box 9	PAX9	15466
PAX3 and PAX7 binding protein 1	PAXBP1	15467
polybromo 1	PBRM1	15468
pre-B-cell leukemia homeobox 1	PBX1	15469
pre-B-cell leukemia homeobox 2	PBX2	15470
pre-B-cell leukemia homeobox 3	PBX3	15471
pre-B-cell leukemia homeobox 4	PBX4	15472
poly(rC) binding protein 1	PCBP1	15473
poly(rC) binding protein 2	PCBP2	15474
poly(rC) binding protein 3	PCBP3	15475
poly(rC) binding protein 4	PCBP4	15476
poly comb group ring finger 6	PCGF6	15477
pancreatic and duodenal homeobox 1	PDX1	15478-15479
paternally expressed 3	PEG3	15480
progesterone receptor	PGR	15481
prohibitin	PHB	15482
prohibitin 2	PHB2	15483
PHD finger protein 20	PHF20	15484
PHD finger protein 5A	PHF5A	15485
paired like homeobox 2a	PHOX2A	15486
paired like homeobox 2b	PHOX2B	15487
putative homeodomain transcription factor 1	PHTF1	15488
putative homeodomain transcription factor 2	PHTF2	15489
paired like homeodomain 1	PITX1	15490
paired like homeodomain 2	PITX2	15491
paired like homeodomain 3	PITX3	15492
PBX/knotted 1 homeobox 1	PKNOX1	15493
PBX/knotted 1 homeobox 2	PKNOX2	15494
PLAG1 zinc finger	PLAG1	15495
PLAG1 like zinc finger 1	PLAGL1	15496
PLAG1 like zinc finger 2	PLAGL2	15497
pleckstrin	PLEK	15498
promyelocytic leukaemia zinc finger	PLZF	15499
pogo transposable element with ZNF domain	POGZ	15500
POU class 1 homeobox 1	POU1F1	15501
POU class 2 associating factor 1	POU2AF1	15502
POU class 2 homeobox 1	POU2F1	15503
POU class 2 homeobox 2	POU2F2	15504
POU class 2 homeobox 3	POU2F3	15505
POU class 3 homeobox 1	POU3F1	15506
POU class 3 homeobox 2	POU3F2	15507
POU class 3 homeobox 3	POU3F3	15508
POU class 3 homeobox 4	POU3F4	15509
POU class 4 homeobox 1	POU4F1	15510
POU class 4 homeobox 2	POU4F2	15511
POU class 4 homeobox 3	POU4F3	15512
POU class 5 homeobox 1	POU5F1	15513
POU class 5 homeobox 1B	POU5F1B	15514
POU domain class 5, transcription factor 2	POU5F2	15515
POU class 6 homeobox 1	POU6F1	15516
POU class 6 homeobox 2	POU6F2	15517
peroxisome proliferator activated receptor alpha	PPARA	15518
peroxisome proliferator activated receptor delta	PPARD	15519
peroxisome proliferator activated receptor gamma	PPARG	15520
protein phosphatase 1 regulatory subunit 13 like	PPP1R13L	15521
PR domain 1	PRDM1	15522
PR domain 10	PRDM10	15523
PR domain 11	PRDM11	15524
PR domain 12	PRDM12	15525
PR domain 13	PRDM13	15526
PR domain 14	PRDM14	15527
PR domain 15	PRDM15	15528
PR domain 16	PRDM16	15529
PR domain 2	PRDM2	15530
PR domain 4	PRDM4	15531
PR domain 5	PRDM5	15532
PR domain 6	PRDM6	15533
PR domain 7	PRDM7	15534

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TABLE 4-continued

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Full Name	Abbreviation	SEQ ID NO:
PR domain 8	PRDM8	15535
PR domain 9	PRDM9	15536
prolactin regulatory element binding	PREB	15537
PROP paired-like homeobox 1	PROP1	15538
prospero homeobox 1	PROX1	15539
prospero homeobox 2	PROX2	15540
paired related homeobox 1	PRRX1	15541
paired related homeobox 2	PRRX2	15542
paraspeckle component 1	PSPC1	15543
pancreas specific transcription factor, 1a	PTF1A	15544
purine-rich element binding protein A	PURA	15545
purine-rich element binding protein B	PURB	15546
purine-rich element binding protein G	PURG	15547
retinoic acid receptor alpha	RARA	15548
retinoic acid receptor beta	RARB	15549
retinoic acid receptor gamma	RARG	15550
retina and anterior neural fold homeobox	RAX	15551-15552
retina and anterior neural fold homeobox 2	RAX2	15553
RB associated KRAB zinc finger	RBAK	15554
RNA binding motif protein 22	RBM22	15555
recombination signal binding protein for immunoglobulin kappa J region	RBPJ	15556
recombination signal binding protein for immunoglobulin kappa J region-like	RBPJL	15557
ring finger and CCCH-type domains 1	RC3H1	15558
ring finger and CCCH-type domains 2	RC3H2	15559
REST corepressor 1	RCOR1	15560
REST corepressor 2	RCOR2	15561
REST corepressor 3	RCOR3	15562
v-rel avian reticuloendotheliosis viral oncogene homolog	REL	15563
v-rel avian reticuloendotheliosis viral oncogene homolog A	RELA	15564
v-rel avian reticuloendotheliosis viral oncogene homolog B	RELB	15565
arginine-glutamic acid di peptide (RE) repeats	RERE	15566
RE1-silencing transcription factor	REST	15567
regulatory factor X1	RFX1	15568
regulatory factor X2	RFX2	15569
regulatory factor X3	RFX3	15570
regulatory factor X4	RFX4	15571
regulatory factor X5	RFX5	15572
regulatory factor X6	RFX6	15573
regulatory factor X7	RFX7	15574
RFX family member 8, lacking RFX DNA binding domain	RFX8	15575
regulatory factor X associated ankyrin containing protein	RFXANK	15576
regulatory factor X associated protein	RFXAP	15577
Rhox homeobox family member 1	RHOXF1	15578
Rhox homeobox family member 2	RHOXF2	15579
Rhox homeobox family member 2B	RHOXF2B	15580
rearranged L-myc fusion	RLF	15581-15582
RAR related orphan receptor A	RORA	15583
RAR related orphan receptor B	RORB	15584
RAR related orphan receptor C	RORC	15585
retinoic acid receptor-related orphan nuclear receptor gamma	RORgT	15586
ras responsive element binding protein 1	RREB1	15587
runt related transcription factor 1	RUNX1	15588
runt related transcription factor 1; translocated to, 1 (cyclin D related)	RUNX1T1	15589
runt related transcription factor 2	RUNX2	15590
runt related transcription factor 3	RUNX3	15591
retinoid X receptor alpha	RXRA	15592
retinoid X receptor beta	RXRB	15593
retinoid X receptor gamma	RXRG	15594
spalt-like transcription factor 1	SALL1	15595
spalt-like transcription factor 2	SALL2	15596
spalt-like transcription factor 3	SALL3	15597
spalt-like transcription factor 4	SALL4	15598
SATB homeobox 1	SATB1	15599
SATB homeobox 2	SATB2	15600
S-phase cyclin A-associated protein in the ER	SCAPER	15601
scratch family zinc finger 1	SCRT1	15602
scratch family zinc finger 2	SCRT2	15603

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
scleraxis bHLH transcription factor	SCX	15604
SEBOX homeobox	SEBOX	15605
SET binding protein 1	SETBP1	15606
splicing factor proline/glutamine-rich	SFPQ	15607
short stature homeobox	SHOX	15608
short stature homeobox 2	SHOX2	15609
single-minded family bHLH transcription factor 1	SIM1	15610
single-minded family bHLH transcription factor 2	SIM2	15611
SIX homeobox 1	SIX1	15612
SIX homeobox 2	SIX2	15613
SIX homeobox 3	SIX3	15614
SIX homeobox 4	SIX4	15615
SIX homeobox 5	SIX5	15616
SIX homeobox 6	SIX6	15617
SKI proto-oncogene	SKI	15618
SKI-like proto-oncogene	SKIL	15619
SKI family transcriptional corepressor 1	SKOR1	15620
SKI family transcriptional corepressor 2	SKOR2	15621
solute carrier family 30 (zinc transporter), member 9	SLC30A9	15622
SMAD family member 1	SMAD1	15623
SMAD family member 2	SMAD2	15624
SMAD family member 3	SMAD3	15625
SMAD family member 4	SMAD4	15626
SMAD family member 5	SMAD5	15627
SMAD family member 6	SMAD6	15628
SMAD family member 7	SMAD7	15629
SMAD family member 9	SMAD9	15630
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	SMARCA1	15631
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	15632
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	SMARCA4	15633
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SMARCA5	15634
SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	SMARCAD1	15635
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	SMARCAL1	15636
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1	15637
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SMARCC1	15638
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	SMARCC2	15639
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	SMARCD1	15640
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	SMARCD2	15641
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	SMARCD3	15642
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	SMARCE1	15643
snail family zinc finger 1	SNAI1	15644
snail family zinc finger 2	SNAI2	15645
snail family zinc finger 3	SNAI3	15646
small nuclear RNA activating complex polypeptide 4	SNAPC4	15647
spermatogenesis and oogenesis specific basic helix-loop-helix 1	SOHLH1	15648
spermatogenesis and oogenesis specific basic helix-loop-helix 2	SOHLH2	15649
SRY-box 1	SOX1	15650
SRY-box 10	SOX10	15651
SRY-box 11	SOX11	15652
SRY-box 12	SOX12	15653
SRY-box 13	SOX13	15654
SRY-box 14	SOX14	15655
SRY-box 15	SOX15	15656
SRY-box 17	SOX17	15657
SRY-box 18	SOX18	15658
SRY-box 2	SOX2	15659
SRY-box 21	SOX21	15660
SRY-box 3	SOX3	15661
SRY-box 30	SOX30	15662
SRY-box 4	SOX4	15663

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
SRY-box 5	SOX5	15664
SRY-box 6	SOX6	15665
SRY-box 7	SOX7	15666
SRY-box 8	SOX8	15667
SRY-box 9	SOX9	15668
Sp1 transcription factor	SP1	15669-15670
SP100 nuclear antigen	SP100	15671
SP110 nuclear body protein	SP110	15672
SP140 nuclear body protein	SP140	15673
SP140 nuclear body protein like	SP140L	15674
Sp2 transcription factor	SP2	15675
Sp3 transcription factor	SP3	15676
Sp4 transcription factor	SP4	15677
Sp5 transcription factor	SP5	15678
Sp6 transcription factor	SP6	15679
Sp7 transcription factor	SP7	15680
Sp8 transcription factor	SP8	15681
Sp9 transcription factor	SP9	15682
SAM pointed domain containing ETS transcription factor	SPDEF	15683
Spi-1 proto-oncogene	SPI1	15684
Spi-B transcription factor (Spi-1/PU.1 related)	SPIB	15685
Spi-C transcription factor (Spi-1/PU.1 related)	SPIC	15686
spermatogenesis leucine zipper 1	SPZ1	15687
sterol regulatory element binding transcription factor 1	SREBF1	15688
sterol regulatory element binding transcription factor 2	SREBF2	15689
serum response factor	SRF	15690
sex determining region Y	SRY	15691
structure specific recognition protein 1	SSRP1	15692
suppression of tumorigenicity 18, zinc finger	ST18	15693
signal transducer and activator of transcription 1	STAT1	15694
signal transducer and activator of transcription 2	STAT2	15695
signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	15696
signal transducer and activator of transcription 4	STAT4	15697
signal transducer and activator of transcription 5	STAT5	15698
signal transducer and activator of transcription 5A	STAT5A	15699
signal transducer and activator of transcription 5B	STAT5B	15700
signal transducer and activator of transcription 6, interleukin-4 induced	STAT6	15701
transcriptional adaptor 2A	TADA2A	15702
transcriptional adaptor 2B	TADA2B	15703
TATA-box binding protein associated factor 1	TAF1	15704
T-cell acute lymphocytic leukemia 1	TAL1	15705
T-cell acute lymphocytic leukemia 2	TAL2	15706
Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP1	15707
Tax1 (human T-cell leukemia virus type I) binding protein 3	TAX1BP3	15708
T-box transcription factor T-bet	Tbet	15709
TATA-box binding protein	TBP	15710
TATA-box binding protein like 1	TBPL1	15711
TATA-box binding protein like 2	TBPL2	15712
T-box, brain 1	TBR1	15713
T-box 1	TBX1	15714
T-box 10	TBX10	15715
T-box 15	TBX15	15716
T-box 18	TBX18	15717
T-box 19	TBX19	15718
T-box 2	TBX2	15719
T-box 20	TBX20	15720
T-box 21	TBX21	15721
T-box 22	TBX22	15722
T-box 3	TBX3	15723
T-box 4	TBX4	15724
T-box 5	TBX5	15725
T-box 6	TBX6	15726
transcription factor 12	TCF12	15727
transcription factor 15 (basic helix-loop-helix)	TCF15	15728
transcription factor 19	TCF19	15729
transcription factor 20 (AR1)	TCF20	15730
transcription factor 21	TCF21	15731
transcription factor 23	TCF23	15732
transcription factor 24	TCF24	15733
transcription factor 25 (basic helix-loop-helix)	TCF25	15734
transcription factor 3	TCF3	15735

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
transcription factor 4	TCF4	15736
transcription factor 7 (T-cell specific, HMG-box, TCF1)	TCF7	15737
transcription factor 7 like 1	TCF7L1	15738
transcription factor 7 like 2	TCF7L2	15739
transcription factor-like 5 (basic helix-loop-helix)	TCFL5	15740
TEA domain transcription factor 1	TEAD1	15741
TEA domain transcription factor 2	TEAD2	15742
TEA domain transcription factor 3	TEAD3	15743
TEA domain transcription factor 4	TEAD4	15744
thyrotrophic embryonic factor	TEF	15745
telomeric repeat binding factor (NIMA-interacting) 1	TERF1	15746
telomeric repeat binding factor 2	TERF2	15747
tet methylcytosine dioxygenase 1	TET1	15748
tet methylcytosine dioxygenase 2	TET2	15749
tet methylcytosine dioxygenase 3	TET3	15750
transcription factor A, mitochondrial	TFAM	15751
transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	TFAP2A	15752
transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	TFAP2B	15753
transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	TFAP2C	15754
transcription factor AP-2 delta (activating enhancer binding protein 2 delta)	TFAP2D	15755
transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)	TFAP2E	15756
transcription factor AP-4 (activating enhancer binding protein 4)	TFAP4	15757
transcription factor B1, mitochondrial	TFB1M	15758
transcription factor B2, mitochondrial	TFB2M	15759
transcription factor CP2	TCFP2	15760
transcription factor CP2-like 1	TCFP2L1	15761
transcription factor Dp-1	TFDP1	15762
transcription factor Dp-2 (E2F dimerization partner 2)	TFDP2	15763
transcription factor Dp family member 3	TFDP3	15764
transcription factor binding to IGHM enhancer 3	TFE3	15765
transcription factor EB	TFEB	15766
transcription factor EC	TFEC	15767
TGFB induced factor homeobox 1	TGIF1	15768
TGFB induced factor homeobox 2	TGIF2	15769
TGFB induced factor homeobox 2 like, X-linked	TGIF2LX	15770
TGFB induced factor homeobox 2 like, Y-linked	TGIF2LY	15771
THAP domain containing, apoptosis associated protein 1	THAP1	15772
THAP domain containing 10	THAP10	15773
THAP domain containing 11	THAP11	15774
THAP domain containing 12	THAP12	15775
THAP domain containing, apoptosis associated protein 2	THAP2	15776
THAP domain containing, apoptosis associated protein 3	THAP3	15777
THAP domain containing 4	THAP4	15778
THAP domain containing 5	THAP5	15779
THAP domain containing 6	THAP6	15780
THAP domain containing 7	THAP7	15781
THAP domain containing 8	THAP8	15782
THAP domain containing 9	THAP9	15783
Th inducing POZ-Kruppel Factor	ThPOK	15784
thyroid hormone receptor, alpha	THRA	15785
thyroid hormone receptor, beta	THRΒ	15786
T-cell leukemia homeobox 1	TLX1	15787
T-cell leukemia homeobox 2	TLX2	15788
T-cell leukemia homeobox 3	TLX3	15789
target of EGR1, member 1 (nuclear)	TOE1	15790
tonsoku-like, DNA repair protein	TONSL	15791
topoisomerase I binding, arginine-serine-rich, E3	TOPORS	15792
ubiquitin protein ligase		
thymocyte selection associated high mobility group box	TOX	15793
TOX high mobility group box family member 2	TOX2	15794
TOX high mobility group box family member 3	TOX3	15795
TOX high mobility group box family member 4	TOX4	15796
tumor protein p53	TP53	15797
tumor protein p63	TP63	15798
tumor protein p73	TP73	15799

