CARTYRIN COMPOSITIONS AND METHODS FOR USE

RELATED APPLICATIONS

[01] This application claims the priority benefit of United States provisional application No. 62/639,978 filed March, 7, 2018, United States provisional application No. 62/745,151 filed October 12, 2018 and United States provisional application No. 62/783,140 filed December 20, 2018, the contents of each of which are herein incorporated by reference in their entirety.

INCORPORATION-BY-REFERENCE OF SEQUENCE LISTING

[02] The contents of the file named "POTH-033_001WO_SequenceListing_ST25_R.txt", which was created on March 7, 2019, and is 6 KB in size are hereby incorporated by reference in their entirety.

FIELD OF THE DISCLOSURE

[03] The disclosure is directed to molecular biology, and more, specifically, to chimeric antigen receptors, and to transposons containing one or more CARTyrins, as well as methods of making and using the same.

BACKGROUND

[04] There has been a long-felt but unmet need in the art for a method of directing the specificity of an immune cell without using traditional antibody sequences or fragments thereof. The disclosure provides a superior chimeric antigen receptor.

SUMMARY

[05] The disclosure provides a chimeric antigen receptor (CAR) comprising: (a) an ectodomain comprising an antigen recognition region, wherein the antigen recognition region comprises at least one Centyrin; (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. As used throughout the disclosure, a CAR comprising a Centryin is referred to as a CARTyrin. In certain embodiments, the antigen recognition region may comprise two Centyrins to produce a bi-specific or tandem

CARTyrin. In certain embodiments, the antigen recognition region may comprise three Centyrins to produce a tri-specific CARTyrin. 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 recognition region and the transmembrane 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 recognition region and the transmembrane domain.

[06] The disclosure provides a chimeric antigen receptor (CAR) comprising: (a) an ectodomain comprising an antigen recognition region, wherein the antigen recognition region comprises at least one Centyrin and wherein the at least one Centyrin specifically binds to a sequence of Prostate-Specific Membrane Antigen (PSMA); (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. As used throughout the disclosure, a CAR comprising a Centryin is referred to as a CARTyrin. In certain embodiments, the antigen recognition region may comprise two Centyrins to produce a bi-specific or tandem CARTyrin. In certain embodiments, including those wherein the antigen recognition region may comprise two Centyrins to produce a bi-specific or tandem CARTyrin, one or both of the two Centyrins specifically bind(s) to a sequence of PSMA. In some embodiments, a first Centyrin may specifically bind to a first sequence of PSMA and a second Centyrin may specifically bind to a second sequence of PSMA. In some embodiments, the first sequence of PSMA and the second sequence of PSMA are identical. In some embodiments, the first sequence of PSMA and the second sequence of PSMA are not identical. In certain embodiments, the antigen recognition region may comprise three Centyrins to produce a tri-specific CARTyrin. In certain embodiments, including those wherein the antigen recognition region may comprise three Centyrins to produce a tri-specific or tandem CARTyrin, one, two, or three of the three Centyrins specifically bind(s) to a sequence of PSMA. In certain embodiments, a first Centyrin may specifically bind to a first sequence of PSMA, a second Centyrin may specifically bind to a second sequence of PSMA and a third Centyrin may specifically bind to a third sequence of PSMA. In certain embodiments, the ectodomain may further comprise a signal peptide. In certain embodiments, two or more of the first, second or third sequences of PSMA are identical. In

certain embodiments, two or more of the first, second or third sequences of PSMA are not identical. In certain embodiments, the first sequence of PSMA, the second sequence of PSMA and the third sequence of PSMA are not identical. Alternatively, or in addition, in certain embodiments, the ectodomain may further comprise a hinge between the antigen recognition region and the transmembrane 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 recognition region and the transmembrane domain. As used herein, the term "anti-PSMA CARTyrin" refers to a CARTyrin comprising at least one centyrin that specifically binds a sequence of PSMA.

[07] In certain embodiments of an anti-PSMA CARTyrins of the disclosure, the Centyrin comprises or consists of the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18000) ("PSMA5 Centyrin") or the nucleic acid sequence of ATGCTGCCTGCACCAAAGAACCTGGTGGTGTCTCGGGTGACCGAGGACTCTGCC AGACTGAGCTGGGACATCGATGAGCAGAGGGATTGGTTCGAGAGCTTTCTGATC CAGTATCAGGAGTCCGAGAAAGTGGGCGAGGCCATCGTGCTGACAGTGCCTGGC AGCGAGCGGTCCTATGACCTGACCGGCCTGAAGCCAGGCACAGAGTACACCGTG TCCATCTACGGCGTGTATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTCAC CACA (SEQ ID NO: 18001) ("PSMA5 Centyrin").

[08] In certain embodiments of an anti-PSMA CARTyrins of the disclosure, the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 70% identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18000). In certain embodiments, the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 97%, 99%, or any percentage in between of identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18000).

[09] In certain embodiments of an anti-PSMA CARTyrins of the disclosure, the Centyrin comprises or consists of the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18002) ("PSMA8 Centyrin") or the nucleic acid sequence of ATGCTGCCTGCACCAAAGAACCTGGTGGTGTCTCGGGTGACCGAGGACTCTGCC AGACTGAGCTGGGCCATCGACGAGCAGAGGGATTGGTTCGAGAGCTTTCTGATC CAGTATCAGGAGTCCGAGAAAGTGGGCGAGGCCATCGTGCTGACAGTGCCTGGC AGCGAGCGGTCCTATGATCTGACCGGCCTGAAGCCAGGCACAGAGTACACCGTG TCCATCTACGGCGTGTATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTCAC CACA (SEQ ID NO: 18003) ("PSMA8 Centyrin").

[010] In certain embodiments of an anti-PSMA CARTyrins of the disclosure, the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 70% identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18002). In certain embodiments, the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 97%, 99%, or any percentage in between of identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18002).

[011] In certain embodiments of the CARTyrins 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 CARTyrins of the disclosure, the signal peptide may comprise a sequence encoding a human CD8α signal peptide. The human CD8α signal peptide may comprise an amino acid sequence comprising MALPVTALLLPLALLLHAARP (SEQ ID NO: 18004). The human CD8α signal peptide may comprise an amino acid sequence comprising MALPVTALLLPLALLLHAARP (SEQ ID NO: 18004) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the an amino acid sequence comprising MALPVTALLLPLALLLHAARP (SEQ ID NO: 18004).

The human CD8α signal peptide may be encoded by a nucleic acid sequence comprising atggcactgccagtcaccgccctgctgctgcctctggctctgctgctgcacgcagctagacca (SEQ ID NO: 18005).

[012] In certain embodiments of the CARTyrins of the disclosure, 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 CARTyrins of the disclosure, the transmembrane domain may comprise a sequence encoding a human CD8α transmembrane domain. The CD8α transmembrane domain may comprise an amino acid sequence comprising IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006). The CD8α transmembrane domain may be encoded by the nucleic acid sequence comprising atctacatttgggcaccactggccgggacctgtggagtgctgctgctgagcctggtcatcacactgtactgc (SEQ ID NO: 18007).

[013] In certain embodiments of the CARTyrins of the disclosure, the endodomain may comprise a human CD3ζ endodomain.

[014] In certain embodiments of the CARTyrins 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 CARTyrins of the disclosure, the at least one costimulatory domain may comprise a CD28 and/or a 4-1BB costimulatory domain. The CD3ζ costimulatory domain may comprise an amino acid sequence comprising RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR (SEQ ID NO: 18008) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR (SEQ ID NO: 18009). The CD3ζ costimulatory domain may be encoded by the nucleic acid sequence comprising cgcgtgaagtttagtcgatcagcagatgccccagcttacaaacagggacagaaccagctgtataacgagctgaatctgggccgccga gaggaatatgacgtgctggataagcggagaggacgcgaccccgaaatgggaggcaagcccaggcgcaaaaaccctcaggaagg

cctgtataacgagctgcagaaggacaaaatggcagaagcctattctgagatcggcatgaaggggagcgacggagaggcaaagg gcacgatgggctgtaccagggactgagcaccgccacaaaggacacctatgatgctctgcatatgcaggcactgcctccaagg (SEQ ID NO: 18010). The 4-1BB costimulatory domain may comprise an amino acid sequence comprising KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 18011) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 18012). The 4-1BB costimulatory domain may be encoded by the nucleic acid sequence comprising aagagaggcaggaagaaactgctgtatattttcaaacagcccttcatgcgccccgtgcagactacccaggaggaagacgggtgctcc tgtcgattccctgaggaagaggaaggcgggtgtgagctg (SEQ ID NO: 18013). The 4-1BB costimulatory domain may be located between the transmembrane domain and the CD28 costimulatory domain.

[015] In certain embodiments of the CARTyrins of the disclosure, the hinge may comprise a sequence derived from a human CD8α, IgG4, and/or CD4 sequence. In certain embodiments of the CARTyrins of the disclosure, the hinge may comprise a sequence derived from a human CD8α sequence. The hinge may comprise a human CD8α amino acid sequence comprising TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18014) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18015). The human CD8α hinge amino acid sequence may be encoded by the nucleic acid sequence comprising ACCACAACCCCTGCCCCCAGACCTCCCACACCCGCCCCTACCATCGCGAGTCAGC CCCTGAGTCTGAGACCTGAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGTGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 18016) or ACCACAACCCCTGCCCCCAGACCTCCCACACCCGCCCCTACCATCGCGAGTCAGC CCCTGAGTCTGAGACCTGAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGTGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 18017).

[016] Centyrins of the disclosure may comprise at least one fibronectin type III (FN3) domain. Centyrins of the disclosure may be capable of specifically binding an antigen. Preferred Centryrins of the disclosure specifically bind a sequence of PSMA. 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 LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDL TGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18018) or MLPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYD LTGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18019). 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: 18020) at positions 13-16 of the consensus sequence; (b) a B-C loop comprising or consisting of the amino acid residues TAPDAAF (SEQ ID NO: 18021) 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: 18022) 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: 18023) 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: 18024) 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: 18025) 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. Centyrins and/or CARTyrins of the disclosure may bind 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. The K_D may be determined by surface plasmon resonance.

[017] The disclosure provides a composition comprising a CARTyrin of the disclosure and at least one pharmaceutically acceptable carrier.

[018] The disclosure provides a transposon comprising the CARTyrin of the disclosure.

[019] Transposons of the disclosure may comprise a selection gene for identification, enrichment and/or isolation of cells that express the transposon. Exemplary selection genes encode any gene product (e.g. transcript, protein, enzyme) essential for cell viability and survival. Exemplary selection genes encode any gene product (e.g. transcript, protein,

enzyme) essential for conferring resistance to a drug challenge against which the cell is sensitive (or which could be lethal to the cell) in the absence of the gene product encoded by the selection gene. Exemplary selection genes encode any gene product (e.g. transcript, protein, enzyme) essential for viability and/or survival in a cell media lacking one or more nutrients essential for cell viability and/or survival in the absence of the selection gene. Exemplary selection genes include, but are not limited to, *neo* (conferring resistance to neomycin), TYMS (encoding Thymidylate Synthetase), MGMT (encoding O(6)-methylguanine-DNA methyltransferase), multidrug resistance gene (MDR1), ALDH1 (encoding Aldehyde dehydrogenase 1 family, member A1), FRANCF, RAD51C (encoding RAD51 Paralog C), GCS (encoding glucosylceramide synthase), and NKX2.2 (encoding NK2 Homeobox 2).

[020] Transposons of the disclosure may comprise an inducible proapoptotic polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a proapoptotic polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, the non-human sequence comprises a restriction site. In certain embodiments, the ligand binding region may be a multimeric ligand binding region. Inducible proapoptotic polypeptides of the disclosure may also be referred to as an "iC9 safety switch". In certain embodiments, transposons of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, transposons of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, transposons of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide. In certain embodiments, the amino acid sequence of the ligand binding region that comprise a FK506 binding protein 12 (FKBP12) polypeptide may comprise a

modification at position 36 of the sequence. The modification may be 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 GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026). In certain embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027). In certain embodiments, the induction agent specific for the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V) comprises AP20187 and/or AP1903, both synthetic drugs.

[021] In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the linker region is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028) or a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029). In certain embodiments, the nucleic acid sequence encoding the linker does not comprise a restriction site.

[022] In certain embodiments of the truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. Alternatively, or in addition, in certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated

caspase 9 polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030) or a nucleic acid sequence comprising GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

[023] In certain embodiments of the inducible proapoptotic polypeptides, wherein the polypeptide comprises a truncated caspase 9 polypeptide, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE

SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18032) or the nucleic acid sequence comprising ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg ccacccagggatcattccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

[024] Transposons of the disclosure may comprise at least one self-cleaving peptide(s) located, for example, between one or more Centyrin(s) or CARTyrin(s) of the disclosure and a selection gene of the disclosure. Transposons of the disclosure may comprise at least one self-cleaving peptide(s) located, for example, between one or more Centyrin(s) or CARTyrin(s) of the disclosure and an inducible proapoptotic polypeptide of the disclosure. Transposons of the disclosure may comprise at least two self-cleaving peptide(s), a first self-cleaving peptide located, for example, upstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure and a second first self-cleaving peptide located, for example, downstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure.

[025] The at least one self-cleaving peptide may comprise, for example, a T2A peptide, 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. A T2A peptide may comprise an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034) or a sequence

having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18035). A GSG-T2A peptide may comprise an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18036) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18037). A GSG-T2A peptide may comprise a nucleic acid sequence comprising ggatctggagagggaaggggaagcctgctgacctgtggagacgtggaggaaaacccaggacca (SEQ ID NO: 18038). An E2A peptide may comprise an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18039) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18040). A GSG-E2A peptide may comprise an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18041) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18042). An F2A peptide may comprise an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18043) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18044). A GSG-F2A peptide may comprise an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18045) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18046). A P2A peptide may comprise an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18047) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18048). A GSG-P2A peptide may comprise an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18049) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18050).

[026] Transposons of the disclosure may comprise a first and a second self-cleaving peptide, the first self-cleaving peptide located, for example, upstream of one or more

Centyrin(s) or CARTyrin(s) of the disclosure the second self-cleaving peptide located, for example, downstream of the one or more Centyrin(s) or CARTyrin(s) of the disclosure. The first and/or the second self-cleaving peptide may comprise, for example, a T2A peptide, 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. A T2A peptide may comprise an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18035). A GSG-T2A peptide may comprise an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18036) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18037). A GSG-T2A peptide may comprise a nucleic acid sequence comprising ggatctggagagggaaggggaagcctgctgacctgtggagacgtggaggaaaacccaggacca (SEQ ID NO: 18038). An E2A peptide may comprise an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18039) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18040). A GSG-E2A peptide may comprise an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18041) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18042). An F2A peptide may comprise an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18043) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18044). A GSG-F2A peptide may comprise an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18045) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18046). A P2A peptide may comprise an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18047) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18048). A GSG-P2A peptide may comprise an

amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18049) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18050).

[027] In some embodiments of the transposons of the disclosure, including those comprising a CAR of the disclosure, the transposon further comprises a sequence encoding a chimeric stimulatory receptor (CSR). In some embodiments, the CSR comprises: (a) an ectodomain comprising an activation component;(b) a transmembrane domain; and (c) an endodomain comprising at least one signal transduction domain; wherein the combination of (a), (b) and (c) is non-naturally occurring. In some embodiments, the activation component of (a) is isolated or derived from a first protein. In some embodiments, the at least one signal transduction domain of (c) is isolated or derived from a second protein. In some embodiments, the first protein and the second protein are not identical. In some embodiments, the Activation component comprises one or more of a component of a human transmembrane receptor, a human cell-surface receptor, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor. In some embodiments, the activation component comprises a portion of one or more of a component of a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor to which an agonist of the Activation component binds. In some embodiments, the activation component comprises a CD2 protein or a portion thereof to which an agonist binds. In some embodiments, the signal transduction domain comprises one or more of a component of a human signal transduction domain, T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor. In some embodiments, the signal transduction domain comprises a CD3 protein. In some embodiments, the CD3 protein comprises a CD3ζ protein. In some embodiments, the endodomain further comprises a cytoplasmic domain. In some embodiments, the cytoplasmic domain is isolated or derived from a third protein. In some embodiments, the first protein and the third protein are identical. In some embodiments, the ectodomain further comprises a

signal peptide. In some embodiments, the signal peptide is derived from a fourth protein. In some embodiments, the first protein and the fourth protein are identical. In some embodiments, the transmembrane domain is isolated or derived from a fifth protein. In some embodiments, the first protein and the fifth protein are identical. In some embodiments, the Activation component does not bind a naturally-occurring molecule. In some embodiments, the CSR does not transduce a signal upon binding of the activation component to a naturally-occurring molecule. In some embodiments, the ectodomain comprises a modification. In some embodiments, the modification comprises a mutation or a truncation of a sequence encoding the activation component when compared to a wild type sequence of the first protein. In some embodiments, the Activation component binds to a non-naturally occurring molecule. In some embodiments, the CSR selectively transduces a signal upon binding of the Activation component to a non-naturally occurring molecule.

[028] In some embodiments of the transposons of the disclosure, the transposon is a piggyBac or a piggyBac-like transposon.

[029] In some embodiments of the transposons of the disclosure, the transposon is a TcBuster transposon.

[030] In some embodiments of the transposons of the disclosure, the transposon is a Sleeping Beauty transposon.

[031] In some embodiments of the transposons of the disclosure, the transposon is a Helraiser transposon.

[032] In some embodiments of the transposons of the disclosure, the transposon is a Tol2 transposon.

[033] The disclosure provides a composition comprising the transposon the disclosure. In certain embodiments, the composition may further comprise a plasmid comprising a sequence encoding a transposase enzyme. The sequence encoding a transposase enzyme may be an mRNA sequence.

[034] The disclosure provides a composition comprising a CAR of the disclosure. In some embodiments, the composition further comprises a CSR of the disclosure or a sequence encoding the CSR. In some embodiments, the sequence encoding the CSR comprises DNA. In some embodiments, the sequence encoding the CSR comprises RNA. In some embodiments, the sequence encoding the CSR comprises messenger RNA (mRNA). In some

embodiments, upon introduction to a cell of the disclosure, the CSR or the sequence encoding the CSR is stably integrated by the cell. In some embodiments, upon introduction to a cell of the disclosure, the CSR or the sequence encoding the CSR is not stably integrated by the cell. In some embodiments, upon introduction to a cell of the disclosure, the CSR or the sequence encoding the CSR is stably expressed by the cell. In some embodiments, upon introduction to a cell of the disclosure, the CSR or the sequence encoding the CSR is transiently expressed by the cell. In some embodiments, upon introduction to a cell of the disclosure, the CSR or the sequence encoding the CSR comprises an RNA or an mRNA and the CSR or the sequence encoding the CSR is transiently expressed by the cell.

[035] The disclosure provides a cell comprising a CAR of the disclosure. In some embodiments, the cell further comprises a CSR of the disclosure or a sequence encoding the CSR. In some embodiments, the sequence encoding the CSR comprises DNA. In some embodiments, the sequence encoding the CSR comprises RNA. In some embodiments, the sequence encoding the CSR comprises messenger RNA (mRNA). In some embodiments, the CSR or the sequence encoding the CSR is stably integrated into a genomic locus or loci of the cell. In some embodiments, the CSR or the sequence encoding the CSR is not stably integrated into a genomic locus or loci of the cell. In some embodiments, the CSR or the sequence encoding the CSR is stably expressed by the cell. In some embodiments, the CSR or the sequence encoding the CSR is transiently expressed by the cell. In some embodiments, the CSR or the sequence encoding the CSR comprises an RNA or an mRNA and the CSR or the sequence encoding the CSR is transiently expressed by the cell.

[036] Transposons of the disclosure may comprise piggyBac transposons. In certain embodiments of this method, the transposon is a plasmid DNA transposon with a sequence encoding the chimeric antigen receptor flanked by two cis-regulatory insulator elements. In certain embodiments, the transposon is a piggyBac or a piggyBac-like transposon.

[037] Transposase enzymes of the disclosure may include piggyBac transposases or compatible enzymes. Transposase enzymes of the disclosure may include piggyBac-like transposases or compatible enzymes. In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac™ or a Super piggyBac™ (SPB) transposase. In certain embodiments, and, in

particular, those embodiments wherein the transposase is a Super piggyBac™ (SPB) transposase, the sequence encoding the transposase is an mRNA sequence.

[038] In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac™ (PB) transposase enzyme. The piggyBac (PB) transposase enzyme may comprise or consist of an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO:
14487).
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[039] In certain embodiments of the methods 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:

```
  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO:
14487).
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[040] In certain embodiments, the transposase enzyme is a piggyBac™ (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 piggyBac™ (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 piggyBac™ (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).

[041] In certain embodiments of the methods of the disclosure, the transposase enzyme is a Super piggyBac™ (sPBo) transposase enzyme. In certain embodiments, the Super piggyBac™ (sPBo) 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 piggyBac™ (sPBo) 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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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
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421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO: 14484).

[042] In certain embodiments of the methods of the disclosure, the transposase enzyme is a TcBuster transposon and wherein the transposase enzyme is a TcBuster transposase enzyme. In some embodiments, the TcBuster transposase enzyme is a hyperactive TcBuster transposase enzyme. In some embodiments, the TcBuster transposase enzyme comprises a sequence having at least 75% identity to:

MMLNWLKSGK LESQSQEQSS CYLENSNCLP PTLDSTDIIG EENKAGTTSR KKRKYDEDYL
NFGFTWTGDK DEPNGLCVIC EQVVNNSSLN PAKLKRHLDT KHPTLKGKSE YFKRKCNELN
QKKHTFERYV RDDNKNLLKA SYLVSLRIAK QGEAYTIAEK LIKPCTKDLT TCVFGEKFAS
KVDLVPLSDT TISRRIEDMS YFCEAVLVNR LENAKCGFTL QMDESTDVAG LAILLVFVRY
IHESSFEEDM LFCKALPTQT TGEEIFNLLN AYFEKHSIPW NLCYHICTDG AKAMVGVIKG
VIARIKKLVP DIKASHCCLH RHALAVKRIP NALHEVLNDA VKMINFIKSR PLNARVFALL
CDDLGSLHKN LLLHTEVRWL SRGKVLTRFW ELRDEIRIFF NEREFAGKLN DTSWLQNLAY
IADIFSYLNE VNLSLQGPNS TIFKVNSRIN SIKSKLKLWE ECITKNNTEC FANLNDFLET
SNTALDPNLK SNILEHLNGL KNTFLEYFPP TCNNISWVEN PFNECGNVDT LPIKEREQLI
DIRTDTTLKS SFVPDGIGPF WIKLMDEFPE ISKRAVKELM PFVTTYLCEK SFSVYVATKT
KYRNRLDAED DMRLQLTTIH PDIDNLCNNK QAQKSH (SEQ ID NO: 17900).

[043] In certain embodiments of the methods of the disclosure, the transposase enzyme is a Sleeping Beauty transposon and the transposase enzyme is a Sleeping Beauty transposase enzyme. In some embodiments, the Sleeping Beauty transposase enzyme comprises the sequence of SEQ ID NO: 14485. In some embodiments, the Sleeping Beauty transposase enzyme is a hyperactive Sleeping Beauty transposase (SB100X). In some embodiments, the hyperactive Sleeping Beauty transposase (SB100X) comprises the sequence of SEQ ID NO: 14486.

[044] In certain embodiments of the methods of the disclosure, the transposase enzyme is a Helraiser transposon and wherein the transposase enzyme is a Helraiser transposase enzyme. In some embodiments, the Helraiser transposase enzyme comprises the sequence of SEQ ID NO: 14501.

[045] In certain embodiments of the methods of the disclosure, the transposase enzyme is a Tol2 transposon and wherein the transposase enzyme is a Tol2 transposase enzyme. In some embodiments, the Tol2 transposase enzyme comprises the sequence of SEQ ID NO: 14502.

[046] The disclosure provides a vector comprising a CARTyrin of the disclosure. In certain embodiments, the vector is a viral vector. The vector may be a recombinant vector.

[047] 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 Centyrin or CARTyrin 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.

[048] Viral vectors of the disclosure may comprise a selection gene. The selection gene may encode a gene product essential for cell viability and survival. The selection gene may encode a gene product essential for cell viability and survival when challenged by selective cell culture conditions. Selective cell culture conditions may comprise a compound harmful to cell viability or survival and wherein the gene product confers resistance to the compound. Exemplary selection genes of the disclosure may include, but are not limited to, *neo* (conferring resistance to neomycin), TYMS (encoding Thymidylate Synthetase), MGMT (encoding O(6)-methylguanine-DNA methyltransferase), multidrug resistance gene (MDR1), ALDH1 (encoding Aldehyde dehydrogenase 1 family, member A1), FRANCF, RAD51C (encoding RAD51 Paralog C), GCS (encoding glucosylceramide synthase), NKX2.2 (encoding NK2 Homeobox 2) or any combination thereof.

[049] Viral vectors of the disclosure may comprise an inducible proapoptotic polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a proapoptotic polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, the non-human sequence comprises a restriction site. In certain

embodiments, the ligand binding region may be a multimeric ligand binding region. Inducible proapoptotic polypeptides of the disclosure may also be referred to as an "iC9 safety switch". In certain embodiments, viral vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, viral vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, viral vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide. In certain embodiments, the amino acid sequence of the ligand binding region that comprise a FK506 binding protein 12 (FKBP12) polypeptide may comprise a modification at position 36 of the sequence. The modification may be 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 GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026). In certain embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027). In certain embodiments, the induction agent specific for the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide having a

substitution of valine (V) for phenylalanine (F) at position 36 (F36V) comprises AP20187 and/or AP1903, both synthetic drugs.

[050] In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the linker region is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028) or a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029). In certain embodiments, the nucleic acid sequence encoding the linker does not comprise a restriction site.

[051] In certain embodiments of the truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. Alternatively, or in addition, in certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030) or a nucleic acid sequence comprising GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA

AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG
TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG
CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG
CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT
CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT
TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA
ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT
GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

[052] In certain embodiments of the inducible proapoptotic polypeptides, wherein the polypeptide comprises a truncated caspase 9 polypeptide, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18032) or the nucleic acid sequence comprising

ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg
ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag
gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg
ccacccagggatcattccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg
ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt
aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta
gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg
gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga
cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat
ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc
tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt
cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga

acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

[053] Viral vectors of the disclosure may comprise at least one self-cleaving peptide. In some embodiments, the vector may comprise at least one self-cleaving peptide and wherein a self-cleaving peptide is located between a CARtyrin and a selection gene. In some embodiments, the vector may comprise at least one self-cleaving peptide and wherein a first self-cleaving peptide is located upstream of a CARtyrin and a second self-cleaving peptide is located downstream of a CARtyrin. Viral vectors of the disclosure may comprise at least one self-cleaving peptide(s) located, for example, between one or more of a CARTyrin, CAR or CAR of the disclosure and an inducible proapoptotic polypeptide of the disclosure. Viral vectors of the disclosure may comprise at least two self-cleaving peptide(s), a first self-cleaving peptide located, for example, upstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure and a second first self-cleaving peptide located, for example, downstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure. The self-cleaving peptide may comprise, for example, a T2A peptide, 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. A T2A peptide may comprise an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18035). A GSG-T2A peptide may comprise an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18036) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18037). A GSG-T2A peptide may comprise a nucleic acid sequence comprising ggatctggagagggaaggggaagcctgctgacctgtggagacgtggaggaaaacccaggacca (SEQ ID NO: 18038). An E2A peptide may comprise an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18039) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18040). A GSG-E2A peptide may comprise an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18041) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid

sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18042). An F2A peptide may comprise an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18043) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18044). A GSG-F2A peptide may comprise an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18045) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18046). A P2A peptide may comprise an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18047) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18048). A GSG-P2A peptide may comprise an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18049) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18050).

[054] The disclosure provides a vector comprising the CARTyrin of the disclosure. In certain embodiments, 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.

[055] Nanoparticle vectors of the disclosure may comprise a selection gene. The selection gene may encode a gene product essential for cell viability and survival. The selection gene may encode a gene product essential for cell viability and survival when challenged by selective cell culture conditions. Selective cell culture conditions may comprise a compound harmful to cell viability or survival and wherein the gene product confers resistance to the compound. Exemplary selection genes of the disclosure may include, but are not limited to, *neo* (conferring resistance to neomycin), TYMS (encoding Thymidylate Synthetase), MGMT

(encoding O(6)-methylguanine-DNA methyltransferase), multidrug resistance gene (MDR1), ALDH1 (encoding Aldehyde dehydrogenase 1 family, member A1), FRANCF, RAD51C (encoding RAD51 Paralog C), GCS (encoding glucosylceramide synthase), NKX2.2 (encoding NK2 Homeobox 2) or any combination thereof.

[056] Nanoparticle vectors of the disclosure may comprise an inducible proapoptotic polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a proapoptotic polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, the non-human sequence comprises a restriction site. In certain embodiments, the ligand binding region may be a multimeric ligand binding region. Inducible proapoptotic polypeptides of the disclosure may also be referred to as an "iC9 safety switch". In certain embodiments, nanoparticle vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, nanoparticle vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments, nanoparticle vectors of the disclosure may comprise an inducible caspase polypeptide comprising (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide. In certain embodiments, the amino acid sequence of the ligand binding region that comprise a FK506 binding protein 12 (FKBP12) polypeptide may comprise a modification at position 36 of the sequence. The modification may be 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 GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026). In certain embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising

GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG
GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG
GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA
GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC
AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC
ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027). In certain embodiments, the induction agent specific for the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V) comprises AP20187 and/or AP1903, both synthetic drugs.

[057] In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the linker region is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028) or a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029). In certain embodiments, the nucleic acid sequence encoding the linker does not comprise a restriction site.

[058] In certain embodiments of the truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. Alternatively, or in addition, in certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030) or a nucleic acid sequence comprising

GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT
TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT
TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA
AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT
GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG
AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT
CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG
AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA
AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG
TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG
CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG
CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT
CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT
TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA
ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT
GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

[059] In certain embodiments of the inducible proapoptotic polypeptides, wherein the polypeptide comprises a truncated caspase 9 polypeptide, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18032) or the nucleic acid sequence comprising ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg ccacccagggatcattccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg

ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

[060] Nanoparticle vectors of the disclosure may comprise at least one self-cleaving peptide. In some embodiments, the nanoparticle vector may comprise at least one self-cleaving peptide and wherein a self-cleaving peptide is located between a CARTyrin and the nanoparticle. In some embodiments, the nanoparticle vector may comprise at least one self-cleaving peptide and wherein a first self-cleaving peptide is located upstream of a CARTyrin and a second self-cleaving peptide is located downstream of a CARTyrin. In some embodiments, the nanoparticle vector may comprise at least one self-cleaving peptide and wherein a first self-cleaving peptide is located between a CARTyrin and the nanoparticle and a second self-cleaving peptide is located downstream of the CARTyrin. In some embodiments, the nanoparticle vector may comprise at least one self-cleaving peptide and wherein a first self-cleaving peptide is located between a CARTyrin and the nanoparticle and a second self-cleaving peptide is located downstream of the CARTyrin, for example, between the CARTyrin and a selection gene.

[061] Nanoparticle vectors of the disclosure may comprise at least one self-cleaving peptide(s) located, for example, between one or more Centyrins(s) or CARTyrin(s) of the disclosure and an inducible proapoptotic polypeptide of the disclosure. Nanoparticle vectors of the disclosure may comprise at least two self-cleaving peptide(s), a first self-cleaving peptide located, for example, upstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure and a second first self-cleaving peptide located, for example, downstream or immediately upstream of an inducible proapoptotic polypeptide of the disclosure. The self-cleaving peptide may comprise, for example, a T2A peptide, 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. A T2A peptide may comprise an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034). A GSG-T2A peptide may comprise an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18036) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18036). A GSG-T2A peptide may comprise a nucleic acid sequence comprising ggatctggagagggaaggggaagcctgctgacctgtggagacgtggaggaaaacccaggacca (SEQ ID NO: 18038). An E2A peptide may comprise an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18039) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18039). A GSG-E2A peptide may comprise an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18041) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18041). An F2A peptide may comprise an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18043) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18043). A GSG-F2A peptide may comprise an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18045) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18045). A P2A peptide may comprise an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18047) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18047). A GSG-P2A peptide may comprise an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18050) or a sequence having at least 70%, 80%, 90%, 95%, or 99% identity to the amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18050).

[062] The disclosure provides a composition comprising a vector of the disclosure. The disclosure provides a cell comprising a CARTyrin of the disclosure. The disclosure provides a cell comprising a transposon of the disclosure. In certain embodiments, the cell comprising a CARTyrin, a transposon, or a vector of the disclosure may express a CARTyrim on the cell surface. The cell may be any type of cell. Preferably, the cell is an immune cell. The immune cell may be a T-cell, a Natural Killer (NK) cell, a Natural Killer (NK)-like cell, Cytokine Induced Killer (CIK) cell), a hematopoeitic progenitor cell, a peripheral blood (PB) derived T cell or an umbilical cord blood (UCB) derived T-cell. Preferably, the immune cell is a T-cell. The T-cell may be an early memory cell, a stem-like T-cell, a T_{SCM}-like cell, a T_{SCM} or a T_{CM}. The T-cell may be a T_{SCM}. The cell may be an artificial antigen presenting cell, which, optionally, may be used to stimulate and expand a modified immune cell or T cell of the disclosure. The cell may be a tumor cell, which, optionally, may be used as an artificial or modified antigen presenting cell.

[063] Modified cells of the disclosure that may be used for adoptive therapy may be autologous or allogeneic.

[064] The disclosure provides a method for expressing a CARTyrin on the surface of a cell, comprising: (a) obtaining a cell population; (b) contacting the cell population to a composition comprising a CARTyrin of the disclosure or a sequence encoding the CARTyrin, under conditions sufficient to transfer the CARTyrin across a cell membrane of at least one cell in the cell population, thereby generating a modified cell population; (c) culturing the modified cell population under conditions suitable for integration of the transposon; and (d) expanding and/or selecting at least one cell from the modified cell population that express the CARTyrin on the cell surface.

[065] In certain embodiments of this method of expressing a CARTyrin, the cell population may comprise leukocytes and/ or CD4+ and CD8+ leukocytes. The cell population may comprise CD4+ and CD8+ leukocytes in an optimized ratio. The optimized ratio of CD4+ to CD8+ leukocytes does not naturally occur *in vivo*. The cell population may comprise a tumor cell.

[066] In certain embodiments of this method of expressing a CARTyrin, a transposon or vector comprises the CARTyrin or the sequence encoding the CARTyrin. In certain embodiments, a transposon comprises an anti-PSMA CARTyrin or the sequence encoding an

anti-PSMA CARTyrin. In certain embodiments, the transposon comprises a piggyBac transposon. In certain embodiments, the transposon further comprises a composition comprising a plasmid comprising a sequence encoding a transposase enzyme. In certain embodiments, including those embodiments wherein the transposase is a piggyBac transposase, the transpose enzyme is an mRNA sequence. In certain embodiments, the piggyBac transposase comprises an amino acid sequence comprising SEQ ID NO: 18017. 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: 18017. In certain embodiments, the amino acid substitution at position 30 of SEQ ID NO: 18017 is a substitution of a valine (V) for an isoleucine (I) (I30V). In certain embodiments, the amino acid substitution at position 165 of SEQ ID NO: 18017 is a substitution of a serine (S) for a glycine (G) (G165S). In certain embodiments, wherein the amino acid substitution at position 282 of SEQ ID NO: 18017 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: 18017 is a substitution of a lysine (K) for an asparagine (N) (N538K). In certain embodiments, the transposase is a Super piggyBac (sPBo) transposase. In certain embodiments, the Super piggyBac (sPBo) transposase comprises an amino acid sequence comprising SEQ ID NO: 14484.

[067] The disclosure provides a vector comprising a CARTyrin or a sequence encoding a CARTyrin of the disclosure. In certain embodiments, the vector comprises an anti-PSMA CARTyrin or a sequence encoding an anti-PSMA CARTyrin of the disclosure.

[068] In certain embodiments of this method of expressing a CARTyrin, the conditions sufficient to transfer the sequence encoding the CARTyrin across a cell membrane of at least one cell in the cell population comprise nucleofection.

[069] In certain embodiments of this method of expressing a CARTyrin, wherein the conditions sufficient to transfer the sequence encoding the CARTyrin across a cell membrane of at least one cell in the cell population comprise at least one of an application of one or more pulses of electricity at a specified voltage, a buffer, and one or more supplemental factor(s). In certain embodiments, the buffer may comprise PBS, HBSS, OptiMEM, BTXpress, Amaxa Nucleofector, Human T cell nucleofection buffer or any combination thereof. In certain embodiments, the one or more supplemental factor(s) may comprise (a) a

recombinant human cytokine, a chemokine, an interleukin or any combination thereof; (b) a salt, a mineral, a metabolite or any combination thereof; (c) a cell medium; (d) an inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof; and (e) a reagent that modifies or stabilizes one or more nucleic acids. The recombinant human cytokine, the chemokine, the interleukin or any combination thereof may comprise 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 or any combination thereof. The salt, the mineral, the metabolite or any combination thereof may comprise 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, Pop313, Crown-5, or any combination thereof. The cell medium 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 or any combination thereof. The inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof comprise 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. The reagent that modifies or stabilizes one or more nucleic acids

comprises a pH modifier, a DNA-binding protein, a lipid, a phospholipid, CaPO4, a net neutral charge DNA binding peptide with or without a NLS sequence, a TREX1 enzyme or any combination thereof.

[070] In certain embodiments of this method of expressing a CARTyrin, the conditions suitable for integration of the CARTyrin or a sequence encoding the CARTyrin of the disclosure comprise at least one of a buffer and one or more supplemental factor(s). In certain embodiments, a transposon or vector of the disclosure comprise the CARTyrin or a sequence encoding the CARTyrin of the disclosure. In certain embodiments, the buffer may comprise PBS, HBSS, OptiMEM, BTXpress, Amaxa Nucleofector, Human T cell nucleofection buffer or any combination thereof. In certain embodiments, the one or more supplemental factor(s) may comprise (a) a recombinant human cytokine, a chemokine, an interleukin or any combination thereof; (b) a salt, a mineral, a metabolite or any combination thereof; (c) a cell medium; (d) an inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof; and (e) a reagent that modifies or stabilizes one or more nucleic acids. The recombinant human cytokine, the chemokine, the interleukin or any combination thereof may comprise 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 or any combination thereof. The salt, the mineral, the metabolite or any combination thereof may comprise 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, Pop313, Crown-5, or any combination thereof. The cell medium 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 or any combination thereof. The inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof comprise 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. The reagent that modifies or stabilizes one or more nucleic acids comprises a pH modifier, a DNA-binding protein, a lipid, a phospholipid, CaPO4, a net neutral charge DNA binding peptide with or without a NLS sequence, a TREX1 enzyme or any combination thereof.

[071] In certain embodiments of this method of expressing a CARTyrin, the expansion and selection steps occur sequentially. The expansion may occur prior to selection. The expansion may occur following selection, and, optionally, a further (i.e. second) selection may occur following expansion.

[072] In certain embodiments of this method of expressing a CARTyrin, the expansion and selection steps may occur simultaneously.

[073] In certain embodiments of this method of expressing a CARTyrin, the expansion may comprise contacting at least one cell of the modified cell population with an antigen to stimulate the at least one cell through the CARTyrin, thereby generating an expanded cell population. The antigen may be presented on the surface of a substrate. The substrate may have any form, including, but not limited to a surface, a well, a bead or a plurality thereof, and a matrix. The substrate may further comprise a paramagnetic or magnetic component. In certain embodiments of this method of expressing a CARTyrin, the antigen may be presented on the surface of a substrate, wherein the substrate is a magnetic bead, and wherein a magnet may be used to remove or separate the magnetic beads from the modified and expanded cell population. The antigen may be presented on the surface of a cell or an artificial antigen presenting cell. Artificial antigen presenting cells of the disclosure may include, but are not limited to, tumor cells and stem cells.

[074] In certain embodiments of this method of expressing a CARTyrin, wherein the transposon or vector comprises a selection gene and wherein the selection step comprises contacting at least one cell of the modified cell population with a compound to which the selection gene confers resistance, thereby identifying a cell expressing the selection gene as surviving the selection and identifying a cell failing to express the selection gene as failing to survive the selection step.

[075] In certain embodiments of this method of expressing a CARTyrin, the expansion and/or selection steps may proceed for a period of 10 to 14 days, inclusive of the endpoints.

[076] The disclosure provides a composition comprising the modified, expanded and selected cell population of the methods of the disclosure.

[077] The disclosure provides a method of treating cancer in a subject in need thereof, comprising administering to the subject a composition of the disclosure, wherein the CARTyrin specifically binds to an antigen on a tumor cell. In certain embodiments, the tumor cell may be a malignant tumor cell. In certain embodiments, comprising administering to the subject the composition comprising a modified cell or cell population of the disclosure, the cell or cell population may be autologous. In certain embodiments, comprising administering to the subject the composition comprising a modified cell or cell population of the disclosure, the cell or cell population may be allogeneic.

[078] The disclosure provides a method of treating cancer in a subject in need thereof, comprising administering to the subject a composition of the disclosure, wherein the anti-PSMA CARTyrin specifically binds to a PSMA antigen on a tumor cell or a component of a vasculature of a tumor cell. In certain embodiments, the tumor cell is a prostate cell. In certain embodiments, the tumor cell may be a malignant tumor cell. In certain embodiments, comprising administering to the subject the composition comprising a modified cell or cell population of the disclosure, the cell or cell population may be autologous. In certain embodiments, comprising administering to the subject the composition comprising a modified cell or cell population of the disclosure, the cell or cell population may be allogeneic.

[079] Methods of modifying a cell therapy of the disclosure may be used to terminate or dampen a therapy in response to, for example, a sign of recovery or a sign of decreasing disease severity/progression, a sign of disease remission/cessation, and/or the occurrence of

an adverse event. Cell therapies of the disclosure may be resumed by inhibiting the induction agent should a sign or symptom of the disease reappear or increase in severity and/or an adverse event is resolved.

BRIEF DESCRIPTION OF THE DRAWINGS

[080] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[081] **Figure 1** is a schematic diagram depicting a piggyBac CARTyrin P-PSMA-101 plasmid of 7738 base pairs that includes an EF1α promoter, a safety switch (iC9), a PSMA CARTyrin and a selection gene casette.

[082] **Figure 2** is a schematic diagram depicting a piggyBac CARTyrin that includes a P-PSMA-101 transposon comprising a PSMA CARTyrin (comprising a CD8α signal peptide, an anti-PSMA Centyrin, a CD8α spacer, a CD8α transmembrane sequence, a 4-1BB costimulatory domain and a CD3ζ costimulatory domain).

[083] **Figure 3A** is a schematic diagram of the amino acid sequence of a P-PSMA5-101 construct of the disclosure.

[084] **Figure 3B** is a schematic diagram of the nucleic acid sequence of a P-PSMA5-101 construct of the disclosure.

[085] **Figure 3C** is a schematic diagram of the nucleic acid sequence of a P-PSMA5-101 construct of the disclosure.

[086] **Figure 4A** is a schematic diagram of the amino acid sequence of a P-PSMA8-101 construct of the disclosure.

[087] **Figure 4B** is a schematic diagram of the amino acid sequence of a P-PSMA8-101 construct of the disclosure.

[088] **Figure 4C** is a schematic diagram of the amino acid sequence of a P-PSMA8-101 construct of the disclosure.

[089] **Figure 5** is a schematic diagram depicting the construction of a CARTyrin of the disclosure and a table contrasting characteristics of Centyrins and antibodies.

[090] **Figure 6A-6E** shows the transient expression and function of PSMA CARTyrins. *In vitro* assays were performed to test the expression and function of the lead PSMA

CARTyrins used to produce P-PSMA5-101 and P-PSMA8-101. PSMA CARTyrins were detected on the surface of primary human T cells that were transiently transfected with mRNA encoding the PSMA CARTyrins the night before (Figure 6A). Briefly, previously activated then frozen Pan T cells were thawed and rested overnight in T cell culture media, cells were electroporated with 10 µg of PSMA CARTyrin mRNA the next evening, and then surface expression analysis was performed the next morning by FACS using soluble recombinant human PSMA protein (rPSMA) for labeling. To test the function of these T cells *in vitro*, cells were co-cultured with a panel of PSMA-expressing cells for 4 hours and then target cell killing was measured by expression of CD107a, which is a marker for degranulation and a surrogate for T cell killing. Surface expression of PSMA was assessed on K562 cells engineered to stably express PSMA (K562.PSMA) and LNCaP, a human prostate cancer cell line that endogenously expressed PSMA (Figure 6B). PSMA CARTyrin-expressing T cells were capable of degranulating against all cell lines expressing PSMA (LNCaP, K562.PSMA) with little to no degranulation above background against PSMA- cell lines (K562, PC-3) (Figure 6C). mRNA encoding PSMA was titrated into a PSMA- cell line, K562, to control for the level of surface expression of PSMA (Figure 6D). PSMA CARTyrin+ cells exhibited strong cytotoxic function against K562 cells expressing various amounts of surface PSMA (Figure 6E). These data show that the PSMA CARTyrins can be expressed on the surface of T cells and facilitate cytotoxic function against PSMA+ cell targets.

[091] **Figure 7A-7F** shows the phenotype and function of piggyBac manufactured P-PSMA-101. To support *in vivo* evaluation of the lead PSMA CARTyrins, P-PSMA-101 was constructed using the piggyBac DNA modification system. PSMA CARTyrin was detected on the surface of primary human T cells from a representative donor that were transposed with either P-PSMA5-101 or P-PSMA8-101 plasmids, but not on cells transposed with the P-BCMA-101 plasmid control (Figure 7A). In both cases, a majority of the CD8+ CAR-T cells were double positive for expression of CD45RA and CD62L, markers commonly associated with a T stem cell memory phenotype (Tscm), following staining and FACS analysis (Figure 7B). Furthermore, these cells (gated on CD8+ or CD4+) expressed low to no levels of PD-1, Tim-3 and Lag-3 by FACS analysis, which are molecules associated with activation and/or functional T cell exhaustion (Figure 7C). Next, the effector function of these CAR-T cells

was assessed *in vitro* following co-culture with PSMA-expressing cells. IFN-γ secretion was measured by standard ELISA after 24 hours and detected in the medium when CAR-T cells (from 3 independent donors) were incubated in the presence of their cognate target antigen; P-BCMA-101 secreted IFN-γ only in the presence of K562 cells engineered to express BCMA on the surface (K562.BCMA), whereas P-PSMA-101 secreted IFN-γ only in the presence of cell tumor lines expressing PSMA on the surface (LNCaP and K562.PSMA) (Figure 7D). In addition, P-PSMA-101 exhibited strong cytotoxic function against LNCaP as measured by a standard killing assay, whereas P-BCMA-101 exhibited little killing capability; data from 2 independent donors (Figure 7E). The capacity for cell proliferation upon co-culture with a several tumor cell lines was assessed after 96 hours. P-PSMA-101 exhibited a robust capacity for proliferation against PSMA+ LNCaP and 22Rv1 and P-BCMA-101 proliferated against BCMA+ H929, whereas neither CAR-T cell proliferated against PSMA-BCMA- cell lines K562 nor DU145 (Figure 7F). These data show that P-PSMA-101 cells expressed the PSMA CARTyrin on the surface and demonstrated cytotoxic function and proliferative capacity *in vitro* against PSMA+ cell targets.

[092] **Figure 8A-8F** shows the pre-clinical evaluation of P-PSMA8-101 using a murine xenograft model. Figure 8A is a schematic of the treatment schedule. A murine xenograft model using a luciferase-expressing LNCaP cell line (LNCaP.luc) injected subcutaneously (SC) into NSG mice was utilized to assess in vivo anti-tumor efficacy of P-PSMA8-101. For these in vivo studies, all CAR-T cells were produced using PB delivery of the P-PSMA8-101 plasmid and the Poseida manufacturing process. Mice were injected in the axilla with LNCaP (n=25 to account for poor LNCaP "take" rate) and treated when tumors were established (100-300 mm^3 by caliper measurement, 17 days post implantation). Mice were treated with several doses including ultra-low (1x10^6), 'stress' (5x10^6), and standard (10x10^6) doses of P-PSMA-101 by IV injection. Figure 8B is a survival curve graph of anti-tumor activity. Figure 8C is a bar graph showing the P-PSMA8-101 CD8+ T cell expansion and detection in the blood. Figure 8D is a series of line graphs showing tumor volume assessment by caliper measurement. Figure 8E is a line graph showing the bioluminescence of LNCaP tumor by BLI. Figure 8F shows representative photographs of the bioluminescense of LNCaP tumor in mice quantified in Figure 8E.

[093] **Figure 9A-9G** shows the preclinical evaluation of lead P-PSMA5-101 and P-PSMA8-101 candidates as a "stress" dose using the murine xenograft model. Figure 9A is a schematic diagram depicting the timeline of a study for the preclinical evaluation of P-PSMA-101 candidates at a 'stress' dose using the Murine Xenograft Model. A murine xenograft model using a luciferase-expressing LNCaP cell line (LNCaP.luc) injected subcutaneously (SC) into NSG mice was utilized to assess in vivo anti-tumor efficacy of P-PSMA5-101 and P-PSMA8-101 at a 'stress' dose (4x10^6) total CAR-T cells. For these in vivo studies, all CAR-T cells were produced using PB delivery of either the P-PSMA5-101 or P-PSMA8-101 plasmid using the Poseida manufacturing process. Mice were injected in the axilla with LNCaP and treated when tumors were established (100-300 mm^3 by caliper measurement). Mice were treated with a 'stress' dose (4x10^6) of P-PSMA-101 by IV injection in order to tease out any possible differences in efficacy between the PSMA5 and the PSMA8 CARs. Anti-tumor activity was evaluated by survival, CD8+ T cell expansion and detection in the blood, tumor volume assessment by caliper measurement, and bioluminescence of LNCaP tumor. P-PSMA5-101 and P-PSMA8-101 at a 'stress' dose demonstrated significantly enhanced anti-tumor efficacy and survival in comparison to the T cells (no CAR) control mice against established SC LNCaP.luc solid tumors in NSG mice. Specifically, there was no survival in T cells (no CAR) control animals, 25% survival in the P-BCMA-101 treated group, 75% survival in the P-PSMA5-101 treated group, and 100% survival in animals treated with a 'stress' dose of P-PSMA8-101. In the peripheral blood, P-PSMA5-101 and P-PSMA8-101 expanded and gave rise to differentiated effector CARTyrin+ T-cells that were concomitant with a decrease in tumor burden below detectable caliper and bioluminescent imaging limits. These cells then contracted, yet persisted in the peripheral blood. Figure 9B is a survival curve graph of anti-tumor activity. Figure 9C is a bar graph showing the P-PSMA5-101 and P-PSMA8-101 CD8+ T cell expansion and detection in the blood. Figure 9D is a series of line graphs showing tumor volume assessment by caliper measurement. The left panel shows the average of the tumor volume data shown in the series of graphs on the right panel. Figure 9E is a line graph showing the bioluminescence of LNCaP tumor by BLI. Figure 9F shows representative photographs of the bioluminescnece of LNCaP tumor mice quantified in Figure 9E. Figure 9G is a series of flow cytometry plots showing that P-PSMA-101 (T_{SCM}/T_{CM}) give rise to CARTyrin+ T_{CM}, T_{EM},

and Teff to attack solid tumor. After solid tumor elimination, a population of P-PSMA-101 T_{SCM} persists.

[094] **Figure 10** is a series of flow cytometry plots depicting the abundance of cells moving from an area of live cells (the gated lower right quadrant) to an area populated by apoptotic cells (the upper left quadrant) as a function of increasing dosage of the induction agent (AP1903) in cells modified to express a therapeutic agent (a CARTyrin) alone or in combination with an inducible caspase polypeptide of the disclosure (encoded by an iC9 construct (also known as a "safety switch") introduced into cells by a piggyBac (PB) transposase) at day 12 post nucleofection.

[095] **Figure 11** is a series of flow cytometry plots depicting the abundance of cells moving from an area of live cells (the gated lower right quadrant) to an area populated by apoptotic cells (the upper left quadrant) as a function of increasing dosage of the induction agent (AP1903) in cells modified to express a therapeutic agent (a CARTyrin) alone or in combination with an inducible caspase polypeptide of the disclosure (encoded by an iC9 construct (also known as a "safety switch") introduced into cells by a piggyBac (PB) transposase) at day 19 post nucleofection.

[096] **Figure 12** is a pair of graphs depicting a quantification of the aggregated results shown either in Figure 10 (left graph) or Figure 11 (right graph). Specifically, these graphs show the impact of the iC9 safety switch on the percent cell viability as a function of the concentration of the induction agent (AP1903) of the iC9 switch for each modified cell type at either day 12 (Figure 10 and left graph) or day 19 (Figure 11 and right graph).

[097] **Figure 13** 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 knockout 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.

[098] **Figure 14** are 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.

[099] **Figure 15A** 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 TGFβRII, 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.

[0100] **Figure 15B** 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 Figure 15A were expressed on the surface of primary human T cells. T cells were stained with either anti-PD1 (top; blue histograms) or anti-TGFβRII (bottom; blue histograms), or isotype control or secondary only (gray histograms). Cells staining positive for PD-1 or TGFβRII 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-1 and 02.8aSP-TGFβRII 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-TGFβRII null receptor exhibited an MFI of 13,809, which is 102-fold higher than endogenous T cell TGFβRII expression and 1.8-fold higher than the wildtype TGFβRII 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).

[0101] **Figure 16A-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.

[0102] **Figure 17** 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 mutein 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 NFκB 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 NFκB activity is lower. GFP expression is still observed at Day 19, which may due to the long half-life of GFP protein (~30hr), or, basal level of NFκB activity through, for example, a TCR, a CAR, a cytokine receptor, or a growth factor receptor signal.

[0103] **Figure 18** 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 mutein 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), BMCA+ (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.

[0104] **Figure 19** 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 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. The x-axes of each of the FACS histograms are depicted in logarithmic scale (0, 10^3, 10^4, 10^5). The samples plotted each of the FACS histograms are NFKB-A08-DHFR_Rev002.fcs, NFKB-A08_DHFR_Rev-RE4X_12.fcs, NFKB-A08_DHFR_Rev-RE3X_011.fcs, NFKB-A08_DHFR_Rev-RE2X_010.fcs, NFKB-A08_DHFR_Rev-RE1X_009.fcs, NFKB-A08_DHFR_Rev-RE0X_008.fcs, NFKB-A08_DHFR_v5_013.fcs and NFKB-A08_DHFR_MOCK_014.fcs, from top to bottom. 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.

[0105] **Figure 20** is a schematic depiction of the Csy4-T2A-Clo051-G4Slinker-dCas9 construct map (Embodiment 2).

[0106] **Figure 21** is a schematic depiction of the pRT1-Clo051-dCas9 Double NLS construct map (Embodiment 1).

[0107] **Figure 22** is a schematic diagram depicting the timeline of a study for the preclinical evaluation of lead P-PSMA-101 candidates in a prostate cancer bone metastasis Murine Xenograft Model. A murine xenograft model using a luciferase-expressing PC3 cell line engineered to express human PSMA protein (PC3.lucGFP.hPSMA) was injected peri-tibially (IT) into NSG mice and was utilized to assess in vivo anti-tumor efficacy of P-PSMA5-101 and P-PSMA8-101 at two different doses- a 'stress' dose of 4x10^6 and standard dose of 12x10^6 total CAR-T cells. As negative controls, T cells alone (not expressing a CAR; 12e6 dose) or P-BCMA-101 T cells (expressing an irrelevant anti-BCMA CAR; 12e6 dose) were also included. For these in vivo studies, all CAR-T cells were produced using PB delivery of either the P-PSMA5-101 or P-PSMA8-101 plasmid using the Poseida manufacturing process. Mice were injected peri-tibially with Pc3.lucGFP.hPSMA and treated with CAR-T cells four days later (all tumor-challenged mice had detectable tumors by bioluminescent imaging (BLI) ranging from 1-5x10^6 in total luminescent flux (p/sec/m^2)).

[0108] **Figure 23** is a graph showing dose efficacy of P-PSMA5-101 and P-PSMA8-101 at either a 'stress' dose or standard dose demonstrated anti-tumor efficacy in comparison to the T cells (no CAR) alone or P-BCMA-101 treated control mice against established IT PC3.lucGFP.hPSMA solid tumors in NSG mice.

[0109] **Figure 24** is a schematic diagram depicting a piggyBac P-PSMA-101 nanotransposon of the disclosure.

[0110] **Figure 25** is a graph showing electroporation (EP) delivery of either P-PSMA-101 piggyBac plasmid (light gray bars) or P-PSMA-101 piggyBac nanotransposon (dark gray bars) in combination with super piggyBac transposase enzyme resulted in high transposition efficiency in human pan T cells (5 days post-EP) as measured by surface expression of PSMA CARTyrin (Percent Transposition (%)).

[0111] **Figure 26** is a series of graphs showing that human CAR-T cells produced using anti-PSMA CAR nanotransposons (NT) were capable of killing target tumor cells. Anti-PSMA CAR T cells produced using either full-sized piggyBac plasmids (FP) or piggyBac nanotransposon (NT) were produced using the standard Poseida process. Killing of K562 cells engineered to express PSMA (K562.PSMA) by CAR-T cells at the indicated effector to

target ratios. These data show that all CAR-T cells, whether produced using FP or NT, were capable of killing target tumor cells in an antigen-dependent manner. This was true for CAR-T cells that were produced from human pan T cells from two different normal donors.

[0112] **Figure 27** is a series of graphs showing that human CAR-T cells produced using anti-PSMA CAR nanotransposons (NT) were comparable in phenotypic composition. Anti-PSMA CAR T cells produced using either full-sized piggyBac plasmids (FP) or piggyBac nanotransposon (NT) were manufactured using the standard Poseida process. Phenotypic analysis of memory T cell markers and activation/exhaustion markers (data not shown) was performed. These data show that all CAR-T cells, whether produced using FP or NT, exhibited a similar phenotypic composition of CD45RA+CD62L+ (Tscm), CD45RA-CD62L+ (Tcm), CD45RA-CD62L- (Tem), and CD45RA+CD62L- (Teff) cells. In addition, comparable levels of expression of CCR7 (CD197), CD127, CD27, LAG3, TIM3, CXCR3, PD-1, and CD25 was observed (data not shown). This was true for CAR-T cells that were produced from human pan T cells from two different normal donors.

[0113] **Figure 28** is a series of graphs showing that human CAR-T cells produced using anti-PSMA CAR nanotransposons (NT) have similar integrated copy number. Anti-PSMA CAR T cells produced using either full-sized piggyBac plasmids (FP) or piggyBac nanotransposon (NT) were manufactured using the standard Poseida process. Average copy number of integrated transposons was measured by quantitative PCR. These data show that in two different donors, all CAR-T cells, whether produced using FP or NT, exhibited a similar integrated copy number of transposons.

[0114] **Figure 29A** is a schematic diagram showing preclinical evaluation of the P-PSMA-101 transposon when delivered by a full-length plasmid (FLP) versus a nanotransposon (NT) at 'stress' doses using the murine xenograft model. The murine xenograft model using a luciferase-expressing LNCaP cell line (LNCaP.luc) injected subcutaneously (SC) into NSG mice was utilized to assess *in vivo* anti-tumor efficacy of the P-PSMA-101 transposon as delivered by a full-length plasmid (FLP) or a nanotransposon (NT) at two different 'stress' doses (2.5x10^6 or 4x10^6) of total CAR-T cells from two different normal donors. All CAR-T cells were produced using piggyBac (PB) delivery of P-PSMA-101 transposon using either FLP or NT delivery. Mice were injected in the axilla with LNCaP and treated when tumors were established (100-200 mm^3 by caliper measurement). Mice were treated with two

different 'stress' doses (2.5x10^6 or 4x10^6) of P-PSMA-101 CAR-Ts by IV injection for greater resolution in detecting possible functional differences in efficacy between transposon delivery by the FLP and the NT.

[0115] **Figure 29B** are a series of graphs showing the tumor volume assessment of mice treated as described in Figure 29A. Tumor volume assessment by caliper measurement for control mice (black), Donor #1 FLP mice (red), Donor #1 NT mice (blue), Donor #2 FLP mice (orange), and Donor #2 NT mice (green) as displayed as group averages with error bars (top) and individual mice (bottom). The y-axis shows the tumor volume (mm^3) assessed by caliper measurement. The x-axis shows the number of days post T cell treatment. Delivered by NT, P-PSMA-101 transposon at a 'stress' dose demonstrated enhanced anti-tumor efficacy as measured by caliper in comparison to the FLP and control mice against established SC LNCaP.luc solid tumors.

[0116] **Figure 30** is a schematic diagram depicting a T-cell receptor (TCR) and co-receptors CD28 and CD2.

[0117] **Figure 31** is a schematic diagram depicting primary and secondary co-stimulation is delivered to T-cell via binding of agonist mAbs (anti-CD3, anti-CD28, and anti-CD2). Full T-cell activation critically depends on TCR engagement in conjunction with a second signal by co-stimulatory receptors that boost the immune response. Primary and secondary co-stimulation can be delivered to T-cell via treatment and engagement of surface receptors with reagents displaying agonist mAbs (E.g. anti-CD3, anti-CD28, anti-CD2, beads conjugated with these mAbs, multimeric complexes of these mAbs, etc…).

[0118] **Figure 32** is a schematic diagram showing that, in absence of TCR, stimulation is enhanced with expression of Chimeric Stimulatory Receptors (CSRs). In the presence of surface-expressed CSR/s, either transiently or stably expressed, enhanced primary and secondary co-stimulatory signals are delivered when T cell is treated with reagents displaying agonist mAbs. Since a fuller T-cell activation is achieved via CSR-mediated stimulatory signals, T cell activation and expansion is enhanced.

[0119] **Figure 33A** is a schematic diagram depicting an exemplary CSR CD28z of the disclosure.

[0120] **Figure 33B** is an amino sequence encoding the CSR CD28z shown in Figure 33A.

[0121] **Figure 33C** is a nucleotide sequence encoding the CSR CD28z shown in Figure 33A.

[0122] **Figure 34A** is a schematic diagram depicting an exemplary CSR CD2z of the disclosure.

[0123] **Figure 34B** is an amino sequence encoding the CSR CD2z shown in Figure 34A.

[0124] **Figure 34C** is a nucleotide sequence encoding the CSR CD2z shown in Figure 34A.

[0125] **Figure 35** is a series of graphs showing that CSRs are expressed on the surface of T cells and do not lead to cellular activation in the absence of exogenous stimulation. Pan T cells from normal blood donors were stimulated with anti-CD3/anti-CD28 beads in standard T cell culture media, then rested. These cells were then electroporated (BTX ECM 830 electroporator @ 500V for 700 μs) with 10 μg of mRNA encoding either CD28 CSR, CD2 CSR, or wild-type CD19 control. Two days later the electroporated cells were examined by flow cytometry for surface-expression of each molecule and data are shown as stacked histograms. In addition, cell size (FSC-A) and CD69 expression was evaluated as a possible indication of cellular activation above the Mock electroporated control cells. Increased surface expression of CD28, CD2, and CD19 were detected in T cells electroporated either with CD28z CSR, CD2z CSR or CD19, respectively. Expression of these molecules on the surface of T cells did not intrinsically activate the cells in the absence of exogenous stimulation.

[0126] **Figure 36** is a graph showing that delivery of CSR enhances the expansion of CAR-T cells. CSRs were delivered to CAR-T cells either transiently by mRNA or stably by piggyBac™. Pan T cells isolated from the blood of a normal donor were genetically modified using the piggyBac™ DNA modification system and the standard Poseida process. Cells were co-electroporated in a single reaction with mRNA encoding the Super piggyBac transposase enzyme (SPB), a transposon encoding a BCMA CAR and selection gene, along with an additional mRNA encoding a CSR (either CD28z or CD2z; resulting in transient expression) or a CD19 mRNA control, or, with a transposon encoding a BCMA CAR, selection gene and a CSR (either CD28z or CD2z; resulting in stable expression). The cells were subsequently stimulated with agonist mAbs anti-CD2, anti-CD3 and anti-CD28, and were later selected for genetic modification over the course of a 19 day culture period. At the end of the initial culture period all T cells expressed the CAR, indicating successful selection