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
tetra-peptide repeat homeobox 1	TPRX1	15800
tetra-peptide repeat homeobox-like	TPRXL	15801
transcriptional regulating factor 1	TRERF1	15802
trichorhinophalangeal syndrome I	TRPS1	15803
TSC22 domain family member 1	TSC22D1	15804
TSC22 domain family member 2	TSC22D2	15805
TSC22 domain family member 3	TSC22D3	15806
TSC22 domain family member 4	TSC22D4	15807
teashirt zinc finger homeobox 1	TSHZ1	15808
teashirt zinc finger homeobox 2	TSHZ2	15809
teashirt zinc finger homeobox 3	TSHZ3	15810
transcription termination factor, RNA polymerase I	TTF1	15811-15812
transcription termination factor, RNA polymerase II	TTF2	15813-15814
tubby bipartite transcription factor	TUB	15815
twist family bHLH transcription factor 1	TWIST1	15816
twist family bHLH transcription factor 2	TWIST2	15817
upstream binding protein 1 (LBP-1a)	UBP1	15818
upstream binding transcription factor, RNA polymerase I	UBTF	15819
upstream binding transcription factor, RNA polymerase I-like 1	UBTFL1	15820
upstream binding transcription factor, RNA polymerase I-like 6 (pseudogene)	UBTFL6	15821
UNC homeobox	UNCX	15822
unkempt family zinc finger	UNK	15823
unkempt family like zinc finger	UNKL	15824
upstream transcription factor 1	USF1	15825
upstream transcription factor 2, c-fos interacting	USF2	15826
upstream transcription factor family member 3	USF3	15827
undifferentiated embryonic cell transcription factor 1	UTF1	15828
ventral anterior homeobox 1	VAX1	15829
ventral anterior homeobox 2	VAX2	15830
vitamin D (1,25-dihydroxyvitamin D3) receptor	VDR	15831
VENT homeobox	VENTX	15832
vascular endothelial zinc finger 1	VEZF1	15833
visual system homeobox 1	VSX1	15834
visual system homeobox 2	VSX2	15835
WD repeat and HMG-box DNA binding protein 1	WDHD1	15836
Wolf-Hirschhorn syndrome candidate 1	WHSC1	15837
widely interspaced zinc finger motifs	WIZ	15838
Wilms tumor 1	WT1	15839
X-box binding protein 1	XBP1	15840
Y-box binding protein 1	YBX1	15841
Y-box binding protein 2	YBX2	15842
Y-box binding protein 3	YBX3	15843
YEATS domain containing 2	YEATS2	15844
YEATS domain containing 4	YEATS4	15845
YY1 transcription factor	YY1	15846
YY2 transcription factor	YY2	15847
zinc finger BED-type containing 1	ZBED1	15848
zinc finger BED-type containing 2	ZBED2	15849
zinc finger BED-type containing 3	ZBED3	15850
zinc finger BED-type containing 4	ZBED4	15851
zinc finger BED-type containing 5	ZBED5	15852
zinc finger, BED-type containing 6	ZBED6	15853
Z-DNA binding protein 1	ZBP1	15854-15855
zinc finger and BTB domain containing 1	ZBTB1	15856
zinc finger and BTB domain containing 10	ZBTB10	15857
zinc finger and BTB domain containing 11	ZBTB11	15858
zinc finger and BTB domain containing 12	ZBTB12	15859
zinc finger and BTB domain containing 14	ZBTB14	15860
zinc finger and BTB domain containing 16	ZBTB16	15861
zinc finger and BTB domain containing 17	ZBTB17	15862
zinc finger and BTB domain containing 18	ZBTB18	15863
zinc finger and BTB domain containing 2	ZBTB2	15864
zinc finger and BTB domain containing 20	ZBTB20	15865
zinc finger and BTB domain containing 21	ZBTB21	15866
zinc finger and BTB domain containing 22	ZBTB22	15867
zinc finger and BTB domain containing 24	ZBTB24	15868
zinc finger and BTB domain containing 25	ZBTB25	15869
zinc finger and BTB domain containing 26	ZBTB26	15870
zinc finger and BTB domain containing 3	ZBTB3	15871
zinc finger and BTB domain containing 32	ZBTB32	15872
zinc finger and BTB domain containing 33	ZBTB33	15873
zinc finger and BTB domain containing 34	ZBTB34	15874
zinc finger and BTB domain containing 37	ZBTB37	15875

TABLE 4-continued

Full Name	Abbreviation	SEQ ID NO:
zinc finger and BTB domain containing 38	ZBTB38	15876
zinc finger and BTB domain containing 39	ZBTB39	15877
zinc finger and BTB domain containing 4	ZBTB4	15878
zinc finger and BTB domain containing 40	ZBTB40	15879
zinc finger and BTB domain containing 41	ZBTB41	15880
zinc finger and BTB domain containing 42	ZBTB42	15881
zinc finger and BTB domain containing 43	ZBTB43	15882
zinc finger and BTB domain containing 44	ZBTB44	15883
zinc finger and BTB domain containing 45	ZBTB45	15884
zinc finger and BTB domain containing 46	ZBTB46	15885
zinc finger and BTB domain containing 47	ZBTB47	15886
zinc finger and BTB domain containing 48	ZBTB48	15887
zinc finger and BTB domain containing 49	ZBTB49	15888
zinc finger and BTB domain containing 5	ZBTB5	15889
zinc finger and BTB domain containing 6	ZBTB6	15890
zinc finger and BTB domain containing 7A	ZBTB7A	15891
zinc finger and BTB domain containing 7B	ZBTB7B	15892
zinc finger and BTB domain containing 7C	ZBTB7C	15893
zinc finger and BTB domain containing 8A	ZBTB8A	15894
zinc finger and BTB domain containing 9	ZBTB9	15895
zinc finger CCCH-type containing 10	ZC3H10	15896
zinc finger CCCH-type containing 11A	ZC3H11A	15897
zinc finger CCCH-type containing 12A	ZC3H12A	15898
zinc finger CCCH-type containing 12B	ZC3H12B	15899
zinc finger CCCH-type containing 13	ZC3H13	15900
zinc finger CCCH-type containing 14	ZC3H14	15901
zinc finger CCCH-type containing 15	ZC3H15	15902
zinc finger CCCH-type containing 18	ZC3H18	15903
zinc finger CCCH-type containing 3	ZC3H3	15904
zinc finger CCCH-type containing 4	ZC3H4	15905
zinc finger CCCH-type containing 6	ZC3H6	15906
zinc finger CCCH-type containing 7A	ZC3H7A	15907
zinc finger CCCH-type containing 7B	ZC3H7B	15908
zinc finger CCCH-type containing 8	ZC3H8	15909
zinc finger CCHC-type containing 11	ZCCHC11	15910
zinc finger CCHC-type containing 6	ZCCHC6	15911
zinc finger E-box binding homeobox 1	ZEB1	15912
zinc finger E-box binding homeobox 2	ZEB2	15913
zinc finger and AT-hook domain containing	ZFAT	15914
zinc finger homeobox 2	ZFHX2	15915
zinc finger homeobox 3	ZFHX3	15916
zinc finger homeobox 4	ZFHX4	15917
ZFP1 zinc finger protein	ZFP1	15918
ZFP14 zinc finger protein	ZFP14	15919
ZFP2 zinc finger protein	ZFP2	15920
ZFP28 zinc finger protein	ZFP28	15921
ZFP3 zinc finger protein	ZFP3	15922
ZFP30 zinc finger protein	ZFP30	15923
ZFP36 ring finger protein-like 1	ZFP36L1	15924
ZFP36 ring finger protein-like 2	ZFP36L2	15925
ZFP37 zinc finger protein	ZFP37	15926
ZFP41 zinc finger protein	ZFP41	15927
ZFP42 zinc finger protein	ZFP42	15928
ZFP57 zinc finger protein	ZFP57	15929
ZFP62 zinc finger protein	ZFP62	15930
ZFP64 zinc finger protein	ZFP64	15931
ZFP69 zinc finger protein	ZFP69	15932-15933
ZFP69 zinc finger protein B	ZFP69B	15934
ZFP82 zinc finger protein	ZFP82	15935
ZFP90 zinc finger protein	ZFP90	15936
ZFP91 zinc finger protein	ZFP91	15937
ZFP92 zinc finger protein	ZFP92	15938
zinc finger protein, FOG family member 1	ZFPM1	15939
zinc finger protein, FOG family member 2	ZFPM2	15940
zinc finger protein, X-linked	ZFX	15941
zinc finger protein, Y-linked	ZFY	15942
zinc finger, FYVE domain containing 26	ZFYVE26	15943
zinc finger, GATA-like protein 1	ZGLP1	15944
zinc finger CCCH-type and G-patch domain containing	ZGPAT	15945
zinc fingers and homeoboxes 1	ZHX1	15946
zinc fingers and homeoboxes 2	ZHX2	15947
zinc fingers and homeoboxes 3	ZHX3	15948
Zic family member 1	ZIC1	15949
Zic family member 2	ZIC2	15950
Zic family member 3	ZIC3	15951

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
Zic family member 4	ZIC4	15952
Zic family member 5	ZIC5	15953
zinc finger protein interacting with K protein 1	ZIK1	15954
zinc finger, imprinted 2	ZIM2	15955
zinc finger, imprinted 3	ZIM3	15956
zinc finger with KRAB and SCAN domains 1	ZKSCAN1	15957
zinc finger with KRAB and SCAN domains 2	ZKSCAN2	15958
zinc finger with KRAB and SCAN domains 3	ZKSCAN3	15959
zinc finger with KRAB and SCAN domains 4	ZKSCAN4	15960
zinc finger with KRAB and SCAN domains 5	ZKSCAN5	15961
zinc finger with KRAB and SCAN domains 7	ZKSCAN7	15962
zinc finger with KRAB and SCAN domains 8	ZKSCAN8	15963
zinc finger matrin-type 1	ZMAT1	15964
zinc finger matrin-type 2	ZMAT2	15965
zinc finger matrin-type 3	ZMAT3	15966
zinc finger matrin-type 4	ZMAT4	15967
zinc finger matrin-type 5	ZMAT5	15968
zinc finger protein 10	ZNF10	15969
zinc finger protein 100	ZNF100	15970
zinc finger protein 101	ZNF101	15971
zinc finger protein 106	ZNF106	15972
zinc finger protein 107	ZNF107	15973
zinc finger protein 112	ZNF112	15974
zinc finger protein 114	ZNF114	15975
zinc finger protein 117	ZNF117	15976
zinc finger protein 12	ZNF12	15977
zinc finger protein 121	ZNF121	15978
zinc finger protein 124	ZNF124	15979
zinc finger protein 131	ZNF131	15980
zinc finger protein 132	ZNF132	15981
zinc finger protein 133	ZNF133	15982
zinc finger protein 134	ZNF134	15983
zinc finger protein 135	ZNF135	15984
zinc finger protein 136	ZNF136	15985
zinc finger protein 137, pseudogene	ZNF137P	15986
zinc finger protein 138	ZNF138	15987
zinc finger protein 14	ZNF14	15988
zinc finger protein 140	ZNF140	15989
zinc finger protein 141	ZNF141	15990
zinc finger protein 142	ZNF142	15991
zinc finger protein 143	ZNF143	15992
zinc finger protein 146	ZNF146	15993
zinc finger protein 148	ZNF148	15994
zinc finger protein 154	ZNF154	15995
zinc finger protein 155	ZNF155	15996
zinc finger protein 157	ZNF157	15997
zinc finger protein 16	ZNF16	15998
zinc finger protein 160	ZNF160	15999
zinc finger protein 165	ZNF165	16000
zinc finger protein 169	ZNF169	16001
zinc finger protein 17	ZNF17	16002
zinc finger protein 174	ZNF174	16003
zinc finger protein 175	ZNF175	16004
zinc finger protein 18	ZNF18	16005
zinc finger protein 180	ZNF180	16006
zinc finger protein 181	ZNF181	16007
zinc finger protein 182	ZNF182	16008
zinc finger protein 184	ZNF184	16009
zinc finger protein 189	ZNF189	16010
zinc finger protein 19	ZNF19	16011
zinc finger protein 195	ZNF195	16012
zinc finger protein 197	ZNF197	16013
zinc finger protein 2	ZNF2	16014
zinc finger protein 20	ZNF20	16015-16016
zinc finger protein 200	ZNF200	16017
zinc finger protein 202	ZNF202	16018
zinc finger protein 205	ZNF205	16019
zinc finger protein 207	ZNF207	16020
zinc finger protein 208	ZNF208	16021
zinc finger protein 211	ZNF211	16022
zinc finger protein 212	ZNF212	16023
zinc finger protein 213	ZNF213	16024
zinc finger protein 214	ZNF214	16025
zinc finger protein 215	ZNF215	16026
zinc finger protein 217	ZNF217	16027
zinc finger protein 219	ZNF219	16028

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 22	ZNF22	16029
zinc finger protein 221	ZNF221	16030
zinc finger protein 223	ZNF223	16031
zinc finger protein 224	ZNF224	16032
zinc finger protein 225	ZNF225	16033-16034
zinc finger protein 226	ZNF226	16035
zinc finger protein 227	ZNF227	16036
zinc finger protein 229	ZNF229	16037
zinc finger protein 23	ZNF23	16038
zinc finger protein 230	ZNF230	16039-16040
zinc finger protein 232	ZNF232	16041
zinc finger protein 233	ZNF233	16042-16043
zinc finger protein 234	ZNF234	16044
zinc finger protein 235	ZNF235	16045
zinc finger protein 236	ZNF236	16046
zinc finger protein 239	ZNF239	16047
zinc finger protein 24	ZNF24	16048
zinc finger protein 248	ZNF248	16049
zinc finger protein 25	ZNF25	16050
zinc finger protein 250	ZNF250	16051
zinc finger protein 251	ZNF251	16052
zinc finger protein 252, pseudogene	ZNF252P	16053
zinc finger protein 253	ZNF253	16054
zinc finger protein 254	ZNF254	16055
zinc finger protein 256	ZNF256	16056
zinc finger protein 257	ZNF257	16057
zinc finger protein 26	ZNF26	16058
zinc finger protein 260	ZNF260	16059
zinc finger protein 263	ZNF263	16060
zinc finger protein 264	ZNF264	16061
zinc finger protein 266	ZNF266	16062
zinc finger protein 267	ZNF267	16063
zinc finger protein 268	ZNF268	16064
zinc finger protein 273	ZNF273	16065
zinc finger protein 274	ZNF274	16066
zinc finger protein 275	ZNF275	16067
zinc finger protein 276	ZNF276	16068
zinc finger protein 277	ZNF277	16069
zinc finger protein 28	ZNF28	16070
zinc finger protein 280A	ZNF280A	16071
zinc finger protein 280B	ZNF280B	16072
zinc finger protein 280C	ZNF280C	16073
zinc finger protein 280D	ZNF280D	16074
zinc finger protein 281	ZNF281	16075
zinc finger protein 282	ZNF282	16076
zinc finger protein 283	ZNF283	16077
zinc finger protein 284	ZNF284	16078
zinc finger protein 285	ZNF285	16079
zinc finger protein 286A	ZNF286A	16080
zinc finger protein 286B	ZNF286B	16081
zinc finger protein 287	ZNF287	16082
zinc finger protein 292	ZNF292	16083
zinc finger protein 296	ZNF296	16084
zinc finger protein 3	ZNF3	16085
zinc finger protein 30	ZNF30	16086
zinc finger protein 300	ZNF300	16087
zinc finger protein 302	ZNF302	16088
zinc finger protein 304	ZNF304	16089
zinc finger protein 311	ZNF311	16090
zinc finger protein 316	ZNF316	16091
zinc finger protein 317	ZNF317	16092
zinc finger protein 318	ZNF318	16093
zinc finger protein 319	ZNF319	16094
zinc finger protein 32	ZNF32	16095
zinc finger protein 320	ZNF320	16096
zinc finger protein 322	ZNF322	16097
zinc finger protein 324	ZNF324	16098
zinc finger protein 324B	ZNF324B	16099
zinc finger protein 326	ZNF326	16100
zinc finger protein 329	ZNF329	16101
zinc finger protein 331	ZNF331	16102
zinc finger protein 333	ZNF333	16103
zinc finger protein 334	ZNF334	16104
zinc finger protein 335	ZNF335	16105
zinc finger protein 337	ZNF337	16106
zinc finger protein 33A	ZNF33A	16107

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 33B	ZNF33B	16108
zinc finger protein 34	ZNF34	16109
zinc finger protein 341	ZNF341	16110
zinc finger protein 343	ZNF343	16111
zinc finger protein 345	ZNF345	16112
zinc finger protein 346	ZNF346	16113
zinc finger protein 347	ZNF347	16114
zinc finger protein 35	ZNF35	16115
zinc finger protein 350	ZNF350	16116
zinc finger protein 354A	ZNF354A	16117
zinc finger protein 354B	ZNF354B	16118
zinc finger protein 354C	ZNF354C	16119
zinc finger protein 355, pseudogene	ZNF355P	16120
zinc finger protein 358	ZNF358	16121
zinc finger protein 362	ZNF362	16122
zinc finger protein 365	ZNF365	16123-16124
zinc finger protein 366	ZNF366	16125
zinc finger protein 367	ZNF367	16126
zinc finger protein 37A	ZNF37A	16127
zinc finger protein 382	ZNF382	16128
zinc finger protein 383	ZNF383	16129
zinc finger protein 384	ZNF384	16130
zinc finger protein 385A	ZNF385A	16131
zinc finger protein 385B	ZNF385B	16132
zinc finger protein 385C	ZNF385C	16133
zinc finger protein 385D	ZNF385D	16134
zinc finger protein 391	ZNF391	16135
zinc finger protein 394	ZNF394	16136
zinc finger protein 395	ZNF395	16137
zinc finger protein 396	ZNF396	16138
zinc finger protein 397	ZNF397	16139
zinc finger protein 398	ZNF398	16140
zinc finger protein 404	ZNF404	16141
zinc finger protein 407	ZNF407	16142
zinc finger protein 408	ZNF408	16143
zinc finger protein 41	ZNF41	16144
zinc finger protein 410	ZNF410	16145
zinc finger protein 414	ZNF414	16146
zinc finger protein 415	ZNF415	16147
zinc finger protein 416	ZNF416	16148
zinc finger protein 417	ZNF417	16149
zinc finger protein 418	ZNF418	16150
zinc finger protein 419	ZNF419	16151
zinc finger protein 420	ZNF420	16152
zinc finger protein 423	ZNF423	16153
zinc finger protein 425	ZNF425	16154
zinc finger protein 426	ZNF426	16155
zinc finger protein 428	ZNF428	16156
zinc finger protein 429	ZNF429	16157
zinc finger protein 43	ZNF43	16158
zinc finger protein 430	ZNF430	16159
zinc finger protein 431	ZNF431	16160
zinc finger protein 432	ZNF432	16161
zinc finger protein 433	ZNF433	16162
zinc finger protein 436	ZNF436	16163
zinc finger protein 438	ZNF438	16164
zinc finger protein 439	ZNF439	16165
zinc finger protein 44	ZNF44	16166
zinc finger protein 440	ZNF440	16167
zinc finger protein 441	ZNF441	16168
zinc finger protein 442	ZNF442	16169
zinc finger protein 443	ZNF443	16170
zinc finger protein 444	ZNF444	16171
zinc finger protein 445	ZNF445	16172
zinc finger protein 446	ZNF446	16173
zinc finger protein 449	ZNF449	16174
zinc finger protein 45	ZNF45	16175
zinc finger protein 451	ZNF451	16176
zinc finger protein 454	ZNF454	16177
zinc finger protein 460	ZNF460	16178
zinc finger protein 461	ZNF461	16179
zinc finger protein 462	ZNF462	16180
zinc finger protein 467	ZNF467	16181
zinc finger protein 468	ZNF468	16182
zinc finger protein 469	ZNF469	16183
zinc finger protein 470	ZNF470	16184