for genetically-modified cells (data not shown). Bars represent total live CAR-T cells in well and numbers indicate fold-enhancement of expansion above CAR-T cells produced in the absence of a CSR or a CD19 mRNA control. In the samples expressing either CD2z or CD28z CSR, either transiently or stably, a greater degree of expansion of the CAR-T cells.

[0127] **Figure 37** is a series of bar graphs showing that expression of CSRs does not significantly affect CAR-T cell cytotoxicity. CSRs were delivered to CAR-T cells either transiently by mRNA or stably by piggyBac™. Pan T cells isolated from the blood of a normal donor were genetically modified using the piggyBac™ DNA modification system and the standard Poseida process. Cells were co-electroporated in a single reaction with mRNA encoding the Super piggyBac transposase enzyme (SPB), a transposon encoding a BCMA CAR and selection gene, along with an additional mRNA encoding a CSR (either CD28z or CD2z; resulting in transient expression), or, with a transposon encoding a BCMA CAR, selection gene and a CSR (either CD28z or CD2z; resulting in stable expression). The cells were subsequently stimulated with agonist mAbs anti-CD2, anti-CD3 and anti-CD28, and were later selected for genetic modification over the course of a 19 day culture period. At the end of the initial culture period all T cells expressed the CAR, indicating successful selection for genetically-modified cells (data not shown). To assess CAR-T cell ability to kill, cells were co-cultured with engineered K562-BCMA-Luciferase (eK562-Luc.BCMA) or negative control line K562-Luciferase (eK562-Luc) for 48 hours at 10:1, 3:1, or 1:1 E:T ratios. Luciferase signal was measured to determine cytotoxicity. Killing of eK562-Luc is shown in bar graph on left, while killing of eK562-Luc.BCMA is shown in bar graph on right. All CAR^+ T cells expressed an anti-BCMA specific CAR and exhibited similar *in vitro* cytotoxicity against BCMA+ target cells. In summary, this activity was not significantly affected by transient or stable CSR co-expression.

DETAILED DESCRIPTION

[0128] The disclosure provides chimeric antigen receptors (CARs) comprising at least one Centyrin (CARTyrin). Chimeric antigen receptors of the disclosure may comprise more than one Centyrin. For example, a bi-specific CARTyrin may comprise two Centyrins that specifically bind two distinct antigens. In preferred embodiments, CARTyrins of the disclosure comprise at least one Centryrin that specifically binds a sequence of PSMA, and,

therefore, are referred to as PSMA-specific Centryins. CARTyrins of the disclosure that comprise at least one PSMA-specific Centryrin are referred to herein as anti-PSMA CARTyrins for specifically binding a sequence of PSMA.

[0129] Centyrins of the disclosure specifically bind to an antigen. Chimeric antigen receptors 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 the specific antigen.

[0130] Centyrins of the disclosure may comprise a consensus sequence comprising LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDL TGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18018).

[0131] Chimeric antigen receptors of the disclosure may comprise a signal peptide of human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BBor GM-CSFR. A hinge/spacer domain of the disclosure may comprise a hinge/spacer/stalk of human CD8α, IgG4, and/or CD4. An intracellular 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, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BBor GM-CSFR transmembrane domain.

[0132] 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 antigens by introducing to these cells a CARTyrin of the disclosure. Cells of the disclosure may be modified by electrotransfer of a transposon encoding a CARTyrin of the disclosure and a plasmid comprising a sequence encoding a transposase of the disclosure (preferably, the sequence encoding a transposase of the disclosure is an mRNA sequence).

Further Modifications of Cell Compositions

[0133] The disclosure provides a chimeric stimulatory receptor (CSR) comprising: (a) an ectodomain comprising an activation component and (b) a transmembrane domain or a cell-membrane attachment region, wherein the combination of (a) and (b) is non-naturally

occurring. In some embodiments, this CSR binds a component of the environment and changes the cellular consequence of that signaling by competing with full-length or transmembrane versions of the receptor to reduce the intracellular signal resulting from binding of the component of the environment to the activation component.

[0134] The disclosure provides a chimeric stimulatory receptor (CSR) comprising: (a) an ectodomain comprising a activation component; (b) a transmembrane domain; and (c) an endodomain comprising at least one signal transduction domain; wherein the combination of (a), (b) and (c) is non-naturally occurring.

[0135] In some embodiments of the CSRs of the disclosure, the activation component of (a) is isolated or derived from a first protein. In some embodiments, the signal transduction domain of (c) is isolated or derived from a second protein. In some embodiments, the first protein and the second protein are not identical.

[0136] In some embodiments of the CSRs of the disclosure, the CSR is a switch receptor that translates binding of the activation component extracellularly with either suppressing a signal or transducing a qualitatively different signal than would be transduced by a wild type, full-length or transmembrane version of the first protein. Because a CSR switch receptor is chimeric with respect to the extracellular and intracellular domains, the CSR can switch the consequence of binding the extracellular activation component from the naturally-occurring scenario to an engineered, non-naturally occurring, scenario.

[0137] In some embodiments of the CSRs of the disclosure, the activation component comprises one or more of a component of a human transmembrane receptor, a human cell-surface receptor, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor. In some embodiments, the Activation component comprises a portion of one or more of a component of a human transmembrane receptor, a human cell-surface receptor, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor to which an agonist of the activation component binds.

[0138] In some embodiments of the CSRs of the disclosure, the agonist comprises one or more of a small organic or inorganic molecule, a nucleic acid, an amino acid, an antibody or

a fragment thereof, an antibody mimetic, an aptamer, a scaffold protein, a ligand, a receptor, a naturally occurring biomolecule, and a non-naturally occurring molecule (organic or inorganic).

[0139] In some embodiments of the CSRs of the disclosure, the Activation component comprises a CD2 protein or a portion thereof to which an agonist binds.

[0140] In some embodiments of the CSRs of the disclosure, the signal transduction domain comprises one or more of a component of human signal transduction domain, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor. In some embodiments, the signal transduction domain comprises a CD3 protein. In some embodiments, the CD3 protein comprises a CD3ζ protein.

[0141] In some embodiments of the CSRs of the disclosure, the endodomain further comprises a cytoplasmic domain. In some embodiments, the sequence encoding the cytoplasmic domain comprises a sequence encoding a co-stimulatory protein. In some embodiments, the cytoplasmic domain is isolated or derived from a third protein. In some embodiments, the first protein and the third protein are identical.

[0142] In some embodiments of the CSRs of the disclosure, the ectodomain further comprises a signal peptide. In some embodiments, the signal peptide is derived from a fourth protein. In some embodiments, the first protein and the fourth protein are identical.

[0143] In some embodiments of the CSRs of the disclosure, the transmembrane domain is isolated or derived from a fifth protein. In some embodiments, the first protein and the fifth protein are identical.

[0144] In some embodiments of the CSRs of the disclosure, the CSR comprises an ectodomain comprising a signal peptide having a sequence isolated or derived from a CD2 protein and a Activation component comprising a sequence isolated or derived from a CD2 protein or a portion thereof to which an agonist binds, a transmembrane domain comprising a sequence isolated or derived from a CD2 protein, and an endodomain comprising a cytoplasmic domain comprising a sequence isolated or derived from a CD2 protein and a signal transduction domain comprising a sequence isolated or derived form a CD3ζ protein.

[0145] In some embodiments of the CSRs of the disclosure, the Activation component does not bind a naturally-occurring molecule.

[0146] In some embodiments of the CSRs of the disclosure, the CSR does not transduce a signal upon binding of the Activation component to a naturally-occurring molecule. In some embodiments, the ectodomain comprises a modification. In some embodiments, the modification comprises a mutation or a truncation of a sequence encoding the Activation component when compared to a wild type sequence of the first protein.

[0147] In some embodiments of the CSRs of the disclosure, the Activation component binds to a non-naturally occurring molecule.

[0148] In some embodiments of the CSRs of the disclosure, the CSR selectively transduces a signal upon binding of the Activation component to a non-naturally occurring molecule.

[0149] The disclosure provides a nucleic acid sequence encoding the CSR of the disclosure.

[0150] The disclosure provides a vector comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0151] The disclosure provides a vector comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0152] The disclosure provides a transposon comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0153] The disclosure provides a cell comprising the CSR of the disclosure.

[0154] The disclosure provides a cell comprising the nucleic acid encoding the CSR of the disclosure.

[0155] The disclosure provides a cell comprising the vector comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0156] The disclosure provides a cell comprising the transposon comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0157] The disclosure provides a composition comprising the CSR of the disclosure.

[0158] The disclosure provides a composition comprising the nucleic acid encoding the CSR of the disclosure.

[0159] The disclosure provides a composition comprising the vector comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0160] The disclosure provides a composition comprising the transposon comprising the nucleic acid sequence encoding the CSR of the disclosure.

[0161] The disclosure provides a composition comprising a cell of the disclosure, including those comprising a sequence encoding a CSR and/or expressing a CSR of the disclosure. The disclosure provides a composition comprising a plurality of cells of the disclosure, including those comprising a sequence encoding a CSR and/or expressing a CSR of the disclosure.

[0162] The disclosure provides a modified cell comprising: (a) a sequence encoding a CSR of the disclosure and (b) a sequence encoding an inducible proapoptotic polypeptide; and wherein the cell is a T-cell.

[0163] The disclosure provides a modified cell comprising: (a) a sequence encoding a CSR of the disclosure and (b) a sequence encoding an inducible proapoptotic polypeptide. In some embodiments of the modified cells of the disclosure, the modified cells further comprise a sequence encoding a non-naturally occurring antigen receptor, and/or a sequence encoding a therapeutic polypeptide.

[0164] In some embodiments of the modified cells of the disclosure, including those wherein the modified cell comprises a sequence encoding a non-naturally occurring antigen receptor, the non-naturally occurring antigen receptor comprises a chimeric antigen receptor (CAR). In some embodiments, the CAR comprises: (a) an ectodomain comprising an antigen recognition region, (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In some embodiments, the ectodomain of (a) of the CAR further comprises a signal peptide. In some embodiments, the ectodomain of (a) of the CAR further comprises a hinge between the antigen recognition region and the transmembrane domain. In some embodiments, the endodomain comprises a human CD3ζ endodomain. In some embodiments, the at least one costimulatory domain comprises a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. In some embodiments, the at least one costimulatory domain comprises a human CD28 and/or a 4-1BB costimulatory domain.

[0165] In some embodiments of the modified cells of the disclosure, a transposon, a vector, a donor sequence or a donor plasmid comprises the sequence encoding the CSR and/or the sequence encoding the inducible proapoptotic polypeptide. In some embodiments, the transposon, the vector, the donor sequence or the donor plasmid further comprises a sequence

encoding a non-naturally occurring antigen receptor or a sequence encoding a therapeutic protein. In some embodiments, the transposon, the vector, the donor sequence, or the donor plasmid further comprises the sequence encoding the selection marker. In some embodiments, the transposon is a piggyBac or a piggy-Bac like transposon.

[0166] In some embodiments of the modified cells of the disclosure, the sequence encoding the CSR is transiently expressed in the cell and wherein the sequence encoding the inducible proapoptotic polypeptide is stably expressed in the cell. In some embodiments, a sequence encoding a non-naturally occurring antigen receptor or a sequence encoding a therapeutic protein is stably expressed in the cell. In some embodiments, a first transposon, a first vector, a first donor sequence, or a first donor plasmid comprises the sequence encoding the CSR. In some embodiments, a second transposon, a second vector, a second donor sequence, or a second donor plasmid comprises one or more of the sequence encoding the inducible proapoptotic polypeptide, the sequence encoding a non-naturally occurring antigen receptor, the sequence encoding a therapeutic protein. In some embodiments, the first transposon, the first vector, the first donor sequence, or the first donor plasmid further comprises a sequence encoding a first selection marker. In some embodiments, the second transposon, the second vector, the second donor sequence, or the second donor plasmid further comprises a sequence encoding a second selection marker. In some embodiments, the first selection marker and the second selection marker are not identical.

[0167] In some embodiments of the modified cells of the disclosure, the selection marker is a cell surface marker. In some embodiments, the cell surface marker distinguishes cells when sorted by the marker or a detectable tag. In some embodiments, the detectable tag is fluorescent or magnetic.

[0168] In some embodiments of the modified cells of the disclosure, the selection marker comprises a protein that is active in dividing cells and not active in non-dividing cells. In some embodiments, the selection marker comprises a metabolic marker. In some embodiments, the selection marker comprises a dihydrofolate reductase (DHFR) mutein enzyme. In some embodiments, the DHFR mutein enzyme comprises or consists of the amino acid sequence of:

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  1 MVGSLNCIVA VSQNMGIGKN GDFPWPPLRN ESRYFQRMTT TSSVEGKQNL
 61 VIMGKKTWFS IPEKNRPLKG RINLVLSREL KEPPQGAHFL SRSLDDALKL
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121 TEQPELANKV DMVWIVGGSS VYKEAMNHPG HLKLFVTRIM QDFESDTFFP
181 EIDLEKYKLL PEYPGVLSDV QEEKGIKYKF EVYEKND (SEQ ID NO: 17012). In some embodiments, theamino acid sequence of the DHFR mutein enzyme further comprises a mutation at one or more of positions 80, 113, or 153. In some embodiments, the amino acid sequence of the DHFR mutein enzyme comprises one or more of a substitution of a Phenylalanine (F) or a Leucine (L) at position 80, a substitution of a Leucine (L) or a Valine (V) at position 113, and a substitution of a Valine (V) or an Aspartic Acid (D) at position 153.

Chimeric Stimulatory Receptors (CSRs)

[0169] The disclosure provides a Chimeric Stimulatory Receptor (CSR) to deliver CD3z primary stimulation to T cells (and, consequently, an endogenous CD3ζ) when stimulated using standard activation/stimulation reagents, including agonist anti-CD3 mAb.

[0170] Chimeric Stimulatory Receptors (CSRs) of the disclosure provide a CD3ζ stimulus to enhance activation and expansion of T cells. In some embodiments, CSRs of the disclosure comprise an agonist mAb epitope extracellularly and a CD3ζ stimulatory domain intracellularly and, functionally, convert an anti-CD28 or anti-CD2 binding event on the surface into a CD3z signaling event in an allogeneic T cell modified to express the CSR. In some embodiments, a CSR comprises a wild type CD28 or CD2 protein and a CD3z intracellular stimulation domain, to produce CD28z CSR and CD2z CSR, respectively. In preferred embodiments, CD28z CSR and/or CD2z CSR further express a non-naturally occurring antigen receptor and/or a therapeutic protein. In preferred embodiments, the non-naturally occurring antigen receptor comprises a Chimeric Antigen Receptor.

[0171] In certain embodiments, the CD28z CSR is encoded by an amino acid sequence comprising
MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHK
GLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFC
KIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLL
VTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSR
SADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE
LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 17910).

[0172] In certain embodiments, the CD28z CSR is encoded by a nucleic acid sequence comprising

atgctgagactgctgctggccctgaatctgttccccagcatccaagtgaccggcaacaagatcctggtcaagcagagccctatgctgg
tggcctacgacaacgccgtgaacctgagctgcaagtacagctacaacctgttcagcagagagttccgggccagcctgcacaaagga
ctggattctgctgtggaagtgtgcgtggtgtacggcaactacagccagcagctgcaggtctacagcaagaccggcttcaactgcgac
ggcaagctgggcaatgagagcgtgaccttctacctgcaaaacctgtacgtgaaccagaccgacatctatttctgcaagatcgaagtga
tgtacccgcctccttacctggacaacgagaagtccaacggcaccatcatccacgtgaagggcaagcacctgtgtccttctccactgttc
cccggacctagcaagcctttctgggtgctcgttgttgttggcggcgtgctggcctgttatagcctgctggttacagtggccttcatcatctt
ttgggtccgaagcaagcggagccggctgctgcacagcgactacatgaacatgaccctagacggcccggaccaaccagaaagca
ctaccagccttacgctcctcctagagacttcgccgcctaccggtccagagtgaagttctccagatccgccgatgctcccgcctataagc
agggccagaaccagctgtacaacgagctgaacctggggagaagagaagagtacgatgtgctggacaagcggagaggcagagatc
ctgagatgggcggcaagcccagacggaagaatcctcaagagggcctgtacaatgaactgcagaaagacaagatggccgaggcct
acagcgagatcggaatgaagggcgagcgcagaagaggcaagggacacgatggactgtaccagggcctgagcaccgccaccaag
gatacctatgatgccctgcacatgcaggccctgcctccaaga (SEQ ID NO: 17911).

[0173] In certain embodiments, the CD2z CSR is encoded by an amino acid sequence comprising

MSFPCKFVASFLLIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDDIDDIK
WEKTSDKKKIAQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGK
NVLEKIFDLKIQERVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVIT
HKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGSLLMVFVALLV
FYITKRKKQRSRRNDEELETRAHRVATEERGRKPHQIPASTPQNPATSQHPPPPPGHR
SQAPSHRPPPPGHRVQHQPQKRPPAPSGTQVHQQKGPPLPRPRVQPKPPHGAAENSL
SPSSNRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR
RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH
MQALPPR (SEQ ID NO: 17912)

[0174] In certain embodiments, the CD2z CSR is encoded by a nucleic acid sequence comprising

atgagcttcccttgcaagttcgtggccagcttcctgctgatcttcaacgtgtcctctaagggcgccgtgtccaaagagatcacaaacgcc
ctggaaacctggggagccctcggccaggatattaacctggacatccccagcttccagatgagcgacgacatcgatgacatcaagtgg
gagaaaaccagcgacaagaagaagatcgcccagttccggaaagagaaagagacattcaaagagaaggacacctacaagctgttca
agaacggcaccctgaagatcaagcacctgaaaaccgacgaccaggacatctataaggtgtccatctacgacaccaagggcaagaa

cgtgctggaaaagatcttcgacctcaagatccaagagcgggtgtccaagcctaagatcagctggacctgcatcaacaccacactgac
ctgcgaagtgatgaacggcacagaccccgagctgaacctgtaccaggatggcaaacacctgaagctgagccagcgcgtgatcacc
cacaagtggacaacaagcctgagcgccaagttcaagtgcaccgccggaaacaaagtgtctaaagagtccagcgtcgagcccgtgtc
ttgccctgaaaaaggactggacatctacctgatcatcggcatctgtggcggcggaagcctgctgatggtgtttgtggctctgctggtgtt
ctacatcaccaagcggaagaagcagcggagcagacggaacgacgaggaactggaaacacgggcccatagagtggccaccgag
gaaagaggcagaaagccccaccagattccagccagcacaccccagaatcctgccacctctcaacaccctccacctccacctggaca
cagatctcaggccccatctcacagacctccaccacctggtcatcgggtgcagcaccagcctcagaaaagacctcctgctcctagcgg
cacacaggtgcaccagcaaaaaggacctccactgcctcggcctagagtgcagcctaaacctcctcatggcgccgctgagaacagcc
tgtctccaagcagcaacagagtgaagttcagccgcagcgccgatgctcctgcctataagcagggacagaaccagctgtacaacgag
ctgaatctggggcgcagagaagagtacgatgtgctggacaagcggagaggcagagatcctgagatgggcggcaagcccagacgg
aagaatcctcaagagggcctgtataatgagctgcagaaagacaagatggccgaggcctacagcgagatcggaatgaagggcgagc
gcagaagaggcaagggacacgatggactgtatcagggcctgagcaccgccaccaaggatacctatgatgccctgcacatgcaggc
cctgcctccaaga (SEQ ID NO: 17913).

[0175] Modified T cells of the disclosure comprising/expressing a CSR of the disclosure improve the expansion of T cells when compared to those cells that do not comprise/express a CSR of the disclosure.

Immune and Immune Precursor Cells

[0176] 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, neutrophils, basophils, eosinophils, monocytes, macrophages, platelets, erythrocytes, red blood cells (RBCs), megakaryocytes or osteoclasts.

[0177] 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)

[0178] 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.

[0179] 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).

[0180] 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.

[0181] 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+.

[0182] 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.

T Cells

[0183] Modified T cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

[0184] 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.

[0185] 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 parental T cell subset with T_{SCM} cells being the most abundant (e.g. T_{SCM} > T_{CM} > T_{EM} > T_E > T_{TE}).

[0186] 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 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.

[0187] In some embodiments of the methods of the disclosure, 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}.

[0188] In some embodiments of the methods of the disclosure, the immune cell is an early memory T cell.

[0189] In some embodiments of the methods of the disclosure, the immune cell is a stem cell like T-cell.

[0190] In some embodiments of the methods of the disclosure, the immune cell is a T_{SCM}.

[0191] In some embodiments of the methods of the disclosure, the immune cell is a T_{CM}.

[0192] 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 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}.

[0193] 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. 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}.

[0194] 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-2Rβ. In certain embodiments, the cell-surface markers comprise one or more of CD45RA, CD95, IL-2Rβ, CCR7, and CD62L.

[0195] 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-2Rβ, CCR7, and CD62L.

[0196] 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.

[0197] 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-2Rβ.

[0198] 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}).

[0199] 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 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, $MgCl_2$, ClNa, Glucose and $Ca(NO_3)_2$ 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 $MgCl_2$, 90 mM ClNa, 10 mM Glucose and 0.4 mM $Ca(NO_3)_2$. In certain embodiments, the buffer comprises 5 mM KCl, 15 mM $MgCl_2$, 90 mM ClNa, 10 mM Glucose and 0.4 mM $Ca(NO_3)_2$ and a supplement comprising 20 mM HEPES and 75 mM Tris/HCl. In certain embodiments, the buffer comprises 5 mM KCl, 15 mM $MgCl_2$, 90 mM ClNa, 10 mM Glucose and 0.4 mM $Ca(NO_3)_2$ and a supplement comprising 40 mM Na_2HPO_4/NaH_2PO_4 at pH 7.2. In certain embodiments, the composition comprising primary human T cells comprises 100 µl of the buffer and between $5x10^6$ and $25x10^6$ cells. In certain embodiments, the composition comprises a scalable ratio of $250x10^6$ primary human T cells per milliliter of buffer or other media during the introduction step.

[0200] 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.

[0201] 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.

[0202] 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 lympokines 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 (INFγ). The one or more cytokine(s) may comprise IL-2.

[0203] 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-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 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 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.

[0204] 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 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 7.56 µmol/kg and a sterol at a concentration of 2.61 µmol/kg.

[0205] 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).

[0206] 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.

[0207] 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.

[0208] 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.

[0209] 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 .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%).

[0210] 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).

[0211] 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 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 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 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 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 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.

[0212] 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 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 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 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 7.56 μmol/kg and a sterol at a concentration of 2.61 μmol/kg.

[0213] 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 the P13K-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 GSK3β such as TWS119 (also known as 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 (BLUEBIRDBIO™). 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 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-aminopyrrolidine, 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)), 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 (Edelfosine (1-O-octadecyl-2-O-methyl-rac-glycero-3-phosphocholine, ET-18-OCH_3) 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), Sulfonamide 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), triciribine 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 1125976, 3-methyl-xanthine, quinoline-4-carboxamide and 2-[4-(cyclohexa-1,3-dien-1-yl)-1H-pyrazol-3-yl]phenol, 3-oxo-tirucallic acid, 3α- and 3β-acetoxy-tirucallic acids, acetoxy-tirucallic 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).

[0214] 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).

[0215] 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 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*.

[0216] In certain embodiments of the methods of producing a modified T cell (e.g. a stem cell-like T cell, a TSCM and/or a TCM) 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).

[0217] 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 lympokines 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 (INFγ). The one or more cytokine(s) may comprise IL-2.

[0218] 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

[0219] 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.

[0220] Modified NK cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

[0221] In certain embodiments, non-activated NK cells are derived from CD3-depleted leukopheresis (containing CD14/CD19/CD56+ cells).

[0222] 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.

[0223] In certain embodiments, 5x10E6 cells were electroporated per electroporation in 100 µL P3 buffer in cuvettes. However, this ratio of cells per volume is scalable for commercial manufacturing methods.

[0224] In certain embodiments, NK cells were stimulated by co-culture with an additional cell line. In certain embodiments, 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.

[0225] In certain embodiments, NK cells express CD56.

B cells

[0226] 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.

[0227] Modified B cells of the disclosure may be derived from modified hematopoietic stem and progenitor cells (HSPCs) or modified HSCs.

[0228] 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.

[0229] 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.

[0230] 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 were cultured with MS-5 feeder cells for 33 days.

Transposition Systems

[0231] 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, Tol2 transposons and transposases and TcBuster transposons and transposases.

[0232] 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 piggyBac™ or a Super piggyBac™ (SPB) transposase. In certain embodiments, and, in particular, those embodiments wherein the transposase is a Super piggyBac™ (SPB) transposase, the sequence encoding the transposase is an mRNA sequence.

[0233] In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac™ (PB) transposase enzyme. The piggyBac (PB) transposase enzyme may comprise or consist of an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 99% or any percentage in between identical to:

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
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241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO: 14487).

[0234] In certain embodiments of the methods 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:

1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SG**T**KYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO: 14487).

[0235] In certain embodiments, the transposase enzyme is a piggyBac™ (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 piggyBac™ (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 piggyBac™ (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).

[0236] In certain embodiments of the methods of the disclosure, the transposase enzyme is a Super piggyBac™ (SPB) transposase enzyme. In certain embodiments, the Super piggyBac™ (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 piggyBac™ (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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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO:
14484).
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[0237] 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™ or Super piggyBac™ 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 piggyBac™ or Super piggyBac™ 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 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 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).

[0238] 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™ transposase enzyme may comprise or the Super piggyBac™ 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 piggyBac™ transposase enzyme may comprise or the Super piggyBac™ 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 piggyBac™ transposase enzyme may comprise or the Super piggyBac™ 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 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 piggyBac™ 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 piggyBac™ transposase enzyme may comprise a substitution of a valine (V) for a methionine (M) at position 194 of SEQ ID NO: 14487, the piggyBac™ 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 piggyBac™ 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 piggyBac™ 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.

[0239] 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.

[0240] 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).

[0241] 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:

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  1 MGKSKEISQD LRKKIVDLHK SGSSLGAISK RLKVPRSSVQ TIVRKYKHHG TTQPSYRSGR
 61 RRVLSPRDER TLVRKVQINP RTTAKDLVKM LEETGTKVSI STVKRVLYRH NLKGRSARKK
121 PLLQNRHKKA RLRFATAHGD KDRTFWRNVL WSDETKIELF GHNDHRYVWR KKGEACKPKN
181 TIPTVKHGGG SIMLWGCFAA GGTGALHKID GIMRKENYVD ILKQHLKTSV RKLKLGRKWV
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241 FQMDNDPKHT SKVVAKWLKD NKVKVLEWPS QSPDLNPIEN LWAELKKRVR ARRPTNLTQL
301 HQLCQEEWAK IHPTYCGKLV EGYPKRLTQV KQFKGNATKY (SEQ ID NO: 14485).

[0242] 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:

1 MGKSKEISQD LRKRIVDLHK SGSSLGAISK RLAVPRSSVQ TIVRKYKHHG TTQPSYRSGR
61 RRVLSPRDER TLVRKVQINP RTTAKDLVKM LEETGTKVSI STVKRVLYRH NLKGHSARKK
121 PLLQNRHKKA RLRFATAHGD KDRTFWRNVL WSDETKIELF GHNDHRYVWR KKGEACKPKN
181 TIPTVKHGGG SIMLWGCFAA GGTGALHKID GIMDAVQYVD ILKQHLKTSV RKLKLGRKWV
241 FQHDNDPKHT SKVVAKWLKD NKVKVLEWPS QSPDLNPIEN LWAELKKRVR ARRPTNLTQL
301 HQLCQEEWAK IHPNYCGKLV EGYPKRLTQV KQFKGNATKY (SEQ ID NO: 14486).

[0243] 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:

1 TCCTATATAA TAAAAGAGAA ACATGCAAAT TGACCATCCC TCCGCTACGC TCAAGCCACG
61 CCCACCAGCC AATCAGAAGT GACTATGCAA ATTAACCCAA CAAAGATGGC AGTTAAATTT
121 GCATACGCAG GTGTCAAGCG CCCCAGGAGG CAACGGCGGC CGCGGGCTCC CAGGACCTTC
181 GCTGGCCCCG GGAGGCGAGG CCGGCCGCGC CTAGCCACAC CCGCGGGCTC CCGGGACCTT
241 CGCCAGCAGA GAGCAGAGCG GGAGAGCGGG CGGAGAGCGG GAGGTTTGGA GGACTTGGCA
301 GAGCAGGAGG CCGCTGGACA TAGAGCAGAG CGAGAGAGAG GGTGGCTTGG AGGGCGTGGC
361 TCCCTCTGTC ACCCCAGCTT CCTCATCACA GCTGTGGAAA 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 ACGTGCGTCT GATCTTGAAA GAAGGCGGCG CCTGCAACAG
661 AATGTATCTG AAGAGCAGCT ACTGGAAAAA CGTCGCTCTG AAGCCGAAAA ACAGCGGCGT
721 CATCGACAGA AAATGTCTAA AGACCAACGT GCCTTTGAAG TTGAAAGAAG GCGGTGGCGA
781 CGACAGAATA TGTCTAGAGA ACAGTCATCA ACAAGTACTA CCAATACCGG TAGGAACTGC
841 CTTCTCAGCA AAAATGGAGT ACATGAGGAT GCAATTCTCG AACATAGTTG TGGTGGAATG
901 ACTGTTCGAT GTGAATTTTG CCTATCACTA AATTTCTCTG ATGAAAAACC ATCCGATGGG
961 AAATTTACTC GATGTTGTAG CAAAGGGAAA GTCTGTCCAA ATGATATACA TTTTCCAGAT
1021 TACCCGGCAT ATTTAAAAAG ATTAATGACA AACGAAGATT CTGACAGTAA AAATTTCATG
1081 GAAAATATTC GTTCCATAAA TAGTTCTTTT GCTTTTGCTT CCATGGGTGC AAATATTGCA
1141 TCGCCATCAG GATATGGGCC ATACTGTTTT AGAATACACG GACAAGTTTA TCACCGTACT
1201 GGAACTTTAC ATCCTTCGGA TGGTGTTTCT CGGAAGTTTG CTCAACTCTA TATTTTGGAT

1261 ACAGCCGAAG CTACAAGTAA AAGATTAGCA ATGCCAGAAA ACCAGGGCTG CTCAGAAAGA
1321 CTCATGATCA ACATCAACAA CCTCATGCAT GAAATAAATG AATTAACAAA ATCGTACAAG
1381 ATGCTACATG AGGTAGAAAA GGAAGCCCAA TCTGAAGCAG CAGCAAAAGG TATTGCTCCC
1441 ACAGAAGTAA CAATGGCGAT TAAATACGAT CGTAACAGTG ACCCAGGTAG ATATAATTCT
1501 CCCCGTGTAA CCGAGGTTGC TGTCATATTC AGAAACGAAG ATGGAGAACC TCCTTTTGAA
1561 AGGGACTTGC TCATTCATTG TAAACCAGAT CCCAATAATC CAAATGCCAC TAAAATGAAA
1621 CAAATCAGTA TCCTGTTTCC TACATTAGAT GCAATGACAT ATCCTATTCT TTTTCCACAT
1681 GGTGAAAAAG GCTGGGGAAC AGATATTGCA TTAAGACTCA GAGACAACAG TGTAATCGAC
1741 AATAATACTA GACAAAATGT AAGGACACGA GTCACACAAA TGCAGTATTA TGGATTTCAT
1801 CTCTCTGTGC GGGACACGTT CAATCCTATT TTAAATGCAG GAAAATTAAC TCAACAGTTT
1861 ATTGTGGATT CATATTCAAA AATGGAGGCC AATCGGATAA ATTTCATCAA AGCAAACCAA
1921 TCTAAGTTGA GAGTTGAAAA ATATAGTGGT TTGATGGATT ATCTCAAATC TAGATCTGAA
1981 AATGACAATG TGCCGATTGG TAAAATGATA ATACTTCCAT CATCTTTTGA GGGTAGTCCC
2041 AGAAATATGC AGCAGCGATA TCAGGATGCT ATGGCAATTG TAACGAAGTA TGGCAAGCCC
2101 GATTTATTCA TAACCATGAC ATGCAACCCC AAATGGGCAG ATATTACAAA CAATTTACAA
2161 CGCTGGCAAA AAGTTGAAAA CAGACCTGAC TTGGTAGCCA GAGTTTTTAA TATTAAGCTG
2221 AATGCTCTTT TAAATGATAT ATGTAAATTC CATTTATTTG GCAAAGTAAT AGCTAAAATT
2281 CATGTCATTG AATTTCAGAA ACGCGGACTG CCTCACGCTC ACATATTATT GATATTAGAT
2341 AGTGAGTCCA AATTACGTTC AGAAGATGAC ATTGACCGTA TAGTTAAGGC AGAAATTCCA
2401 GATGAAGACC AGTGTCCTCG ACTTTTTCAA ATTGTAAAAT CAAATATGGT ACATGGACCA
2461 TGTGGAATAC AAAATCCAAA TAGTCCATGT ATGGAAAATG GAAAATGTTC AAAGGGATAT
2521 CCAAAAGAAT TTCAAAATGC GACCATTGGA AATATTGATG GATATCCCAA ATACAAACGA
2581 AGATCTGGTA GCACCATGTC TATTGGAAAT AAAGTTGTCG ATAACACTTG GATTGTCCCT
2641 TATAACCCGT ATTTGTGCCT TAAATATAAC TGTCATATAA ATGTTGAAGT CTGTGCATCA
2701 ATTAAAAGTG TCAAATATTT ATTTAAATAC ATCTATAAAG GGCACGATTG TGCAAATATT
2761 CAAATTTCTG AAAAAAATAT TATCAATCAT GACGAAGTAC AGGACTTCAT TGACTCCAGG
2821 TATGTGAGCG CTCCTGAGGC TGTTTGGAGA CTTTTTGCAA TGCGAATGCA TGACCAATCT
2881 CATGCAATCA CAAGATTAGC TATTCATTTG CCAAATGATC AGAATTTGTA TTTTCATACC
2941 GATGATTTTG CTGAAGTTTT AGATAGGGCT AAAAGGCATA ACTCGACTTT GATGGCTTGG
3001 TTCTTATTGA ATAGAGAAGA TTCTGATGCA CGTAATTATT ATTATTGGGA GATTCCACAG
3061 CATTATGTGT TTAATAATTC TTTGTGGACA AAACGCCGAA AGGGTGGGAA TAAAGTATTA
3121 GGTAGACTGT TCACTGTGAG CTTTAGAGAA CCAGAACGAT ATTACCTTAG ACTTTTGCTT
3181 CTGCATGTAA AAGGTGCGAT AAGTTTTGAG GATCTGCGAA CTGTAGGAGG TGTAACTTAT
3241 GATACATTTC ATGAAGCTGC TAAACACCGA GGATTATTAC TTGATGACAC TATCTGGAAA
3301 GATACGATTG ACGATGCAAT CATCCTTAAT ATGCCCAAAC AACTACGGCA ACTTTTTGCA
3361 TATATATGTG TGTTTGGATG TCCTTCTGCT GCAGACAAAT TATGGGATGA GAATAAATCT
3421 CATTTTATTG AAGATTTCTG TTGGAAATTA CACCGAAGAG AAGGTGCCTG TGTGAACTGT

3481 GAAATGCATG CCCTTAACGA AATTCAGGAG GTATTCACAT TGCATGGAAT GAAATGTTCA
3541 CATTTCAAAC TTCCGGACTA TCCTTTATTA ATGAATGCAA ATACATGTGA TCAATTGTAC
3601 GAGCAACAAC AGGCAGAGGT TTTGATAAAT TCTCTGAATG ATGAACAGTT GGCAGCCTTT
3661 CAGACTATAA CTTCAGCCAT CGAAGATCAA ACTGTACACC CCAAATGCTT TTTCTTGGAT
3721 GGTCCAGGTG GTAGTGGAAA AACATATCTG TATAAAGTTT TAACACATTA TATTAGAGGT
3781 CGTGGTGGTA CTGTTTTACC CACAGCATCT ACAGGAATTG CTGCAAATTT ACTTCTTGGT
3841 GGAAGAACCT TTCATTCCCA ATATAAATTA CCAATTCCAT TAAATGAAAC TTCAATTTCT
3901 AGACTCGATA TAAAGAGTGA AGTTGCTAAA ACCATTAAAA AGGCCCAACT TCTCATTATT
3961 GATGAATGCA CCATGGCATC CAGTCATGCT ATAAACGCCA TAGATAGATT ACTAAGAGAA
4021 ATTATGAATT TGAATGTTGC ATTTGGTGGG AAAGTTCTCC TTCTCGGAGG GGATTTTCGA
4081 CAATGTCTCA GTATTGTACC ACATGCTATG CGATCGGCCA TAGTACAAAC GAGTTTAAAG
4141 TACTGTAATG TTTGGGGATG TTTCAGAAAG TTGTCTCTTA AAACAAATAT GAGATCAGAG
4201 GATTCTGCTT ATAGTGAATG GTTAGTAAAA CTTGGAGATG GCAAACTTGA TAGCAGTTTT
4261 CATTTAGGAA TGGATATTAT TGAAATCCCC CATGAAATGA TTTGTAACGG ATCTATTATT
4321 GAAGCTACCT TTGGAAATAG TATATCTATA GATAATATTA AAAATATATC TAAACGTGCA
4381 ATTCTTTGTC CAAAAAATGA GCATGTTCAA AAATTAAATG AAGAAATTTT GGATATACTT
4441 GATGGAGATT TTCACACATA TTTGAGTGAT GATTCCATTG ATTCAACAGA TGATGCTGAA
4501 AAGGAAAATT TTCCCATCGA ATTTCTTAAT AGTATTACTC CTTCGGGAAT GCCGTGTCAT
4561 AAATTAAAAT TGAAAGTGGG TGCAATCATC ATGCTATTGA GAAATCTTAA TAGTAAATGG
4621 GGTCTTTGTA ATGGTACTAG ATTTATTATC AAAAGATTAC GACCTAACAT TATCGAAGCT
4681 GAAGTATTAA CAGGATCTGC AGAGGGAGAG GTTGTTCTGA TTCCAAGAAT TGATTTGTCC
4741 CCATCTGACA CTGGCCTCCC ATTTAAATTA ATTCGAAGAC AGTTTCCCGT GATGCCAGCA
4801 TTTGCGATGA CTATTAATAA ATCACAAGGA CAAACTCTAG ACAGAGTAGG AATATTCCTA
4861 CCTGAACCCG TTTTCGCACA TGGTCAGTTA TATGTTGCTT TCTCTCGAGT TCGAAGAGCA
4921 TGTGACGTTA AAGTTAAAGT TGTAAATACT TCATCACAAG GGAAATTAGT CAAGCACTCT
4981 GAAAGTGTTT TTACTCTTAA TGTGGTATAC AGGGAGATAT TAGAATAAGT TTAATCACTT
5041 TATCAGTCAT TGTTTGCATC AATGTTGTTT TTATATCATG TTTTTGTTGT TTTTATATCA
5101 TGTCTTTGTT GTTGTTATAT CATGTTGTTA TTGTTTATTT ATTAATAAAT TTATGTATTA
5161 TTTTCATATA CATTTTACTC ATTTCCTTTC ATCTCTCACA CTTCTATTAT AGAGAAAGGG
5221 CAAATAGCAA TATTAAAATA TTTCCTCTAA TTAATTCCCT TTCAATGTGC ACGAATTTCG
5281 TGCACCGGGC CACTAG (SEQ ID NO: 18061).

[0244] 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.

[0245] An exemplary Helitron transposase of the disclosure comprises an amino acid sequence comprising:

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   1 MSKEQLLIQR SSAAERCRRY RQKMSAEQRA SDLERRRRLQ QNVSEEQLLE KRRSEAEKQR
  61 RHRQKMSKDQ RAFEVERRRW RRQNMSREQS STSTTNTGRN CLLSKNGVHE DAILEHSCGG
 121 MTVRCEFCLS LNFSDEKPSD GKFTRCCSKG KVCPNDIHFP DYPAYLKRLM TNEDSDSKNF
 181 MENIRSINSS FAFASMGANI ASPSGYGPYC FRIHGQVYHR TGTLHPSDGV SRKFAQLYIL
 241 DTAEATSKRL AMPENQGCSE RLMININNLM HEINELTKSY KMLHEVEKEA QSEAAAKGIA
 301 PTEVTMAIKY DRNSDPGRYN SPRVTEVAVI FRNEDGEPPF ERDLLIHCKP DPNNPNATKM
 361 KQISILFPTL DAMTYPILFP HGEKGWGTDI ALRLRDNSVI DNNTRQNVRT RVTQMQYYGF
 421 HLSVRDTFNP ILNAGKLTQQ FIVDSYSKME ANRINFIKAN QSKLRVEKYS GLMDYLKSRS
 481 ENDNVPIGKM IILPSSFEGS PRNMQQRYQD AMAIVTKYGK PDLFITMTCN PKWADITNNL
 541 QRWQKVENRP DLVARVFNIK LNALLNDICK FHLFGKVIAK IHVIEFQKRG LPHAHILLIL
 601 DSESKLRSED DIDRIVKAEI PDEDQCPRLF QIVKSNMVHG PCGIQNPNSP CMENGKCSKG
 661 YPKEFQNATI GNIDGYPKYK RRSGSTMSIG NKVVDNTWIV PYNPYLCLKY NCHINVEVCA
 721 SIKSVKYLFK YIYKGHDCAN IQISEKNIIN HDEVQDFIDS RYVSAPEAVW RLFAMRMHDQ
 781 SHAITRLAIH LPNDQNLYFH TDDFAEVLDR AKRHNSTLMA WFLLNREDSD ARNYYYWEIP
 841 QHYVFNNSLW TKRRKGGNKV LGRLFTVSFR EPERYYLRLL LLHVKGAISF EDLRTVGGVT
 901 YDTFHEAAKH RGLLLDDTIW KDTIDDAIIL NMPKQLRQLF AYICVFGCPS AADKLWDENK
 961 SHFIEDFCWK LHRREGACVN CEMHALNEIQ EVFTLHGMKC SHFKLPDYPL LMNANTCDQL
1021 YEQQQAEVLI NSLNDEQLAA FQTITSAIED QTVHPKCFFL DGPGGSGKTY LYKVLTHYIR
1081 GRGGTVLPTA STGIAANLLL GGRTFHSQYK LPIPLNETSI SRLDIKSEVA KTIKKAQLLI
1141 IDECTMASSH AINAIDRLLR EIMNLNVAFG GKVLLLGGDF RQCLSIVPHA MRSAIVQTSL
1201 KYCNVWGCFR KLSLKTNMRS EDSAYSEWLV KLGDGKLDSS FHLGMDIIEI PHEMICNGSI
1261 IEATFGNSIS IDNIKNISKR AILCPKNEHV QKLNEEILDI LDGDFHTYLS DDSIDSTDDA
1321 EKENFPIEFL NSITPSGMPC HKLKLKVGAI IMLLRNLNSK WGLCNGTRFI IKRLRPNIIE
1381 AEVLTGSAEG EVVLIPRIDL SPSDTGLPFK LIRRQFPVMP AFAMTINKSQ GQTLDRVGIF
1441 LPEPVFAHGQ LYVAFSRVRR ACDVKVKVVN TSSQGKLVKH SESVFTLNVV YREILE (SEQ ID
NO: 14501).
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[0246] 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 5' and 3' 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 GTGCACGAATTTCGTGCACCGGGCCACTAG (SEQ ID NO: 14500).

[0247] Tol2 transposons may be isolated or derived from the genome of the medaka fish, and may be similar to transposons of the hAT family. Exemplary Tol2 transposons of the disclosure are encoded by a sequence comprising about 4.7 kilobases and contain a gene encoding the Tol2 transposase, which contains four exons. An exemplary Tol2 transposase of the disclosure comprises an amino acid sequence comprising the following:

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  1 MEEVCDSSAA ASSTVQNQPQ DQEHPWPYLR EFFSLSGVNK DSFKMKCVLC LPLNKEISAF
 61 KSSPSNLRKH IERMHPNYLK NYSKLTAQKR KIGTSTHASS SKQLKVDSVF PVKHVSPVTV
121 NKAILRYIIQ GLHPFSTVDL PSFKELISTL QPGISVITRP TLRSKIAEAA LIMKQKVTAA
181 MSEVEWIATT TDCWTARRKS FIGVTAHWIN PGSLERHSAA LACKRLMGSH TFEVLASAMN
241 DIHSEYEIRD KVVCTTTDSG SNFMKAFRVF GVENNDIETE ARRCESDDTD SEGCGEGSDG
301 VEFQDASRVL DQDDGFEFQL PKHQKCACHL LNLVSSVDAQ KALSNEHYKK LYRSVFGKCQ
361 ALWNKSSRSA LAAEAVESES RLQLLRPNQT RWNSTFMAVD RILQICKEAG EGALRNICTS
421 LEVPMFNPAE MLFLTEWANT MRPVAKVLDI LQAETNTQLG WLLPSVHQLS LKLQRLHHSL
481 RYCDPLVDAL QQGIQTRFKH MFEDPEIIAA AILLPKFRTS WTNDETIIKR GMDYIRVHLE
541 PLDHKKELAN SSSDDEDFFA SLKPTTHEAS KELDGYLACV SDTRESLLTF PAICSLSIKT
601 NTPLPASAAC ERLFSTAGLL FSPKRARLDT NNFENQLLLK LNLRFYNFE
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(SEQ ID NO: 14502).

[0248] 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:

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   1 CAGAGGTGTA AAGTACTTGA GTAATTTTAC TTGATTACTG TACTTAAGTA TTATTTTTGG
  61 GGATTTTTAC TTTACTTGAG TACAATTAAA AATCAATACT TTTACTTTTA CTTAATTACA
 121 TTTTTTTAGA AAAAAAAGTA CTTTTTACTC CTTACAATTT TATTTACAGT CAAAAAGTAC
 181 TTATTTTTTG GAGATCACTT CATTCTATTT TCCCTTGCTA TTACCAAACC AATTGAATTG
 241 CGCTGATGCC CAGTTTAATT TAAATGTTAT TTATTCTGCC TATGAAAATC GTTTTCACAT
 301 TATATGAAAT TGGTCAGACA TGTTCATTGG TCCTTTGGAA GTGACGTCAT GTCACATCTA
 361 TTACCACAAT GCACAGCACC TTGACCTGGA AATTAGGGAA ATTATAACAG TCAATCAGTG
 421 GAAGAAAATG GAGGAAGTAT GTGATTCATC AGCAGCTGCG AGCAGCACAG TCCAAAATCA
 481 GCCACAGGAT CAAGAGCACC CGTGGCCGTA TCTTCGCGAA TTCTTTTCTT TAAGTGGTGT
 541 AAATAAAGAT TCATTCAAGA TGAAATGTGT CCTCTGTCTC CCGCTTAATA AAGAAATATC
 601 GGCCTTCAAA AGTTCGCCAT CAAACCTAAG GAAGCATATT GAGGTAAGTA CATTAAGTAT
 661 TTTGTTTTAC TGATAGTTTT TTTTTTTTTT TTTTTTTTTT TTTTTGGGTG TGCATGTTTT
 721 GACGTTGATG GCGCGCCTTT TATATGTGTA GTAGGCCTAT TTTCACTAAT GCATGCGATT
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781 GACAATATAA GGCTCACGTA ATAAAATGCT AAAATGCATT TGTAATTGGT AACGTTAGGT
841 CCACGGGAAA TTTGGCGCCT ATTGCAGCTT TGAATAATCA TTATCATTCC GTGCTCTCAT
901 TGTGTTTGAA TTCATGCAAA ACACAAGAAA ACCAAGCGAG AAATTTTTTT CCAAACATGT
961 TGTATTGTCA AAACGGTAAC ACTTTACAAT GAGGTTGATT AGTTCATGTA TTAACTAACA
1021 TTAAATAACC ATGAGCAATA CATTTGTTAC TGTATCTGTT AATCTTTGTT AACGTTAGTT
1081 AATAGAAATA CAGATGTTCA TTGTTTGTTC ATGTTAGTTC ACAGTGCATT AACTAATGTT
1141 AACAAGATAT AAAGTATTAG TAAATGTTGA AATTAACATG TATACGTGCA GTTCATTATT
1201 AGTTCATGTT AACTAATGTA GTTAACTAAC GAACCTTATT GTAAAAGTGT TACCATCAAA
1261 ACTAATGTAA TGAAATCAAT TCACCCTGTC ATGTCAGCCT TACAGTCCTG TGTTTTTGTC
1321 AATATAATCA GAAATAAAAT TAATGTTTGA TTGTCACTAA ATGCTACTGT ATTTCTAAAA
1381 TCAACAAGTA TTTAACATTA TAAAGTGTGC AATTGGCTGC AAATGTCAGT TTTATTAAAG
1441 GGTTAGTTCA CCCAAAAATG AAAATAATGT CATTAATGAC TCGCCCTCAT GTCGTTCCAA
1501 GCCCGTAAGA CCTCCGTTCA TCTTCAGAAC ACAGTTTAAG ATATTTTAGA TTTAGTCCGA
1561 GAGCTTTCTG TGCCTCCATT GAGAATGTAT GTACGGTATA CTGTCCATGT CCAGAAAGGT
1621 AATAAAAACA TCAAAGTAGT CCATGTGACA TCAGTGGGTT AGTTAGAATT TTTTGAAGCA
1681 TCGAATACAT TTTGGTCCAA AAATAACAAA ACCTACGACT TTATTCGGCA TTGTATTCTC
1741 TTCCGGGTCT GTTGTCAATC CGCGTTCACG ACTTCGCAGT GACGCTACAA TGCTGAATAA
1801 AGTCGTAGGT TTTGTTATTT TTGGACCAAA ATGTATTTTC GATGCTTCAA ATAATTCTAC
1861 CTAACCCACT GATGTCACAT GGACTACTTT GATGTTTTTA TTACCTTTCT GGACATGGAC
1921 AGTATACCGT ACATACATTT TCAGTGGAGG GACAGAAAGC TCTCGGACTA AATCTAAAAT
1981 ATCTTAAACT GTGTTCCGAA GATGAACGGA GGTGTTACGG GCTTGGAACG ACATGAGGGT
2041 GAGTCATTAA TGACATCTTT TCATTTTTGG GTGAACTAAC CCTTTAATGC TGTAATCAGA
2101 GAGTGTATGT GTAATTGTTA CATTTATTGC ATACAATATA AATATTTATT TGTTGTTTTT
2161 ACAGAGAATG CACCCAAATT ACCTCAAAAA CTACTCTAAA TTGACAGCAC AGAAGAGAAA
2221 GATCGGGACC TCCACCCATG CTTCCAGCAG TAAGCAACTG AAAGTTGACT CAGTTTTCCC
2281 AGTCAAACAT GTGTCTCCAG TCACTGTGAA CAAAGCTATA TTAAGGTACA TCATTCAAGG
2341 ACTTCATCCT TTCAGCACTG TTGATCTGCC ATCATTTAAA GAGCTGATTA GTACACTGCA
2401 GCCTGGCATT TCTGTCATTA CAAGGCCTAC TTTACGCTCC AAGATAGCTG AAGCTGCTCT
2461 GATCATGAAA CAGAAAGTGA CTGCTGCCAT GAGTGAAGTT GAATGGATTG CAACCACAAC
2521 GGATTGTTGG ACTGCACGTA GAAAGTCATT CATTGGTGTA ACTGCTCACT GGATCAACCC
2581 TGGAAGTCTT GAAAGACATT CCGCTGCACT TGCCTGCAAA AGATTAATGG GCTCTCATAC
2641 TTTTGAGGTA CTGGCCAGTG CCATGAATGA TATCCACTCA GAGTATGAAA TACGTGACAA
2701 GGTTGTTTGC ACAACCACAG ACAGTGGTTC CAACTTTATG AAGGCTTTCA GAGTTTTTGG
2761 TGTGGAAAAC AATGATATCG AGACTGAGGC AAGAAGGTGT GAAAGTGATG ACACTGATTC
2821 TGAAGGCTGT GGTGAGGGAA GTGATGGTGT GGAATTCCAA GATGCCTCAC GAGTCCTGGA
2881 CCAAGACGAT GGCTTCGAAT TCCAGCTACC AAAACATCAA AAGTGTGCCT GTCACTTACT
2941 TAACCTAGTC TCAAGCGTTG ATGCCCAAAA AGCTCTCTCA AATGAACACT ACAAGAAACT

3001 CTACAGATCT GTCTTTGGCA AATGCCAAGC TTTATGGAAT AAAAGCAGCC GATCGGCTCT
3061 AGCAGCTGAA GCTGTTGAAT CAGAAAGCCG GCTTCAGCTT TTAAGGCCAA ACCAAACGCG
3121 GTGGAATTCA ACTTTTATGG CTGTTGACAG AATTCTTCAA ATTTGCAAAG AAGCAGGAGA
3181 AGGCGCACTT CGGAATATAT GCACCTCTCT TGAGGTTCCA ATGTAAGTGT TTTTCCCCTC
3241 TATCGATGTA AACAAATGTG GGTTGTTTTT GTTTAATACT CTTTGATTAT GCTGATTTCT
3301 CCTGTAGGTT TAATCCAGCA GAAATGCTGT TCTTGACAGA GTGGGCCAAC ACAATGCGTC
3361 CAGTTGCAAA AGTACTCGAC ATCTTGCAAG CGGAAACGAA TACACAGCTG GGGTGGCTGC
3421 TGCCTAGTGT CCATCAGTTA AGCTTGAAAC TTCAGCGACT CCACCATTCT CTCAGGTACT
3481 GTGACCCACT TGTGGATGCC CTACAACAAG GAATCCAAAC ACGATTCAAG CATATGTTTG
3541 AAGATCCTGA GATCATAGCA GCTGCCATCC TTCTCCCTAA ATTTCGGACC TCTTGGACAA
3601 ATGATGAAAC CATCATAAAA CGAGGTAAAT GAATGCAAGC AACATACACT TGACGAATTC
3661 TAATCTGGGC AACCTTTGAG CCATACCAAA ATTATTCTTT TATTTATTTA TTTTTGCACT
3721 TTTTAGGAAT GTTATATCCC ATCTTTGGCT GTGATCTCAA TATGAATATT GATGTAAAGT
3781 ATTCTTGCAG CAGGTTGTAG TTATCCCTCA GTGTTTCTTG AAACCAAACT CATATGTATC
3841 ATATGTGGTT TGGAAATGCA GTTAGATTTT ATGCTAAAAT AAGGGATTTG CATGATTTTA
3901 GATGTAGATG ACTGCACGTA AATGTAGTTA ATGACAAAAT CCATAAAATT TGTTCCCAGT
3961 CAGAAGCCCC TCAACCAAAC TTTTCTTTGT GTCTGCTCAC TGTGCTTGTA GGCATGGACT
4021 ACATCAGAGT GCATCTGGAG CCTTTGGACC ACAAGAAGGA ATTGGCCAAC AGTTCATCTG
4081 ATGATGAAGA TTTTTTCGCT TCTTTGAAAC CGACAACACA TGAAGCCAGC AAAGAGTTGG
4141 ATGGATATCT GGCCTGTGTT TCAGACACCA GGGAGTCTCT GCTCACGTTT CCTGCTATTT
4201 GCAGCCTCTC TATCAAGACT AATACACCTC TTCCCGCATC GGCTGCCTGT GAGAGGCTTT
4261 TCAGCACTGC AGGATTGCTT TTCAGCCCCA AAAGAGCTAG GCTTGACACT AACAATTTTG
4321 AGAATCAGCT TCTACTGAAG TTAAATCTGA GGTTTTACAA CTTTGAGTAG CGTGTACTGG
4381 CATTAGATTG TCTGTCTTAT AGTTTGATAA TTAAATACAA ACAGTTCTAA AGCAGGATAA
4441 AACCTTGTAT GCATTTCATT TAATGTTTTT TGAGATTAAA AGCTTAAACA AGAATCTCTA
4501 GTTTTCTTTC TTGCTTTTAC TTTTACTTCC TTAATACTCA AGTACAATTT TAATGGAGTA
4561 CTTTTTTACT TTTACTCAAG TAAGATTCTA GCCAGATACT TTTACTTTTA ATTGAGTAAA
4621 ATTTTCCCTA AGTACTTGTA CTTTCACTTG AGTAAAATTT TTGAGTACTT TTTACACCTC
4681 TG (SEQ ID NO: 18062).

[0249] Exemplary transposon/transposase systems of the disclosure include, but are not limited to, piggyBac and piggyBac-like transposons and transposases.

[0250] 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 TTAA 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.

[0251] In certain embodiments, and, in particular, those embodiments wherein the transposon is a piggyBac transposon, the transposase is a piggyBac™, Super piggyBac™ (SPB) transposase. In certain embodiments, and, in particular, those embodiments wherein the transposase is a piggyBac™, Super piggyBac™ (SPB), the sequence encoding the transposase is an mRNA sequence.

[0252] In certain embodiments of the methods of the disclosure, the transposase enzyme is a piggyBac or piggyBac-like transposase enzyme.

[0253] 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:

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID
NO: 14487).
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[0254] 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:

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
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421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO: 14487).

[0255] 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 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).

[0256] 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, 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 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:

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO:
14484).
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[0257] 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 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 piggyBac™, Super piggyBac™ 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 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 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).

[0258] 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™ or piggyBac-like transposase enzyme or may comprise or the Super piggyBac™ 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 piggyBac™ or piggyBac-like transposase enzyme may comprise or the Super piggyBac™ 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 piggyBac™ or piggyBac-like transposase enzyme may comprise or the Super piggyBac™ 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 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 piggyBac™ 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 piggyBac™ 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 piggyBac™ 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 piggyBac™ 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 piggyBac™ 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.

[0259] 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: 16796), *Argyrogramma agnata* (GenBank Accession No. GU477713; SEQ ID NO: 14534, SEQ ID NO: 16797), *Anopheles gambiae* (GenBank Accession No. XP_312615 (SEQ ID NO: 16798); GenBank Accession No. XP_320414 (SEQ ID NO: 16799); GenBank Accession No. XP_310729 (SEQ ID NO: 16800)), *Aphis gossypii* (GenBank Accession No. GU329918; SEQ ID NO: 16801, SEQ ID NO: 16802), *Acyrthosiphon pisum* (GenBank Accession No. XP_001948139; SEQ ID NO: 16803), *Agrotis ipsilon* (GenBank Accession No. GU477714; SEQ ID NO: 14537, SEQ ID NO: 16804), *Bombyx mori* (GenBank Accession No. BAD11135; SEQ ID NO: 14505), *Chilo suppressalis* (GenBank Accession No. JX294476; SEQ ID NO: 16805, SEQ ID NO: 16806), *Drosophila melanogaster* (GenBank Accession No. AAL39784; SEQ ID NO: 16807), *Helicoverpa armigera* (GenBank Accession No. ABS18391; SEQ ID NO: 14525), *Heliothis virescens* (GenBank Accession No. ABD76335; SEQ ID NO: 16808), *Macdunnoughia crassisigna* (GenBank Accession No. EU287451; SEQ ID NO: 16809, SEQ ID NO: 16810), *Pectinophora gossypiella* (GenBank Accession No. GU270322; SEQ ID NO: 14530, SEQ ID NO: 16811), *Tribolium castaneum* (GenBank Accession No. XP_001814566; SEQ ID NO: 16812), *Ctenoplusia agnata* (also called *Argyrogramma agnata*), *Messour bouvieri*, *Megachile rotundata*, *Bombus impatiens*, *Mamestra brassicae*, *Mayetiola destructor* or *Apis mellifera*.

[0260] 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).

[0261] 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).

[0262] 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: 16813).

[0263] 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: 14518), *Homo sapiens* (GenBank Accession No. NP_689808; SEQ ID NO: 16814), *Mus musculus* (GenBank Accession No. NP_741958; SEQ ID NO: 16815), *Macaca fascicularis* (GenBank Accession No. AB179012; SEQ ID NO: 16816, SEQ ID NO: 16817), *Rattus norvegicus* (GenBank Accession No. XP_220453; SEQ ID NO: 16818) or *Myotis lucifugus*.

[0264] 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: 16819).

[0265] 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).

[0266] 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).

[0267] In certain embodiments, the target sequence of the piggyBac 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', 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'-CACA-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'.

[0268] 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:

```
  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 LKDLWRTDGT GVDIFRTTMS LQRFQFLQNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FDVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELSANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRANKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KHSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14504).
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[0269] 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:

```
  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 LKDLWRTDGT GVDIFRTTMS LQRFQFLQNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14505).
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[0270] 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 piggyBac or piggyBac-like transposase fused to a nuclear localization signal is encoded by a polynucleotide sequence comprising:

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   1 atggcaccca aaaagaaacg taaagtgatg gacattgaaa gacaggaaga aagaatcagg
  61 gcgatgctcg aagaagaact gagcgactac tccgacgaat cgtcatcaga ggatgaaacc
 121 gaccactgta gcgagcatga ggttaactac gacaccgagg aggagagaat cgactctgtg
 181 gatgtgccct ccaactcacg ccaagaagag gccaatgcaa ttatcgcaaa cgaatcggac
 241 agcgatccag acgatgatct gccactgtcc ctcgtgcgcc agcgggccag cgcttcgaga
 301 caagtgtcag gtccattcta cacttcgaag gacggcacta agtggtacaa gaattgccag
 361 cgacctaacg tcagactccg ctccgagaat atcgtgaccg aacaggctca ggtcaagaat
 421 atcgcccgcg acgcctcgac tgagtacgag tgttggaata tcttcgtgac ttcggacatg
 481 ctgcaagaaa ttctgacgca caccaacagc tcgattaggc atcgccagac caagactgca
 541 gcggagaact catcggccga aacctccttc tatatgcaag agactactct gtgcgaactg
 601 aaggcgctga ttgcactgct gtacttggcc ggcctcatca aatcaaatag gcagagcctc
 661 aaagatctct ggagaacgga tggaactgga gtggatatct ttcggacgac tatgagcttg
 721 cagcggttcc agtttctgca aaacaatatc agattcgacg acaagtccac ccgggacgaa
 781 aggaaacaga ctgacaacat ggctgcgttc cggtcaatat tcgatcagtt tgtgcagtgc
 841 tgccaaaacg cttatagccc atcggaattc ctgaccatcg acgaaatgct tctctccttc
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 901 cgggggcgct gcctgttccg agtgtacatc ccgaacaagc cggctaaata cggaatcaaa
 961 atcctggccc tggtggacgc caagaatttc tacgtcgtga atctcgaagt gtacgcagga
1021 aagcaaccgt cgggaccgta cgctgtttcg aaccgcccgt ttgaagtcgt cgagcggctt
1081 attcagccgg tggccagatc ccaccgcaat gttaccttcg acaattggtt caccggctac
1141 gagctgatgc ttcaccttct gaacgagtac cggctcacta gcgtggggac tgtcaggaag
1201 aacaagcggc agatcccaga atccttcatc cgcaccgacc gccagcctaa ctcgtccgtg
1261 ttcggatttc aaaaggatat cacgcttgtc tcgtacgccc ccaagaaaaa caaggtcgtg
1321 gtcgtgatga gcaccatgca tcacgacaac agcatcgacg agtcaaccgg agaaaagcaa
1381 aagcccgaga tgatcacctt ctacaattca actaaggccg gcgtcgacgt cgtggatgaa
1441 ctgtgcgcga actataacgt gtcccggaac tctaagcggt ggcctatgac tctcttctac
1501 ggagtgctga atatggccgc aatcaacgcg tgcatcatct accgcaccaa caagaacgtg
1561 accatcaagc gcaccgagtt catcagatcg ctgggtttga gcatgatcta cgagcacctc
1621 cattcacgga acaagaagaa gaatatccct acttacctga ggcagcgtat cgagaagcag
1681 ttgggagaac caagcccgcg ccacgtgaac gtgccggggc gctacgtgcg gtgccaagat
1741 tgcccgtaca aaaaggaccg caaaaccaaa agatcgtgta acgcgtgcgc caaacctatc
1801 tgcatggagc atgccaaatt tctgtgtgaa aattgtgctg aactcgattc ctccctg
(SEQ ID NO: 14629).
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[0271] 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 *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:

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  1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
 61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQMSGPHYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSASTS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLQNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSHL (SEQ ID NO: 14576).
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[0272] 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:

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  1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
 61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVHNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YEVMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
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541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAHLDS (SEQ ID NO: 14630).
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[0273] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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  1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
 61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSASTS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIAM QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14631).
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[0274] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