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 471	ZNF471	16185
zinc finger protein 473	ZNF473	16186
zinc finger protein 474	ZNF474	16187-16188
zinc finger protein 479	ZNF479	16189
zinc finger protein 48	ZNF48	16190
zinc finger protein 480	ZNF480	16191
zinc finger protein 483	ZNF483	16192
zinc finger protein 484	ZNF484	16193
zinc finger protein 485	ZNF485	16194
zinc finger protein 486	ZNF486	16195
zinc finger protein 487	ZNF487	16196
zinc finger protein 488	ZNF488	16197
zinc finger protein 490	ZNF490	16198
zinc finger protein 491	ZNF491	16199
zinc finger protein 492	ZNF492	16200
zinc finger protein 493	ZNF493	16201
zinc finger protein 496	ZNF496	16202
zinc finger protein 497	ZNF497	16203
zinc finger protein 500	ZNF500	16204
zinc finger protein 501	ZNF501	16205
zinc finger protein 502	ZNF502	16206
zinc finger protein 503	ZNF503	16207
zinc finger protein 506	ZNF506	16208
zinc finger protein 507	ZNF507	16209
zinc finger protein 510	ZNF510	16210
zinc finger protein 511	ZNF511	16211
zinc finger protein 512	ZNF512	16212
zinc finger protein 512B	ZNF512B	16213
zinc finger protein 513	ZNF513	16214
zinc finger protein 514	ZNF514	16215
zinc finger protein 516	ZNF516	16216
zinc finger protein 517	ZNF517	16217
zinc finger protein 518A	ZNF518A	16218
zinc finger protein 518B	ZNF518B	16219
zinc finger protein 519	ZNF519	16220
zinc finger protein 521	ZNF521	16221
zinc finger protein 524	ZNF524	16222
zinc finger protein 526	ZNF526	16223
zinc finger protein 527	ZNF527	16224
zinc finger protein 528	ZNF528	16225
zinc finger protein 529	ZNF529	16226
zinc finger protein 530	ZNF530	16227
zinc finger protein 532	ZNF532	16228
zinc finger protein 534	ZNF534	16229
zinc finger protein 536	ZNF536	16230
zinc finger protein 540	ZNF540	16231
zinc finger protein 541	ZNF541	16232
zinc finger protein 542, pseudogene	ZNF542P	16233
zinc finger protein 543	ZNF543	16234
zinc finger protein 544	ZNF544	16235
zinc finger protein 546	ZNF546	16236
zinc finger protein 547	ZNF547	16237
zinc finger protein 548	ZNF548	16238
zinc finger protein 549	ZNF549	16239
zinc finger protein 550	ZNF550	16240
zinc finger protein 552	ZNF552	16241
zinc finger protein 554	ZNF554	16242
zinc finger protein 555	ZNF555	16243
zinc finger protein 556	ZNF556	16244
zinc finger protein 557	ZNF557	16245
zinc finger protein 558	ZNF558	16246
zinc finger protein 559	ZNF559	16247
zinc finger protein 56	ZNF56	16248
zinc finger protein 560	ZNF560	16249
zinc finger protein 561	ZNF561	16250
zinc finger protein 562	ZNF562	16251
zinc finger protein 563	ZNF563	16252
zinc finger protein 564	ZNF564	16253
zinc finger protein 565	ZNF565	16254
zinc finger protein 566	ZNF566	16255
zinc finger protein 567	ZNF567	16256
zinc finger protein 568	ZNF568	16257
zinc finger protein 569	ZNF569	16258
zinc finger protein 57	ZNF57	16259
zinc finger protein 570	ZNF570	16260
zinc finger protein 571	ZNF571	16261

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 572	ZNF572	16262
zinc finger protein 573	ZNF573	16263
zinc finger protein 574	ZNF574	16264
zinc finger protein 575	ZNF575	16265
zinc finger protein 576	ZNF576	16266-16267
zinc finger protein 577	ZNF577	16268
zinc finger protein 578	ZNF578	16269
zinc finger protein 579	ZNF579	16270
zinc finger protein 580	ZNF580	16271
zinc finger protein 581	ZNF581	16272
zinc finger protein 582	ZNF582	16273
zinc finger protein 583	ZNF583	16274
zinc finger protein 584	ZNF584	16275
zinc finger protein 585A	ZNF585A	16276
zinc finger protein 585B	ZNF585B	16277
zinc finger protein 586	ZNF586	16278
zinc finger protein 587	ZNF587	16279
zinc finger protein 589	ZNF589	16280
zinc finger protein 592	ZNF592	16281
zinc finger protein 593	ZNF593	16282
zinc finger protein 594	ZNF594	16283
zinc finger protein 595	ZNF595	16284
zinc finger protein 596	ZNF596	16285
zinc finger protein 597	ZNF597	16286
zinc finger protein 598	ZNF598	16287
zinc finger protein 599	ZNF599	16288
zinc finger protein 600	ZNF600	16289
zinc finger protein 605	ZNF605	16290
zinc finger protein 606	ZNF606	16291
zinc finger protein 607	ZNF607	16292
zinc finger protein 608	ZNF608	16293
zinc finger protein 609	ZNF609	16294
zinc finger protein 610	ZNF610	16295
zinc finger protein 611	ZNF611	16296
zinc finger protein 613	ZNF613	16297
zinc finger protein 614	ZNF614	16298
zinc finger protein 615	ZNF615	16299
zinc finger protein 616	ZNF616	16300
zinc finger protein 618	ZNF618	16301
zinc finger protein 619	ZNF619	16302
zinc finger protein 620	ZNF620	16303
zinc finger protein 621	ZNF621	16304
zinc finger protein 622	ZNF622	16305
zinc finger protein 623	ZNF623	16306
zinc finger protein 624	ZNF624	16307
zinc finger protein 625	ZNF625	16308
zinc finger protein 626	ZNF626	16309
zinc finger protein 627	ZNF627	16310
zinc finger protein 628	ZNF628	16311
zinc finger protein 629	ZNF629	16312
zinc finger protein 639	ZNF639	16313
zinc finger protein 641	ZNF641	16314
zinc finger protein 644	ZNF644	16315
zinc finger protein 645	ZNF645	16316
zinc finger protein 646	ZNF646	16317
zinc finger protein 648	ZNF648	16318
zinc finger protein 649	ZNF649	16319
zinc finger protein 652	ZNF652	16320
zinc finger protein 653	ZNF653	16321
zinc finger protein 654	ZNF654	16322
zinc finger protein 655	ZNF655	16323
zinc finger protein 658	ZNF658	16324
zinc finger protein 658B (pseudogene)	ZNF658B	16325
zinc finger protein 66	ZNF66	16326
zinc finger protein 660	ZNF660	16327
zinc finger protein 662	ZNF662	16328
zinc finger protein 664	ZNF664	16329
zinc finger protein 665	ZNF665	16330
zinc finger protein 667	ZNF667	16331
zinc finger protein 668	ZNF668	16332
zinc finger protein 669	ZNF669	16333
zinc finger protein 670	ZNF670	16334
zinc finger protein 671	ZNF671	16335
zinc finger protein 672	ZNF672	16336
zinc finger protein 674	ZNF674	16337
zinc finger protein 675	ZNF675	16338

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 676	ZNF676	16339
zinc finger protein 677	ZNF677	16340
zinc finger protein 678	ZNF678	16341
zinc finger protein 679	ZNF679	16342
zinc finger protein 680	ZNF680	16343
zinc finger protein 681	ZNF681	16344
zinc finger protein 682	ZNF682	16345
zinc finger protein 683	ZNF683	16346
zinc finger protein 684	ZNF684	16347
zinc finger protein 687	ZNF687	16348
zinc finger protein 688	ZNF688	16349
zinc finger protein 689	ZNF689	16350
zinc finger protein 69	ZNF69	16351
zinc finger protein 691	ZNF691	16352
zinc finger protein 692	ZNF692	16353
zinc finger protein 695	ZNF695	16354
zinc finger protein 696	ZNF696	16355
zinc finger protein 697	ZNF697	16356
zinc finger protein 699	ZNF699	16357
zinc finger protein 7	ZNF7	16358
zinc finger protein 70	ZNF70	16359
zinc finger protein 701	ZNF701	16360
zinc finger protein 702, pseudogene	ZNF702P	16361
zinc finger protein 703	ZNF703	16362
zinc finger protein 704	ZNF704	16363
zinc finger protein 705A	ZNF705A	16364
zinc finger protein 705D	ZNF705D	16365
zinc finger protein 705E	ZNF705E	16366
zinc finger protein 705G	ZNF705G	16367
zinc finger protein 706	ZNF706	16368
zinc finger protein 707	ZNF707	16369
zinc finger protein 708	ZNF708	16370
zinc finger protein 709	ZNF709	16371
zinc finger protein 71	ZNF71	16372
zinc finger protein 710	ZNF710	16373
zinc finger protein 711	ZNF711	16374
zinc finger protein 713	ZNF713	16375
zinc finger protein 714	ZNF714	16376
zinc finger protein 716	ZNF716	16377
zinc finger protein 717	ZNF717	16378
zinc finger protein 718	ZNF718	16379
zinc finger protein 720	ZNF720	16380
zinc finger protein 721	ZNF721	16381
zinc finger protein 724, pseudogene	ZNF724P	16382
zinc finger protein 726	ZNF726	16383
zinc finger protein 727	ZNF727	16384
zinc finger protein 729	ZNF729	16385
zinc finger protein 730	ZNF730	16386
zinc finger protein 732	ZNF732	16387
zinc finger protein 735	ZNF735	16388
zinc finger protein 737	ZNF737	16389
zinc finger protein 74	ZNF74	16390
zinc finger protein 740	ZNF740	16391
zinc finger protein 746	ZNF746	16392
zinc finger protein 747	ZNF747	16393
zinc finger protein 749	ZNF749	16394
zinc finger protein 750	ZNF750	16395
zinc finger protein 75a	ZNF75A	16396
zinc finger protein 75D	ZNF75D	16397
zinc finger protein 76	ZNF76	16398
zinc finger protein 761	ZNF761	16399
zinc finger protein 763	ZNF763	16400
zinc finger protein 764	ZNF764	16401
zinc finger protein 765	ZNF765	16402
zinc finger protein 766	ZNF766	16403
zinc finger protein 768	ZNF768	16404
zinc finger protein 77	ZNF77	16405
zinc finger protein 770	ZNF770	16406
zinc finger protein 771	ZNF771	16407
zinc finger protein 772	ZNF772	16408
zinc finger protein 773	ZNF773	16409
zinc finger protein 774	ZNF774	16410
zinc finger protein 775	ZNF775	16411
zinc finger protein 776	ZNF776	16412
zinc finger protein 777	ZNF777	16413
zinc finger protein 778	ZNF778	16414

TABLE 4-continued

Exemplary Transcription Factors.		
Full Name	Abbreviation	SEQ ID NO:
zinc finger protein 780A	ZNF780A	16415
zinc finger protein 780B	ZNF780B	16416
zinc finger protein 781	ZNF781	16417
zinc finger protein 782	ZNF782	16418
zinc finger family member 783	ZNF783	16419
zinc finger protein 784	ZNF784	16420
zinc finger protein 785	ZNF785	16421
zinc finger protein 786	ZNF786	16422
zinc finger protein 787	ZNF787	16423
zinc finger family member 788	ZNF788	16424
zinc finger protein 789	ZNF789	16425
zinc finger protein 79	ZNF79	16426
zinc finger protein 790	ZNF790	16427
zinc finger protein 791	ZNF791	16428
zinc finger protein 792	ZNF792	16429
zinc finger protein 793	ZNF793	16430
zinc finger protein 799	ZNF799	16431
zinc finger protein 8	ZNF8	16432
zinc finger protein 80	ZNF80	16433
zinc finger protein 800	ZNF800	16434
zinc finger protein 804A	ZNF804A	16435
zinc finger protein 804B	ZNF804B	16436
zinc finger protein 805	ZNF805	16437
zinc finger protein 806	ZNF806	16438
zinc finger protein 808	ZNF808	16439
zinc finger protein 81	ZNF81	16440
zinc finger protein 813	ZNF813	16441
zinc finger protein 814	ZNF814	16442
zinc finger protein 816	ZNF816	16443
zinc finger protein 821	ZNF821	16444
zinc finger protein 823	ZNF823	16445
zinc finger protein 827	ZNF827	16446
zinc finger protein 829	ZNF829	16447
zinc finger protein 83	ZNF83	16448
zinc finger protein 830	ZNF830	16449
zinc finger protein 831	ZNF831	16450
zinc finger protein 833, pseudogene	ZNF833P	16451
zinc finger protein 835	ZNF835	16452
zinc finger protein 836	ZNF836	16453
zinc finger protein 837	ZNF837	16454
zinc finger protein 839	ZNF839	16455
zinc finger protein 84	ZNF84	16456
zinc finger protein 840, pseudogene	ZNF840P	16457
zinc finger protein 841	ZNF841	16458
zinc finger protein 843	ZNF843	16459
zinc finger protein 844	ZNF844	16460
zinc finger protein 845	ZNF845	16461
zinc finger protein 846	ZNF846	16462
zinc finger protein 85	ZNF85	16463
zinc finger protein 853	ZNF853	16464
zinc finger protein 860	ZNF860	16465
zinc finger protein 876, pseudogene	ZNF876P	16466
zinc finger protein 878	ZNF878	16467
zinc finger protein 879	ZNF879	16468
zinc finger protein 880	ZNF880	16469
zinc finger protein 891	ZNF891	16470
zinc finger protein 90	ZNF90	16471
zinc finger protein 91	ZNF91	16472
zinc finger protein 92	ZNF92	16473
zinc finger protein 93	ZNF93	16474
zinc finger protein 98	ZNF98	16475
zinc finger protein 99	ZNF99	16476
zinc finger, NFX1-type containing 1	ZNFX1	16477
zinc finger and SCAN domain containing 1	ZSCAN1	16478
zinc finger and SCAN domain containing 10	ZSCAN10	16479
zinc finger and SCAN domain containing 12	ZSCAN12	16480
zinc finger and SCAN domain containing 16	ZSCAN16	16481
zinc finger and SCAN domain containing 18	ZSCAN18	16482
zinc finger and SCAN domain containing 2	ZSCAN2	16483
zinc finger and SCAN domain containing 20	ZSCAN20	16484
zinc finger and SCAN domain containing 21	ZSCAN21	16485
zinc finger and SCAN domain containing 22	ZSCAN22	16486
zinc finger and SCAN domain containing 23	ZSCAN23	16487
zinc finger and SCAN domain containing 25	ZSCAN25	16488
zinc finger and SCAN domain containing 26	ZSCAN26	16489
zinc finger and SCAN domain containing 29	ZSCAN29	16490

TABLE 4-continued

Exemplary Transcription Factors.

Full Name	Abbreviation	SEQ ID NO:
zinc finger and SCAN domain containing 30	ZSCAN30	16491
zinc finger and SCAN domain containing 31	ZSCAN31	16492
zinc finger and SCAN domain containing 32	ZSCAN32	16493
zinc finger and SCAN domain containing 4	ZSCAN4	16494
zinc finger and SCAN domain containing 5A	ZSCAN5A	16495
zinc finger and SCAN domain containing 5B	ZSCAN5B	16496
zinc finger and SCAN domain containing 5C, pseudogene	ZSCAN5CP	16497
zinc finger and SCAN domain containing 9	ZSCAN9	16498
zinc finger with UFM1-specific peptidase domain	ZUFSP	16499
zinc finger, X-linked, duplicated A	ZXDA	16500
zinc finger, X-linked, duplicated B	ZXDB	16501
ZXD family zinc finger C	ZXDC	16502
zinc finger ZZ-type containing 3	ZZZ3	16503

In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding a cell death or cell apoptosis receptor to produce an armored T-cell of the disclosure. Interaction of a death receptor and its endogenous ligand results in the initiation of apoptosis. Disruption of an expression, an activity, or an interaction of a cell death and/or cell apoptosis receptor and/or ligand render an armored T-cell of the disclosure less

receptive to death signals, consequently, making the armored T cell of the disclosure more efficacious in a tumor environment. An exemplary cell death receptor which may be modified in an armored T cell of the disclosure is Fas (CD95). Exemplary cell death and/or cell apoptosis receptors and ligands of the disclosure include, but are not limited to, the exemplary receptors and ligands provided in Table 5.

TABLE 5

Exemplary Cell Death and/or Cell Apoptosis Receptors and Ligands.

Full Name	Abbreviation	SEQ ID NO:
Cluster of Differentiation 120	CD120a	16504-16505
Death receptor 3	DR3	16506
Death receptor 6	DR6	16507
first apoptosis signal (Fas) receptor	Fas (CD95/AP0-1)	16508-16509
Fas Ligand	FasL	16510
cellular tumor antigen p53	p53	16511
Tumor necrosis factor receptor 1	TNF-R1	16512
Tumor necrosis factor receptor 2	TNF-R2	16513
Tumor necrosis factor-related apoptosis-inducing ligand receptor 1	TRAIL-R1 (DR4)	16514
Tumor necrosis factor-related apoptosis-inducing ligand receptor 2	TRAIL-R2 (DR5)	16515
Fas-associated protein with death domain	FADD	16516
Tumor necrosis factor receptor type 1-associated DEATH domain protein	TRADD	16517
Bc1-2-associated X protein	Bax	16518
Bc1-2 homologous killer	BAK	16519
14-3-3 protein	14-3-3	16520
B-cell lymphoma 2	Bcl-2	16521
Cytochrome C	Cyt C	16522
Second mitochondria-derived activator of caspase	Smac/Diablo	16523
High temperature requirement protein A2	HTRA2/Omi	16524
Apoptosis inducing factor	AIF	16525
Endonuclease G	EXOG	16526
Caspase 9	Cas9	16527
Caspase 2	Cas2	16528
Caspase 8	Cas8	16529
Caspase 10	Cas10	16530
Caspase 3	Cas3	16531
Caspase 6	Cas6	16532
Caspase 7	Cas7	16533
Tumor Necrosis Factor alpha	TNF-alpha	16534
TNF-related weak inducer of apoptosis	TWEAK	16535
TNF-related weak inducer of apoptosis receptor	TWEAK-R	16536
Tumor necrosis factor-related apoptosis-inducing ligand	TRAIL	16537
TNF ligand-related molecule 1	TL1A	16538
Receptor-interacting serine/threonine-protein kinase 1	RIP1	16539
Cellular inhibitor of apoptosis 1	cIAP-1	16540
TNF receptor-associated factor 2	TRAF-2	16541

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In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding a metabolic sensing protein to produce an armored T-cell of the disclosure. Disruption to the metabolic sensing of the immunosuppressive tumor microenvironment (characterized by low levels of oxygen pH glucose and other molecules) by an armored T-cell of the disclosure leads to extended retention of T-cell function and, consequently,

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more tumor cells killed per armored cell. For example, HIF1a and VHL play a role in T-cell function while in a hypoxic environment. An armored T-cell of the disclosure may have silenced or reduced expression of one or more genes encoding HIF1a or VHL. Genes and proteins involved in metabolic sensing include, but are not limited to the exemplary genes and proteins provided in Table 6.