```
  1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
 61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRWRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYI AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFQFLLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVKNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKTQIPENF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14632).
```

[0275] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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

[0276] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

```
  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 LKDLWRTDGT GVDIFRTTMS LQRFQFLQNN
```

```
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN DYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSSRHV NVKGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14634).
```

[0277] 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 96%, at least 97%, at least 98%, or at least 99% or any percentage in between identical to SEQ ID NO: 14505.

[0278] 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, 507,5 23, 527, 528, 543, 549, 550, 557,6 01, 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.

[0279] 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, R402XT403X, D404X, R405X, Q406X, P407X, N408X, S409X, S410X, V411X, F412X, F414X, Q415X, I418X, T419X, L420X, N428XV432X, 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 US patent No. 10,041,077, the contents of which are incorporated herein by reference in their entirety.

[0280] 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.

[0281] 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, A87X, S88X, A89X,S90X,R91X, Q92X, V93X, S94X, G95X, P96X, F97X, Y98X, T99X, W012X, G103X, Y107X, K108X, L117X, I122X, Q128X, I312X, D135X, S137X, E139X, Y140X, I145X, S149X, D150X, Q153X, E154X, T157X, S161X, 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, L211X, 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, R402XT403X, D404X, R405X, Q406X, P407X, N408X, S409X, S410X, Q415X,K416X, A424X, K426X, N428X, V430X, V432X, V433X, M434X, D436X, D440X, N441X, S442X, I443X, D444X, E445X, S446X, T447X, 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, E601X, 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 US patent No. 10,041,077, the contents of which are incorporated by reference in their entirety.

[0282] In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence of:

```
  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 LKDLWRKDGT GVDIFRTTMS LQRFQFLLNN
241 IRFDDISTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKKWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMMYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPVPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14606).
```

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

```
  1 MDIERQEERI RAMLEEELSD YSDESSSEDE TDHCSEHEVN YDTEEERIDS VDVPSNSRQE
 61 EANAIIANES DSDPDDDLPL SLVRQRASAS RQVSGPFYTS KDGTKWYKNC QRPNVRLRSE
121 NIVTEQAQVK NIARDASTEY ECWNIFVTSD MLQEILTHTN SSIRHRQTKT AAENSSAETS
181 FYMQETTLCE LKALIGLLYL AGLIKSNRQS LKDLWRTDGT GVDIFRTTMS LQRFYFLQNN
241 IRFDDKSTLD ERKQTDNMAA FRSIFDQFVQ SCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN FYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YELMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKRWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIYEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NYPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 VNCAELDSSL (SEQ ID NO: 14607).
```

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

```
  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 LKDLWRKDGT GVDIFRTTMS LQRFQFLLNN
241 IRFDDKSTRD ERKQTDNMAA FRSIFDQFVQ CCQNAYSPSE FLTIDEMLLS FRGRCLFRVY
301 IPNKPAKYGI KILALVDAKN DYVVNLEVYA GKQPSGPYAV SNRPFEVVER LIQPVARSHR
361 NVTFDNWFTG YECMLHLLNE YRLTSVGTVR KNKRQIPESF IRTDRQPNSS VFGFQKDITL
421 VSYAPKKNKV VVVMSTMHHD NSIDESTGEK QKPEMITFYN STKAGVDVVD ELCANYNVSR
481 NSKKWPMTLF YGVLNMAAIN ACIIYRTNKN VTIKRTEFIR SLGLSMIKEH LHSRNKKKNI
541 PTYLRQRIEK QLGEPSPRHV NVPGRYVRCQ DCPYKKDRKT KRSCNACAKP ICMEHAKFLC
601 ENCAELDSSL (SEQ ID NO: 14608).
```

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

[0283] 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:

```
   1 ttatcccggc gagcatgagg cagggtatct catacctgg taaaatttta aagttgtgta
  61 ttttataaaa ttttcgtctg acaacactag cgcgctcagt agctggaggc aggagcgtgc
 121 gggaggggat agtggcgtga tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc
 181 aaacctgttt cgggtatgtt ataccctgcc tcattgttga cgtatttttt ttatgtaatt
 241 tttccgatta ttaatttcaa ctgttttatt ggtattttta tgttatccat tgttcttttt
 301 ttatgattta ctgtatcggt tgtctttcgt tcctttagtt gagtttttt ttattatttt
 361 cagtttttga tcaaa (SEQ ID NO: 14506).
```

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

```
   1 tcatattttt agtttaaaaa aataattata tgttttataa tgaaaagaat ctcattatct
  61 ttcagtatta ggttgattta tattccaaag aataatattt ttgttaaatt gttgattttt
 121 gtaaacctct aaatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
 181 taataatttc ataattaaaa acttctttca ttgaatgcca ttaaataaac cattatttta
 241 caaaataaga tcaacataat tgagtaaata ataataagaa caatattata gtacaacaaa
 301 atatgggtat gtcataccct gccacattct tgatgtaact ttttttcacc tcatgctcgc
 361 cgggttat (SEQ ID NO: 14507).
```

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

```
   1 ttatcccggc gagcatgagg cagggtatct catacctgg taaaatttta aagttgtgta
  61 ttttataaaa ttttcgtctg acaacactag cgcgctcagt agctggaggc aggagcgtgc
 121 gggaggggat agtggcgtga tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc
 181 aaacctgttt cgggtatgtt ataccctgcc tcat (SEQ ID NO: 14508).
```

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

```
   1 taaataataa taatttcata attaaaaact tctttcattg aatgccatta aataaaccat
  61 tattttacaa aataagatca acataattga gtaaataata ataagaacaa tattatagta
 121 caacaaaata tgggtatgtc ataccctgcc acattcttga tgtaactttt tttcacctca
 181 tgctcgccgg gttat (SEQ ID NO: 14509).
```

[0284] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 5' sequence corresponding to SEQ ID NO: 14506 and a 3' 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 5' and 3' 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 inverted in the orientation in the two ends. In certain embodiments, 5' transposon end begins with a sequence comprising 5'-TTATCCCGGCGAGCATGAGG-3 (SEQ ID NO: 14511), and the 3' transposon ends with a sequence comprising the reverse complement of this sequence: 5'-CCTCATGCTCGCCGGGTTAT-3' (SEQ ID NO: 14512).

[0285] 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.

[0286] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
  1 ttaacccggc gagcatgagg cagggtatct cataccctgg taaaatttta aagttgtgta
 61 ttttataaaa ttttcgtctg acaacactag cgcgctcagt agctggaggc aggagcgtgc
121 gggaggggat agtggcgtga tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc
181 aaacctgttt cgggtatgtt ataccctgcc tcattgttga cgtatttttt ttatgtaatt
241 tttccgatta ttaatttcaa ctgttttatt ggtattttta tgttatccat tgttcttttt
301 ttatgattta ctgtatcggt tgtctttcgt tcctttagtt gagtttttt ttattatttt
361 cagtttttga tcaaa (SEQ ID NO: 14515).
```

[0287] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
  1 tcatattttt agtttaaaaa aataattata tgttttataa tgaaaagaat ctcattatct
 61 ttcagtatta ggttgattta tattccaaag aataatattt ttgttaaatt gttgattttt
121 gtaaacctct aaatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
181 taataatttc ataattaaaa acttctttca ttgaatgcca ttaaataatt cattatttta
241 caaaataaga tcaacataat tgagtaaata ataataagaa caatattata gtacaacaaa
301 atatgggtat gtcataccct ttttttttt ttttttttt ttttttcggg tagagggccg
361 aacctcctac gaggtccccg cgcaaaaggg gcgcgcgggg tatgtgagac tcaacgatct
421 gcatggtgtt gtgagcagac cgcgggccca aggattttag agcccaccca ctaaacgact
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```
481 cctctgcact cttacacccg acgtccgatc ccctccgagg tcagaacccg gatgaggtag
541 gggggctacc gcggtcaaca ctacaaccag acggcgcggc tcaccccaag gacgcccagc
601 cgacggagcc ttcgaggcga atcgaaggct ctgaaacgtc ggccgtctcg gtacggcagc
661 ccgtcgggcc gcccagacgg tgccgctggt gtcccggaat accccgctgg accagaacca
721 gcctgccggg tcgggacgcg atacaccgtc gaccggtcgc tctaatcact ccacggcagc
781 gcgctagagt gctggta (SEQ ID NO: 14516).
```

[0288] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of CCCGGCGAGCATGAGG (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 CCTCATGCTCGCCGGGTTAT (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 CCTCATGCTCGCCGGGTTAA (SEQ ID NO: 14514).

[0289] 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.

[0290] 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.

[0291] 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 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 transposase. 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.

[0292] 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:

```
  1 cccggcgagc atgaggcagg gtatctcata ccctggtaaa attttaaagt tgtgtatttt
 61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
121 ggggatagtg gcgtgatcgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
181 ctgtttcggg tatgttatac cctgcctcat tgttgacgta t (SEQ ID NO: 14577).
```

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

```
  1 tttaagaaaa agattaataa ataataataa tttcataatt aaaaacttct ttcattgaat
 61 gccattaaat aaaccattat tttacaaaat aagatcaaca taattgagta aataataata
121 agaacaatat tatagtacaa caaaatatgg gtatgtcata ccctgccaca ttcttgatgt
181 aacttttttt cacctcatgc tcgccggg (SEQ ID NO: 14578).
```

In certain embodiments, the transposon comprises at least 16 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:

```
   1 cccggcgagc atgaggcagg gtatctcata ccctggtaaa attttaaagt tgtgtatttt
  61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
 121 ggggatagtg gcgtgatcgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
 181 ctgtttcggg tatgttatac cctgcctcat tgttgacgta ttttttttat gtaatttttc
 241 cgattattaa tttcaactgt tttattggta tttttatgtt atccattgtt ctttttttat
 301 gatttactgt atcggttgtc tttcgttcct ttagttgagt tttttttttat tattttcagt
 361 ttttgatcaa a (SEQ ID NO: 14595).
```

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

```
   1 tcatattttt agtttaaaaa aataattata tgttttataa tgaaaagaat ctcattatct
  61 ttcagtatta ggttgattta tattccaaag aataatattt ttgttaaatt gttgatttct
 121 gtaaacctct aaatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
 181 taataatttc ataattaaaa acttctttca ttgaatgcca ttaaataaac cattatttta
 241 caaaataaga tcaacataat tgagtaaata ataataagaa caatattata gtacaacaaa
 301 atatgggtat gtcataccct gccacattct tgatgtaact ttttttcacc tcatgctcgc
 361 cggg (SEQ ID NO: 14596).
```

[0293] 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, 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.

[0294] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
   1 cccggcgagc atgaggcagg gtatctcata ccctggtaaa attttaaagt tgtgtatttt
  61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
 121 ggggatagtg gcgtgatcgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
 181 ctgtttcggg tatgttatac cctgcctcat tgttgacgta ttttttttat gtaatttttc
 241 cgattattaa tttcaactgt tttattggta tttttatgtt atccattgtt ctttttttat
 301 g (SEQ ID NO: 14597).
```

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

```
   1 cagggtatct cataccctgg taaaatttta aagttgtgta ttttataaaa ttttcgtctg
  61 acaacactag cgcgctcagt agctggaggc aggagcgtgc gggaggggat agtggcgtga
 121 tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc aaacctgttt cgggtatgtt
 181 ataccctgcc tcattgttga cgtatttttt ttatgtaatt tttccgatta ttaatttcaa
 241 ctgttttatt ggtattttta tgttatccat tgttcttttt ttatg (SEQ ID NO:
14598).
```

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

```
   1 cagggtatct cataccctgg taaaatttta aagttgtgta ttttataaaa ttttcgtctg
  61 acaacactag cgcgctcagt agctggaggc aggagcgtgc gggaggggat agtggcgtga
```

```
121 tcgcagtgtg gcacgggaca ccggcgagat attcgtgtgc aaacctgttt cgggtatgtt
181 ataccctgcc tcattgttga cgtat (SEQ ID NO: 14599).
```

In certain embodiments, the 5' end of the piggyBac or piggyBac-like transposon comprises a sequence of SEQ ID NO: 14577, SEQ ID NO: 14595, or SEQ ID NOs: 14597-14599. In certain embodiments, the 5' end of the piggyBac or piggyBac-like transposon is preceded by a 5' target sequence.

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

```
  1 tcatattttt agtttaaaaa aataattata tgttttataa tgaaaagaat ctcattatct
 61 ttcagtatta ggttgattta tattccaaag aataatattt ttgttaaatt gttgattttt
121 gtaaacctct aaatgtttgt tgctaaaatt actgtgttta agaaaaagat taataaataa
181 taataatttc ataattaaaa acttctttca ttgaatgcca ttaaataaac cattatttta
241 caaaataaga tcaacataat tgagtaaata ataataagaa caatattata gtacaacaaa
301 atatgggtat gtcataccct gccacattct tgatgtaact ttttttcacc tcatgctcgc
361 cggg (SEQ ID NO: 14600).
```

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

```
  1 tttaagaaaa agattaataa ataataataa tttcataatt aaaaacttct ttcattgaat
 61 gccattaaat aaaccattat tttacaaaat aagatcaaca taattgagta aataataata
121 agaacaatat tatagtacaa caaaatatgg gtatgtcata ccctgccaca ttcttgatgt
181 aacttttttt ca (SEQ ID NO: 14601).
```

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

```
  1 cccggcgagc atgaggcagg gtatctcata ccctggtaaa attttaaagt tgtgtatttt
 61 ataaaatttt cgtctgacaa cactagcgcg ctcagtagct ggaggcagga gcgtgcggga
121 ggggatagtg gcgtgatcgc agtgtggcac gggacaccgg cgagatattc gtgtgcaaac
181 ctgtttcggg tatgttatac cctgcctcat tgttgacgta ttttttttat gtaatttttc
241 cgattattaa tttcaactgt tttattggta tttttatgtt atccattgtt ctttttttat
301 gatttactgt atcggttgtc tttcgttcct ttagttgagt tttttttttat tattttcagt
361 ttttgatcaa a (SEQ ID NO: 14602).
```

[0295] In certain embodiments, the 3' end of the piggyBac or piggyBac-like transposon comprises a sequence of SEQ ID NO: 14578, SEQ ID NO: 14596, or SEQ ID NOs: 14600-14601. In certain embodiments, the 3' end of the piggyBac or piggyBac-like transposon is followed by a 3' target sequence. In certain embodiments, the transposon is transposed by the transposase of SEQ ID NO: 14505. In certain embodiments, the 5' and 3' 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 5' transposon end begins with SEQ ID NO: 14510, and the 3' transposon end ends with the reverse complement of SEQ ID NO: 14510, 5'-CCTCATGCTCGCCGGG-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 5' transposon end comprising a sequence selected from SEQ ID NOs: 14577, 14595 or 14597 and a 3' transposon end comprising SEQ ID NO: 14578 or 14596 followed by a target sequence. in certain embodiments, the piggyBac or piggyBac like transposon comprises one end that comprises a sequence that is at least 90%, at least 95% or at least 99% or any percentage in between identical to SEQ ID NO: 14577 and one end that comprises a sequence that is at least 90%, at least 95% or at least 99% or any percentage in 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.

[0296] 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.

[0297] 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 embodiments, the piggyBac or piggyBac-like transposon 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.

[0298] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 5' 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), ATACCCTGCC (SEQ ID NO: 14617), TAAAATTTTA (SEQ ID NO: 14618), ATTTTATAAAAT (SEQ ID NO: 14619), TCATACCCTG (SEQ ID NO: 14620) and TAAATAATAATAA (SEQ ID NO: 14621). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 3' end comprising 1, 2 or 3 sequences selected from SEQ ID NO: 14617, SEQ ID NO: 14620 and SEQ ID NO: 14621.

[0299] 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:

```
  1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHY (SEQ ID NO:
14517).
```

[0300] 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:

```
  1 MAKRFYSAEE AAAHCMAPSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWNTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPDHD RLHKLRPLID
```

```
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLR FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
361 PACGTINRTR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT SAWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMLP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHY (SEQ ID NO:
14518).
```

[0301] 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:

```
  1 MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFANVY TPCQNICIDE SLMLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPD SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
14572).
```

[0302] 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:

```
  1 MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFANVY TPCQNICIDE SLMLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPD SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
14572).
```

[0303] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

```
  1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
```

```
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
14624).
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[0304] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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  1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLKIPVFSAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHY (SEQ ID NO:
14625).
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[0305] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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  1 MAKRFYSAEE AAAHCMASSS EQTSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SIESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFANVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRKPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
14627).
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[0306] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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  1 MAKRFYSAEE AAAHCSASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
 61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRG ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
181 SLESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
241 SLSERFANVY TPCQNICIDE SLMLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSTGYTSYF
301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
14628).
```

[0307] In certain embodiments, the hyperactive piggyBac or piggyBac-like transposase comprises a sequence of:

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      1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
     61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
    121 FMTEAILQDM VLYTNVYAEQ YLTQNPLTRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
    181 SLESYWDTTT VLSIPVFGAT MSRNRYQLLL RFLHFNNNAT AVPPDQPGHD RLHKLRPLID
    241 SLSERFANVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
    301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLNT
    361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
    421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RHWYKKVGIY LIQMALRNSY
    481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
    541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCRKPCF EIYHTQLHY (SEQ ID NO:
16820).
```

[0308] 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, Yl41Q, Y141A, N145E, N145V, P146T, P146V, P146K, P148T, P148H, Y150G, Y150S, Y150C, H157Y, A162C, A179K, L182I, L182V, T189G, L192H, S193N, S193K, V196I, S198G, T200W, L210H, F212N, N218E, A248N, L263M, Q270L, S294T, T297M, S308R, L310R, L333M, Q336M, A354H, C357V, L358F, D359N, L377I, V 423H, P426K, K428R, S438A, T447G, T447A, L450V, A462H, A462Q, I469V, I472L, Q498M, L502V, E5171, 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).

[0309] 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, A13X, 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, L172X, A173X, M174X, I177X, A179X, L182X, D187X, T188X, T189X, T190X, L192X, S193X, I194X, P195X, V196X, S198X, A199X, T200X, S202X, L208X, L209X, L210X, R211X, 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, S293XS294X, 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, V482XY483X, K484X, A485X, A486X, V487X, P488X, P490X, K491X, S493X, Y494X, Y495X, K496X, Y497T, 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, I533X, 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 US patent No. 10,041,077, the contents of which are incorporated by reference in their entirety.

[0310] 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 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.

[0311] 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 :

```
      1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
     61 DEDVDDLEDQ EAGDRVDAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
    121 FMTEAILQDM VLYTNVYAEQ YLTQNPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
    181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL KFLHFNNEAT AVPPDQPGHD RLHKLRPLID
    241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
    301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
    361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
    421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
    481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
    541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHYG RR (SEQ ID
NO: 14605).
```

[0312] In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

```
      1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
     61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
    121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
    181 SLESYWDTTT VLNIPVFSAT MSRNRYQLLL RFLEFNNEAT AVPPDQPGHD RLHKLRPLID
    241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
    301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
    361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
    421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
    481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
    541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHY (SEQ ID NO:
14604).
```

[0313] In certain embodiments, the integration deficient piggyBac or piggyBac-like transposase comprises a sequence that is at least 90% identical to a sequence of:

```
      1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
     61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
```

```
     121 FMTEAILQDM VLYTNVYAEQ YLTQNVLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
     181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNDAT AVPPDQPGHD RLHKLRPLID
     241 SLTERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
     301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
     361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
     421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
     481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
     541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHYG RR (SEQ ID
NO: 14611).
```

[0314] In certain embodiments, the integration deficient piggyBac 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:

```
       1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
      61 DEDVDDLEDQ EAGDRADAAP GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
     121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
     181 SLESYWDTTT VLSIPVFSAT MSRNRYQLLL RFLHFNNEAT AVPPDQPGHD RLHKLRPLID
     241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
     301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
     361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
     421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
     481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
     541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHYG RR (SEQ ID
NO: 14612).
```

[0315] In certain embodiments, the integration deficient piggyBac 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:

```
       1 MAKRFYSAEE AAAHCMASSS EEFSGSDSEY VPPASESDSS TEESWCSSST VSALEEPMEV
      61 DEDVDDLEDQ EAGDRADAAA GGEPAWGPPC NFPPEIPPFT TVPGVKVDTS NFEPINFFQL
     121 FMTEAILQDM VLYTNVYAEQ YLTQVPLPRY ARAHAWHPTD IAEMKRFVGL TLAMGLIKAN
     181 SLESYWDTTT VLNIPVFSAT MSRNRYQLLL RFLEFNNNAT AVPPDQPGHD RLHKLRPLID
     241 SLSERFAAVY TPCQNICIDE SLLLFKGRLQ FRQYIPSKRA RYGIKFYKLC ESSSGYTSYF
     301 LIYEGKDSKL DPPGCPPDLT VSGKIVWELI SPLLGQGFHL YVDNFYSSIP LFTALYCLDT
     361 PACGTINRNR KGLPRALLDK KLNRGETYAL RKNELLAIKF FDKKNVFMLT SIHDESVIRE
     421 QRVGRPPKNK PLCSKEYSKY MGGVDRTDQL QHYYNATRKT RAWYKKVGIY LIQMALRNSY
     481 IVYKAAVPGP KLSYYKYQLQ ILPALLFGGV EEQTVPEMPP SDNVARLIGK HFIDTLPPTP
     541 GKQRPQKGCK VCRKRGIRRD TRYYCPKCPR NPGLCFKPCF EIYHTQLHYG RR (SEQ ID
NO: 14613).
```

[0316] In certain embodiments, the integration deficient piggyBac 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).

[0317] 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, 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, T123X, E124X, A125X, L127X, Q128X, D129X, L132X, Y133X, V126X, Y127X, E139X, Q140X, Y141X, L142X, T143X, Q144X, N145X, P146X, L147X, P148X, R149X, Y150X, A151X, H154X, H157X, P158X, T159X, D160X, I161X, A162X, E163X, M164X, K165X, R166X, F167X, V168X, G169X, L170X, T171X, L172X, A173X, M174X, G175X, L176X, I177X, K178X, A179X, N180X, S181X, L182X, S184X, Y185X, D187X, T188X, T189X, 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, 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, R384XG385X, 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, 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, I533X, D534X, T535X, L536X, P537X, P538X, T539X, P540X, G541X, F542X, Q543X, R544X, P545X, Q546X, K547X, G548X, C549X, K550X, V551X, C552X, R553X, K554X, R555X, G556X, I557X, 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 US patent No. 10,041,077, the contents of which are incorporated by reference in their entirety.

[0318] 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:

```
   1 atggcaccca aaaagaaacg taaagtgatg gccaaaagat tttacagcgc cgaagaagca
  61 gcagcacatt gcatggcatc gtcatccgaa gaattctcgg ggagcgattc cgaatatgtc
 121 ccaccggcct cggaaagcga ttcgagcact gaggagtcgt ggtgttcctc ctcaactgtc
 181 tcggctcttg aggagccgat ggaagtggat gaggatgtgg acgacttgga ggaccaggaa
 241 gccggagaca gggccgacgc tgccgcggga ggggagccgg cgtggggacc tccatgcaat
 301 tttcctcccg aaatcccacc gttcactact gtgccgggag tgaaggtcga cacgtccaac
 361 ttcgaaccga tcaatttctt tcaactcttc atgactgaag cgatcctgca agatatggtg
 421 ctctacacta atgtgtacgc cgagcagtac ctgactcaaa acccgctgcc tcgctacgcg
 481 agagcgcatg cgtggcaccc gaccgatatc gcggagatga agcggttcgt gggactgacc
 541 ctcgcaatgg gcctgatcaa ggccaacagc ctcgagtcat actgggatac cacgactgtg
 601 cttagcattc cggtgttctc cgctaccatg tcccgtaacc gctaccaact cctgctgcgg
 661 ttcctccact tcaacaacaa tgcgaccgct gtgccacctg accagccagg acacgacaga
 721 ctccacaagc tgcggccatt gatcgactcg ctgagcgagc gattcgccgc ggtgtacacc
 781 ccttgccaaa acatttgcat cgacgagtcg cttctgctgt ttaaaggccg gcttcagttc
 841 cgccagtaca tcccatcgaa gcgcgctcgc tatggtatca aattctacaa actctgcgag
 901 tcgtccagcg gctacacgtc atacttcttg atctacgagg ggaaggactc taagctggac
 961 ccaccggggt gtccaccgga tcttactgtc tccggaaaaa tcgtgtggga actcatctca
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    1021 cctctcctcg gacaaggctt tcatctctac gtcgacaatt tctactcatc gatccctctg
    1081 ttcaccgccc tctactgcct ggatactcca gcctgtggga ccattaacag aaaccggaag
    1141 ggtctgccga gagcactgct ggataagaag ttgaacaggg gagagactta cgcgctgaga
    1201 aagaacgaac tcctcgccat caaattcttc gacaagaaaa atgtgtttat gctcacctcc
    1261 atccacgacg aatccgtcat ccgggagcag cgcgtgggca ggccgccgaa aaacaagccg
    1321 ctgtgctcta aggaatactc caagtacatg gggggtgtcg accggaccga tcagctgcag
    1381 cattactaca acgccactag aaagacccgg gcctggtaca agaaagtcgg catctacctg
    1441 atccaaatgg cactgaggaa ttcgtatatt gtctacaagg ctgccgttcc gggcccgaaa
    1501 ctgtcatact acaagtacca gcttcaaatc ctgccggcgc tgctgttcgg tggagtggaa
    1561 gaacagactg tgcccgagat gccgccatcc gacaacgtgg cccggttgat cggaaagcac
    1621 ttcattgata ccctgcctcc gacgcctgga aagcagcggc cacagaaggg atgcaaagtt
    1681 tgccgcaagc gcggaatacg gcgcgatacc cgctactatt gcccgaagtg cccccgcaat
    1741 cccggactgt gtttcaagcc ctgttttgaa atctaccaca cccagttgca ttac (SEQ
ID NO: 14626).
```

[0319] 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:

```
       1 ttaacctttt tactgccaat gacgcatggg atacgtcgtg gcagtaaaag ggcttaaatg
      61 ccaacgacgc gtcccatacg ttgttggcat tttaagtctt ctctctgcag cggcagcatg
     121 tgccgccgct gcagagagtt tctagcgatg acagcccctc tgggcaacga gccgggggggg
     181 ctgtc (SEQ ID NO: 14519).
```

[0320] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
       1 tttgcatttt tagacattta gaagcctata tcttgttaca gaattggaat tacacaaaaa
      61 ttctaccata ttttgaaagc ttaggttgtt ctgaaaaaaa caatatattg ttttcctggg
     121 taaactaaaa gtcccctcga ggaaaggccc ctaaagtgaa acagtgcaaa acgttcaaaa
     181 actgtctggc aatacaagtt ccactttgac caaaacggct ggcagtaaaa gggttaa
(SEQ ID NO: 14520).
```

[0321] 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:

```
       1 ttaacccttt gcctgccaat cacgcatggg atacgtcgtg gcagtaaaag ggcttaaatg
      61 ccaacgacgc gtcccatacg ttgttggcat tttaagtctt ctctctgcag cggcagcatg
     121 tgccgccgct gcagagagtt tctagcgatg acagcccctc tgggcaacga gccgggggggg
     181 ctgtc (SEQ ID NO: 14521).
```

[0322] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
     1 tttgcatttt tagacattta gaagcctata tcttgttaca gaattggaat tacacaaaaa
      61 ttctaccata ttttgaaagc ttaggttgtt ctgaaaaaaa caatatattg ttttcctggg
     121 taaactaaaa gtcccctcga ggaaaggccc ctaaagtgaa acagtgcaaa acgttcaaaa
     181 actgtctggc aatacaagtt ccactttggg acaaatcggc tggcagtgaa agggttaa
(SEQ ID NO: 14522).
```

[0323] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
  1 ttaacctttt tactgccaat gacgcatggg atacgtcgtg gcagtaaaag ggcttaaatg
 61 ccaacgacgc gtcccatacg ttgttggcat tttaattctt ctctctgcag cggcagcatg
121 tgccgccgct gcagagagtt tctagcgatg acagcccctc tgggcaacga gccgggggggg
181 ctgtc (SEQ ID NO: 14523).
```

[0324] 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.

[0325] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCTTTTTACTGCCA (SEQ ID NO: 14524). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCCTTTGCCTGCCA (SEQ ID NO: 14526). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCYTTTTACTGCCA (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 TGGCAGTGAAAGGGTTAA (SEQ ID NO: 14531). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of TTAACCYTTTKMCTGCCA (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 piggyBac™ (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 piggyBac™ (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 piggyBac like transposon comprises SEQ ID NO: 14533 in inverted orientation in the two transposon ends.

[0326] 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.

[0327] In certain embodiments, the piggyBac or piggyBac-like transposase recognizes a transposon end with a 5' sequence corresponding to SEQ ID NO: 14519, and a 3' 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 5' end of one transposon end to the 5'-TTAA-3' at the 3' 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 5' and 3' transposon ends will also function as part of a transposon that can be transposed by the piggyBac or piggyBac-like transposase. For example, the 5' transposon end can be replaced by a sequence corresponding to SEQ ID NO: 14521 or SEQ ID NO: 14523, the 3' transposon end can be replaced by a shorter sequence corresponding to SEQ ID NO: 14522. In certain embodiments, the 5' and 3' transposon ends share an 18 bp almost perfectly repeated sequence at their ends (5'-TTAACCYTTTKMCTGCCA: 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 5' transposon end begins with the sequence 5'-TTAACCTTTTTACTGCCA-3' (SEQ ID NO: 14524), or in SEQ ID NO: 14521 the 5' transposon end begins with the sequence 5'-TTAACCCTTTGCCTGCCA-3' (SEQ ID NO: 14526); the 3' transposon ends with approximately the reverse 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'-TGGCAGTGAAAGGGTTAA-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 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.