TABLE 6

Exemplary Metabolic Sensing Genes (and encoded Proteins).			
Full Name	Metabolite	Abbreviation	SEQ ID NO:
hypoxia-inducible factor 1α	Low oxygen	HIF-1α	16542
von Hippel-Lindau tumor suppressor	Low oxygen	VHL	16543
Prolyl-hydroxylase domain proteins	High oxygen	PHD proteins	
Glucose transporter 1	glucose	GLUT1	16544
Linker of Activated T cells	Amino acid (leucine)	LAT	16545
CD98 glycoprotein	Amino acid (leucine)	CD98	16546
Alanine, serine, cysteine-preferring transporter 2	Cationic Amino acid (glutamine)	ASCT2/Slc1a5	16547
Solute carrier family 7 member 1	Cationic Amino acids	Slc7a1	16548
Solute carrier family 7 member 2	Cationic Amino acids	Slc7a2	16549
Solute carrier family 7 member 3	Cationic Amino acids	Slc7a3	16550
Solute carrier family 7 member 4	Cationic Amino acids	Slc7a4	16551
Solute carrier family 7 member 5	Glycoprotein associated Amino acids	Slc7a5	16552
Solute carrier family 7 member 6	Glycoprotein associated Amino acids	Slc7a6	16553
Solute carrier family 7 member 7	Glycoprotein associated Amino acids	Slc7a7	16554
Solute carrier family 7 member 8	Glycoprotein associated Amino acids	Slc7a8	16555
Solute carrier family 7 member 9	Glycoprotein associated Amino acids	Slc7a9	16556
Solute carrier family 7 member 10	Glycoprotein associated Amino acids	Slc7a10	16557
Solute carrier family 7 member 11	Glycoprotein associated Amino acids	Slc7a11	16558
Solute carrier family 7 member 13	Glycoprotein associated Amino acids	Slc7a13	16559
Solute carrier family 7 member 14	Cationic Amino acids	Slc7a14	16560
Solute carrier family 3 member 2	Amino acid	Slc3a2	16561
Calcium transport protein 2	Cationic Amino acid (arginine)	CAT2	16562
Calcium transport protein 3	Cationic Amino acid (arginine)	CAT3	16563
Calcium transport protein 4	Cationic Amino acid (arginine)	CAT4	16564
Bromodomain adjacent to zinc finger domain protein 1B	Amino acid (arginine)	BAZ1B	16565
PC4 and SFRS1-interacting protein	Amino acid (arginine)	PSIP1	16566
Translin	Amino acid (arginine)	TSN	16567
G-protein-coupled receptors	Fatty Acid and Cholesterol	GPCRs	
T-cell Receptor, subunit alpha	Fatty Acid and Cholesterol	TCR alpha	16568
T-cell Receptor, subunit beta	Fatty Acid and Cholesterol	TCR beta	16569
T-cell Receptor, subunit zeta	Fatty Acid and Cholesterol	TCR zeta	16570
T-cell Receptor, subunit CD3 epsilon	Fatty Acid and Cholesterol	TCR CD3 epsilon	16571
T-cell Receptor, subunit CD3 gamma	Fatty Acid and Cholesterol	TCR CD3 gamma	16572
T-cell Receptor, subunit CD3 delta	Fatty Acid and Cholesterol	TCR CD3 delta	16573
peroxisome proliferator-activated receptors	Fatty Acid and Cholesterol	PPARs	
AMP-activated protein kinase	Energy homeostasis (intracellular AMP to ATP ratio)	AMPK	16574-16575
P2X purinoceptor 7	Redox homeostasis	P2X7	16576

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In some embodiments a T-cell of the disclosure is modified to silence or reduce therapy, including a monoclonal antibody, to produce an armored T-cell of the disclosure. Thus an armored T-cell of the disclosure can function and may demonstrate superior function or efficacy whilst in the presence of a cancer therapy (e.g. a chemotherapy, a monoclonal antibody therapy, or another anti-tumor treatment). Proteins involved in conferring sensitivity to a cancer therapy include, but are not limited to, the exemplary proteins provided in Table 7.

TABLE 7

Exemplary Proteins that Confer Sensitivity to a Cancer Therapeutic.

Full Name	Abbreviation	SEQ ID NO:
Copper-transporting ATPase 2	ATP7B	16577
Breakpoint cluster region protein	BCR	16578
Abelson tyrosine-protein kinase 1	ABL	16579
Breast cancer resistance protein	BCRP	16580
Breast cancer type 1 susceptibility protein	BRCA1	16581
Breast cancer type 2 susceptibility protein	BRCA2	16582
CAMPATH-1 antigen	CD52	16583
Cytochrome P450 2D6	CYP2D6	16584
Deoxycytidine kinase	dCK	16585
Dihydrofolate reductase	DHFR	16586
Dihydropyrimidine dehydrogenase [NADP (+)]	DPYD	16587
Epidermal growth factor receptor	EGFR	16588
DNA excision repair protein ERCC-1	ERCC1	16589
Estrogen Receptor	ESR	16590
Low affinity immunoglobulin gamma Fc region receptor III-A	FCGR3A	16591
Receptor tyrosine-protein kinase erbB-2	HER2 or ERBB2	16592
Insulin-like growth factor 1 receptor	IGF1R	16593
GTPase KRas	KRAS	16594
Multidrug resistance protein 1	MDR1 or ABCB1	16595
Methylated-DNA--protein-cysteine methyltransferase	MGMT	16596
Multidrug resistance-associated protein 1	MRP1 or ABCC1	16597
Progesterone Receptor	PGR	16598
Regulator of G-protein signaling 10	RGS10	16599
Suppressor of cytokine signaling 3	SOCS-3	16600
Thymidylate synthase	TYMS	16601
UDP-glucuronosyltransferase 1-1	UGT1A1	16602

In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding a growth advantage factor to produce an armored T-cell. Silencing or reducing expression of an oncogene can confer a growth advantage for an armored T-cell of the disclosure. For example, silencing or reducing expression (e.g. disrupting expression) of a TET2 gene during a CAR-T manufacturing process results in the generation of an armored CAR-T with a significant capacity for expansion and subsequent eradication of a tumor when compared to an un-armored CAR-T lacking this capacity for expansion. This strategy may be coupled to a safety switch (e.g. an iC9 safety switch of the disclosure), which allows for the targeted disruption of an armored CAR-T-cell in the event of an adverse reaction from a subject or uncontrolled growth of the armored CAR-T. Exemplary growth advantage factors include, but are not limited to, the factors provided in Table 8.

TABLE 8

Exemplary Growth Advantage Factors.

Full Name	Abbreviation	SEQ ID NO:
Ten Eleven Translocation 2	TET2	16603
DNA (cytosine-5)-methyltransferase 3A	DNMT3A	16604
Transforming protein RhoA	RHOA	16605

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TABLE 8-continued

Exemplary Growth Advantage Factors.		
Full Name	Abbreviation	SEQ ID NO:
Proto-oncogene vav	VAV1	16606
Rhombotin-2	LMO2	16607
T-cell acute lymphocytic leukemia protein 1	TAL1	16608
Suppressor of cytokine signaling 1	SOCS1	16609

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TABLE 8-continued

Exemplary Growth Advantage Factors.

Full Name	Abbreviation	SEQ ID NO:
herpes virus entry mediator	HVEM	16610
T cell death-associated gene 8	TDAG8	16611
BCL6 corepressor	BCOR	16612
B and T cell attenuator	BTLA	16613
SPARC-like protein 1	SPARCL1	16614
Msh homeobox 1-like protein	MSX1	16615

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Armored T-Cells “Null or Switch Receptor” Strategy
In some embodiments, a T-cell of the disclosure is modified to express a modified/chimeric checkpoint receptor to produce an armored T-cell of the disclosure.

In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor. A null receptor, decoy receptor or dominant negative receptor of the disclosure may be modified/chimeric receptor/protein. A null receptor, decoy receptor or dominant negative receptor of the disclosure may be truncated for expression of the intracellular signaling domain. Alternatively, or in addition, a null receptor, decoy receptor or dominant negative receptor of the disclosure may be mutated within an intracellular signaling domain at one or more amino acid positions that are determinative or required for effective signaling. Truncation or mutation of null recep-

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tor, decoy receptor or dominant negative receptor of the disclosure may result in loss of the receptor's capacity to convey or transduce a checkpoint signal to the cell or within the cell.

For example, a dilution or a blockage of an immunosuppressive checkpoint signal from a PD-L1 receptor expressed on the surface of a tumor cell may be achieved by expressing a modified/chimeric PD-1 null receptor on the surface of an armored T-cell of the disclosure, which effectively competes with the endogenous (non-modified) PD-1 receptors also expressed on the surface of the armored T-cell to reduce or inhibit the transduction of the immunosuppressive checkpoint signal through endogenous PD-1 receptors of the armored T cell. In this exemplary embodiment, competition between the two different receptors for binding to PD-L1 expressed on the tumor cell reduces or diminishes a level of effective checkpoint signaling, thereby enhancing a therapeutic potential of the armored T-cell expressing the PD-1 null receptor.

In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is a transmembrane receptor.

In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or domi-

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nant negative receptor that is a membrane-associated or membrane-linked receptor/protein.

In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is an intracellular receptor/protein.

In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is an intracellular receptor/protein. Exemplary null, decoy, or dominant negative intracellular receptors/proteins of the disclosure include, but are not limited to, signaling components downstream of an inhibitory checkpoint signal (as provided, for example, in Tables 2 and 3), a transcription factor (as provided, for example, in Table 4), a cytokine or a cytokine receptor, a chemokine or a chemokine receptor, a cell death or apoptosis receptor/ligand (as provided, for example, in Table 5), a metabolic sensing molecule (as provided, for example, in Table 6), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 7), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 8). Exemplary cytokines, cytokine receptors, chemokines and chemokine receptors of the disclosure include, but are not limited to, the cytokines and cytokine receptors as well as chemokines and chemokine receptors provided in Table 9.

TABLE 9

Exemplary Cytokines, Cytokine receptors, Chemokines and Chemokine Receptors.		
Full Name	Abbreviation	SEQ ID NO:
4-1BB Ligand	4-1BBL	16616
Tumor necrosis factor receptor superfamily member 25	Apo3 or TNFRSF25	16617
Tumor necrosis factor receptor superfamily member 13	APRIL or TNFRSF13	16618
Bc12-associated agonist of cell death	Bc1-xL or BAD	16619
Tumor necrosis factor receptor superfamily member 17	BCMA or TNFRS17	16620
C-C motif chemokine 1	CCL1	16621
C-C motif chemokine 11	CCL11	16622
C-C motif chemokine 13	CCL13	16623
C-C motif chemokine 14	CCL14	16624
C-C motif chemokine 15	CCL15	16625
C-C motif chemokine 16	CCL16	16626
C-C motif chemokine 17	CCL17	16627
C-C motif chemokine 18	CCL18	16628
C-C motif chemokine 19	CCL19	16629
C-C motif chemokine 2	CCL2	16630
C-C motif chemokine 20	CCL20	16631
C-C motif chemokine 21	CCL21	16632
C-C motif chemokine 22	CCL22	16633
C-C motif chemokine 23	CCL23	16634
C-C motif chemokine 24	CCL24	16635
C-C motif chemokine 25	CCL25	16636
C-C motif chemokine 26	CCL26	16637
C-C motif chemokine 27	CCL27	16638
C-C motif chemokine 28	CCL28	16639
C-C motif chemokine 3	CCL3	16640
C-C motif chemokine 4	CCL4	16641
C-C motif chemokine 5	CCL5	16642
C-C motif chemokine 7	CCL7	16643
C-C motif chemokine 8	CCL8	16644
C-C chemokine receptor type 1	CCR1	16645
C-C chemokine receptor type 10	CCR10	16646
C-C chemokine receptor type 11	CCR11	16647
C-C chemokine receptor type 2	CCR2	16648
C-C chemokine receptor type 3	CCR3	16649
C-C chemokine receptor type 4	CCR4	16650
C-C chemokine receptor type 5	CCR5	16651
C-C chemokine receptor type 6	CCR6	16652
C-C chemokine receptor type 7	CCR7	16653
C-C chemokine receptor type 8	CCR8	16654
C-C chemokine receptor type 9	CCR9	16655

TABLE 9-continued

Exemplary Cytokines, Cytokine receptors, Chemokines and Chemokine Receptors.		
Full Name	Abbreviation	SEQ ID NO:
Granulocyte colony-stimulating factor receptor	CD114 or CSF3R	16656
Macrophage colony-stimulating factor 1 receptor	CD115 or CSF1R	16657
Granulocyte-macrophage colony-stimulating factor receptor subunit alpha	CD116 or CSF2RA	16658
Mast/stem cell growth factor receptor Kit	CD117 or KIT	16659
Leukemia inhibitory factor receptor	CD118 or LIFR	16660
Tumor necrosis factor receptor superfamily member 1A	CD120a or TNFRSF1A	16661
Tumor necrosis factor receptor superfamily member 1B	CD120b or TNFRSF1B	16662
Interleukin-1 receptor type 1	CD121a or IL1R1	16663
Interleukin-2 receptor subunit beta	CD122 or IL2RB	16664
Interleukin-3 receptor subunit alpha	CD123 or IL3RA	16665
Interleukin-4 receptor subunit alpha	CD124 or IL4R	16666
Interleukin-6 receptor subunit alpha	CD126 or IL6R	16667
Interleukin-7 receptor subunit alpha	CD127 or IL7R	16668
Interleukin-6 receptor subunit beta	CD130 or IL6ST	16669
Cytokine receptor common subunit gamma	CD132 or IL2RG	16670
Tumor necrosis factor ligand superfamily member 8	CD153 or TNFSF8	16671
CD40 ligand	CD154 or CD40L	16672
Tumor necrosis factor ligand superfamily member 6	CD178 or FASLG	16673
Interleukin-12 receptor subunit beta-1	CD212 or IL12RB1	16674
Interleukin-13 receptor subunit alpha-1	CD213a1 or IL13RA1	16675
Interleukin-13 receptor subunit alpha-2	CD213a2 or IL13RA2	16676
Interleukin-2 receptor subunit alpha	CD25 or IL2RA	16677
CD27 antigen	CD27	16678
Tumor necrosis factor receptor superfamily member 8	CD30 or TNFRSF	16679
T-cell surface glycoprotein CD4	CD4	16680
Tumor necrosis factor receptor superfamily member 5	CD40 or TNFRSF5	16681
CD70 antigen	CD70	16682
Tumor necrosis factor receptor superfamily member 6	CD95 or FAS or FNFRSF6	16683
Granulocyte-macrophage colony-stimulating factor receptor subunit alpha	CDw116 or CSF2RA	16684
Interferon gamma receptor 1	CDw119 or IFNGR1	16685
Interleukin-1 receptor type 2	CDw12b or IL1R2	16686
Interleukin-5 receptor subunit alpha	CDw125 or IL5RA	16687
Cytokine receptor common subunit beta	CDw131 or CSF2RB	16688
Tumor necrosis factor receptor superfamily member 9	CDw137 or TNFRSF9	16689
Interleukin-10 receptor	CDw210 or IL1OR	16690
Interleukin-17 receptor A	CDw217 or IL17RA	16691
C-X3-C motif chemokine 1	CX3CL1	16692
C-X3-C chemokine receptor 1	CX3CR1	16693
C-X-C motif chemokine 1	CXCL1	16694
C-X-C motif chemokine 10	CXCL10	16695
C-X-C motif chemokine 11	CXCL11	16696
C-X-C motif chemokine 12	CXCL12	16697
C-X-C motif chemokine 13	CXCL13	16698
C-X-C motif chemokine 14	CXCL14	16699
C-X-C motif chemokine 16	CXCL16	16700
C-X-C motif chemokine 2	CXCL2	16701
C-X-C motif chemokine 3	CXCL3	16702
C-X-C motif chemokine 4	CXCL4	16703
C-X-C motif chemokine 5	CXCL5	16704
C-X-C motif chemokine 6	CXCL6	16705
C-X-C motif chemokine 7	CXCL7	16706
C-X-C motif chemokine 8	CXCL8	16707
C-X-C motif chemokine 9	CXCL9	16708
C-X-C chemokine receptor type 1	CXCR1	16709
C-X-C chemokine receptor type 2	CXCR2	16710
C-X-C chemokine receptor type 3	CXCR3	16711
C-X-C chemokine receptor type 4	CXCR4	16712
C-X-C chemokine receptor type 5	CXCR5	16713
C-X-C chemokine receptor type 6	CXCR6	16714
C-X-C chemokine receptor type 7	CXCR7	16715
Atypical chemokine receptor 1	DARC or ACKR1	16716

TABLE 9-continued

Exemplary Cytokines, Cytokine receptors, Chemokines and Chemokine Receptors.		
Full Name	Abbreviation	SEQ ID NO:
Erythropoietin	Epo	16717
Erythropoietin receptor	EpoR	16718
Receptor-type tyrosine-protein kinase Flt-3	Flt-3	16719
FLT3		
FLT3 Ligand	Flt-3L	16720
Granulocyte colony-stimulating factor receptor	G-CSF or GSF3R	16721
Tumor necrosis factor receptor superfamily member 18	GITR or TNERSFI8	16722
GITR Ligand	GITRL	16723
Cytokine receptor common subunit beta	GM-CSF or CSF2RB	16724
Interleukin-6 receptor subunit beta	gp130 or IL6ST	16725
Tumor necrosis factor receptor superfamily member 14	HVEM or TNFRSF14	16726
Interferon gamma	IFN γ	16727
Interferon gamma receptor 2	IFNGR2	16728
Interferon-alpha	IFN- α	16729
Interferon-beta	IFN- β	16730
Interleukin-1 alpha	IL1	16731
Interleukin-10	IL10	16732
Interleukin-10 receptor	IL10R	16733
Interleukin-11	IL-11	16734
Interleukin-11 receptor alpha	IL-11Ra	16735
Interleukin-12	IL12	16736
Interleukin-13	IL13	16737
Interleukin-13 receptor	IL13R	16738
Interleukin-14	IL-14	16739
Interleukin-15	IL15	16740
Interleukin-15 receptor alpha	IL-15Ra	16741
Interleukin-16	IL-16	16742
Interleukin-17	IL17	16743
Interleukin-17 receptor	IL17R	16744
Interleukin-18	IL18	16745
Interleukin-1 receptor alpha	IL-1RA	16746
Interleukin-1 alpha	IL-1 α	16747
Interleukin-1 beta	IL-1 β	16748
interleukin-2	IL2	16749
interleukin-20	IL-20	16750
Interleukin-20 receptor alpha	IL-20R α	16751
Interleukin-20 receptor beta	IL-20R β	16752
Interleukin-21	IL21	16753
Interleukin-3	IL-3	16754
interleukin-35	IL35	16755
Interleukin-4	IL4	16756
Interleukin-4 receptor	IL4R	16757
Interleukin-5	IL5	16758
Interleukin-5 receptor	IL5R	16759
Interleukin-6	IL6	16760
Interleukin-6 receptor	IL6R	16761
Interleukin-7	IL7	16762
Interleukin-9 receptor	IL-9R	16763
Leukemia inhibitory factor	LIF	16764
Leukemia inhibitory factor receptor	LIFR	16765
tumor necrosis factor superfamily member 14	LIGHT or TNFSF14	16766
Tumor necrosis factor receptor superfamily member 3	LT β R or INFRSF3	16767
Lymphotoxin-beta	LT- β	16768
Macrophage colony-stimulating factor 1	M-CSF	16769
Tumor necrosis factor receptor superfamily member 11B	OPG or TNFRSF11B	16770
Oncostatin-M	OSM	16771
Oncostatin-M receptor	OSMR	16772
Tumor necrosis factor receptor superfamily member 4	OX40 or TNFRSF4	16773
Tumor necrosis factor ligand superfamily member 4	OX40L or TNFSF4	16774
Tumor necrosis factor receptor superfamily member 11A	RANK or TNFRSF11A	16775
Kit Ligana	SCF or KITLG	16776
Tumor necrosis factor receptor superfamily member 13B	TACI or TNFRSF13B	16777
Tumor necrosis factor ligand superfamily member -13B	TALL-I or TNFSF13B	16778
TGF-beta receptor type-1	TGF- β R1	16779

TABLE 9-continued

Exemplary Cytokines, Cytokine receptors, Chemokines
and Chemokine Receptors.