[0328] In certain embodiments, the piggyBac™ (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:

```
  1 ccctttgcct gccaatcacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgtt (SEQ ID NO: 14573).
```

[0329] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 cctgggtaaa ctaaaagtcc cctcgaggaa aggcccctaa agtgaaacag tgcaaaacgt
 61 tcaaaaactg tctggcaata caagttccac tttgggacaa atcggctggc agtgaaaggg
```

(SEQ ID NO: 14574).

[0330] 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 CCYTTTBMCTGCCA (SEQ ID NO: 14575).

[0331] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 ccctttgcct gccaatcacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta agtcttctct ctgcagcggc agcatgtgcc
121 gccgctgcag agagtttcta gcgatgacag cccctctggg caacgagccg gggggctgt
181 c (SEQ ID NO: 14579).
```

[0332] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 cctttttact gccaatgacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta attcttctct ctgcagcggc agcatgtgcc
121 gccgctgcag agagtttcta gcgatgacag cccctctggg caacgagccg gggggctgt
181 c (SEQ ID NO: 14580).
```

[0333] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 cctttttact gccaatgacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta agtcttctct ctgcagcggc agcatgtgcc
121 gccgctgcag agagtttcta gcgatgacag cccctctggg caacgagccg gggggctgt
181 c (SEQ ID NO: 14581).
```

[0334] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 cctttttact gccaatgacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta agtcttctct ctgcagcggc agcatgtgcc
121 gccgctgcag agag (SEQ ID NO: 14582).
```

[0335] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 cctttttact gccaatgacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta agtctt (SEQ ID NO: 14583).
```

[0336] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
  1 ccctttgcct gccaatcacg catgggatac gtcgtggcag taaaagggct taaatgccaa
 61 cgacgcgtcc catacgttgt tggcatttta agtctt (SEQ ID NO: 14584).
```

[0337] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 ttatcctttt tactgccaat gacgcatggg atacgtcgtg gcagtaaaag ggcttaaatg
     61 ccaacgacgc gtcccatacg ttgttggcat tttaagtctt ctctctgcag cggcagcatg
    121 tgccgccgct gcagagagtt tctagcgatg acagcccctc tgggcaacga gccgggggggg
    181 ctgtc (SEQ ID NO: 14585).
```

[0338] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 tttgcatttt tagacattta gaagcctata tcttgttaca gaattggaat tacacaaaaa
     61 ttctaccata ttttgaaagc ttaggttgtt ctgaaaaaaa caatatattg ttttcctggg
    121 taaactaaaa gtcccctcga ggaaaggccc ctaaagtgaa acagtgcaaa acgttcaaaa
    181 actgtctggc aatacaagtt ccactttggg acaaatcggc tggcagtgaa aggg (SEQ
ID NO: 14586).
```

[0339] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 5' transposon end sequence selected from SEQ ID NO: 14573 and SEQ ID NOs: 14579-14585. In certain embodiments, the 5' transposon end sequence is preceded by a 5' target sequence. In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 tttgcatttt tagacattta gaagcctata tcttgttaca gaattggaat tacacaaaaa
     61 ttctaccata ttttgaaagc ttaggttgtt ctgaaaaaaa caatatattg ttttcctggg
    121 taaactaaaa gtcccctcga ggaaaggccc ctaaagtgaa acagtgcaaa acgttcaaaa
    181 actgtctggc aatacaagtt ccactttgac caaaacggct ggcagtaaaa ggg (SEQ ID
NO: 14587).
```

[0340] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 ttgttctgaa aaaaacaata tattgttttc ctgggtaaac taaaagtccc ctcgaggaaa
     61 ggcccctaaa gtgaaacagt gcaaaacgtt caaaaactgt ctggcaatac aagttccact
    121 ttgaccaaaa cggctggcag taaaaggg (SEQ ID NO: 14588).
```

[0341] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 tttgcatttt tagacattta gaagcctata tcttgttaca gaattggaat tacacaaaaa
     61 ttctaccata ttttgaaagc ttaggttgtt ctgaaaaaaa caatatattg ttttcctggg
    121 taaactaaaa gtcccctcga ggaaaggccc ctaaagtgaa acagtgcaaa acgttcaaaa
    181 actgtctggc aatacaagtt ccactttgac caaaacggct ggcagtaaaa gggttat
(SEQ ID NO: 14589).
```

[0342] In certain embodiments, the piggyBac or piggyBac-like transposon comprises at a sequence of:

```
      1 ttgttctgaa aaaaacaata tattgttttc ctgggtaaac taaaagtccc ctcgaggaaa
```

```
 61 ggcccctaaa gtgaaacagt gcaaaacgtt caaaaactgt ctggcaatac aagttccact
121 ttgggacaaa tcggctggca gtgaaaggg (SEQ ID NO: 14590).
```

[0343] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 3' transposon end sequence selected from SEQ ID NO: 14574 and SEQ ID NOs: 14587-14590. In certain embodiments, the 3' transposon end sequence is followed by a 3' target sequence. In certain embodiments, the 5' and 3' transposon ends share a 14 repeated sequence inverted in orientation in the two ends (SEQ ID NO: 14575) adjacent to the target sequence. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a 5' transposon end comprising a target sequence and a sequence that is selected from SEQ ID NOs: 14582-14584 and 14573, and a 3' transposon end comprising a sequence selected from SEQ ID NOs: 14588-14590 and 14574 followed by a 3' target sequence.

[0344] In certain embodiments, the 5' transposon end of the piggyBac or piggyBac-like transposon comprises

```
  1 atcacgcatg ggatacgtcg tggcagtaaa agggcttaaa tgccaacgac gcgtcccata
 61 cgtt
```

(SEQ ID NO: 14591), and an ITR. In certain embodiments, the 5' transposon end comprises

```
  1 atgacgcatg ggatacgtcg tggcagtaaa agggcttaaa tgccaacgac gcgtcccata
 61 cgttgttggc attttaagtc tt
```

(SEQ ID NO: 14592) and an ITR. In certain embodiments, the 3' transposon end of the piggyBac or piggyBac-like transposon comprises

```
  1 cctgggtaaa ctaaaagtcc cctcgaggaa aggcccctaa agtgaaacag tgcaaaacgt
 61 tcaaaaactg tctggcaata caagttccac tttgggacaa atcggc
```

(SEQ ID NO: 14593) and an ITR. In certain embodiments, the 3' transposon end comprises

```
  1 ttgttctgaa aaaaacaata tattgttttc ctgggtaaac taaaagtccc ctcgaggaaa
 61 ggcccctaaa gtgaaacagt gcaaaacgtt caaaaactgt ctggcaatac aagttccact
121 ttgaccaaaa cggc
```

(SEQ ID NO: 14594) and an ITR.

[0345] 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.

[0346] In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence selected from of SEQ ID 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.

[0347] In certain embodiments, the piggyBac or piggyBac-like transposon comprises ITRs of CCCTTTGCCTGCCA (SEQ ID NO: 14622) (5' ITR) and TGGCAGTGAAAGGG (SEQ ID NO: 14623) (3' ITR) adjacent to the target sequences.

[0348] 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:

```
       1 MASRQRLNHD EIATILENDD DYSPLDSESE KEDCVVEDDV WSDNEDAIVD FVEDTSAQED
      61 PDNNIASRES PNLEVTSLTS HRIITLPQRS IRGKNNHVWS TTKGRTTGRT SAINIIRTNR
     121 GPTRMCRNIV DPLLCFQLFI TDEIIHEIVK WTNVEIIVKR QNLKDISASY RDTNTMEIWA
     181 LVGILTLTAV MKDNHLSTDE LFDATFSGTR YVSVMSRERF EFLIRCIRMD DKTLRPTLRS
     241 DDAFLPVRKI WEIFINQCRQ NHVPGSNLTV DEQLLGFRGR CPFRMYIPNK PDKYGIKFPM
     301 MCAAATKYMI DAIPYLGKST KTNGLPLGEF YVKDLTKTVH GTNRNITCDN WFTSIPLAKN
     361 MLQAPYNLTI VGTIRSNKRE MPEEIKNSRS RPVGSSMFCF DGPLTLVSYK PKPSKMVFLL
     421 SSCDENAVIN ESNGKPDMIL FYNQTKGGVD SFDQMCKSMS ANRKTNRWPM AVFYGMLNMA
     481 FVNSYIIYCH NKINKQEKPI SRKEFMKKLS IQLTTPWMQE RLQAPTLKRT LRDNITNVLK
     541 NVVPASSENI SNEPEPKKRR YCGVCSYKKR RMTKAQCCKC KKAICGEHNI DVCQDCI
(SEQ ID NO: 14525).
```

[0349] In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Helicoverpa armigera*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
       1 ttaaccctag aagcccaatc tacgtaaatt tgacgtatac cgcggcgaaa tatctctgtc
      61 tctttcatgt ttaccgtcgg atcgccgcta acttctgaac caactcagta gccattggga
```

```
121 cctcgcagga cacagttgcg tcatctcggt aagtgccgcc attttgttgt actctctatt
181 acaacacacg tcacgtcacg tcgttgcacg tcattttgac gtataattgg gctttgtgta
241 acttttgaat ttgtttcaaa ttttttatgt ttgtgattta tttgagttaa tcgtattgtt
301 tcgttacatt tttcatataa taataatatt ttcaggttga gtacaaa (SEQ ID NO:
```

14570). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
  1 agactgtttt tttctaagag acttctaaaa tattattacg agttgattta attttatgaa
 61 aacatttaaa actagttgat tttttttata attacataat tttaagaaaa agtgttagag
121 gcttgatttt tttgttgatt ttttctaaga tttgattaaa gtgccataat agtattaata
181 aagagtattt tttaacttaa aatgtatttt atttattaat taaaacttca attatgataa
241 ctcatgcaaa aatatagttc attaacagaa aaaaatagga aaactttgaa gttttgtttt
301 tacacgtcat ttttacgtat gattgggctt tatagctagt taaatatgat tgggcttcta
361 gggttaa (SEQ ID NO: 14528).
```

[0350] 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:

```
  1 MDLRKQDEKI RQWLEQDIEE DSKGESDNSS SETEDIVEME VHKNTSSESE VSSESDYEPV
 61 CPSKRQRTQI IESEESDNSE SIRPSRRQTS RVIDSDETDE DVMSSTPQNI PRNPNVIQPS
121 SRFLYGKNKH KWSSAAKPSS VRTSRRNIIH FIPGPKERAR EVSEPIDIFS LFISEDMLQQ
181 VVTFTNAEML IRKNKYKTET FTVSPTNLEE IRALLGLLFN AAAMKSNHLP TRMLFNTHRS
241 GTIFKACMSA ERLNFLIKCL RFDDKLTRNV RQRDDRFAPI RDLWQALISN FQKWYTPGSY
301 ITVDEQLVGF RGRCSFRMYI PNKPNKYGIK LVMAADVNSK YIVNAIPYLG KGTDPQNQPL
361 ATFFIKEITS TLHGTNRNIT MDNWFTSVPL ANELLMAPYN LTLVGTLRSN KREIPEKLKN
421 SKSRAIGTSM FCYDGDKTLV SYKAKSNKVV FILSTIHDQP DINQETGKPE MIHFYNSTKG
481 AVDTVDQMCS SISTNRKTQR WPLCVFYNML NLSIINAYVV YVYNNVRNNK KPMSRRDFVI
541 KLGDQLMEPW LRQRLQTVTL RRDIKVMIQD ILGESSDLEA PVPSVSNVRK IYYLCPSKAR
601 RMTKHRCIKC KQAICGPHNI DICSRCIE (SEQ ID NO: 14530).
```

[0351] 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:

```
  1 ttaaccctag ataactaaac attcgtccgc tcgacgacgc gctatgccgc gaaattgaag
 61 tttacctatt attccgcgtc ccccgccccc gccgcttttt ctagcttcct gatttgcaaa
121 atagtgcatc gcgtgacacg ctcgaggtca cacgacaatt aggtcgaaag ttacaggaat
181 ttcgtcgtcc gctcgacgaa agtttagtaa ttacgtaagt ttggcaaagg taagtgaatg
241 aagtattttt ttataattat tttttaattc tttatagtga taacgtaagg tttatttaaa
301 tttattactt ttatagttat ttagccaatt gttataaatt ccttgttatt gctgaaaaat
361 ttgcctgttt tagtcaaaat ttattaactt ttcgatcgtt ttttag (SEQ ID NO:
```

14532). In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
      1 tttcactaag taattttgtt cctatttagt agataagtaa cacataatta ttgtgatatt
     61 caaaacttaa gaggtttaat aaataataat aaaaaaaaaa tggtttttat ttcgtagtct
    121 gctcgacgaa tgtttagtta ttacgtaacc gtgaatatag tttagtagtc tagggttaa
(SEQ ID NO: 14571).
```

[0352] 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:

```
      1 MASRQHLYQD EIAAILENED DYSPHDTDSE MEDCVTQDDV RSDVEDEMVD NIGNGTSPAS
     61 RHEDPETPDP SSEASNLEVT LSSHRIIILP QRSIREKNNH IWSTTKGQSS GRTAAINIVR
    121 TNRGPTRMCR NIVDPLLCFQ LFIKEEIVEE IVKWTNVEMV QKRVNLKDIS ASYRDTNEME
    181 IWAIISMLTL SAVMKDNHLS TDELFNVSYG TRYVSVMSRE RFEFLLRLLR MGDKLLRPNL
    241 RQEDAFTPVR KIWEIFINQC RLNYVPGTNL TVDEQLLGFR GRCPFRMYIP NKPDKYGIKF
    301 PMVCDAATKY MVDAIPYLGK STKTQGLPLG EFYVKELTQT VHGTNRNVTC DNWFTSVPLA
    361 KSLLNSPYNL TLVGTIRSNK REIPEEVKNS RSRQVGSSMF CFDGPLTLVS YKPKPSKMVF
    421 LLSSCNEDAV VNQSNGKPDM ILFYNQTKGG VDSFDQMCSS MSTNRKTNRW PMAVFYGMLN
    481 MAFVNSYIIY CHNMLAKKEK PLSRKDFMKK LSTDLTTPSM QKRLEAPTLK RSLRDNITNV
    541 LKIVPQAAID TSFDEPEPKK RRYCGFCSYK KKRMTKTQCF KCKKPVCGEH NIDVCQDCI
(SEQ ID NO: 14534).
```

[0353] In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Ctenoplusia agnata*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
      1 ttaaccctag aagcccaatc tacgtcattc tgacgtgtat gtcgccgaaa atactctgtc
     61 tctttctcct gcacgatcgg attgccgcga acgctcgatt caacccagtt ggcgccgaga
    121 tctattggag gactgcggcg ttgattcggt aagtcccgcc attttgtcat agtaacagta
    181 ttgcacgtca gcttgacgta tatttgggct ttgtgttatt tttgtaaatt ttcaacgtta
    241 gtttattatt gcatcttttt gttacattac tggtttattt gcatgtatta ctcaaatatt
    301 atttttattt tagcgtagaa aataca (SEQ ID NO: 14535).
```

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

```
      1 agactgtttt ttttgtattt gcattatata ttatattcta aagttgattt aattctaaga
     61 aaaacattaa aataagtttc tttttgtaaa atttaattaa ttataagaaa aagtttaagt
    121 tgatctcatt ttttataaaa atttgcaatg tttccaaagt tattattgta aaagaataaa
    181 taaaagtaaa ctgagtttta attgatgttt tattatatca ttatactata tattacttaa
    241 ataaaacaat aactgaatgt atttctaaaa ggaatcacta gaaaatatag tgatcaaaaa
    301 tttacacgtc atttttgcgt atgattgggc tttataggtt ctaaaaatat gattgggcct
    361 ctagggttaa (SEQ ID NO: 14536).
```

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

[0354] 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 *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:

```
   1 MESRQRLNQD EIATILENDD DYSPLDSDSE AEDRVVEDDV WSDNEDAMID YVEDTSRQED
  61 PDNNIASQES ANLEVTSLTS HRIISLPQRS ICGKNNHVWS TTKGRTTGRT SAINIIRTNR
 121 GPTRMCRNIV DPLLCFQLFI TDEIIHEIVK WTNVEMIVKR QNLIDISASY RDTNTMEMWA
 181 LVGILTLTAV MKDNHLSTDE LFDATFSGTR YVSVMSRERF EFLIRCMRMD DKTLRPTLRS
 241 DDAFIPVRKL WEIFINQCRL NYVPGGNLTV DEQLLGFRGR CPFRMYIPNK PDKYGIRFPM
 301 MCDAATKYMI DAIPYLGKST KTNGLPLGEF YVKELTKTVH GTNRNVTCDN WFTSIPLAKN
 361 MLQAPYNLTI VGTIRSNKRE IPEEIKNSRS RPVGSSMFCF DGPLTLVSYK PKPSRMVFLL
 421 SSCDENAVIN ESNGKPDMIL FYNQTKGGVD SFDQMCKSMS ANRKTNRWPM AVFYGMLNMA
 481 FVNSYIIYCH NKINKQKKPI NRKEFMKNLS TDLTTPWMQE RLKAPTLKRT LRDNITNVLK
 541 NVVPPSPANN SEEPGPKKRS YCGFCSYKKR RMTKTQFYKC KKAICGEHNI DVCQDCV
(SEQ ID NO: 14537).
```

[0355] 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:

```
   1 ttaaccctag aagcccaatc tacgtaaatt tgacgtatac cgcggcgaaa tatatctgtc
  61 tctttcacgt ttaccgtcgg attcccgcta acttcggaac caactcagta gccattgaga
 121 actcccagga cacagttgcg tcatctcggt aagtgccgcc attttgttgt aatagacagg
 181 ttgcacgtca ttttgacgta taattgggct ttgtgtaact tttgaaatta tttataattt
 241 ttattgatgt gatttatttg agttaatcgt attgtttcgt tacatttttc atatgatatt
 301 aatattttca gattgaatat aaa (SEQ ID NO: 14538).
```

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

```
   1 agactgtttt ttttaaaagg cttataaagt attactattg cgtgatttaa ttttataaaa
  61 atatttaaaa ccagttgatt tttttaataa ttacctaatt ttaagaaaaa atgttagaag
 121 cttgatattt ttgttgattt ttttctaaga tttgattaaa aggccataat tgtattaata
 181 aagagtattt ttaacttcaa atttatttta tttattaatt aaaacttcaa ttatgataat
 241 acatgcaaaa atatagttca tcaacagaaa aatataggaa aactctaata gttttatttt
 301 tacacgtcat ttttacgtat gattgggctt tatagctagt caaatatgat tgggcttcta
 361 gggttaa (SEQ ID NO: 14539).
```

[0356] 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:

```
   1 MNGKDSLGEF YLDDLSDCLD CRSASSTDDE SDSSNIAIRK RCPIPLIYSD SEDEDMNNNV
```

```
 61 EDNNHFVKES NRYHYQIVEK YKITSKTKKW KDVTVTEMKK FLGLIILMGQ VKKDVLYDYW
121 STDPSIETPF FSKVMSRNRF LQIMQSWHFY NNNDISPNSH RLVKIQPVID YFKEKFNNVY
181 KSDQQLSLDE CLIPWRGRLS IKTYNPAKIT KYGILVRVLS EARTGYVSNF CVYAADGKKI
241 EETVLSVIGP YKNMWHHVYQ DNYYNSVNIA KIFLKNKLRV CGTIRKNRSL PQILQTVKLS
301 RGQHQFLRNG HTLLEVWNNG KRNVNMISTI HSAQMAESRN RSRTSDCPIQ KPISIIDYNK
361 YMKGVDRADQ YLSYYSIFRK TKKWTKRVVM FFINCALFNS FKVYTTLNGQ KITYKNFLHK
421 AALSLIEDCG TEEQGTDLPN SEPTTTRTTS RVDHPGRLEN FGKHKLVNIV TSGQCKKPLR
481 QCRVCASKKK LSRTGFACKY CNVPLHKGDC FERYHSLKKY (SEQ ID NO: 14540).
```

[0357] 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:

```
  1 ttaaataatg cccactctag atgaacttaa cactttaccg accggccgtc gattattcga
 61 cgtttgctcc ccagcgctta ccgaccggcc atcgattatt cgacgtttgc ttcccagcgc
121 ttaccgaccg gtcatcgact tttgatcttt ccgttagatt tggttaggtc agattgacaa
181 gtagcaagca tttcgcattc tttattcaaa taatcggtgc ttttttctaa gctttagccc
241 ttagaa (SEQ ID NO: 14541).
```

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

```
  1 acaacttctt ttttcaacaa atattgttat atggattatt tatttattta tttatttatg
 61 gtatatttta tgtttattta tttatggtta ttatggtata ttttatgtaa ataataaact
121 gaaaacgatt gtaatagatg aaataaatat tgttttaaca ctaatataat taaagtaaaa
181 gattttaata aatttcgtta ccctacaata acacgaagcg tacaatttta ccagagttta
241 ttaa (SEQ ID NO: 14542).
```

[0358] 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:

```
  1 MNEKNGIGEF YLDDLSDCPD SYSRSNSGDE SDGSDTIIRK RGSVLPPRYS DSEDDEINNV
 61 EDNANNVENN DDIWSTNDEA IILEPFEGSP GLKIMPSSAE SVTDNVNLFF GDDFFEHLVR
121 ESNRYHYQVM EKYKIPSKAK KWTDITVPEM KKFLGLIVLM GQIKKDVLYD YWSTDPSIET
181 PFFSQVMSRN RFVQIMQSWH FCNNDNIPHD SHRLAKIQPV IDYFRRKFND VYKPCQQLSL
241 DESIIPWRGR LSIKTYNPAK ITKYGILVRV LSEAVTGYVC NFDVYAADGK KLEDTAVIEP
301 YKNIWHQIYQ DNYYNSVKMA RILLKNKVRV CGTIRKNRGL PRSLKTIQLS RGQYEFRRNH
361 QILLEVWNNG RRNVNMISTI HSAQLMESRS KSKRSDVPIQ KPNSIIDYNK YMKGVDRADQ
421 YLAYYSIFRK TKKWTKRVVM FFINCALFNS FRVYTILNGK NITYKNFLHK VAVSWIEDGE
481 TNCTEQDDNL PNSEPTRRAP RLDHPGRLSN YGKHKLINIV TSGRSLKPQR QCRVCAVQKK
541 RSRTCFVCKF CNVPLHKGDC FERYHTLKKY (SEQ ID NO: 14543).
```

[0359] 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:

```
   1 ttaatttttt aacattttac cgaccgatag ccgattaatc gggtttttgc cgctgacgct
  61 taccgaccga taacctatta atcggctttt tgtcgtcgaa gcttaccaac ctatagccta
 121 cctatagtta atcggttgcc atggcgataa acaatctttc tcattatatg agcagtaatt
 181 tgttatttag tactaaggta ccttgctcag ttgcgtcagt tgcgttgctt tgtaagctcc
 241 cacagtttta taccaattcg aaaaacttac cgttcgcg (SEQ ID NO: 14544).
```

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

```
   1 actatttcac atttgaacta aaaaccgttg taatagataa aataaatata atttagtatt
  61 aatattatgg aaacaaaaga ttttattcaa tttaattatc ctatagtaac aaaaagcggc
 121 caatttttatc tgagcatacg aaaagcacag atactcccgc ccgacagtct aaaccgaaac
 181 agagccggcg ccagggagaa tctgcgcctg agcagccggt cggacgtgcg tttgctgttg
 241 aaccgctagt ggtcagtaaa ccagaaccag tcagtaagcc agtaactgat cagttaacta
 301 gattgtatag ttcaaattga acttaatcta gtttttaagc gtttgaatgt tgtctaactt
 361 cgttatatat tatattcttt ttaa (SEQ ID NO: 14545).
```

[0360] 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:

```
   1 MFSFVPNKEQ TRTVLIFCFH LKTTAAESHR PLVEAFGEQV PTVKTCERWF QRFKSGDFDV
  61 DDKEHGKPPK RYEDAELQAL LDEDDAQTQK QLAEQLEVSQ QAVSNRLREG GKIQKVGRWV
 121 PHELNERQRE RRKNTCEILL SRYKRKSFLH RIVTGEEKWI FFVNPKRKKS YVDPGQPATS
 181 TARPNRFGKK TRLCVWWDQS GVIYYELLKP GETVNTARYQ QQLINLNRAL QRKRPEYQKR
 241 QHRVIFLHDN APSHTARAVR DTLETLNWEV LPHAAYSPDL APSDYHLFAS MGHALAEQRF
 301 DSYESVEEWL DEWFAAKDDE FYWRGIHKLP ERWDNCVASD GKYFE (SEQ ID NO:
14546).
```

[0361] 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:

```
   1 ttattgggtt gcccaaaaag taattgcgga tttttcatat acctgtcttt taaacgtaca
  61 tagggatcga actcagtaaa actttgacct tgtgaaataa caaacttgac tgtccaacca
 121 ccatagtttg gcgcgaattg agcgtcataa ttgttttgac tttttgcagt caac (SEQ
ID NO: 14547).
```

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

```
   1 atgatttttt ctttttaaac caattttaat tagttaattg atataaaaat ccgcaattac
  61 tttttgggca acccaataa (SEQ ID NO: 14548).
```

[0362] 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 *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:

```
  1 MENFENWRKR RHLREVLLGH FFAKKTAAES HRLLVEVYGE HALAKTQCFE WFQRFKSGDF
 61 DTEDKERPGQ PKKFEDEELE ALLDEDCCQT QEELAKSLGV TQQAISKRLK AAGYIQKQGN
121 WVPHELKPRD VERRFCMSEM LLQRHKKKSF LSRIITGDEK WIHYDNSKRK KSYVKRGGRA
181 KSTPKSNLHG AKVMLCIWWD QRGVLYYELL EPGQTITGDL YRTQLIRLKQ ALAEKRPEYA
241 KRHGAVIFHH DNARPHVALP VKNYLENSGW EVLPHPPYSP DLAPSDYHLF RSMQNDLAGK
301 RFTSEQGIRK WLDSFLAAKP AKFFEKGIHE LSERWEKVIA SDGQYFE (SEQ ID NO:
14549).
```

[0363] In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Mayetiola destructor*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
  1 taagacttcc aaaatttcca cccgaacttt accttccccg cgcattatgt ctctcttttc
 61 accctctgat ccctggtatt gttgtcgagc acgatttata ttgggtgtac aacttaaaaa
121 ccggaattgg acgctagatg tccacactaa cgaatagtgt aaaagcacaa atttcatata
181 tacgtcattt tgaaggtaca tttgacagct atcaaaatca gtcaataaaa ctattctatc
241 tgtgtgcatc atatttttt attaact (SEQ ID NO: 14550).
```

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

```
  1 tgcattcatt cattttgtta tcgaaataaa gcattaattt tcactaaaaa attccggttt
 61 ttaagttgta cacccaatat catccttagt gacaattttc aaatggcttt cccattgagc
121 tgaaaccgtg gctctagtaa gaaaaacgcc caacccgtca tcatatgcct ttttttctc
181 aacatccg (SEQ ID NO: 14551).
```

[0364] 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:

```
  1 MENQKEHYRH ILLFYFRKGK NASQAHKKLC AVYGDEALKE RQCQNWFDKF RSGDFSLKDE
 61 KRSGRPVEVD DDLIKAIIDS DRHSTTREIA EKLHVSHTCI ENHLKQLGYV QKLDTWVPHE
121 LKEKHLTQRI NSCDLLKKRN ENDPFLKRLI TGDEKWVVYN NIKRKRSWSR PREPAQTTSK
181 AGIHRKKVLL SVWWDYKGIV YFELLPPNRT INSVVYIEQL TKLNNAVEEK RPELTNRKGV
241 VFHHDNARPH TSLVTRQKLL ELGWDVLPHP PYSPDLAPSD YFLFRSLQNS LNGKNFNNDD
301 DIKSYLIQFF ANKNQKFYER GIMMLPERWQ KVIDQNGQHI TE (SEQ ID NO: 14552).
```

[0365] 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:

```
  1 ttgggttggc aactaagtaa ttgcggattt cactcataga tggcttcagt tgaattttta
 61 ggtttgctgg cgtagtccaa atgtaaaaca cattttgtta tttgatagtt ggcaattcag
121 ctgtcaatca gtaaaaaaag ttttttgatc ggttgcgtag ttttcgtttg gcgttcgttg
181 aaaa (SEQ ID NO: 14553).
```

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

```
   1 agttatttag ttccatgaaa aaattgtctt tgattttcta aaaaaaatcc gcaattactt
  61 agttgccaat ccaa (SEQ ID NO: 14554).
```

[0366] 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 *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:

```
   1 MSSFVPENVH LRHALLFLFH QKKRAAESHR LLVETYGEHA PTIRTCETWF RQFKCGDFNV
  61 QDKERPGRPK TFEDAELQEL LDEDSTQTQK QLAEKLNVSR VAICERLQAM GKIQKMGRWV
 121 PHELNDRQME NRKIVSEMLL QRYERKSFLH RIVTGDEKWI YFENPKRKKS WLSPGEAGPS
 181 TARPNRFGRK TMLCVWWDQI GVVYYELLKP GETVNTDRYR QQMINLNCAL IEKRPQYAQR
 241 HDKVILQHDN APSHTAKPVK EMLKSLGWEV LSHPPYSPDL APSDYHLFAS MGHALAEQHF
 301 ADFEEVKKWL DEWFSSKEKL FFWNGIHKLS ERWTKCIESN GQYFE (SEQ ID NO:
14555).
```

[0367] In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Messor bouvieri*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
   1 agtcagaaat gacacctcga tcgacgacta atcgacgtct aatcgacgtc gattttatgt
  61 caacatgtta ccaggtgtgt cggtaattcc tttccggttt ttccggcaga tgtcactagc
 121 cataagtatg aaatgttatg atttgataca tatgtcattt tattctactg acattaacct
 181 taaaactaca caagttacgt tccgccaaaa taacagcgtt atagatttat aatttttga
 241 aa (SEQ ID NO: 14556).
```

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

```
   1 ataaatttga actatccatt ctaagtaacg tgttttcttt aacgaaaaaa ccggaaaaga
  61 attaccgaca ctcctggtat gtcaacatgt tattttcgac attgaatcgc gtcgattcga
 121 agtcgatcga ggtgtcattt ctgact (SEQ ID NO: 14557).
```

[0368] 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%, 90%, 95%, 99% or any percentage in between identical to:

```
   1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
  61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
 121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
 181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
 241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
```

```
     301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
     361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
     421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
     481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
     541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ
ID NO: 14558).
```

[0369] In certain embodiments, the piggyBac or piggyBac-like transposon is isolated or derived from *Trichoplusia ni*. In certain embodiments, the piggyBac or piggyBac-like transposon comprises a sequence of:

```
       1 ttaaccctag aaagatagtc tgcgtaaaat tgacgcatgc attcttgaaa tattgctctc
      61 tctttctaaa tagcgcgaat ccgtcgctgt gcatttagga catctcagtc gccgcttgga
     121 gctcccgtga ggcgtgcttg tcaatgcggt aagtgtcact gattttgaac tataacgacc
     181 gcgtgagtca aaatgacgca tgattatctt ttacgtgact tttaagattt aactcatacg
     241 ataattatat tgttatttca tgttctactt acgtgataac ttattatata tatattttct
     301 tgttatagat atc (SEQ ID NO: 14559).
```

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

```
       1 tttgttactt tatagaagaa attttgagtt tttgtttttt tttaataaat aaataaacat
      61 aaataaattg tttgttgaat ttattattag tatgtaagtg taaatataat aaaacttaat
     121 atctattcaa attaataaat aaacctcgat atacagaccg ataaaacaca tgcgtcaatt
     181 ttacgcatga ttatctttaa cgtacgtcac aatatgatta tctttctagg gttaa (SEQ
ID NO: 14560).
```

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

```
       1 ccctagaaag atagtctgcg taaaattgac gcatgcattc ttgaaatatt gctctctctt
      61 tctaaatagc gcgaatccgt cgctgtgcat ttaggacatc tcagtcgccg cttggagctc
     121 ccgtgaggcg tgcttgtcaa tgcggtaagt gtcactgatt ttgaactata acgaccgcgt
     181 gagtcaaaat gacgcatgat tatcttttac gtgactttta agatttaact catacgataa
     241 ttatattgtt atttcatgtt ctacttacgt gataacttat tatatatata ttttcttgtt
     301 atagatatc (SEQ ID NO: 14561).
```

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

```
       1 tttgttactt tatagaagaa attttgagtt tttgtttttt tttaataaat aaataaacat
      61 aaataaattg tttgttgaat ttattattag tatgtaagtg taaatataat aaaacttaat
     121 atctattcaa attaataaat aaacctcgat atacagaccg ataaaacaca tgcgtcaatt
     181 ttacgcatga ttatctttaa cgtacgtcac aatatgatta tctttctagg g (SEQ ID
NO: 14562).
```

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

```
       1 tctaaatagc gcgaatccgt cgctgtgcat ttaggacatc tcagtcgccg cttggagctc
      61 ccgtgaggcg tgcttgtcaa tgcggtaagt gtcactgatt ttgaactata acgaccgcgt
     121 gagtcaaaat gacgcatgat tatcttttac gtgactttta agatttaact catacgataa
     181 ttatattgtt atttcatgtt ctacttacgt gataacttat tatatatata ttttcttgtt
     241 atagatatc (SEQ ID NO: 14609).
```

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

```
       1 tttgttactt tatagaagaa attttgagtt tttgtttttt tttaataaat aaataaacat
      61 aaataaattg tttgttgaat ttattattag tatgtaagtg taaatataat aaaacttaat
```

121 atctattcaa attaataaat aaacctcgat atacagaccg ataaaacaca tgcgtcaatt
181 ttacgcatga ttatctttaa cgtacgtcac aatatgatta tctttctagg g (SEQ ID NO: 14610).

[0370] 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.

[0371] 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).

[0372] 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).

[0373] 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 CCCTTAATTACTCGCG (SEQ ID NO: 14567).

[0374] 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 CCCTAGATAACTAAAC (SEQ ID NO: 14568).

[0375] 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 CCCTAGAAAGATA (SEQ ID NO: 14569).

[0376] DNA transposons in the hAT family are widespread in plants and animals. A number of active hAT transposon systems have been identified and found to be functional, including but not limited to, the Hermes transposon, Ac transposon, hobo transposon, and the Tol2 transposon. The hAT family is composed of two families that have been classified as the AC subfamily and the Buster subfamily, based on the primary sequence of their transposases. Members of the hAT family belong to Class II transposable elements. Class II

mobile elements use a cut and paste mechanism of transposition. hAT elements share similar transposases, short terminal inverted repeats, and an eight base-pairs duplication of genomic target.