Full Name	Abbreviation	SEQ ID NO:
TGF-beta receptor type-2	TGF- β R2	16780
TGF-beta receptor type-3	TGF- β R3	16781
Transforming growth factor beta-1	TGF- β 1	16782
Transforming growth factor beta-2	TGF- β 2	16783
Transforming growth factor beta-3	TGF- β 3	16784
Tumor necrosis factor alpha	TNF or TNF- α	16785
Tumor necrosis factor beta	TNF- β	16786
Thyroid peroxidase	Tpo	16787
Thyroid peroxidase receptor	TpoR	16788
Tumor necrosis factor ligand superfamily member 10	TRAIL or TNFSF10	16789
Tumor necrosis factor receptor superfamily member 10A	TRAILR1 or TNFRSF10A	16790
Tumor necrosis factor receptor superfamily member 10B	TRAILR2 or TNFRSF10B	16791
Tumor necrosis factor ligand superfamily member 11	TRANCE or TNFSF11	16792
Tumor necrosis factor ligand superfamily member 12	TWEAK or TNFSF11	16793
Lymphotactin	XCL1	16794
Cytokine SCM-1 beta	XCL2	16795

In some embodiments, the modified/chimeric checkpoint receptor comprises a switch receptor. Exemplary switch receptors may comprise a modified chimeric receptor/protein of the disclosure wherein a native or wild type intracellular signaling domain is switched or replaced with a different intracellular signaling domain that is either non-native to the protein and/or not a wild-type domain. For example, replacement of an inhibitory signaling domain with a stimulatory signaling domain would switch an immunosuppressive signal into an immunostimulatory signal. Alternatively, replacement of an inhibitory signaling domain with a different inhibitory domain can reduce or enhance the level of inhibitory signaling. Expression or overexpression, of a switch receptor can result in the dilution and/or blockade of a cognate checkpoint signal via competition with an endogenous wildtype checkpoint receptor (not a switch receptor) for binding to the cognate checkpoint receptor expressed within the immunosuppressive tumor microenvironment. Armored T cells of the disclosure may comprise a sequence encoding switch receptors of the disclosure, leading to the expression of one or more switch receptors of the disclosure, and consequently, altering an activity of an armored T-cell of the disclosure. Armored T cells of the disclosure may express a switch receptor of the disclosure that targets an intracellularly expressed protein downstream of a checkpoint receptor, a transcription factor, a cytokine receptor, a death receptor, a metabolic sensing molecule, a cancer therapy, an oncogene, and/or a tumor suppressor protein or gene of the disclosure.

Exemplary switch receptors of the disclosure may comprise or may be derived from a protein including, but are not limited to, the signaling components downstream of an inhibitory checkpoint signal (as provided, for example, in Tables 2 and 3), a transcription factor (as provided, for example, in Table 4), a cytokine or a cytokine receptor, a chemokine or a chemokine receptor, a cell death or apoptosis receptor/ligand (as provided, for example, in Table 5), a metabolic sensing molecule (as provided, for example, in Table 6), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 7), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 8). Exemplary cytokines, cytokine receptors, chemokines

and chemokine receptors of the disclosure include, but are not limited to, the cytokines and cytokine receptors as well as chemokines and chemokine receptors provided in Table 9. 30 Armored T-Cells “Synthetic Gene Expression” Strategy

In some embodiments, a T-cell of the disclosure is modified to express chimeric ligand receptor (CLR) or a chimeric antigen receptor (CAR) that mediates conditional gene expression to produce an armored T-cell of the disclosure. The combination of the CLR/CAR and the condition gene expression system in the nucleus of the armored T cell constitutes a synthetic gene expression system that is conditionally activated upon binding of cognate ligand(s) with CLR or cognate antigen(s) with CAR. This system may help to ‘armor’ or enhance therapeutic potential of modified T cells by reducing or limiting synthetic gene expression at the site of ligand or antigen binding, at or within the tumor environment for example.

Exogenous Receptors

In some embodiments, the armored T-cell comprises a composition comprising (a) an inducible transgene construct, comprising a sequence encoding an inducible promoter and a sequence encoding a transgene, and (b) a receptor construct, comprising a sequence encoding a constitutive promoter and a sequence encoding an exogenous receptor, such as a CLR or CAR, wherein, upon integration of the construct of (a) and the construct of (b) into a genomic sequence of a cell, the exogenous receptor is expressed, and wherein the exogenous receptor, upon binding a ligand or antigen, transduces an intracellular signal that targets directly or indirectly the inducible promoter regulating expression of the inducible transgene (a) to modify gene expression.

In some embodiments of a synthetic gene expression system of the disclosure, the composition modifies gene expression by decreasing gene expression. In some embodiments, the composition modifies gene expression by transiently modifying gene expression (e.g. for the duration of binding of the ligand to the exogenous receptor). In some embodiments, the composition modifies gene expression acutely (e.g. the ligand reversibly binds to the exogenous receptor). In some embodiments, the composition modifies

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gene expression chronically (e.g. the ligand irreversibly binds to the exogenous receptor).

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises an endogenous receptor with respect to the genomic sequence of the cell. Exemplary receptors include, but are not limited to, intracellular receptors, cell-surface receptors, transmembrane receptors, ligand-gated ion channels, and G-protein coupled receptors.

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In some embodiments, the non-naturally occurring receptor is a synthetic, modified, recombinant, mutant or chimeric receptor. In some embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a T-cell receptor (TCR). In some embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a scaffold protein. In some embodiments, including those wherein the non-naturally occurring receptor does not comprise a transmembrane domain, the non-naturally occurring receptor interacts with a second transmembrane, membrane-bound and/or an intracellular receptor that, following contact with the non-naturally occurring receptor, transduces an intracellular signal.

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In some embodiments, the non-naturally occurring receptor is a synthetic, modified, recombinant, mutant or chimeric receptor. In some embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a T-cell receptor (TCR). In some embodiments, the non-naturally occurring receptor comprises one or more sequences isolated or derived from a scaffold protein. In some embodiments, the non-naturally occurring receptor comprises a transmembrane domain. In some embodiments, the non-naturally occurring receptor interacts with an intracellular receptor that transduces an intracellular signal. In some embodiments, the non-naturally occurring receptor comprises an intracellular signalling domain. In some embodiments, the non-naturally occurring receptor is a chimeric ligand receptor (CLR). In some embodiments, the CLR is a chimeric antigen receptor (CAR).

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In some embodiments, the CLR is a chimeric antigen receptor (CAR). In some embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In some embodiments, the ectodomain of (a) further comprises a signal peptide. In some embodiments, the ectodomain of (a) further comprises a hinge between the ligand recognition region and the transmembrane domain.

In some embodiments of the CLR/CARs of the disclosure, the signal peptide comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3, CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1 BB or GM-CSFR signal peptide. In some embodiments, the signal peptide comprises a sequence encoding a human CD8 α signal peptide. In some embodiments, the signal peptide comprises an amino acid sequence comprising MALPTALLPLALLHAARP (SEQ ID NO: 17000). In some embodiments, the signal peptide is encoded

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by a nucleic acid sequence comprising atggcactgccagt-caccgcctgtctgcctctggctgctgcacgcagctagatcca (SEQ ID NO: 17001).

In some embodiments of the CLR/CARs of the disclosure, the transmembrane domain comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1BB or GM-CSFR transmembrane domain. In some embodiments, the transmembrane domain comprises a sequence encoding a human CD8 α transmembrane domain. In some embodiments, the transmembrane domain comprises an amino acid sequence comprising IYI-WAPLAGTCGVLLSLVITLYC (SEQ ID NO: 17002). In some embodiments, the transmembrane domain is encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17003)
atctacattttggccaccactggccggggacctgtggag
tgctgctgtgtggcatcacactgtactgc.

In some embodiments of the CLR/CARs of the disclosure, the endodomain comprises a human CD3 ζ endodomain. In some embodiments, the at least one costimulatory domain comprises a human 4-1BB, CD28, CD3 ζ , CD40, ICOS, MyD88, OX-40 intracellular segment, or an) combination thereof. In some embodiments, the at least one costimulatory domain comprises a human CD3 ζ and/or a 4-1 BB costimulatory domain. In some embodiments, the CD3 ζ costimulatory domain comprises an amino acid sequence comprising RVKFSRSADAPAYKQGQNQLY-NELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRGKGHDGLYQGLSTATKDTYDALHMQALP PR (SEQ ID NO: 17004). In some embodiments, the CD3 ζ costimulatory domain is encoded by a nucleic acid sequence comprising

(SEQ ID NO: 17005)
cgctgtgaagtttagtcgtatcagcagatgccccagtttacaaaca
gggacagaaccagctgtataacgagctgtatctggccggccgag
agaaatatgacgtgtggataagcggagaggacgcgaccggaa
atggggaggcaagcccaggcgcaaaaaaccctcaggaaggcgtta
taacgagctgcagaaggacaaaatggcagaagcctattctgaga
tggcatgaagggggggcgacggagaggcaaggcgcacatgg
ctgttaccaggactgagcaccccacaaaggacaccttatgtgc
tctgcataatgcaggcactgtgttccagg.

In some embodiments, the 4-1BB costimulatory domain comprises an amino acid sequence comprising KRGRKKL-LYIFKQPMPVQTTQEEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 17006). In some embodiments, the 4-1BB costimulatory domain is encoded by a nucleic acid sequence comprising aagagaggcaggaagaactgtgtatatttcaaacagcccttcatgegccccgtgcagactaccaggaggagaacgggtgtcc ttgcgttccctgaggaaggaggaggcgggtgtgactg (SEQ ID NO: 17007). In some embodiments, the 4-1BB costimulatory domain is located between the transmembrane domain and the CD3 ζ costimulatory domain.

In some embodiments of the CLR/CARs of the disclosure, the hinge comprises a sequence derived from a human CD8 α , IgG4, and/or CD4 sequence. In some embodiments, the hinge comprises a sequence derived from a human

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CD8 α sequence. In some embodiments, the hinge comprises an amino acid sequence comprising

(SEQ NO: 17008) 5
 TTTPAPRPPPTPAPTIASQPLSLR
 PEACRPAAGGAVHTRGLDFACD,

In some embodiments, the hinge is encoded by a nucleic acid sequence comprising actaccacaccaggcacctagaccac- 10 caactccagtcacaaccatcgcgagtccggcctgagtcgagacct- gaggccgtcaggcc agctcgaggaggagg- etgtgcacaccaggggctggacttcgcctgagac (SEQ ID NO: 17028). In some embodiments, the hinge is encoded by a nucleic acid sequence comprising ACCACAACCCCTGCCCA- 15 GACCTCCCACACCCGCCCTAC- CATCGCGAGTCAGCCCTGAGTCTGA GACCT- GAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGT- GCACACCAGGGCCTGGACTTCGCCTGC GAC (SEQ ID NO: 17009). In some embodiments, the at least one protein scaffold specifically binds the ligand.

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In some embodiments, the CLR is a chimeric antigen receptor (CAR). In some embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In some embodiments, the at least one protein scaffold comprises an antibody, an antibody fragment, a single domain antibody, a single chain antibody, an antibody mimetic, or a Centyrin (referred to herein as a CARTyrin). In some embodiments, the ligand recognition region comprises one or more of an antibody, an antibody fragment, a single domain antibody, a single chain antibody, an antibody mimetic, and a Centyrin. In some embodiments, the single domain antibody comprises or consists of a VHH or a VH (referred to herein as a VCAR). In some embodiments, the single domain antibody comprises or consists of a VHH or a VH comprising human complementarity determining regions (CDRs). In some embodiments, the VH is a recombinant or chimeric protein. In some embodiments, the VH is a recombinant or chimeric human protein. In some embodiments, the antibody mimetic comprises or consists of an affibody, an affilin, an affimer, an affitin, an alphabody, an anticalin, an avimer, a DARPin, a Fynomeric, a Kunitz domain peptide or a monobody. In some embodiments, the Centyrin comprises or consists of a consensus sequence of at least one fibronectin type III (FN3) domain.

In some embodiments of the compositions of the disclosure, the exogenous receptor of (b) comprises a non-naturally occurring receptor. In some embodiments, the CLR is a chimeric antigen receptor (CAR). In some embodiments, the chimeric ligand receptor comprises (a) an ectodomain comprising a ligand recognition region, wherein the ligand recognition region comprises at least scaffold protein; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In some embodiments, the Centyrin comprises or consists of a consensus sequence of at least one fibronectin type III (FN3) domain. In some embodiments, the at least one fibronectin type III (FN3) domain is derived from a human protein. In some embodiments, the human protein is Tenascin-C. In some embodiments, the consensus sequence comprises LPAPKNLVV- 60 SEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVG- 65

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AINLTVPGSERSYDL
 TGLKPGTEYTVSIYGVKGGRHSNPLSAEFTT (SEQ ID NO: 17010). In some embodiments, the consensus sequence comprises MLPAPKNLVVSEVTEDSLRLSWTAPDAAF- DSFLIQYQESEKVGAEAINLTVPGSERSYD
 LTGLKPGTEYTVSIYGVKGGRHSNPLSAEFTT (SEQ ID NO: 17011). In some embodiments, the consensus sequence is modified at one or more positions within (a) a A-B loop comprising or consisting of the amino acid residues TEDS at positions 13-16 of the consensus sequence; (b) a B-C loop comprising or consisting of the amino acid residues TAPDAAF at positions 22-28 of the consensus sequence; (c) a C-D loop comprising or consisting of the amino acid residues SEKVGE at positions 38-43 of the consensus sequence; (d) a D-E loop comprising or consisting of the amino acid residues GSER at positions 51-54 of the consensus sequence; (e) a E-F loop comprising or consisting of the amino acid residues GLKPG at positions 60-64 of the consensus sequence; (f) a F-G loop comprising or consisting of the amino acid residues KGGHRSN at positions 75-81 of the consensus sequence; or (g) any combination of (a)-(f). In some embodiments, the Centyrin comprises a consensus sequence of at least 5 fibronectin type III (FN3) domains. In some embodiments, the Centyrin comprises a consensus sequence of at least 10 fibronectin type III (FN3) domains. In some embodiments, the Centyrin comprises a consensus sequence of at least 15 fibronectin type III (FN3) domains. In some embodiments, the scaffold binds an antigen with at least one affinity selected from a K_D of less than or equal to 10^{-9} M, less than or equal to 10^{-10} M, less than or equal to 10^{-11} M, less than or equal to 10^{-12} M, less than or equal to 10^{-13} M, less than or equal to 10^{-14} M, and less than or equal to 10^{-15} M. In some embodiments, the K_D is determined by surface plasmon resonance.

Inducible Promoters

In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an NF κ B promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an interferon (IFN) promoter or a sequence encoding an interleukin-2 promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding a nuclear receptor subfamily 4 group A member 1 (NR4A1; also known as NUR77) promoter or a sequence encoding a NR4A1 promoter. In certain embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding a T-cell surface glycoprotein CD5 (CD5) promoter or a sequence encoding a CD5 promoter. In certain embodiments, the interferon (IFN) promoter is an IFN γ promoter. In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a cytokine or a chemokine. In certain embodiments, the cytokine or chemokine comprises IL2, IL3, IL4, IL5, IL6, IL10, IL12, IL13, IL17A/F, IL21, IL22, IL23, transforming growth factor beta (TGF β), colony stimulating factor 2 (GM-CSF), interferon gamma (IFN γ), Tumor necrosis factor (TNF α), LT α , perforin, Granzyme C (Gzmc), Granzyme B (Gzmb), C-C motif chemokine ligand 5 (CCL5), C-C motif chemokine ligand 4 (CCL4), C-C motif chemokine ligand 3 (CCL3), X-C motif chemokine ligand 1 (XCL1) and LIF interleukin 6 family cytokine (Lif).

In certain embodiments of the compositions of the disclosure, including those wherein the sequence encoding the inducible promoter of (a) comprises a sequence encoding a NR4A1 promoter or a sequence encoding a NR4A1 promoter, the NR4A1 promoter is activated by T-cell Receptor

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(TCR) stimulation in T cells and by B-cell Receptor (BCR) stimulation in B cells, therefore, inducing expression of any sequence under control of the NR4A1 promoter upon activation of a T-cell or B-cell of the disclosure through a TCR or BCR, respectively.

In certain embodiments of the compositions of the disclosure, including those wherein the sequence encoding the inducible promoter of (a) comprises a sequence encoding a CD5 promoter or a sequence encoding a CD5 promoter, the CD5 promoter is activated by T-cell Receptor (TCR) stimulation in T cells, therefore, inducing expression of any sequence under control of the CD5 promoter upon activation of a T-cell of the disclosure through a TCR.

In certain embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene comprising a surface protein involved in cell differentiation, activation, exhaustion and function. In certain embodiments, the gene comprises CD69, 15 CD71, CTLA4, PD-1, TIGIT, LAG3, TIM-3, GITR, MHCII, COX-2, FASL and 4-1BB.