[0377] Compositions and methods of the disclosure may comprise a TcBuster transposon and/or a TcBuster transposase.

[0378] Compositions and methods of the disclosure may comprise a TcBuster transposon and/or a hyperactive TcBuster transposase. A hyperactive TcBuster transposase demonstrates an increased excision and/or increased insertion frequency when compared to an excision and/or insertion frequency of a wild type TcBuster transposase. A hyperactive TcBuster transposase demonstrates an increased transposition frequency when compared to a transposition frequency of a wild type TcBuster transposase.

[0379] In some embodiments of the compositions and methods of the disclosure, a wild type TcBuster transposase comprises or consists of the amino acid sequence of:

```
  1 MMLNWLKSGK LESQSQEQSS CYLENSNCLP PTLDSTDIIG EENKAGTTSR KKRKYDEDYL
 61 NFGFTWTGDK DEPNGLCVIC EQVVNNSSLN PAKLKRHLDT KHPTLKGKSE YFKRKCNELN
121 QKKHTFERYV RDDNKNLLKA SYLVSLRIAK QGEAYTIAEK LIKPCTKDLT TCVFGEKFAS
181 KVDLVPLSDT TISRRIEDMS YFCEAVLVNR LENAKCGFTL QMDESTDVAG LAILLVFVRY
241 IHESSFEEDM LFCKALPTQT TGEEIFNLLN AYFEKHSIPW NLCYHICTDG AKAMVGVIKG
301 VIARIKKLVP DIKASHCCLH RHALAVKRIP NALHEVLNDA VKMINFIKSR PLNARVFALL
361 CDDLGSLHKN LLLHTEVRWL SRGKVLTRFW ELRDEIRIFF NEREFAGKLN DTSWLQNLAY
421 IADIFSYLNE VNLSLQGPNS TIFKVNSRIN SIKSKLKLWE ECITKNNTEC FANLNDFLET
481 SNIALDPNLK SNILEHLNGL KNTFLEYFPP TCNNISWVEN PFNECGNVDI LPIKEREQLI
541 DIRTDTTLKS SFVPDGIGPF WIKLMDEFPE ISKRAVKELM PFVTTYLCEK SFSVYVATKT
601 KYRNRLDAED DMRLQLTTIH PDIDNLCNNK QAQKSH
```

(GenBank Accession No. ABF20545 and SEQ ID NO: 17900).

[0380] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase comprises or consists of a sequence having at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or any percentage identity in between to a wild type TcBuster transposase comprising or consisting of the amino acid sequence of:

```
  1 MMLNWLKSGK LESQSQEQSS CYLENSNCLP PTLDSTDIIG EENKAGTTSR KKRKYDEDYL
 61 NFGFTWTGDK DEPNGLCVIC EQVVNNSSLN PAKLKRHLDT KHPTLKGKSE YFKRKCNELN
121 QKKHTFERYV RDDNKNLLKA SYLVSLRIAK QGEAYTIAEK LIKPCTKDLT TCVFGEKFAS
181 KVDLVPLSDT TISRRIEDMS YFCEAVLVNR LENAKCGFTL QMDESTDVAG LAILLVFVRY
241 IHESSFEEDM LFCKALPTQT TGEEIFNLLN AYFEKHSIPW NLCYHICTDG AKAMVGVIKG
301 VIARIKKLVP DIKASHCCLH RHALAVKRIP NALHEVLNDA VKMINFIKSR PLNARVFALL
361 CDDLGSLHKN LLLHTEVRWL SRGKVLTRFW ELRDEIRIFF NEREFAGKLN DTSWLQNLAY
421 IADIFSYLNE VNLSLQGPNS TIFKVNSRIN SIKSKLKLWE ECITKNNTEC FANLNDFLET
481 SNIALDPNLK SNILEHLNGL KNTFLEYFPP TCNNISWVEN PFNECGNVDI LPIKEREQLI
541 DIRTDTTLKS SFVPDGIGPF WIKLMDEFPE ISKRAVKELM PFVTTYLCEK SFSVYVATKT
```

```
601 KYRNRLDAED DMRLQLTTIH PDIDNLCNNK QAQKSH
```

(GenBank Accession No. ABF20545 and SEQ ID NO: 17900).

[0381] In some embodiments of the compositions and methods of the disclosure, a wild type TcBuster transposase is encoded by a nucleic acid sequence comprising or consisting of:

```
   1 atgatgttga attggctgaa aagtggaaag cttgaaagtc aatcacagga acagagttcc
  61 tgctaccttg agaactctaa ctgcctgcca ccaacgctcg attctacaga tattatcggt
 121 gaagagaaca aagctggtac cacctctcgc aagaagcgga aatatgacga ggactatctg
 181 aacttcggtt ttacatggac tggcgacaag gatgagccca acggactttg tgtgatttgc
 241 gagcaggtag tcaacaattc ctcacttaac ccggccaaac tgaaacgcca tttggacaca
 301 aagcatccga cgcttaaagg caagagcgaa tacttcaaaa gaaaatgtaa cgagctcaat
 361 caaaagaagc atacttttga gcgatacgta agggacgata acaagaacct cctgaaagct
 421 tcttatctcg tcagtttgag aatagctaaa cagggcgagg catataccat agcggagaag
 481 ttgatcaagc cttgcaccaa ggatctgaca acttgcgtat ttggagaaaa attcgcgagc
 541 aaagttgatc tcgtcccctt gtccgacacg actatttcaa ggcgaatcga agacatgagt
 601 tacttctgtg aagccgtgct ggtgaacagg ttgaaaaatg ctaaatgtgg gtttacgctg
 661 cagatggacg agtcaacaga tgttgccggt cttgcaatcc tgcttgtgtt tgttaggtac
 721 atacatgaaa gctcttttga ggaggatatg ttgttctgca aagcacttcc cactcagacg
 781 acagggggagg agattttcaa tcttctcaat gcctatttcg aaaagcactc catcccatgg
 841 aatctgtgtt accacatttg cacagacggt gccaaggcaa tggtaggagt tattaaagga
 901 gtcatagcga gaataaaaaa actcgtccct gatataaaag ctagccactg ttgcctgcat
 961 cgccacgctt tggctgtaaa gcgaataccg aatgcattgc acgaggtgct caatgacgct
1021 gttaaaatga tcaacttcat caagtctcgg ccgttgaatg cgcgcgtctt cgctttgctg
1081 tgtgacgatt tggggagcct gcataaaaat cttcttcttc ataccgaagt gaggtggctg
1141 tctagaggaa aggtgctgac ccgattttgg gaactgagag atgaaattag aattttcttc
1201 aacgaaaggg aatttgccgg gaaattgaac gacaccagtt ggttgcaaaa tttggcatat
1261 atagctgaca tattcagtta tctgaatgaa gttaatcttt ccctgcaagg gccgaatagc
1321 acaatcttca aggtaaatag ccgcattaac agtattaaat caaagttgaa gttgtgggaa
1381 gagtgtataa cgaaaaataa cactgagtgt tttgcgaacc tcaacgattt tttggaaact
1441 tcaaacactg cgttggatcc aaacctgaag tctaatattt tggaacatct caacggtctt
1501 aagaacacct ttctggagta ttttccacct acgtgtaata atatctcctg ggtggagaat
1561 cctttcaatg aatgcggtaa cgtcgataca ctcccaataa aagagaggga acaattgatt
1621 gacatacgga ctgatacgac attgaaatct tcattcgtgc ctgatggtat aggaccattc
1681 tggatcaaac tgatggacga atttccagaa attagcaaac gagctgtcaa agagctcatg
1741 ccatttgtaa ccacttacct ctgtgagaaa tcatttttccg tctatgtagc cacaaaaaca
1801 aaatatcgaa atagacttga tgctgaagac gatatgcgac tccaacttac tactatccat
1861 ccagacattg acaacctttg taacaacaag caggctcaga aatcccactg a
```

(GenBank Accession No. DQ481197 and SEQ ID NO: 17901).