In some embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a gene involved in CD metabolism and differentiation. In some embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived 25 from the promoter of Nr4a1, Nr4a3, Tnfrsf9 (4-1BB), Sema7a, Zfp3612, Gadd45b, Dusp5, Dusp6 and Neto2. Inducible Transgene

In some embodiments, the inducible transgene construct comprises or drives expression of a signaling component 30 downstream of an inhibitory checkpoint signal (as provided, for example, in Tables 2 and 3), a transcription factor (as provided, for example, in Table 4), a cytokine or a cytokine receptor, a chemokine or a chemokine receptor, a cell death or apoptosis receptor/ligand (as provided, for example, in 35 Table 5), a metabolic sensing molecule (as provided, for example, in Table 6), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 7 and/or 1), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 8). Exemplary cytokines, cytokine receptors, chemokines and chemokine receptors of the disclosure include, but are not limited to, the cytokines and cytokine receptors as well as chemokines and chemokine receptors provided in Table 9.

Cas-Clover

The disclosure provides a composition comprising a guide RNA and a fusion protein or a sequence encoding the fusion protein wherein the fusion protein comprises a dCas9 and a Clo051 endonuclease or a nuclease domain thereof.

Small Cas9 (SaCas9)

The disclosure provides compositions comprising a small, Cas9 (Cas9) operatively-linked to an effector. In certain embodiments, the disclosure provides a fusion protein comprising, consisting essentially of or consisting of a DNA localization component and an effector molecule, wherein the effector comprises a small, Cas9 (Cas9). In certain embodiments, a small Cas9 construct of the disclosure may comprise an effector comprising a type IIS endonuclease.

Amino acid sequence of *Staphylococcus aureus* Cas9 with an active catalytic site.

(SEQ ID NO: 17074)
1 mkrnyilgld igitsvgyg i dyetrdvid
agvrlfkean vennegrsk rgarrlkrrr

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-continued

61 rhriqrvkkl lfdynlltdh selsginpye
arvkglsqkl seeefsaall hlakrrgvhn
121 vneveedtgn elstkeqisr nskaleekyv
aeglqlerlkk dgevrsgsinr fktsdyvkea
181 kgllkvqkay hqldqsfidt yidlletrrt
yyegpgegsp fgwkdikewy emlmghctyf
241 peelrsvkya ynadlynaln dlnnlvitrd
enekeyyek fqiienvfq kkkptlkqia
301 keilvneedi kgvrvtstgk peftnlkvhy
dikditarke iienaelldq iakiltivqs
361 sedigeeltn inseltqeei egisnikgyt
gthnlslkai nlildelwht ndnqiaifnr
421 lk1vpkkvd1 sqqkeipttl vddfilspvv
krsfiqsikv inaiikkylg pndiiielar
481 eknnskdaqkm inemqkrnrq tnerieeiir
ttgkenakyl iekiklhdmq egkclyslea
541 ipledllnnp fnyevdhiip rsvsfdnsfn
nkvlvkqeen skkgnrtpfq ylsssdskis
601 yetfkkhln lakgkgrisk tkkeylleer
dinrfsqvkd finrnldvtr yatrglmnll
661 rsyfrvnld vkvksinggf tsflrrkwkf
kkernkgykh haedaliian adfifkewkk
721 ldkakkvmen qmfeekqaes mpeieteqey
keifitphqi khikdfkdyk yshrvdkkpn
781 relindtlys trkddkgntl ivnnlnglyd
kdndk1kkli nkspekllmv hhdpqtyqkl
841 klimeqyde knplykyyee tgnyltkysk
kdngpvikk kyygnlnah 1ditddypns
901 rnkvvvklslk pyrfdvylnd gvykfvtvkn
ldvikkenyy evnskcyeea kklkkisnqa
961 efiasfynnd likingelyr vigvnndl
rievnmidit yreyienmnd krpprikti
1021 asktqskky stdilgnlve vkskkhpqii
kkg

Inactivated, Small Cas9 (dSaCas9)

The disclosure provides compositions comprising an inactivated, small, Cas9 (dSaCas9) operatively-linked to an effector. In certain embodiments, the disclosure provides a fusion protein comprising, consisting essentially of or consisting of a DNA localization component and an effector molecule, wherein the effector comprises a small, inactivated Cas9 (dSaCas9). In certain embodiments, a small, inactivated Cas9 (dSaCas9) construct of the disclosure may 60 comprise an effector comprising a type IIS endonuclease.

dSaCas9 Sequence: D10A and N580A mutations (bold, capitalized, and underlined) inactivate the catalytic site.

US 12,385,061 B2

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(SEQ ID NO: 17075)

1	mkrnviigla	igitsvgysi	idyetrvid
	agvrlfkean	vennegrrsk	rgarrlkrrr
61	rhrigrvkkl	lfdvnlltdh	selsginpye
	arvkglsql	seeefsaall	hlakrrgahn
121	vneveedtgn	elstkeqisr	nskaleekv
	aelqlerlkk	dgevrgsinr	fktstdyvkea
181	kglkvqkay	hqlqsfidt	yidlletrrt
	yyegpgegsp	fgwkdikewy	eumlmgchctyf
241	peelrvky	ynadlynaln	dlnnlvitrd
	enekeyyek	fqienvfk	kkptlkqia
301	keilvneedi	kgyrvtstqk	peftnlkvhy
	dikditarke	iienaelldq	iakiltiyqs
361	sediqueelt	lnseltqeei	eqisnlkgyt
	gthnlslkai	nlidelwht	ndnqiaifnr
421	lklvpkkvd	sqqkeipttl	vddfilspvv
	krsfiqsikv	inaiikk	ygipndiielar
481	eknskdaqkm	inemqkrnq	tnerieeiir
	ttgkenakyl	iekiklhdmq	egkclyslea
541	ipledllnnp	fnyevdhiip	rsvsfdnsfn
	nkvlvkqee	skkgnrtpf	ylssssdkis
601	yetfkkhilm	lakgkgrisk	tkkeylleer
	dinrfsvqkd	finrnldvtr	yatrglmnll

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661	rsyfrvnnld	vkvksinggf	tsflrrkwkf
	kkernkgykh	haedaliian	adfifkewkk
721	ldkakkvmen	qmfeekqaes	mpeieteqey
	keifitphqi	khikdfkdyk	yshrvdkpn
781	relindtlys	trkddkgntl	ivnnlnlyd
	kdndklkkli	nkspekkllmy	hdpqtyqkl
841	klimeqygd	knplykyee	tnylnlkysk
	kdngpvikk	kyygnklnah	lditddypns
901	rnkvvklslk	pyrfdvyldn	gvykfvtvkn
	ldvikkenyy	evnskcyeeaa	kkkkkisenqa
961	efiasfynnd	likingelyr	vigvnndl
	rievnmidit	yreylenmnd	krppriiki
1021	asktgsikky	stdilgnlye	vkskkhpqii
	kkg		

Inactivated Cas9 (dCas9)

25 The disclosure provides compositions comprising an inactivated Cas9 (dCas9) operatively-linked to an effector. In certain embodiments, the disclosure provides a fusion protein comprising, consisting essentially of or consisting of a DNA localization component and an effector molecule, 30 wherein the effector comprises an inactivated Cas9 (dCas9). In certain embodiments, an inactivated Cas9 (dCas9) construct of the disclosure may comprise an effector comprising a type IIIS endonuclease.

In certain embodiments, the dCas9 of the disclosure 35 comprises a dCas9 isolated or derived from *Staphylococcus pyogenes*. In certain embodiments, the dCas9 comprises a dCas9 with substitutions at positions 10 and 840 of the amino acid sequence of the dCas9 which deactivate the catalytic site. In certain embodiments, these substitutions are D10A and H840A. In certain embodiments, the amino acid sequence of the dCas9 comprises the sequence of:

(SEQ ID NO: 17076)

1	XDKKYSIGLA	IGTNSVGWAV	ITDEYKVPSK	KFKVGLNTDR	HSIKKNLIGA	LLFDSGETAE
61	ATRLKRTARR	RYTRRKNRIC	YLQEIFSNEM	AKVDDSPFHR	LEESFLVEED	KKHERHPIFG
121	NIVDEVAYHE	KYPTTYHLRK	KLDSTDKD	LRLIYALAH	MIKFRGHFL	EGDLNPNDN
181	VDKLFIQLVQ	TYNQLFEENP	INASGVDAKA	ILSARLSKSR	RLENLIAQLP	GEKKNGLFGN
241	LIALSLGLTP	NFKSNFDLAE	DAKLQLSKDT	YDDLDNLNA	QIGDQYADLF	LAAKNLSDAI
301	LLSDILRVNT	EITKAPLSAS	MIKRYDEHHQ	DLLTLKALVR	QQLPEKYKEI	FFDQSKHGYA
361	GYIDGGASQE	EFYKFIKPIL	EKMDGTEELL	VKLNREDLLR	KQRTFDNGSI	PHQIHLGELH
421	AILRRQEDFY	PFLKDNREKI	EKILTFRIPY	YVGPLARGKS	RFAWMTRKSE	ETITPWNFEE
481	VVDKGASAQS	FIERMTNFDK	NLPNEKVLPK	HSLLYEYFTV	YNELTKVKYV	TEGMRKPAFL
541	SGEQKKAIVD	LLFKTNRKVT	VKQLKEDYFK	KIECFDSVEI	SGVEDRFNAS	LGTYHDLLKI
601	IKDKDFLDNE	ENEDILEDIV	LTLTLFEDRE	MIEERLKTYA	HLFDDKVMKQ	LKRRRTGWG
661	RLSRKLINGI	RDKQSGKTIL	DFLKSDGFAN	RNFMQLIHDD	SLTFKEDIQK	AQVSGQGDSL
721	HEHIAMLAGS	PAIKKGILQT	VKVVDELVKV	MGRHKPENIV	IEMARENQTT	QKGQKNSRER
781	MKRIEEGIKE	LGSQILKEHP	VENTQLQNEK	LYLYYLQNGR	DMYVDQELDI	NRLSDYDVDA
841	IVPQSFLKDD	SIDNKVLTRS	DKNRGKSDNV	PSEEVVKKMK	NYWRQLLNAK	LITQRKFDSL

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901 TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILDLSRMN TKYDENDKLI REVKVITLKS
 961 KLVSDPRKDF QFYKVREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
 1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGDRF
 1081 ATVRKVL SMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
 1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDLIIKLPK
 1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLGSPE DNEQKQLFVE
 1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRSK PIREQAENII HLFTLTNLGA
 1321 PAAFKYFDTT IDRKYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD.

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In certain embodiments, the amino acid sequence of the dCas9 comprises the sequence of:

(SEQ ID NO: 17077
 1 MBKKYSIGLA IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSETAE
 61 ATRLRRRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSSFFKR LEESFLVEED KKHERHPIFG
 121 NIVDEVAYHE KYPTIYHLRK KLVDSTDKAD LRLIYLALAH MIKFRGHFLI EGDLNPNDSD
 181 VDKLFITQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
 241 LIALSLGLTP NFKNFNDLAE DAKLQLSKDT YDDDDLDNLLA QIGDQYADLF LAAKNLSDAI
 301 LLSDILRVNT EITKAPLAS MIKRYDEHHQ DLTLKALVR QQLPEKYKEI FFDQSKNGYA
 361 GYIDGGASQE EFYKFIKPIL EKMDGTEELL VKLNREDLLR KORTFDNGSI PKQIHLGELH
 421 AILRRQEDFY PFLKDNREKI EKILTFRIPY YVGPLARGNS RFAMTRKSE ETITPWNFEE
 481 VVDKGASAQS FIERMTMFDK NLPNEKVLPK HSLLYEYFTV YNEELTKVKYV TEGMRKPAFL
 541 SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLLKI
 601 IKDKDFLDNE ENEDILEDIV LTTLTFEDRE MIEERLKTYA HLFDDKVMQ LKRRRTGWG
 661 RLSRKLINGI RDKQSGKTI DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGDSDL
 721 HEHIANLAGS PAIKKGILQT VKVVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER
 781 MKRIEEGIKE LGSQILKEHP VENTOLQNEK LYLYYYLQNGR DMVVDQELDI NRRLSDYDVDA
 841 IVPQSFLKDD SIDNKVLTRS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDSL
 901 TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILDLSRMN TKYDENDKLI REVKVITLKS
 961 KLVSDPRKDF QFYKVREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
 1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGDRF
 1081 ATVRKVL SMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
 1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDLIIKLPK
 1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLGSPE DNEQKQLFVE
 1281 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRSK PIREQAENII HLFTLTNLGA
 1321 PAAFKYFDTT IDRKYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD.

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Clo051 Endonuclease

An exemplary Clo051 nuclease domain may comprise, consist essentially of or consist of, the amino acid sequence of:

(SEQ ID NO: 17078)
EGIKSNISLLKDELRGQISHEYL**LIDLA**FDS**KQNRLF**
EMKV**LELLVNEYGFGRHLGGSRKPDGIV**STTLEDNFG**I**
VDTKAYSEGYSLPISQA**DEMERYVRENSRDEEVNP**NKWW
NFSEEVKYYFVFISGSFKGKFEQLRRLSMTTGNGSAVN
WNLLGAEKIRSGEMTIEELERAMFNSEFILKY

Cas-Clover Fusion Protein

In certain embodiments, an exemplary dCas9-Clo051 fusion protein (embodiment 1) may comprise, consist essentially of or consist of, the amino acid sequence of (Clo051 sequence underlined, linker bold italics, dCas9 sequence (*Streptococcus pyogenes*) in italics):

(SEQ ID NO: 17079)
MAPKKKRKVEGIKSNISLLKDELRGQI**SHEYL****LIDLA**FDS**KQNRL**
FEMKVLELLVNEYGFGRHLGGSRKPDGIV**Y**STTLEDNFG**I****IVD**T**KAYS**
EGYS**LPISQA****DEMERYVRENSRDEEVNP**NKWW**ENFSEEVKYYFVFIS**
GSF**KGK**FEQLRRLSMTTGNGSAVN**VNNLLGAEKIRSGEMTIEELER**
AMP**NNSEFILKY****GGGGS****DKKYSIGLAI**GTN**SVGWAVITDEYKVPSK****KF**
KVLGNTDRHSIKKNLICALLFDSG**ETAEATR**LKR**TARR**YTR**RKNR****ICYL**
QEIFS**NEMAKVDD**SSFFHR**LEESFLVEED**KKHER**HPIFGN**I**DEVAYHEK**
YPTIYHLRKKLV**DSTDKADL**R**L**I**Y**LALAH**MIKFRGH**FL**IEGL**DNPD**N**
VDKLFIQ**L**V**QTYNQ**LFEE**NPINASGV**DA**KAIL**SAR**L**SKS**R**LEN**LIA**
PGEKKNGLFGNLIALSGLTPNF**KSNFD**LA**EDAKL**Q**LSK**D**TYDD**LD**N**
LAQIGDQYADLFLAA**KNLSDA**ILL**SDIL**RV**NT**E**ITKAP**LSAS**MIKRY****DE**

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HHQDLTLLKALVRQQLP**E**KIFFDQS**KNGYAGYIDGGASQEEFYKF**I
KPILEKMDGTEELLV**KLNRED**LLRK**QRTFDNGS**IP**HQI**HIGEL**HAIL**RR
5 QEDFYPFLKD**NREKIE**KILT**FRI**PYVG**PLARGNSRFAWMTRK**SEET**IT**
PWNFEVV**DKGASAGSFIER**MT**NFDKNLPNE**K**VLPKH**SLLYEYFTV**YNE**
LTKVKV**Y**TE**CMRKP**A**FLSGEQ**KK**AI**V**DLLFK**TK**NRK**V**TKQ**L**KED**Y**FK****KI**
10 ECFDS**V**E**ISGV**EDRF**N**AS**L**G**TY**HD**LLK**I**I**K**D**K**F**LD**N**EE**N**E**D**ILED**I****VL**
TL**T**LF**E**D**R**E**M**IE**E**ERL**K**T**Y**A**H**LF**DD**K**V**M**K**Q**L**K**R**R**Y**T**G**W**G**R**L**S**R**K**L****ING**
RD**K**Q**S**G**K**T**I**LD**FL**K**S**D**G**F**AN**R**N**F**M**Q**L**I**H**DD**S**LT**F**K**E**D**I**Q**K**Q**S**G**Q****G****D**
15 L**HE**H**I**AN**L**AG**S**PA**I**KK**G**I**L**Q**T**V**K**V**V**DEL**V**K**V**M**R**H**K**P**E**N**I**V**E**M**A****R****EN****Q**
TTQ**K**Q**K**N**S**R**E**R**M**K**R**I**E**E**G**I**K**L**G**S**Q****I****L**K**H**P**V**E**N**T**Q****L**Q**N**E**K**L**Y****Y****L****Q**
NGR**D**M**V**D**Q****E****L**D**I****N**R**L**S**D****Y****D**V**D**A**I****V**P**Q****S****F**L**K****D****D****S****I****D**N**K**V**L****T****R****S****D****K****N****R****G**
20 SD**N**V**P****S****E****V**V**K**K**M**N**Y**W**R**Q**L**N**A****K****L****I****T****Q****R****K****F****D****N****L****T****K****A****E****R****G****G****L****S****E****L****D****K****A**
F**I****K****R****Q****L****V****E****T****R****Q****I****T****K****H****V****A****Q****I****L****D****S****R****M****N****T****K****Y****D****E****N****D****K****L****I****R****E****V****K****V****I****T****L****K****S****K****L****V****S**
D**F****R****K****D****F****Q****F****Y****K****V****R****E****I****N****N****Y****H****A****H****D****A****Y****L****N****A****V****G****T****A****L****I****K****K****P****K****E****S****F****V****G****D**
25 K**V****Y****D****V****R****K****M****I****A****K****S****E****Q****E****I****G****K****A****T****Y****F****F****S****N****I****M****N****F****F****K****T****E****I****T****L****A****N****G****E****I****R****K****R****P**
I**E****T****N****G****E****T****G****E****I****V****W****D****X****G****R****D****F****A****T****V****R****K****V****L****S****M****P****Q****V****N****I****V****K****K****T****E****V****Q****T****G****G****F****S****K****E****S****I**
P**K****R****N****S****D****K****L****I****A****R****K****K****D****W****D****P****K****K****Y****G****F****D****S****P****T****V****A****S****V****L****V****V****A****K****V****E****K****G****K****S****K****K****L****K****S**
30 K**E****L****L****G****I****T****M****E****R****S****F****E****K****N****P****I****D****F****L****E****A****K****G****Y****K****E****V****K****K****D****L****I****I****K****L****P****K****Y****S****L****F****E****L****E****N**
R**K****R****M****L****A****S****A****G****E****L****Q****K****G****N****E****L****A****P****S****K****Y****V****N****F****L****Y****L****A****S****H****Y****E****K****L****K****G****S****P****E****D****N****E****Q****K****Q****L****F**
V**E****Q****H****K****Y****L****D****E****I****I****Q****I****S****E****F****K****R****V****I****L****A****D****N****L****K****V****L****S****A****Y****N****K****R****D****K****P****I****R****Q****A****E**
35 N**I****I****H****L****F****T****L****N****L****G****A****P****A****A****F****K****Y****F****D****T****I****D****R****K****Y****T****S****T****K****E****V****L****D****A****T****L****I****H****Q****S****I****T****G****Y**
E**T****R****I****D****L****S****Q****L****G****G****D****G****S****P****K****K****R****K****V****S**
In certain embodiments, an exemplary dCas9-Clo051 fusion protein (embodiment 1) may comprise, consist essentially of or consist of, the nucleic acid sequence of (dCas9 sequence derived from *Streptococcus pyogenes*):

(SEQ ID NO: 17080)
1 atggcaccaa agaagaaaag aaaagtggag ggcataagt caaacatcag cctgctgaa
61 gacgaactgc gggacagat tagtcacatc agtcacgagt acctgtcact gattgtatct
121 gccttcgaca gcaagcaga tagactgttt gagatgaaag tgctgaaact gctggtaac
181 gagtatggct tcaaggcag acatctggc gggcttagga aacctgacgg catcgatc
241 agtaccacac tggagacaa ctccggatc attgtcgata ccaaggctta ttccggaggc
301 tactgtgtc caatttagtca ggcagatggat atggaaaggat acgtgcgcga aaactcaaa
361 agggacgagg aagtcaaccc caataagtggat tgggagaatt tcagcggagg agtgaagaaa
421 tactacttcg tctttatctc aggagcttc aaaggaaaggat ttggagggaca gctgcggaga
481 ctgtccatga ctaccggggta gaacggatct gctgtcaac tggctcaatc gctgtgggc
541 gcagaaaaga tcaggtccgg ggagatgaca attggagaaac tggAACCGCAG catgttcaac
601 aattctgagt ttatcctgaa gtatggaggc gggggaaagcg ataagaaaata ctccatcgaa
661 ctggccattg gcaccaattc cgtggctgg gctgtcatca cagacgagta caaggtggca
721 agcaagaagt tcaaggcttc ggggaacacc gatgccaca gtatcaagaa aaatctgatt
781 ggagccctgc tgttcgactc aggccgagact gctgaagcaa cccgactgaa cggcggactgt

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841 aggccgcgat atacccggag aaaaaatcggtatctgtacc tgccaggaaat ttccagcaac
 901 gagatggcca aggtggacga tagtttcttt caccgcctgg aggaatcatt cctgggtggag
 961 aaagataaga aacacgagcg gcatccccatc tttggcaaca ttgtggacga agtcgcttat
 1021 cacgagaagt accctactat ctatcatctg aggaagaaac ttgtggactc caccgataag
 1081 gcagacctgc gcctgatcta tctggccctg gtcacatga tcaagttccg ggggcatttt
 1141 ctgatcgagg gagatctgaa ccctgacaat tctgatgtgg acaagctgtt catccagctg
 1201 gtccagacat acaatcagct gtttggagaa aacccaatta atgcctcagg cgtggacgca
 1261 aaggccatcc tgagggcccg actgtccaa tctaggcgcc ttggaaaacct gatcgctcag
 1321 ctgccaggag agaagaaaaa cggcctgttt gggaatctga ttgcactgtc cctggccctg
 1381 acacccaaact tcaagtctaa ttttgatctg gccgaggacg ctaagctgca gctgtccaaa
 1441 gacacttatg acgatgaccc ggataaacctg ctggctcaga tcggcgtca gtacgcagac
 1501 ctgttccctgg ccgctaagaa tctgagtgtac gccatccctgc tgcagatata tctgcgcgtg
 1561 aacacagaga ttactaaggc cccactgagt gcttcaatga tcaaaagata tgacgagcac
 1621 catcaggatc tgaccctgtc gaaggctctg gtgaggcagc agctgcccga gaaatacaag
 1681 gaaatttctt ttgatcagag caagaatggta tacggccgct atattgacgg cggggcttcc
 1741 caggaggagt tctacaagtt catcaagccc attctggaaa agatggacgg caccgagggaa
 1801 ctgctggta agctgaatcg ggaggacctg ctgagaaaaac agaggacatt tgataacgg
 1861 agcatccctc accagattca tctggcgaa ctgcacgcca tcctgcgacg gcaggaggac
 1921 ttctaccat ttctgaagga taaccgcgaa aaaatcgaaa agatcctgtac ttctcagaatc
 1981 ccctactatg tggggctct ggacggggaa aatagtagat ttgcctggat gacaagaaaag
 2041 tcagagggaaa ctatcacccc ctggaaacttc gaggaagtgg tcgataaaagg cgctagcgca
 2101 cagtccttca ttgaaaggat gacaaatttt gacaagaacc tgccaaatga gaaggtgt
 2161 cccaaacaca gcgtgtgtc cgaatatttc acagtgtata acgagctgtac taaagtgaag
 2221 tacgttaccg aaggatgtcg caagcccgaa ttctgtccg gagagcagaa gaaagccatc
 2281 gtggacctgc tttttaaagac aaatcgaaa gtgactgtca aacagctgaa ggaagactat
 2341 ttcaagaaaa ttgagttttt cgattcagtg gaaatcagcg gcgtcgagga caggtttac
 2401 gcctccctgg ggacccatcca cgatctgtc aagatcatca aggataaggg cttccctggac
 2461 aacgagggaaa atgaggacat cctggaggac atttgtgtca cactgactct gtttgggat
 2521 cgcgaaatga tcgagggaaacg actgaagact tatggccatc tggatgtca caaagtgtat
 2581 aagcagctga aaagaaggcg ctacaccggaa tggggacgccc tgagccgaaa actgtatcaat
 2641 gggatttagag acaacgacag cggaaaaactt atccctggact ttctgaagtc cgatggcttc
 2701 gccaacagga acttcatgtc gctgatttac gatgactctc tgacattcaa ggaggacatc
 2761 cagaaacgcac aggtgtctgg ccaggggggac agtctgcacg agcatatcgca aacacccgt
 2821 ggcagccccg ccataaagaa agggattctg cagacccgtga aggtgggtggaa cgaactggtc
 2881 aaggtcatgg gacgacacaa acctggaaac atcgtgatttgg agatggcccg cgaaaatcg
 2941 acaactcaga agggccagaa aaacagtgcga gaacggatgtca agagaatcgaa ggaaggcatc
 3001 aaggagactgg ggtcacatcgtt cctgaaggag catcctgtgg aaaacactca gctgcagaat
 3061 gagaaactgt atctgtacta tctgcagaat ggacgggata ttgtacgtggaa ccaggagctg
 3121 gatattaaaca gactgagtgtca ttatgacgtgtac gatgcctcgatc tccctcagatc ttctcgt
 3181 gatgactcca ttgacaacaa ggtgtgtacc aggtccgacaa agaaccgcgg caaatcagat
 3241 aatgtgcacaa gcggaggaaatgtcaagaaaa atgaagaact actggaggca gctgctgtat

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3301 gccaagctga tcacacagcg gaaatttgat aacctgacta aggcagaaaag aggaggggtg
 3361 tctgagctgg acaaggccgg cttcatcaag cgccagctgg tggagacaag acagatcact
 3421 aagcacgtcg ctcagattct ggatagcaga atgaacacaa agtacgatga aaacgacaag
 3461 ctgatcaggg aggtgaaagt cattactctg aaatccaagc tggtgtctga cttagaaag
 3541 gattccagt ttataaaagt cagggagata aacaactacc accatgctca tgacgcatac
 3601 ctgaacgcag tggtccggac cgcctgatt aagaataacc ccaagctgga gtccgagttc
 3661 gtgtacggag actataaaagt gtacgatgtc cggaaagatga tcgccaaatc tgacgagaa
 3721 attggcaagg ccaccgctaa gtatttctt tacagtaaca tcataatctt cttaagacc
 3781 gaaatcacac tggcaaatgg ggagatcaga aaaaggcctc tgattgagac caacggggag
 3841 acaggagaaa tcgttgaaa caagggaaagg gattttgcta cctgtcgcaaa agtctgtcc
 3901 atgccccaaag tgaatattgt caagaaaact gaagtgcaga cccggggatt ctctaaggag
 3961 agtattctgc ctaagcgaaa ctctgataaa ctgategccc ggaagaaaga ctgggacccc
 4021 aagaagtatg gcgggttcga ctctccaaaca gtggcttaca gtgtctgg ggtcgcaag
 4081 gtggaaaagg ggaagtccaa gaaactgaag tctgtcaaag agtgcgtgg aatcactatt
 4141 atggaacgca gtccttcga gaagaatcct atcgattttc tggaaagccaa gggctataaa
 4201 gaggtgaaga aagacctgat cattaagctg cccaaataact cactgtttga gctggaaaac
 4261 ggacgaaagc gaatgctggc aagcgcgggaaactgcaga agggcaatga gctggccctg
 4321 ccctccaaat acgtgaacctt cctgttatctg gctagccact acgagaaact gaaggggtcc
 4381 cctgaggata acgaacagaa gcagctgtt gtggagcagc acaaacatta tctggacgag
 4441 atcattgaac agattcaga gttcagcaag agagtgttcc tggctgacgc aatctggat
 4501 aaagtctga ggcatacaa caagcaccga gacaaaccaa tccggagca ggcggaaaat
 4561 atcattcatac tgttcaccc gacaaacctg ggcgcctg cagccttcaa gtattttgac
 4621 accacaatcg atcggaaagag atacacttct accaaagagg tgctggatgc taccctgtac
 4681 caccagagta ttacccgcgtatgagaca cgcacgcacc tgacacagct gggaggcgat
 4741 gggagccca agaaaaagcg gaaggtgtct agttaa

In certain embodiments, the nucleic acid sequence encoding a dCas9-Clo051 fusion protein (embodiment 1) of the disclosure may comprise a DNA. In certain embodiments, the nucleic acid sequence encoding a dCas9-Clo051 fusion protein (embodiment 1) of the disclosure may comprise an RNA.

In certain embodiments, an exemplary dCas9-Clo051 fusion protein (embodiment 2) may comprise, consist essentially of or consist of, the amino acid sequence of (Clo051 sequence underlined, linker bold italics, dCas9 sequence (*Streptococcus pyogenes*) in italics):

(SEQ ID NO: 17081)
 1 MPKKKRKVEG IKSNISSLKD ELRGQISHIS HEYLSLIDLA
FDSKQNPLFE MKVLELLVNE
 61 YGFKGRHLGG SRKPDGIVYS TTLEDNFGII VDTKAYSEGY
SLPISQADEM ERYVRENSNR
 121 DEEVNPNKWW ENFSEEVKKY YFVFISGSFK GKFREEQLRRL
SMTTGVNGSA VNVVNLLGA

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181 EKIRSGEMTI EELERAMFNN SEFILKY**GGG** GS**DKKYSIGL**
 AIGTNSVGWA VITDEYKVPS
 241 KKFVKVLGNTD RHSIKKNLIG ALLFDSDGETA EATRLKRTAR
 RRYTRRFNRI CYLQEIFSNE
 301 MAKVDDSSFFH RLEESFLVEE DKKHERHPIF GNIVDEVAYH
 EKYPTIYHLR KKLVDSTDKA
 361 DLRLIYLALA HMIKFRGHFL IEGDLNPDNS DVDKLFIQLV
 QTYNQLFEEN PINASGVDAK
 421 AILSARLSKS RRLENLIAQL PGEKKNGLFG NLIALSLGLT
 PNFKSNFDLA EDAKLQLSKD
 481 TYDDDLDNLL AQIGDQYADL FLAAKNLSDA ILLSDILRVN
 TEITKAPLSA SMIKRYDEHH
 541 QDLTLIKALV RQQLPEKYKE IFFDQSKNY AGYIDGGASQ
 EEFYKFIKPI LEKMDGTEEL

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601 *LVKLNREDLL RKQRTFDNGS IPHQIHLGEL HAILRRQEDF*
 YPFLKDNRK *IEKILITFRIP*
 661 *YYVGPLARGN SRFAWMTRKS EETITPWNFE EVVDKGASAQ*
SFIERMTNFD KNLPNEKVLP
 721 *KHSLLYEYFT VYNELTKVKY VTEGMRKPAF LSGEQEEAIV*
DLLFKTNRKV TVKQLKEDYF
 781 *KKIECFDSVE ISGVEDRFA SLGYHDLNK IIKDKDFLDN*
EENEDILEDI VLTLTFEDR
 841 *EMIEERLKTY AHLFDDKVMK QLKRRRYTGW GRLSRKLING*
IRDKQSGKTI LDFLKSDGFA
 901 *NRNFMQLIHD DSLTFKEDIQ KAQVSGQQDS LHEHIANLAG*
SPAIKKGILQ TVKVVDDELVK
 961 *VMGRHKPENI VIEMARENQT TQKGQKNSRE RMKRIEEGIK*
ELGSQILKEH PVENTQLQNE
 1021 *KLYLYYLQNG RDMYVDQELD INRLSDYDVD AIVPQSFLKD*
DSIDNKVLTR SDKNRGKSDN

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1061 *VPSEEVVKKM KNYWRQLLNA KLITQRKF DN LTKAERGGLS*
ELDKAGFIKR QLVETRQITK
 5 *1141 HVAQILDSSRM NTKYDENDKL IREVKVITLK SKLVSDFRKD*
FQFYKVREIN NYHHAHDAYL
 1201 *NAVVGTLAK KYPKLESEFV YGDYKVYDVR KMIAKSEQEI*
 10 *GKATAKYFFY SNIMNFFKTE*
 1261 *ITLANGEIRK RPLIETNGET GEIVWDKG RD FATVRKVLSM*
PQVNIVKKTE VQTGGFSKES
 15 *1321 ILPKRNSDKL IARKKDWDPK KYGGFDSPTV AYSVLVVAKV*
EKGKSKKLKS VKELLGITIM
 1381 *ERSSFEKNPI DFLEAKGYKE VKKDLIKDP KYSLFELENG*
RKRMLASAGE LQKGNELALP
 20 *1441 SKYVNFLYLA SHYEKLKGSP EDNEQKQLFV EQHKHYLDEI*
IEQISEFSKR VILADANL DK
 25 *1501 VLSAYNKHRD KPIREQAENI IHLFTLTNLG APAAFKYFDT*
TIDRKRYTST KEVLDATLIIH
 1561 *QSITGLYETR IDSQLGGDG SPKKRKV.*

In certain embodiments, an exemplary dCas9-Clo051 fusion protein (embodiment 2) may comprise, consist essentially of or consist of, the nucleic acid sequence of (dCas9 sequence derived from *Streptococcus pyogenes*):

(SEQ ID NO: 17082)

1 atgcctaaga agaagcggaa ggtgaaaggc atcaaaggca acatctccct cctgaaagac
 61 gaactccggg ggcagattag ccacattagt cacgaataacc tctccctcat cgacctggct
 121 ttccatagca agcagaacag gtccttttag atgaaagtgc tggactgtcg ctgtcaatag
 181 tacgggttca agggtcgaca cctcgccgaa tctaggaaac cagacggcat cgtgtata
 211 accacactgg aagacaactt tggatcatt gtggatacca aggcatactc tgagggttat
 231 agtctgcca ttccacaggc cgacgagatg gaacggtaac tgccgcgaaa ctcaaata
 361 gatgagaaatg tcaaccctaa caagtggtag gagaacttct ctgagaaatgaa
 421 tactcgtct ttatcagcggt gtccttcaag ggttaatttg aggaacagct caggagact
 481 agcatgacta cccgcgtgaa tggcagcgcc gtcacatcggt tcaatctgtc cctggggct
 541 gaaaagattc ggacgggaga gatgaccatc gaagagctgg agagggcaat gtttata
 501 agcgatgttta tcctgaaata cgggtgggggt ggatccgata aaaagtattt tattggtt
 661 gccatcgca ctaattccga tggatggct gtcataaccg atgaatacaa agtacattca
 721 aagaaattta aggtgttggg gaacacagac cgtcattcgta taaaaagaa tcttacgt
 781 gccctcctat tcgatagttt cgaaacggca gagggcactc gcctgaaacg aaccgcgt
 841 agaaggata cacgtcgaa gaaccgata tgtaacttac aagaaattt tagcaatgag
 901 atggccaaag ttgacgattc tttcttcac cggttggaaag agtccttcct tgtcgaag
 961 gacaagaaac atgaacggca cccatcttt ggaaacatag tagatgagg ggcataatcat
 1021 gaaaagtacc caacgatttta tcacctcaga aaaaagctag ttgactcaac tgataaaagcg
 1081 gacctgaggtaatctactt ggctcttgcc catatgataa agttccgtgg gcactttctc
 1141 attgagggtg atctaaatcc ggacaactcg gatgtcgaca aactgttcat ccagtttagta

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1201 caaacctata atcagttgtt tgaagagaac cctataaaatg caagtggcgt ggatgcgaag
 1261 gctattctta ggcggccct ctctaaatcc cgacggctag aaaacctgtat cgccacaatta
 1321 cccggagaga agaaaaatgg gttgtcggt aaccttagat cgctctcaact aggcttgaca
 1381 ccaaatttta agtcaactt cgacttagt gaagatgcca aattgcagct tagtaaggac
 1441 acgtacgatg acgatctcgaa caatctactg gcacaaatttgg gagatcagta tgccggactta
 1501 tttttggctg cccaaaacct tagcgatgca atccctctat ctgacataact gagatgttat
 1561 actgagatata ccaaggcgcc gttatccgt tcaatgtatca aaaggtaacgta tgaacatcac
 1621 caagacttga cacttctcaa ggcctctatgc cgtcagcaac tgccctgagaa atataaggaa
 1681 atattcttg atcagtcgaa aaacgggtac gcagggtata ttgacggcgag aegcagtc
 1741 gaggaattct acaagtttat caaacccata ttagagaaga tggatgggac ggaagagttg
 1801 cttgtaaaac tcaatcgca agatctactg cgaaaggcgc ggactttcgaa caacggtagc
 1861 attccacatc aaatccactt aggcgaatttgcatgtatac tttagaaggca ggaggatttt
 1921 tatccgttcc tcaaagacaa tcgtgaaaag attgagaaaa tcttaaccctt tcgcataacct
 1981 tactatgtgg gacccttggc ccgagggaaac tctcggttgc catggatgac aagaaagtcc
 2041 gaagaaacgta ttactccatg gaattttgag gaagttgtcg ataaagggtgc gtcagctaa
 2101 tcgttcatcg agaggatgac caactttgc aagaattttc cgaacgaaaa agtattgcct
 2161 aagcacagtt tactttacgat gtatttcaca gtgtacaatg aactcacgaa agttaagtat
 2221 gtcactaagg gcatcgtaa accggccctt ctaagcgaag aacagaagaa agcaatagta
 2281 gatctgttat tcaagaccaa ccgcaaaatgtg acagttaaacg aattgaaaga ggactactt
 2341 aagaaaatttgc aatgttgcgat ttctgtcgat atctccgggg tagaagatcg attaatgc
 2401 tcacttggta cgtatcatgaa cctctctaaatg ataattaaag ataaggactt cctggataac
 2461 gaagagaatg aagatatactt agaagatata gtgttactc ttacccttgc tgaagatgg
 2521 gaaatgatttgg agggaaagact aaaaacatac gtcacccgt tcgacgataa gtttatgaaa
 2581 cagttaaaga ggcgtcgcta taacgggctgg ggacgattgt cgccggaaact tatcaacggg
 2641 ataagagaca agcaaaatgtg taaaactattt ctcgattttc taaagagcga cggcttcgccc
 2701 aataggaaact ttatgcgatc gatccatgat gactctttaa ccttcaaaga ggatatacaa
 2761 aaggcacagg ttccggaca aggggactca ttgcacgaaac atattgcgaa tcttgctgg
 2821 tcgccagcca tcaaaaaggcatactccatg acagtcaaaatg tagtggatgaa gctagttaa
 2881 gtcatgggac gtcacaaacc gggaaacattt gtaatcgaa tggcacgcaaaatcaac
 2941 actcagaagg ggcaaaaaaaa cagtcgagag cggatgaaaga gaatagaaga gggattttaaa
 3001 gaactgggca gccagatctt aaaggagcat cctgtggaaa ataccaattt gcagaacgag
 3061 aaactttacc tctattacactt acaaaaatgggaa agggacatgt atggttgcata ggaactggac
 3121 ataaaccgtt tatctgatcgat cgcattgtac cccatccctt tttgaaggac
 3181 gattcaatcg acaataaaatgc gcttacacgc tcggataaga accggggaa aagtgcataat
 3241 gttccaaatgcg aggaagtcgtt aaagaaaatg aagaactattt ggcggcagctt cctaaatgc
 3301 aaactgataa cgcaaaagaaa gttcgataac ttaactaaatg ctgagaggggg tggcttgct
 3361 gaacttgcata gggccggattt tattaaacgt cagctcggttgg aaacccggcca aatcacaat
 3421 catgttgcac agataactaga ttcccgatgtt aatacgaaat acgacgagaa cgataagctg
 3481 attcggaaatg tcaaaatgttgc tcaaaaatgg tgcggactt cagaaaggat
 3541 tttcaatttctt ataaaggatgg gggatataat aactaccacc atgcgcacgta cgcttatctt

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3601 aatgccgtcg tagggaccgc actcattaag aaatacccgaa agctagaaaag ttagtttgta
3661 tatggtgatt acaaaggtaa tgacgtccgt aagatgatcg cgaaaagcga acaggagata
3721 ggcaaggcta cagccaaata ctcttttat tctaaccatta tgaatttct taagacggaa
3781 atcactctgg caaacggaga gatacgaaaa cgacctttaa ttgaaaccaa tggggagaca
3841 ggtgaaatcg tatggataa gggccgggac ttgcgcacgg tgagaaaagt ttgtccatg
3901 ccccaagtca acatagtaaa gaaaacttag gtgcagacccg gagggtttc aaaggaatcg
3961 attctccaa aaaggaatag tgataagctc atcgctcgta aaaaggactg ggacccgaaa
4021 aagtacggtg gcttcgtat ccctacagtt gcctattctg tcctagtagt ggcaaaagtt
4081 gagaaggaa aatccaagaa actgaagtca gtcaaagaat tattggggat aacgattatg
4141 gagcgctcgt ctggaaaaa gaaccccatc gacttccttg aggcgaaagg ttacaaggaa
4201 gtaaaaaaaaagg atctcataat taaaactacca aagtatagtc tggggatggtttggc
4261 cggaaaacgaa tggtggctag cgccggagat cttcaaaagg ggaacgaaact cgcaactaccg
4321 tctaaatacg tgaatttcat gtatttagcg tccattacg agaagttgaa aggttcaccc
4381 gaagataacg aacagaagca actttttgtt gacgacgaca aacattatct cgacgaaatc
4441 atagagcaaa ttccggaaatt cagtaagaga gtcatccttag ctgatgccaa tctggacaaa
4501 gtattaaacgc catacaacaa gcacaggat aaacccatac gtgagcaggc ggaaaatatt
4561 atccatttgtt ttactcttac caacctcggc gctccagccg cattcaagta ttttgacaca
4621 acgatagatc gcaaacgata cacttctacc aaggaggtgc tagacgcgcac actgattcac
4681 caatccatca cgggattata tggaaactcg atagatttgt cacagttgg ggggtgacggaa
4741 tcccccaaga agaagaggaa agtctga.

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In certain embodiments, the nucleic acid sequence encoding a dCas9-Clo051 fusion protein (embodiment 2) of the disclosure may comprise a DNA. In certain embodiments, the nucleic acid sequence encoding a dCas9-Clo051 fusion protein (embodiment 2) of the disclosure may comprise an RNA.

EXAMPLES

Example 1: Design of NF-KB Inducible Vectors for Expression in Modified T-Cells

Two T cell activation NF-KB inducible vectors were developed (FIGS. 1A and B); one with the gene expression system (GES) in the forward orientation (A) and the other in the complementary direction (B), both preceding the constitutive EF1a promoter. These vectors also direct expression of a CAR molecule and a DHFR selection gene, separated by a T2A sequence. Both the conditional NF-KB inducible system and the EF1a directed genes are a part of a piggyBac transposon which can be permanently integrated into T cells using EP. Once integrated into the genome, the T cells constitutively express the CAR on the membrane surface and the DHFR within the cell, while expression of the NF-KB inducible gene, GFP, will be expressed to the highest level only upon T cell activation.

Example 2: NF-KB Inducible Vectors for GFP Expression in Modified T-Cells

T cells were nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR murein gene under control of an EF1a promoter along with the absence (No

35 gene expression system (GES) control) or presence of an NF-KB inducible expression system driving GFP expression in either the forward (pNFKB-GFP forward) or reverse orientation (pNFKB-GFP reverse). Cells were cultured in the presence of methotrexate selection until the cells were
40 almost completely resting (Day 19) and GFP expression was assessed at Day 5 and Day 19. At Day 5, all T cells are proliferating and highly stimulated, with cells harboring the NF-KB inducible expression cassette producing high levels of GFP due to strong NF κ B activity (see FIG. 2). The No
45 GES control cells did not express detectable levels of GFP. By Day 19, the GES T cells were almost fully resting and GFP expression was significantly lower than Day 5 (~1/8 MFI), since NF κ B activity is lower. GFP expression is still observed at Day 19, which may be due to the long half-life of GFP protein (~30 hr), or, basal level of NF κ B activity through, for example, a TCR, a CAR, a cytokine receptor, or a growth factor receptor signal.

Example 3: NF-KB Inducible Vectors for Anti-BCMA CAR-Mediated GFP Expression in Modified T-Cells

55 T cells were either unmodified (Mock T cells) or nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR murein gene under control of an EF1a promoter along with the absence (No gene expression system (GES) control) or presence of an NF-KB inducible expression system driving GFP expression in either the forward (pNFKB-GFP forward) or reverse orientation (pNFKB-GFP reverse). All cells were cultured for 22 days, either with or without methotrexate selection (Mock T cells), until the cells were almost completely resting. Cells were
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then stimulated for 3 days in the absence (No stimulation) or presence of BCMA- (K562). BCMA+ (RPMI 8226), or positive control anti-CD3 anti-CD28 activation reagent (CD3/28 stimulation). GFP expression was undetectable under all conditions with the No GES control or Mock T cells. However, while pNFkB-GFP forward- and reverse-transposed cells exhibited little GFP expression over the No stimulation control when cultured with BCMA-K562 cells, they both demonstrated dramatic upregulation of gene expression either in the presence of BCMA+ tumor cells or under positive control conditions (FIG. 3). Little difference in GFP expression was observed between the pNFkB-GFP forward- and reverse-transposed cells that were cocultured with BCMA+ tumor cells.

Example 4: Control of Anti-BCMA CAR-Mediated Expression in Modified T-Cells

The expression level of inducible gene can be regulated by the number of response elements upstream or preceding the inducible promoter. T cells were nucleofected with a piggyBac vector encoding an anti-BCMA CARTyrin followed by a selection gene, both under control of a human EF a promoter (FIG. 4). Further, vectors either additionally encoded the conditional NF-KB inducible gene expression system driving expression of a truncated CD19 protein (dCD19) and included a number of NFkB response elements (RE) varying from 0-5, no GES (No GES), or received an electroporation pulse but no piggyBac nucleic acid (Mock). Data are shown for only the GES in the reverse (opposite) direction/orientation. All cells were cultured for 18 days and included selection for piggyBac-modified T cells using methotrexate addition. Cells were then stimulated for 3 days using anti-CD3 anti-CD28 bead activation reagent and dCD19 surface expression was assessed by FACS at Days 0, 3 and 18, and data are shown as FACS histograms and MFI of target protein staining. Surface dCD19 expression was detected at low levels at Day 0 in all T cells transposed with vectors encoding the GES. At 3 days post-stimulation, dramatic upregulation of dCD19 expression was observed for all T cells expressing the GES, with a greater fold increase in surface expression in those with higher numbers of REs. Thus, surface dCD19 expression was directly proportional with the number of REs encoded in the GES. No dCD19 was detected on the surface of T cells that did not harbor the GES: No GES and Mock controls.

Example 5: Expression of Human Factor IX in Modified T-Cells

Genetic deficiencies in Factor IX (FIG. 5) lead to a life threatening disease called Hemophilia B. Hemophilia B is a rare disease that affects between 1 in 25,000 and 1 in 30,000 people. Prior to the development of the compositions and methods of the disclosure, the standard treatment for Hemophilia B involved an infusion of recombinant Factor IX protein every 2-3 days, at a cost of around \$250,000 per year.

T cells are maintained in humans for several decades, and are therefore an ideal vehicle to secrete Factor IX, supplying the Factor IX missing in Hemophilia B patients without the need for frequent transfusions. T cells were transposed with PiggyBac to secrete Factor IX. When transgenic T cells encoding a human Factor IX transgene were examined for T cell markers using FACS (FIG. 6). These modified T cells were able to secrete human Factor IX (FIG. 7A), and this secreted Factor IX provided clotting activity (FIG. 7B).

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Example 6: Knock Down Efficiency of Checkpoint Signaling Proteins on Armored T-Cells

Another strategy to produce armored T-cells is to reduce or inhibit endogenous checkpoint signaling by expressing various modified/chimeric checkpoint receptors that have an altered or absent intracellular signaling domain. One mechanism to produce armored T-cells is to inhibit checkpoint signaling is to knockout various checkpoint receptors. The Cas-CLOVER™ platform was used to target and knockout the checkpoint receptors PD-1, TGF β R2, LAG-3, Tim-3, and CTLA-4 in resting (or quiescent) primary pan T cells. As measured by flow cytometry, gene editing resulted in 30-70% loss of protein expression at the cell surface (FIG. 10). These results show that Cas-CLOVER™ is able to efficiently target the knockout of these genes resulting in loss of target protein expression on the T-cell surface. Knockout efficiency can significantly be increased by further optimization of guide RNA pairs, or by using additional guide RNA pairs targeting the same gene and/or regulators or promoters of the target gene.

Example 7: Strategies for the Expression of Null or Switch Intracellular Signaling Proteins on Armored T-Cells

Another strategy to produce armored T-cells is to reduce or inhibit endogenous checkpoint signaling by expressing various modified/chimeric checkpoint receptors that have an altered or absent intracellular signaling domain. Checkpoint signals that could be targeted using this strategy include PD-1 or TGF β RII of T-cells, which bind to the PD-L1 ligand and TGF β cytokine, respectively. FIG. 11 shows a schematic diagram of various strategies for producing decoy/null/dominant negative receptor (Null receptors) for two different inhibitory receptors (PD-1 (top panel) and TGF β RII (bottom panel)). To design Null receptors, the intracellular domain (ICD) of PD1 or TGF β RII can be mutated (mutated null) or deleted (truncated null). As a result, binding of the cognate ligand(s) of the null receptor does not result in delivery of the checkpoint signal to the T-cells. Furthermore, since the Null receptor competes with wildtype receptors for binding of the endogenous ligand(s), any binding by the Null receptor sequesters endogenous ligand(s) from binding the wild-type receptor. This results in dilution of the overall level of checkpoint signaling effectively delivered to the T-cell, thus, reducing or blocking checkpoint inhibition. FIG. 11 also shows switch receptor design strategies for the inhibitory receptors PD-1 (top panel) and TGF β RII (bottom panel). In switch receptors, wildtype ICD is replaced with the ICD from either an immuno-stimulatory molecule (Co-stimulatory switch) or a different inhibitory molecule (Inhibitory switch). Immuno-stimulatory molecules include but are not limited to CD3z, CD28, 4-1BB and the examples listed in Table 2. Inhibitory molecules include but are not limited to CTLA4, PD1, Lag3 and the examples listed in Table 2. In the former case, binding of the endogenous ligand by the modified switch receptor results in the delivery of a positive signal to the T-cells, thereby helping to enhance stimulation of the T-cell, facilitating continuation of tumor targeting and killing. In the latter case, binding of the endogenous ligand by the modified switch receptor results in the delivery of a negative signal to the T-cells, thereby helping to reduce stimulation and activity of the T-cell.

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Example 8: Enhancing Surface Expression of PD1 and TGF β RII Null or Switch Intracellular Signaling Proteins on Armored T-Cells

To create armored T-cells, a number of truncated null receptors expressing alternative signal peptides (SP) and transmembrane domains (TM) were designed and tested for maximal expression on the surface of modified T-cells. FIG. 12 shows schematic diagrams of several null receptor constructs for PD-1 (top) and TGF β RII (bottom). Extracellular domains (ECD) of these proteins were modified such that the wildtype signal peptide (SP) and/or the transmembrane domains (TM) were replaced with that from the human T cell CD8 α receptor (red arrows). Each of the six truncated null constructs shown in FIG. 12 were DNA synthesized and then subcloned into an mRNA IVT DNA vector (pRT). High quality mRNA was produced via IVT for each. Transfection of mRNA encoding each of the six molecules was performed using electroporation (EP) delivery into primary human T cells and FACS analysis was performed 24 hours post-EP to evaluate expression level of each construct on the cell surface (FIG. 13). By flow cytometry, replacement of the WT SP with the alternative CD8 α (02.8aSP-PD-1 and 02.8aSP-TGF β RII) resulted in the highest level of expression at the T cell surface. 02.8aSP-PD-1 Null receptor exhibited an MFI of 43,680, which is 177-fold higher than endogenous T cell PD-1 expression and 2.8-fold higher than the WT PD-1 Null receptor. 02.8aSP-TGF β RII Null receptor exhibited an MFI of 13,809, which is 102-fold higher than endogenous T cell TGF β RII expression and 1.8-fold higher than the WT TGF β RII Null receptor. These results show that

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replacement of wildtype SP with the alternative CD8 α SP for both PD1 and TGF β RII inhibitory proteins leads to enhanced surface expression of the Null or Switch receptor. This in turn will maximize checkpoint inhibition or co-stimulation, respectively, upon binding of the natural ligand (s).

INCORPORATION BY REFERENCE

10 Every document cited herein, including any cross referenced or related patent or application is hereby incorporated herein by reference in its entirety unless expressly excluded or otherwise limited. The citation of any document is not an admission that it is prior art with respect to any invention disclosed or claimed herein or that it alone, or in any combination with any other reference or references, teaches, suggests or discloses any such invention. Further, to the extent that any meaning or definition of a term in this document conflicts with any meaning or definition of the same term in a document incorporated by reference, the meaning or definition assigned to that term in this document shall govern.

OTHER EMBODIMENTS

25 While particular embodiments of the disclosure have been illustrated and described, various other changes and modifications can be made without departing from the spirit and scope of the disclosure. The scope of the appended claims includes all such changes and modifications that are within the scope of this disclosure.

SEQUENCE LISTING

The patent contains a lengthy sequence listing. A copy of the sequence listing is available in electronic form from the USPTO web site (<https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US12385061B2>). An electronic copy of the sequence listing will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A method of expressing a transgene comprising:
 - a) providing a population of T-cells wherein a plurality of T-cells in the population comprise at least one chimeric antigen receptor (CAR) and at least one inducible transgene construct, wherein the CAR is a transmembrane protein comprising
 - (i) an ectodomain comprising a signal peptide and a ligand recognition region, wherein the ligand recognition region comprises at least one scaffold protein;
 - (ii) a transmembrane domain; and
 - (iii) an endodomain comprising at least one costimulatory domain, wherein the at least one inducible transgene construct comprises a sequence encoding an NF κ B-inducible promoter and a transgene; and
 - b) contacting the population of T-cells with a ligand that binds to the ligand recognition region of the at least one CAR, wherein upon binding of the ligand to the ligand recognition region, the endodomain of the at least one CAR transduces an intracellular signal that targets the NF κ B-inducible promoter and results in expression of the transgene within the plurality of T-cells.
- 45 2. The method of claim 1, wherein the ectodomain of (i) further comprises a hinge between the ligand recognition region and the transmembrane domain.
- 50 3. The method of claim 1, wherein the at least one scaffold protein comprises an antibody, an antibody fragment, a single domain antibody, a single chain antibody, an antibody mimetic, a single chain variable fragment (scFv), a VH, a VHH or a Centyrin.
- 55 4. The method of claim 1, wherein the CAR specifically binds to BCMA or MUC-1.
5. The method of claim 1, wherein the transgene comprises a sequence that is endogenous with respect to the genomic sequence of the T-cell.
- 60 6. The method of claim 1, wherein the transgene comprises a sequence that is exogenous with respect to the genomic sequence of the T-cell.
7. The method of claim 6, wherein the exogenous sequence is a synthetic, modified, recombinant, chimeric or non-naturally occurring sequence with respect to the genome of the cell.
- 65 8. The method of claim 1, wherein the transgene encodes a secreted protein.

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9. The method of claim 8, wherein the secreted protein is Factor IX.

10. The method of claim 1, wherein, the signal peptide comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1BB or GM- 5 CSFR signal peptide.

11. The method of claim 1, wherein the transmembrane domain comprises a sequence encoding a human CD2, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD8 α , CD19, CD28, 4-1BB or GM-CSFR transmembrane domain. 10

12. The method of claim 1, wherein the endodomain comprises a human CD3 ζ endodomain.

13. The method of claim 1, wherein the at least one costimulatory domain comprises a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any 15 combination thereof.

14. The method of claim 1, wherein the NF κ B-inducible promoter comprises 1, 2, 3, 4 or 5 repeats of the NF κ B response element.

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