[0382] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase comprises or consists of a sequence having at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or any percentage identity in between to a wild type TcBuster transposase encoded by a nucleic acid sequence comprising or consisting of:

```
   1 atgatgttga attggctgaa aagtggaaag cttgaaagtc aatcacagga acagagttcc
  61 tgctaccttg agaactctaa ctgcctgcca ccaacgctcg attctacaga tattatcggt
 121 gaagagaaca aagctggtac cacctctcgc aagaagcgga aatatgacga ggactatctg
 181 aacttcggtt ttacatggac tggcgacaag gatgagccca acggactttg tgtgatttgc
 241 gagcaggtag tcaacaattc ctcacttaac ccggccaaac tgaaacgcca tttggacaca
 301 aagcatccga cgcttaaagg caagagcgaa tacttcaaaa gaaaatgtaa cgagctcaat
```

```
 361 caaaagaagc atacttttga gcgatacgta agggacgata acaagaacct cctgaaagct
 421 tcttatctcg tcagtttgag aatagctaaa cagggcgagg catataccat agcggagaag
 481 ttgatcaagc cttgcaccaa ggatctgaca acttgcgtat ttggagaaaa attcgcgagc
 541 aaagttgatc tcgtcccccc gtccgacacg actatttcaa ggcgaatcga agacatgagt
 601 tacttctgtg aagccgtgct ggtgaacagg ttgaaaaatg ctaaatgtgg gtttacgctg
 661 cagatggacg agtcaacaga tgttgccggt cttgcaatcc tgcttgtgtt tgttaggtac
 721 atacatgaaa gctcttttga ggaggatatg ttgttctgca aagcacttcc cactcagacg
 781 acaggggagg agattttcaa tcttctcaat gcctatttcg aaaagcactc catcccatgg
 841 aatctgtgtt accacatttg cacagacggt gccaaggcaa tggtaggagt tattaaagga
 901 gtcatagcga gaataaaaaa actcgtccct gatataaaag ctagccactg ttgcctgcat
 961 cgccacgctt tggctgtaaa gcgaataccg aatgcattgc acgaggtgct caatgacgct
1021 gttaaaatga tcaacttcat caagtctcgg ccgttgaatg cgcgcgtctt cgctttgctg
1081 tgtgacgatt tggggagcct gcataaaaat cttcttcttc ataccgaagt gaggtggctg
1141 tctagaggaa aggtgctgac ccgattttgg gaactgagag atgaaattag aattttcttc
1201 aacgaaaggg aatttgccgg gaaattgaac gacaccagtt ggttgcaaaa tttggcatat
1261 atagctgaca tattcagtta tctgaatgaa gttaatcttt ccctgcaagg gccgaatagc
1321 acaatcttca aggtaaatag ccgcattaac agtattaaat caaagttgaa gttgtgggaa
1381 gagtgtataa cgaaaaataa cactgagtgt tttgcgaacc tcaacgattt tttggaaact
1441 tcaaacactg cgttggatcc aaacctgaag tctaatattt tggaacatct caacggtctt
1501 aagaacacct ttctggagta ttttccacct acgtgtaata atatctcctg ggtggagaat
1561 cctttcaatg aatgcggtaa cgtcgataca ctcccaataa aagagaggga acaattgatt
1621 gacatacgga ctgatacgac attgaaatct tcattcgtgc ctgatggtat aggaccattc
1681 tggatcaaac tgatggacga atttccagaa attagcaaac gagctgtcaa agagctcatg
1741 ccatttgtaa ccacttacct ctgtgagaaa tcattttccg tctatgtagc cacaaaaaca
1801 aaatatcgaa atagacttga tgctgaagac gatatgcgac tccaacttac tactatccat
1861 ccagacattg acaacctttg taacaacaag caggctcaga aatcccactg a
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(GenBank Accession No. DQ481197 and SEQ ID NO: 17901).

[0383] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase comprises or consists of a naturally occurring amino acid sequence.

[0384] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase comprises or consists of a non-naturally occurring amino acid sequence.

[0385] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase is encoded by a sequence comprising or consisting of a naturally occurring nucleic acid sequence.

[0386] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase is encoded by a sequence comprising or consisting of a non-naturally occurring nucleic acid sequence.

[0387] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the wild type TcBuster Transposase comprises or consists of the amino acid sequence of SEQ ID NO: 17900. In some

embodiments, the wild type TcBuster Transposase is encoded by a sequence comprising or consisting of the nucleic acid sequence of SEQ ID NO: 17901. In some embodiments, the one or more sequence variations comprises one or more of a substitution, inversion, insertion, deletion, transposition, and frameshift. In some embodiments, the one or more sequence variations comprises a modified, synthetic, artificial or non-naturally occurring amino acid. In some embodiments, the one or more sequence variations comprises a modified, synthetic, artificial or non-naturally occurring nucleic acid.

[0388] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises an amino acid substitution in one or more of a DNA Binding and Oligomerization domain, an insertion domain and a Zn-BED domain.

[0389] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises an amino acid substitution that increases a net charge a neutral pH when compared to a wild type TcBuster Transposase. In some embodiments, the wild type TcBuster Transposase comprises or consists of the amino acid sequence of SEQ ID NO: 17900. In some embodiments, the wild type TcBuster Transposase is encoded by a sequence comprising or consisting of the nucleic acid sequence of SEQ ID NO: 17901. In some embodiments, the one or more sequence variations comprises an amino acid substitution of the aspartic acid (D) at position 223 (D223), the aspartic acid (D) at position 289 (D289) and the aspartic acid (E) at position 589 (E289) of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 223, 289 and/or 289 of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 70 amino acids of position 223, 289 and/or 289 of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 80 amino acids of position 223, 289 and/or 289 of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution of an aspartic acid (D) or a aspartic

acid (E) to a neutral amino acid, a lysine (L) or an arginine (R) (e.g. D223L, D223R, D289L, D289R, E289L, E289R of SEQ ID NO: 17900).

[0390] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of Q82E, N85S,D99A, D132A, Q151S, Q151A, E153K, E153R, A154P, Y155H, E159A, T171K, T171R, K177E, D183K, D183R, D189A, T191E, S193K, S193R, Y201A, F202D, F202K, C203I, C203V, Q221T, M222L, I223Q, E224G, S225W, D227A, R239H, E243A, E247K, P257K, P257R, Q258T, E263A, E263K, E263R, E274K, E274R, S278K, N281E, L282K, L282R, K292P, V297K, K299S, A303T, H322E, A332S, A358E, A358K, A358S, D376A, V377T, L380N, I398D, I398S, I398K, F400L, V431L, S447E, N450K, N450R, I452F, E469K, K469K, P510D, P510N, E517R, R536S, V553S, P554T, P559D, P559S, P559K, K573E, E578L, K590T, Y595L, V596A, T598I, K599A, Q615A, T618K, T618K, T618R, D622K and D622R of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 154, 155, 159, 171, 177, 183, 189, 191, 193, 201, 202, 203, 221, 223, 224, 225, 227, 239, 243, 247, 257, 258, 263, 274, 278, 281, 282, 292, 297, 299, 303, 322, 332, 358, 376, 377, 380, 398, 400, 431, 447, 450, 452, 469, 510, 517, 536, 553, 554, 559, 573, 578, 590, 595, 596, 598, 599, 615, 618, and 622 of SEQ ID NO: 17900.

[0391] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of E247K, V297K, A358K, S278K, E247R, E274R, V297R, A358R, S278R, T171R, D183R, S193R, P257K, E263R, L282K, T618K, D622R, E153K, N450K, T171K, D183K, S193K, P257R, E263K, L282R, T618R, D622K, E153R and N450R of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 153, 171, 183, 193, 247, 257, 263, 274, 278, 282, 297, 358, 450, 618, 622 of SEQ ID NO: 17900.

[0392] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of V377T/E469K, V377T/E469K/R536S, A332S, V553S/P554T, E517R, K299S, Q615A/T618K, S278K, A303T, P510D, P510N, N281S, N281E, K590T, Q258T, E247K, S447E, N85S, V297K, A358K, I452F, V377T/E469K/D189A, K573E/E578L, I452F/V377T/E469K/D189A, A358K/V377T/E469K/D189A, K573E/E578L/V377T/E469K/D189A, T171R, D183R, S193R, P257K, E263R, L282K, T618K, D622R, E153K, N450K, T171K, D183K, S193K, P257R, E263K, L282R, T618R, D622K, E153R, N450R, E247K/E274K/V297K/A358K of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 85, 153, 171, 189, 193, 247, 257, 258, 263, 274, 278, 281, 282, 297, 299, 303, 332, 358, 377, 450, 469, 447, 452, 469, 510, 517, 536, 553, 554, 573, 578, 590, 615, 618, 622 of SEQ ID NO: 17900.

[0393] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of V377T/E469K, V377T/E469K/R536S, V553S/P554T, Q615A/T618K, S278K, A303T, P510D, P510N, N281S, N281E, K590T, Q258T, E247K, S447E, N85S, V297K, A358K, I452F, V377T/E469K/D189A and K573E/E578L. In some embodiments, the one or more sequence variations comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 85, 189, 247, 258, 278, 281, 297, 303, 358, 377, 447, 452, 469, 510, 536, 553, 554, 573, 578, 590, 615, 618 of SEQ ID NO: 17900.

[0394] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of Q151S, Q151A, A154P, Q615A, V553S, Y155H, Y201A, F202D, F202K, C203I, C203V, F400L, I398D, I398S, I398K, V431L, P559D, P559S, P559K, M222L of SEQ ID NO: 17900. In some embodiments, the one or more sequence variations

comprises an amino acid substitution within 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of amino acids in between of position 151, 154, 615, 553, 155, 201, 202, 203, 400, 398, 431, 559, 222 of SEQ ID NO: 17900.

[0395] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of V377T, E469K, and D189A, when numbered in accordance with SEQ ID NO: 17900.

[0396] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of K573E and E578L, when numbered in accordance with SEQ ID NO: 17900.

[0397] In some embodiments, the mutant TcBuster transposase comprises amino acid substitution I452K, when numbered in accordance with SEQ ID NO: 17900.

[0398] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of A358K, when numbered in accordance with SEQ ID NO: 17900.

[0399] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of V297K, when numbered in accordance with SEQ ID NO: 17900.

[0400] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of N85S, when numbered in accordance with SEQ ID NO: 17900.

[0401] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations

comprises one or more of I452F, V377T, E469K, and D189A, when numbered in accordance with SEQ ID NO: 17900.

[0402] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of A358K, V377T, E469K, and D189A, when numbered in accordance with SEQ ID NO: 17900.

[0403] In some embodiments of the compositions and methods of the disclosure, a mutant TcBuster Transposase comprises one or more sequence variations when compared to a wild type TcBuster Transposase. In some embodiments, the one or more sequence variations comprises one or more of V377T, E469K, D189A, K573E and E578L, when numbered in accordance with SEQ ID NO: 17900.

[0404] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 5' inverted repeat comprising or consisting of the sequence of:

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  1 Cagtgttctt caacctttgc catccggcgg aacccttttgt cgagatattt ttttttatgg
 61 aacccttcat ttagtaatac acccagatga gattttaggg acagctgcgt tgacttgtta
121 cgaacaaggt gagcccgtgc tttggtctag ccaagggcat ggtaaagact atattcgcgg
181 cgttgtgaca atttaccgaa caactccgcg gccgggaagc cgatctcggc ttgaacgaat
241 tgttaggtgg cggtacttgg gtcgatatca aagtgcatca cttcttcccg tatgcccaac
301 tttgtataga gagccactgc gggatcgtca ccgtaatctg cttgcacgta gatcacataa
361 gcaccaagcg cgttggcctc atgcttgagg agattgatga gcgcggtggc aatgccctgc
421 ctccggtgct cgccggagac tgcgagatca tagatata
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(SEQ ID NO: 17902).

[01] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 3' inverted repeat comprising or consisting of the sequence of:

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  1 gatatcaagc ttatcgatac cgtcgacctc gagatttctg aacgattcta ggttaggatc
 61 aaacaaaata caatttattt taaaactgta agttaactta cctttgcttg tctaaaccaa
121 aaacaacaac aaaactacga ccacaagtac agttacatat ttttgaaaat taaggttaag
181 tgcagtgtaa gtcaactatg cgaatggata acatgtttca acatgaaact ccgattgacg
241 catgtgcatt ctgaagagcg gcgcggccga cgtctctcga attgaagcaa tgactcgcgg
301 aaccccgaaa gcctttgggt ggaaccctag ggttccgcgg aacacaggtt gaagaacact
361 g
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(SEQ ID NO: 17903).

[0405] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 5' inverted repeat comprising or consisting of the

sequence of SEQ ID NO: 17902 and a 3' inverted repeat comprising or consisting of the sequence of SEQ ID NO: 17903.

[0406] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 5' inverted repeat comprising or consisting of the sequence of:

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  1 Cctgcaggag tgttcttcaa cctttgccat ccggcggaac cctttgtcga gatatttttt
 61 tttatggaac ccttcattta gtaatacacc cagatgagat tttagggaca gctgcgttga
121 cttgttacga acaaggtgag cccgtgcttt ggtaataaaa actctaaata agatttaaat
181 ttgcatttat ttaaacaaac tttaaacaaa aagataaata ttccaaataa aataatatat
241 aaaataaaaa ataaaaatta atgacttttt tgcgcttgct tattattgca caaattatca
301 atatcgggat ggatcgttgt ttttt
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(SEQ ID NO: 17904).

[0407] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 3' inverted repeat comprising or consisting of the sequence of:

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  1 Gagccaattc agcatcatat ttctgaacga ttctaggtta ggatcaaaca aaatacaatt
 61 tattttaaaa ctgtaagtta acttaccttt gcttgtctaa acctaaaaca acaacaaaac
121 tacgaccaca agtacagtta catatttttg aaaattaagg ttaagtgcag tgtaagtcaa
181 ctatgcgaat ggataacatg tttcaacatg aaactccgat tgacgcatgt gcattctgaa
241 gagcggcgcg gccgacgtct ctcgaattga agcaatgact cgcggaaccc cgaaagcctt
301 tgggtggaac cctagggttc cgcggaacac aggttgaaga acactg
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(SEQ ID NO: 17905).

[0408] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a 5' inverted repeat comprising or consisting of the sequence of SEQ ID NO: 17904 and a 3' inverted repeat comprising or consisting of the sequence of SEQ ID NO: 17905.

[0409] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes an inverted repeat comprising or consisting of a sequence having at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95,% 97%, 99% or any percentage identify in between to one or more of SEQ ID NO: 17902, 17903, 17904 or 17905.

[0410] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes an inverted repeat comprising or consisting of a sequence having at least In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes an inverted repeat comprising or consisting of a sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 99

or any number of contiguous nucleotides in between having between 90 and 100% identity to SEQ ID NO: 17902, 17903, 17904 or 17905 or any portion thereof.

[0411] In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes an inverted repeat comprising or consisting of a sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 97, 99 or any number of discontinuous nucleotides in between having between 90 and 100% identity to SEQ ID NO: 17902, 17903, 17904 or 17905 or any portion thereof.

[0412] In some embodiments of the compositions and methods of the disclosure, a TcBuster transposon comprises a 3' inverted repeat and a 5' inverted repeat. In some embodiments of the compositions and methods of the disclosure, a TcBuster Transposase recognizes a TcBuster transposon comprising a 3' inverted repeat and a 5' inverted repeat comprising or consisting of a sequence having at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80 85, 90, 95, 97, 99 or any number of discontinuous nucleotides in between having between 90 and 100% identity to SEQ ID NO: 17902, 17903, 17904 or 17905 or any portion thereof.

Non-Transposition Based Methods of Genetic Modification

[0413] In some embodiments of the methods of the disclosure, a modified HSCor modified HSC descendent cell of the disclosure may be produced by introducing a transgene into an HSC or an HSC descendent cell of the disclosure. The introducing step may comprise delivery of a nucleic acid sequence and/or a genomic editing construct via a non-transposition delivery system.

[0414] In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell *ex vivo*, *in vivo*, *in vitro* or *in situ* comprises one or more of topical delivery, adsorption, absorption, electroporation, spin-fection, co-culture, transfection, mechanical delivery, sonic delivery, vibrational delivery, magnetofection or by nanoparticle-mediated delivery. In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell *ex vivo*, *in vivo*, *in vitro* or *in situ* comprises liposomal transfection, calcium phosphate transfection, fugene transfection, and dendrimer-mediated transfection. In some embodiments of the methods of the disclosure,

introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell *ex vivo*, *in vivo*, *in vitro* or *in situ* by mechanical transfection comprises cell squeezing, cell bombardment, or gene gun techniques. In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell *ex vivo*, *in vivo*, *in vitro* or *in situ* by nanoparticle-mediated transfection comprises liposomal delivery, delivery by micelles, and delivery by polymerosomes.

[0415] In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell *ex vivo*, *in vivo*, *in vitro* or *in situ* comprises a non-viral vector. In some embodiments, the non-viral vector comprises a nucleic acid. 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, the non-viral vector comprises a transposon of the disclosure.

[0416] In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell ex vivo, in vivo, in vitro or in situ comprises a viral vector. In some embodiments, the viral vector is a non-integrating non-chromosomal vector. 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. Integrating chromosomal vectors include, but are not limited to, adeno-associated vectors (AAV), Lentiviruses, and gamma-retroviruses.

[0417] In some embodiments of the methods of the disclosure, introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell ex vivo, in vivo, in vitro or in situ comprises a combination of vectors. 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 an RNA and a reverse transcriptase, a combination of a transposon and a transposase, a combination of a

non-viral vector and an endonuclease, and a combination of a viral vector and an endonuclease.

[0418] In some embodiments of the methods of the disclosure, genome modification comprising introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell ex vivo, in vivo, in vitro or in situ stably integrates a nucleic acid sequence, transciently integrates a nucleic acid sequence, produces site-specific integration a nucleic acid sequence, or produces a biased integration of a nucleic acid sequence. In some embodiments, the nucleic acid sequence is a transgene.

[0419] In some embodiments of the methods of the disclosure, genome modification comprising introducing a nucleic acid sequence and/or a genomic editing construct into an HSC or HSC descendent cell ex vivo, in vivo, in vitro or in situ stably integrates 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 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 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.

[0420] In some embodiments, the site-specific transgene integration occurs at a site that disrupts expression of a target gene. 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, PDI, any immunosuppressive gene, and genes involved in allo-rejection.

[0421] In some embodiments, the 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.

[0422] In some embodiments of the methods 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).

[0423] In some embodiments of the methods of the disclosure, the 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 gamma-retroviral vector.

[0424] In some embodiments of the methods of the disclosure, the 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.

[0425] In some embodiments of the methods of the disclosure, the genome modification is 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.

[0426] In some embodiments, 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.

[0427] In some embodiments of the methods of the disclosure, the genome modification is a semi-stable or persistent non-chromosomal integration of a transgene. In some 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.

[0428] In some embodiments of the methods of the disclosure, the 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.

[0429] In some embodiments of the methods of the disclosure, the 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.

[0430] In gene editing systems that involve inserting new or existing nucleotides/nucleic acids, insertion tools (e.g. DNA template vectors, transposable elements (transposons or retrotransposons) must be delivered to the cell in addition to the cutting enzyme (e.g. a nuclease, recombinase, integrase or transposase). Examples of such insertion tools for a recombinase may include a DNA vector. Other gene editing systems require the delivery of an integrase along with an insertion vector, a transposase along with a transposon/retrotransposon, etc. In some embodiments, an example recombinase that may be used as a cutting enzyme is the CRE recombinase. In various embodiments, example integrases that may be used in insertion tools include viral based enzymes taken from any of a number of viruses including, but not limited to, AAV, gamma retrovirus, and lentivirus.

Example transposons/retrotransposons that may be used in insertion tools include, but are not limited to, the piggyBac transposon, Sleeping Beauty transposon, and the L1 retrotransposon.

[0431] In certain embodiments of the methods of the disclosure, the transgene is delivered in vivo. In certain embodiments of the methods of the disclosure, in vivo transgene delivery can occur by: topical delivery, adsorption, absorption, electroporation, spin-fection, co-culture, transfection, mechanical delivery, sonic delivery, vibrational delivery, magnetofection or by nanoparticle-mediated delivery. In certain embodiments of the methods of the disclosure, in vivo transgene delivery by transfection can occur by liposomal transfection, calcium phosphate transfection, fugene transfection, and dendrimer-mediated transfection. In certain embodiments of the methods of the disclosure, in vivo mechanical transgene delivery can occur by cell squeezing, bombardment, and gene gun. In certain embodiments of the methods of the disclosure, in vivo nanoparticle-mediated transgene delivery can occur by liposomal delivery, delivery by micelles, and delivery by polymerosomes. In various embodiments, nucleases that may be used as cutting enzymes include, but are not limited to, Cas9, transcription activator-like effector nucleases (TALENs) and zinc finger nucleases.

[0432] In certain embodiments of the methods of the disclosure, non-viral vectors are used for transgene delivery. In certain embodiments, the non-viral vector is a nucleic acid. In certain embodiments, the nucleic acid non-viral vector is 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 certain embodiments, the non-viral vector is a transposon. In certain embodiments, the transposon is piggyBac™.

[0433] In certain embodiments of the methods of the disclosure, transgene delivery can occur via viral vector. In certain embodiments, the viral vector is a non-integrating non-chromosomal vectors. Non-integrating non-chromosomal vectors can include adeno-associated virus (AAV), adenovirus, and herpes viruses. In certain embodiments, the viral vector is an integrating chromosomal vectors. Integrating chromosomal vectors can include adeno-associated vectors (AAV), Lentiviruses, and gamma-retroviruses.

[0434] In certain embodiments of the methods of the disclosure, transgene delivery can occur by a combination of vectors. Exemplary but non-limiting vector combinations can include: viral plus non-viral vectors, more than one non-viral vector, or more than one viral vector. Exemplary but non-limiting vectors combinations can include: DNA-derived plus RNA-derived vectors, RNA plus reverse transcriptase, a transposon and a transposase, a non-viral vectors plus an endonuclease, and a viral vector plus an endonuclease.

[0435] In certain embodiments of the methods of the disclosure, the genome modification can be a stable integration of a transgene, a transient integration of a transgene, a site-specific integration of a transgene, or a biased integration of a transgene.

[0436] In certain embodiments of the methods of the disclosure, the genome modification can be a stable chromosomal integration of a transgene. In certain embodiments, the stable chromosomal integration can be a random integration, a site-specific integration, or a biased integration. In certain embodiments, the site-specific integration can be non-assisted or assisted. In certain embodiments, the assisted site-specific integration is co-delivered with a site-directed nuclease. In certain embodiments, the site-directed nuclease comprises a transgene with 5' and 3' nucleotide sequence extensions that contain homology to upstream and downstream regions of the site of genomic integration. In certain embodiments, the transgene with homologous nucleotide extensions enable genomic integration by homologous recombination, microhomology-mediated end joining, or nonhomologous end-joining. In certain embodiments the site-specific integration occurs at a safe harbor site. Genomic safe harbor sites are able to accommodate the 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.

[0437] In certain embodiments, the site-specific transgene integration occurs at a site that disrupts expression of a target gene. In certain 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 certain embodiments, exemplary target genes targeted by site-specific integration include but are not limited to TRAC, TRAB, PDI, any immunosuppressive gene, and genes involved in allo-rejection.

[0438] In certain embodiments, the site-specific transgene integration occurs at a site that results in enhanced expression of a target gene. In certain 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.

[0439] In certain embodiments of the methods of the disclosure, enzymes may be used to create strand breaks in the host genome to facilitate delivery or integration of the transgene. In certain embodiments, enzymes create single-strand breaks. In certain embodiments, enzymes create double-strand breaks. In certain 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 certain 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).

[0440] In certain embodiments of the methods of the disclosure, the site-specific transgene integration is controlled by a vector-mediated integration site bias. In certain embodiments vector-mediated integration site bias is controlled by the chosen lentiviral vector. In certain embodiments vector-mediated integration site bias is controlled by the chosen gamma-retroviral vector.

[0441] In certain embodiments of the methods of the disclosure, the site-specific transgene integration site is a non-stable chromosomal insertion. In certain embodiments, the integrated transgene may become silenced, removed, excised, or further modified. In certain embodiments of the methods of the disclosure, the genome modification is a non-stable integration of a transgene. In certain 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 certain embodiments, the transient non-chromosomal insertion can be epi-chromosomal or cytoplasmic. In certain embodiments, 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.

[0442] In certain embodiments of the methods of the disclosure, the genome modification is a semi-stable or persistent non-chromosomal integration of a transgene. In certain 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.

[0443] In certain embodiments of the methods of the disclosure, the genome modification is a non-stable chromosomal integration of a transgene. In certain embodiments, the integrated transgene may become silenced, removed, excised, or further modified.

[0444] In certain embodiments of the methods of the disclosure, the 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 certain embodiments, the modification to the genome by transgene insertion can occur via CRISPR-Cas9, TALEN, ZFNs, Cas-CLOVER, and cpf1.

[0445] In certain embodiments of the methods of the disclosure, a cell with an in vivo or ex vivo genomic modification can be a germline cell or a somatic cell. In certain embodiments the modified cell can be a human, non-human, mammalian, rat, mouse, or dog cell. In certain embodiments, the modified cell can be differentiated, undifferentiated, or immortalized. In certain embodiments, the modified undifferentiated cell can be a stem cell. In certain embodiments, the modified cell can be differentiated, undifferentiated, or immortalized. In certain embodiments, the modified undifferentiated cell can be an induced pluripotent stem cell. In certain embodiments, the modified cell can be a T cell, a hematopoietic stem cell, a natural killer cell, a macrophage, a dendritic cell, a monocyte, a megakaryocyte, or an osteoclast. In certain embodiments, the modified cell can be modified while the cell is quiescent, in an activated state, resting, in interphase, in prophase, in metaphase, in anaphase, or in telophase. . In certain embodiments, the modified cell can be fresh, cryopreserved, bulk,

sorted into sub-populations, from whole blood, from leukapheresis, or from an immortalized cell line.

Centyrins

[0446] Centyrins 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 Centyrin 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 invention is a consensus sequence of 15 FN3 domains. The Centyrins of the disclosure can be designed to bind various molecules, for example, a cellular target protein. In a preferred embodiment, the Centyrins of the disclosure can be designed to bind an epitope of a wild type and/or variant form of an antigen.

[0447] Centyrins 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 Centyrins of the disclosure may be bound to a nucleic acid molecule that may encode the Centyrin.

[0448] The disclosure provides at least one method for expressing at least one Centyrin based on a consensus sequence of multiple FN3 domains, in a host cell, comprising culturing a host cell as described herein under conditions wherein at least one protein scaffold is expressed in detectable and/or recoverable amounts.

[0449] The disclosure provides at least one composition comprising (a) a Centyrin 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.

[0450] The disclosure provides a method of generating libraries of a Centyrin 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 Centyrins by altering (by mutation) the amino acids or the number of amino acids in the molecules in particular positions in portions of the Centyrin, 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 Centyrin 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.

[0451] Centyrins 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.

[0452] The disclosure provides a method of generating a Centyrin molecule that binds to a particular target by panning the Centyrin 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 Centyrins 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 Centyrin residues, random mutagenesis due to error-prone PCR, DNA shuffling, and/or a combination of these techniques.

[0453] The disclosure provides an isolated, recombinant and/or synthetic Centyrin based on a consensus sequence of fibronectin type III (FN3) repeat protein, including, without limitation, mammalian-derived Centyrins, as well as compositions and encoding nucleic acid molecules comprising at least one polynucleotide encoding a Centyrin based on the consensus FN3 sequence. The disclosure further includes, but is not limited to, methods of making and using such nucleic acids and Centyrins, including diagnostic and therapeutic compositions, methods and devices.

[0454] The Centyrins 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.

[0455] Moreover, the Centyrins 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.

[0456] Three of the six loops of the Centyrin 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 SEQ ID NO: 18018. Preferably, the loop regions at or about residues 22-28, 51-54, and 75-81 of SEQ ID NO: 18018 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.

[0457] In certain embodiments of the disclosure, PSMA-specific Centyrins are designed, evolved and/or selected for their ability to specifically bind to a sequence of PSMA. In certain embodiments, the PSMA-specific Centyrins are capable of binding to a sequence of PSMA with a comparable affinity to that of an anti-PSMA antibody binding an epitope of PSMA. In certain embodiments, the PSMA-specific Centyrins are capable of binding to a sequence of PSMA with a stronger affinity to that of an anti-PSMA antibody binding an epitope of PSMA. In certain embodiments, the PSMA-specific Centyrins are capable of binding to a sequence of PSMA to which an antibody is not capable of binding. For example the sequence of PSMA may be discontinuous or may have a secondary structure.

Production and Generation of CARTyrins

[0458] At least one CARTyrin 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).

[0459] Amino acids from a CARTyrin 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.

[0460] Optionally, CARTyrins can be engineered with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, the CARTyrins 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 Centyrin or CARTyrin 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), is achieved. Alternatively, or in addition to, the above procedures, other suitable methods of engineering can be used.

Screening of CARTyrin Proteins

[0461] Screening Centyrins or CARTyrins 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. The Centyrins CARTyrins of the disclosure can bind human or other mammalian proteins with a wide range of affinities (KD). In a preferred embodiment, at least one Centyrin of the present invention 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) X 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 Kinexa method, as practiced by those of skill in the art.

[0462] The affinity or avidity of a Centyrin or CARTyrin for an antigen 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 Centyrin-antigen or Centyrin-antigen 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, Kon, Koff) are preferably made with standardized solutions of Centyrins or CARTyrins and antigen, and a standardized buffer, such as the buffer described herein.

[0463] Competitive assays can be performed with the Centyrin or CARTyrin of the disclosure in order to determine what proteins, antibodies, and other antagonists compete for binding to a target protein with the Centyrin or CARTyrin of the present invention 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 Centyrin or CARTyrin to the target protein, e.g., whether

the Centyrin or CARTyrin molecule 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.

Nucleic Acid Molecules

[0464] Nucleic acid molecules of the disclosure encoding Centyrins or CARTyrins 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.

[0465] 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 CARTyrin; nucleic acid molecules comprising the coding sequence for a CARTyrin; 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 CARTyrin 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 CARTyrins of the present invention. See, e.g., Ausubel, et al., supra, and such nucleic acid variants are included in the present invention.

[0466] As indicated herein, nucleic acid molecules of the disclosure which comprise a nucleic acid encoding a CARTyrin can include, but are not limited to, those encoding the amino acid sequence of a Centyrin fragment, by itself; the coding sequence for the entire CARTyrin or a portion thereof; the coding sequence for a Centyrin, 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 CARTyrin can be fused to a marker sequence, such as a sequence encoding a peptide that facilitates purification of the fused CARTyrin comprising a Centyrin fragment or portion.

Polynucleotides Selectively Hybridizing to a Polynucleotide as Described Herein

[0467] 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.

[0468] 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.

[0469] Optionally, polynucleotides of this invention will encode at least a portion of a CARTyrin 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 CARTyrin of the present invention. See, e.g., Ausubel, supra; Colligan, supra, each entirely incorporated herein by reference.

Construction of Nucleic Acids

[0470] 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.

[0471] 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 optionally a vector, adapter, or linker for cloning and/or expression of a polynucleotide of the disclosure.

[0472] 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, 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

[0473] 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 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

[0474] 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, 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 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.

[0475] 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.

[0476] 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.; 4,795,699 and 4,921,794 to Tabor, et al; 5,142,033 to Innis; 5,122,464 to Wilson, et al.; 5,091,310 to Innis; 5,066,584 to Gyllensten, et al; 4,889,818 to Gelfand, et al; 4,994,370 to Silver, et al; 4,766,067 to Biswas; 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.)

[0477] 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.

Synthetic Methods for Constructing Nucleic Acids

[0478] 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

[0479] 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 CARTyrin 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.

[0480] 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.

Nanotransposons

[0481] The disclosure provides a nanotransposon comprising: (a) a sequence encoding a transposon insert, comprising a sequence encoding a first inverted terminal repeat (ITR), a sequence encoding a second inverted terminal repeat (ITR), and an intra-ITR sequence; (b) a sequence encoding a backbone, wherein the sequence encoding the backbone comprises a sequence encoding an origin of replication having between 1 and 450 nucleotides, inclusive

of the endpoints, and a sequence encoding a selectable marker having between 1 and 200 nucleotides, inclusive of the endpoints, and (c) an inter-ITR sequence. In some embodiments, the inter-ITR sequence of (c) comprises the sequence of (b). In some embodiments, the intra-ITR sequence of (a) comprises the sequence of (b).

[0482] In some embodiments of the nanotransposons of the disclosure, the sequence encoding the backbone comprises between 1 and 600 nucleotides, inclusive of the endpoints. In some embodiments, the sequence encoding the backbone consists of between 1 and 50 nucleotides, between 50 and 100 nucleotides, between 100 and 150 nucleotides, between 150 and 200 nucleotides, between 200 and 250 nucleotides, between 250 and 300 nucleotides, between 300 and 350 nucleotides, between 350 and 400 nucleotides, between 400 and 450 nucleotides, between 450 and 500 nucleotides, between 500 and 550 nucleotides, between 550 and 600 nucleotides, each range inclusive of the endpoints.

[0483] In some embodiments of the nanotransposons of the disclosure, the inter-ITR sequence comprises between 1 and 1000 nucleotides, inclusive of the endpoints. In some embodiments, the inter-ITR sequence consists of between 1 and 50 nucleotides, between 50 and 100 nucleotides, between 100 and 150 nucleotides, between 150 and 200 nucleotides, between 200 and 250 nucleotides, between 250 and 300 nucleotides, between 300 and 350 nucleotides, between 350 and 400 nucleotides, between 400 and 450 nucleotides, between 450 and 500 nucleotides, between 500 and 550 nucleotides, between 550 and 600 nucleotides, between 600 and 650 nucleotides, between 650 and 700 nucleotides, between 700 and 750 nucleotides, between 750 and 800 nucleotides, between 800 and 850 nucleotides, between 850 and 900 nucleotides, between 900 and 950 nucleotides, or between 950 and 1000 nucleotides, each range inclusive of the endpoints.

[0484] In some embodiments of the nanotransposons of the disclosure, including the short nanotransposons (SNTs) of the disclosure, the inter-ITR sequence comprises between 1 and 200 nucleotides, inclusive of the endpoints. In some embodiments, the inter-ITR sequence consists of between 1 and 10 nucleotides, between 10 and 20 nucleotides, between 20 and 30 nucleotides, between 30 and 40 nucleotides, between 40 and 50 nucleotides, between 50 and 60 nucleotides, between 60 and 70 nucleotides, between 70 and 80 nucleotides, between 80 and 90 nucleotides, or between 90 and 100 nucleotides, each range inclusive of the endpoints.

[0485] In some embodiments of the nanotransposons of the disclosure, the selectable marker having between 1 and 200 nucleotides, inclusive of the endpoints, comprises a sequence encoding a sucrose-selectable marker. In some embodiments, the sequence encoding a sucrose-selectable marker comprises a sequence encoding an RNA-OUT sequence. In some embodiments, the sequence encoding an RNA-OUT sequence comprises or consists of 137 base pairs (bp). In some embodiments, the selectable marker having between 1 and 200 nucleotides, inclusive of the endpoints, comprises a sequence encoding a fluorescent marker. In some embodiments, the selectable marker having between 1 and 200 nucleotides, inclusive of the endpoints, comprises a sequence encoding a cell surface marker.

[0486] In some embodiments of the nanotransposons of the disclosure, the sequence encoding an origin of replication having between 1 and 450 nucleotides, inclusive of the endpoints, comprises a sequence encoding a mini origin of replication. In some embodiments, the sequence encoding an origin of replication having between 1 and 450 nucleotides, inclusive of the endpoints, comprises a sequence encoding an R6K origin of replication. In some embodiments, the R6K origin of replication comprises an R6K gamma origin of replication. In some embodiments, the R6K origin of replication comprises an R6K mini origin of replication. In some embodiments, the R6K origin of replication comprises an R6K gamma mini origin of replication. In some embodiments, the R6K gamma mini origin of replication comprises or consists of 281 base pairs (bp).

[0487] In some embodiments of the nanotransposons of the disclosure, the sequence encoding the backbone does not comprise a recombination site, an excision site, a ligation site or a combination thereof. In some embodiments, neither the nanotransposon nor the sequence encoding the backbone comprises a product of a recombination site, an excision site, a ligation site or a combination thereof. In some embodiments, neither the nanotransposon nor the sequence encoding the backbone is derived from a recombination site, an excision site, a ligation site or a combination thereof.

[0488] In some embodiments of the nanotransposons of the disclosure, a recombination site comprises a sequence resulting from a recombination event. In some embodiments, a recombination site comprises a sequence that is a product of a recombination event. In some embodiments, the recombination event comprises an activity of a recombinase (e.g., a recombinase site).

[0489] In some embodiments of the nanotransposons of the disclosure, the sequence encoding the backbone does not further comprise a sequence encoding foreign DNA.

[0490] In some embodiments of the nanotransposons of the disclosure, the inter-ITR sequence does not comprise a recombination site, an excision site, a ligation site or a combination thereof. In some embodiments, the inter-ITR sequence does not comprise a product of a recombination event, an excision event, a ligation event or a combination thereof. In some embodiments, the inter-ITR sequence is not derived from a recombination event, an excision event, a ligation event or a combination thereof.

[0491] In some embodiments of the nanotransposons of the disclosure, the inter-ITR sequence comprises a sequence encoding foreign DNA.

[0492] In some embodiments of the nanotransposons of the disclosure, the intra-ITR sequence comprises at least one sequence encoding an insulator and a sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell. In some embodiments, the mammalian cell is a human cell.

[0493] In some embodiments of the nanotransposons of the disclosure, the intra-ITR sequence comprises a first sequence encoding an insulator, a sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell and a second sequence encoding an insulator.

[0494] In some embodiments of the nanotransposons of the disclosure, the intra-ITR sequence comprises a first sequence encoding an insulator, a sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell, a polyadenosine (polyA) sequence and a second sequence encoding an insulator.

[0495] In some embodiments of the nanotransposons of the disclosure, the intra-ITR sequence comprises a first sequence encoding an insulator, a sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell, at least one exogenous sequence, a polyadenosine (polyA) sequence and a second sequence encoding an insulator.

[0496] In some embodiments of the nanotransposons of the disclosure, the sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell is capable of expressing an exogenous sequence in a human cell. In some embodiments, the sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell comprises a sequence encoding a constitutive promoter. In some embodiments, the

sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell comprises a sequence encoding an inducible promoter. In some embodiments, the intra-ITR sequence comprises a first sequence encoding a first promoter capable of expressing an exogenous sequence in a mammalian cell and a second sequence encoding a second promoter capable of expressing an exogenous sequence in mammalian cell, wherein the first promoter is a constitutive promoter, wherein the second promoter is an inducible promoter, and wherein the first sequence encoding the first promoter and the second sequence encoding the second promoter are oriented in opposite directions. In some embodiments, the sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell comprises a sequence encoding a cell-type or tissue-type specific promoter. In some embodiments, the sequence encoding a promoter capable of expressing an exogenous sequence in a mammalian cell comprises a sequence encoding an EF1a promoter, a sequence encoding a CMV promoter, a sequence encoding an MND promoter, a sequence encoding an SV40 promoter, a sequence encoding a PGK1 promoter, a sequence encoding a Ubc promoter, a sequence encoding a CAG promoter, a sequence encoding an H1 promoter, or a sequence encoding a U6 promoter.

[0497] In some embodiments of the nanotransposons of the disclosure, the polyadenosine (polyA) sequence is isolated or derived from a viral polyA sequence. In some embodiments, the polyadenosine (polyA) sequence is isolated or derived from an (SV40) polyA sequence.

[0498] In some embodiments of the nanotransposons of the disclosure, the at least one exogenous sequence comprises an inducible proapoptotic polypeptide. In some embodiments, the inducible caspase polypeptide comprises (a) a ligand binding region, (b) a linker, and (c) a caspase polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence. In some embodiments, the inducible caspase polypeptide comprises (a) a ligand binding region, (b) a linker, and (c) a truncated caspase 9 polypeptide, wherein the inducible proapoptotic polypeptide does not comprise a non-human sequence.

[0499] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide, the ligand binding region comprises a FK506 binding protein 12 (FKBP12) polypeptide. In some embodiments, the amino acid sequence of the ligand binding region comprises a FK506 binding protein 12 (FKBP12) polypeptide. In some embodiments, the

FK506 binding protein 12 (FKBP12) polypeptide comprises a modification at position 36 of the sequence. In some embodiments, the modification comprises a substitution of valine (V) for phenylalanine (F) at position 36 (F36V). In some embodiments, the FKBP12 polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 14635). In some embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 14636).

[0500] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide, the linker region is encoded by an amino acid comprising GGGGS (SEQ ID NO: 14637) or a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 14638). In some embodiments, the nucleic acid sequence encoding the linker does not comprise a restriction site.

[0501] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. In some embodiments, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In some embodiments, the truncated caspase 9 polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE

SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE
TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 14639). In some embodiments, the truncated caspase 9 polypeptide is encoded by a nucleic acid sequence comprising
GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT
TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT
TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA
AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT
GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG
AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT
CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG
AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA
AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG
TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG
CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG
CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT
CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT
TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA
ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT
GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 14640).

[0502] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising
GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI
RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS
GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR
RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG
AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE
SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE
TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID

NO: 14641). In some embodiments, the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising

ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg
ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag
gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg
ccacccagggatcattccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg
ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt
aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta
gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg
gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga
cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat
ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc
tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt
cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga
acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc
cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc (SEQ ID NO: 14642).

[0503] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide, the exogenous sequence further comprises a sequence encoding a selectable marker. In some embodiments, the sequence encoding the selectable marker comprises a sequence encoding a detectable marker. In some embodiments, the detectable marker comprises a fluorescent marker or a cell-surface marker. In some embodiments, the sequence encoding the selectable marker comprises a sequence encoding a protein that is active in dividing cells and not active in non-dividing cells. In some embodiments, the sequence encoding the selectable marker comprises a sequence encoding a metabolic marker. In some embodiments, the sequence encoding the selectable marker comprises a sequence encoding a dihydrofolate reductase (DHFR) mutein enzyme. In some embodiments, the DHFR mutein enzyme comprises or consists of the amino acid sequence of:

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  1 MVGSLNCIVA VSQNMGIGKN GDFPWPPLRN ESRYFQRMTT TSSVEGKQNL
 61 VIMGKKTWFS IPEKNRPLKG RINLVLSREL KEPPQGAHFL SRSLDDALKL
121 TEQPELANKV DMVWIVGGSS VYKEAMNHPG HLKLFVTRIM QDFESDTFFP
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181 EIDLEKYKLL PEYPGVLSDV QEEKGIKYKF EVYEKND (SEQ ID NO: 17012). In some embodiments, the DHFR mutein enzyme is encoded by a the nucleic acid sequence comprising or consisting of atggtcgggtctctgaattgtatcgtcgccgtgagtcagaacatgggcattgggaagaatggcgatttcccatggccacctctgcgcaa cgagtcccgatactttcagcggatgacaactacctcctctgtggaagggaaacagaatctggtcatcatgggaaagaaaacttggttca gcattccagagaagaaccggcccctgaaaggcagaatcaatctggtgctgtcccgagaactgaaggagccaccacagggagctca ctttctgagccggtccctggacgatgcactgaagctgacagaacagcctgagctggccaacaaagtcgatatggtgtggatcgtcgg gggaagttcagtgtataaggaggccatgaatcaccccggccatctgaaactgttcgtcacacggatcatgcaggactttgagagcgat actttctttcctgaaattgacctggagaagtacaaactgctgcccgaatatcctggcgtgctgtccgatgtccaggaagagaaaggcatc aaatacaagttcgaggtctatgagaagaatgac (SEQ ID NO: 17095). In some embodiments, the amino acid sequence of the DHFR mutein enzyme further comprises a mutation at one or more of positions 80, 113, or 153. In some embodiments, the amino acid sequence of the DHFR mutein enzyme comprises one or more of a substitution of a Phenylalanine (F) or a Leucine (L) at position 80, a substitution of a Leucine (L) or a Valine (V) at position 113, and a substitution of a Valine (V) or an Aspartic Acid (D) at position 153.

[0504] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide and/or the exogenous sequence comprises a sequence encoding a selectable marker, the exogenous sequence further comprises a sequence encoding a non-naturally occurring antigen receptor, and/or a sequence encoding a therapeutic polypeptide. In some embodiments, the non-naturally occurring antigen receptor comprises a T cell Receptor (TCR). In some embodiments, a sequence encoding the TCR comprises one or more of an insertion, a deletion, a substitution, an invertion, a transposition or a frameshift compared to a corresponding wild type sequence. In some embodiments, a sequence encoding the TCR comprises a chimeric or recombinant sequence. In some embodiments, the non-naturally occurring antigen receptor comprises a chimeric antigen receptor (CAR). In some embodiments, the CAR comprises: (a) an ectodomain comprising an antigen recognition region, (b) a transmembrane domain, and (c) an endodomain comprising at least one costimulatory domain. In some embodiments, the ectodomain of (a) of the CAR further comprises a signal peptide. In some embodiments, the ectodomain of (a) of the CAR further comprises a hinge between the antigen recognition region and the transmembrane domain. In

some embodiments, the endodomain comprises a human CD3ζ endodomain. In some embodiments, the at least one costimulatory domain comprises a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. In some embodiments, the at least one costimulatory domain comprises a human CD28 and/or a 4-1BB costimulatory domain. In some embodiments, the antigen recognition region comprises one or more of a scFv, a VHH, a VH, and a Centyrin.

[0505] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises an inducible proapoptotic polypeptide and/or the exogenous sequence comprises a sequence encoding a selectable marker, the exogenous sequence further comprises a sequence encoding a transposase.

[0506] In some embodiments of the nanotransposons of the disclosure, the intra-ITR sequence comprises a sequence encoding a selectable marker, an exogenous sequence, a sequence encoding an inducible caspase polypeptide, and at least one sequence encoding a self-cleaving peptide. In some embodiments, the at least one sequence encoding a self-cleaving peptide is positioned between one or more of: (a) the sequence encoding a selectable marker and the exogenous sequence, (b) the sequence encoding a selectable marker and the inducible caspase polypeptide, and (c) the exogenous sequence and the inducible caspase polypeptide. In some embodiments, a first sequence encoding a self-cleaving peptide is positioned between the sequence encoding a selectable marker and the exogenous sequence and a second sequence encoding a self-cleaving peptide is positioned between the exogenous sequence and the inducible caspase polypeptide.

[0507] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a piggyBac transposase or a piggyBac-like transposase. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a piggyBac transposase. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a piggyBac-like transposase. In some embodiments, the sequence

encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprise a TTAA, a TTAT or a TTAX recognition sequence. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprise a TTAA, a TTAT or a TTAX recognition sequence and a sequence having at least 50% identity to a sequence isolated or derived from a piggyBac transposase or a piggyBac-like transposase. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprise at least 2 nucleotides (nts), 3 nts, 4 nts, 5 nts, 6 nts, 7 nts, 8 nts, 9 nts, 10 nts, 11 nts, 12 nts, 13 nts, 14 nts, 15 nts, 16 nts, 17 nts, 18 nts, 19 nts, or 20 nts.

[0508] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a piggyBac transposase or a piggyBac-like transposase. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprises the sequence of CCCTAGAAAGATAGTCTGCGTAAAATTGACGCATG (SEQ ID NO: 17096) or a sequence having at least 70% identity to the sequence of CCCTAGAAAGATAGTCTGCGTAAAATTGACGCATG (SEQ ID NO: 17096). In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprises the sequence of CCCTAGAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG (SEQ ID NO: 17097). In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprises the sequence of CCCTAGAAAGATAGTCTGCGTAAAATTGACGCATG (SEQ ID NO: 17096) and comprises the sequence of CCCTAGAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG (SEQ ID NO: 17097). In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprises the sequence of CCCTAGAAAGATAGTCTGCGTAAAATTGACGCATG

(SEQ ID NO: 17096) and comprises the sequence of CCCTAGAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGTGTAAAATT GACGCATG (SEQ ID NO: 17098). In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) comprises the sequence of CCCTAGAAAGATAGTCTGCGTAAAATTGACGCATG (SEQ ID NO: 17096) and comprises the sequence of TTAACCCTAGAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGTGTAA AATTGACGCATGTGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAAT AGATATTAAGTTTTATTATATTTACACTTACATACTAATAATAAATTCAACAAAC AATTTATTTATGTTTATTTATTTATTAAAAAAAACAAAAACTCAAAATTTCTTCTA TAAAGTAACAAAACTTTTA (SEQ ID NO: 17099).

[0509] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a piggyBac transposase or a piggyBac-like transposase. In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) is recognized by a piggyBac transposase having an amino acid sequence of at least 20% identity to the amino acid sequence of

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID
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NO: 14487). In some embodiments, the sequence encoding a first inverted terminal repeat

(ITR) or the sequence encoding a second inverted terminal repeat (ITR) is recognized by a piggyBac transposase having the amino acid sequence of

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEI SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTGATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RMYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPNEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID
NO: 14487).
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In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) is recognized by a piggyBac transposase having an amino acid sequence of at least 20% identity to the amino acid sequence of

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO:
14484).
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In some embodiments, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) is recognized by a piggyBac transposase having the amino acid sequence of

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  1 MGSSLDDEHI LSALLQSDDE LVGEDSDSEV SDHVSEDDVQ SDTEEAFIDE VHEVQPTSSG
 61 SEILDEQNVI EQPGSSLASN RILTLPQRTI RGKNKHCWST SKSTRRSRVS ALNIVRSQRG
121 PTRMCRNIYD PLLCFKLFFT DEIISEIVKW TNAEISLKRR ESMTSATFRD TNEDEIYAFF
181 GILVMTAVRK DNHMSTDDLF DRSLSMVYVS VMSRDRFDFL IRCLRMDDKS IRPTLRENDV
241 FTPVRKIWDL FIHQCIQNYT PGAHLTIDEQ LLGFRGRCPF RVYIPNKPSK YGIKILMMCD
301 SGTKYMINGM PYLGRGTQTN GVPLGEYYVK ELSKPVHGSC RNITCDNWFT SIPLAKNLLQ
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361 EPYKLTIVGT VRSNKREIPE VLKNSRSRPV GTSMFCFDGP LTLVSYKPKP AKMVYLLSSC
421 DEDASINEST GKPQMVMYYN QTKGGVDTLD QMCSVMTCSR KTNRWPMALL YGMINIACIN
481 SFIIYSHNVS SKGEKVQSRK KFMRNLYMSL TSSFMRKRLE APTLKRYLRD NISNILPKEV
541 PGTSDDSTEE PVMKKRTYCT YCPSKIRRKA NASCKKCKKV ICREHNIDMC QSCF (SEQ ID NO: 14484).

[0510] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a Sleeping Beauty transposase. In some embodiments, the Sleeping Beauty transposase is a hyperactive Sleeping Beauty transposase (SB100X).

[0511] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a Helitron transposase.

[0512] In some embodiments of the nanotransposons of the disclosure, including those wherein the at least one exogenous sequence comprises one or more of an inducible proapoptotic polypeptide, a sequence encoding a selectable marker, and an exogenous sequence, the sequence encoding a first inverted terminal repeat (ITR) or the sequence encoding a second inverted terminal repeat (ITR) are recognized by a Tol2 transposase.

[0513] The disclosure provides a cell comprising a nanotransposon of the disclosure. In some embodiments, the cell further comprises a transposase composition. In some embodiments, the transposase composition comprises a transposase or a sequence encoding the transposase that is capable of recognizing the first ITR or the second ITR of the nanotransposon. In some embodiments, the transposase composition comprises a nanotransposon comprising the sequence encoding the transposase. In some embodiments, the cell comprises a first nanotransposon comprising an exogenous sequence and a second nanotransposon comprising a sequence encoding a transposase. In some embodiments, the cell is an allogeneic cell.

[0514] The disclosure provides a composition comprising the nanotransposon of the disclosure.

[0515] The disclosure provides a composition comprising the cell of the disclosure. In some embodiments, the cell comprises a nanotransposon of the disclosure. In some embodiments, the cell is not further modified. In some embodiments, the cell is allogeneic.

[0516] The disclosure provides a composition comprising the cell of the disclosure. In some embodiments, the cell comprises a nanotransposon of the disclosure. In some embodiments, the cell is not further modified. In some embodiments, the cell is autologous.

[0517] The disclosure provides a composition comprising a plurality of cells of the disclosure. In some embodiments, at least one cell of the plurality of cells comprises a nanotransposon of the disclosure. In some embodiments, a portion of the plurality of cells comprises a nanotransposon of the disclosure. In some embodiments, the portion comprises at least 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or any percentage in between of the plurality of cells. In some embodiments, each cell of the plurality of cells comprises a nanotransposon of the disclosure. In some embodiments, the plurality of cells does not comprise a modified cell of the disclosure. In some embodiments, at least one cell of the plurality of cells is not further modified. In some embodiments, none of the plurality of cells is not further modified. In some embodiments, plurality of cells is allogeneic. In some embodiments, an allogeneic plurality of cells are produced according to the methods of the disclosure. In some embodiments, plurality of cells is autologous. In some embodiments, an autologous plurality of cells are produced according to the methods of the disclosure.

[0518] The disclosure provides a modified cell comprising: (a) a nanotransposon of the disclosure; (b) a sequence encoding an inducible proapoptotic polypeptide; and wherein the cell is a T cell, (c) a modification of an endogenous sequence encoding a T cell Receptor (TCR), wherein the modification reduces or eliminates a level of expression or activity of the TCR. In some embodiments, the cell further comprises: (d) a non-naturally occurring sequence comprising an HLA class I histocompatibility antigen, alpha chain E (HLA-E), and (e) a modification of an endogenous sequence encoding Beta-2-Microglobulin (B2M), wherein the modification reduces or eliminates a level of expression or activity of a major histocompatibility complex (MHC) class I (MHC-I).

[0519] The disclosure provides a modified cell comprising: (a) a nanotransposon of the disclosure; (b) a sequence encoding an inducible proapoptotic polypeptide; (c) a non-naturally occurring sequence comprising an HLA class I histocompatibility antigen, alpha chain E (HLA-E), and (e) a modification of an endogenous sequence encoding Beta-2-Microglobulin (B2M), wherein the modification reduces or eliminates a level of expression or activity of a major histocompatibility complex (MHC) class I (MHC-I).

[0520] In some embodiments of the modified cells of the disclosure, the non-naturally occurring sequence comprising a HLA-E further comprises a sequence encoding a B2M signal peptide. In some embodiments, the non-naturally occurring sequence comprising an HLA-E further comprises a linker, wherein the linker is positioned between the sequence encoding the sequence encoding a B2M polypeptide and the sequence encoding the HLA-E. In some embodiments, the non-naturally occurring sequence comprising an HLA-E further comprises a sequence encoding a peptide and a sequence encoding a B2M polypeptide. In some embodiments, the non-naturally occurring sequence comprising an HLA-E further comprises a first linker positioned between the sequence encoding the B2M signal peptide and the sequence encoding the peptide, and a second linker positioned between the sequence encoding the B2M polypeptide and the sequence encoding the HLA-E.

[0521] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a mammalian cell.

[0522] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a human cell.

[0523] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a stem cell.

[0524] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a differentiated cell.

[0525] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a somatic cell.

[0526] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is an immune cell or an immune cell precursor. In some embodiments, the immune cell is a lymphoid progenitor cell, a natural killer (NK) cell, a cytokine induced killer (CIK) cell, a T lymphocyte (T cell), a B lymphocyte (B-cell) or an antigen presenting

cell (APC). In some embodiments, the immune cell is a T cell, an early memory T cell, a stem cell-like T cell, a stem memory T cell (Tscm), or a central memory T cell (Tcm). In some embodiments, the immune cell precursor is a hematopoietic stem cell (HSC). In some embodiments, the cell is an antigen presenting cell (APC).

[0527] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell further comprises a gene editing composition. In some embodiments, the gene editing composition comprises a sequence encoding a DNA binding domain and a sequence encoding a nuclease protein or a nuclease domain thereof. In some embodiments, the gene editing composition comprises a sequence encoding a nuclease protein or a sequence encoding a nuclease domain thereof. In some embodiments, the e sequence encoding a nuclease protein or the sequence encoding a nuclease domain thereof comprises a DNA sequence, an RNA sequence, or a combination thereof. In some embodiments, the nuclease or the nuclease domain thereof comprises one or more of a CRISPR/Cas protein, a Transcription Activator-Like Effector Nuclease (TALEN), a Zinc Finger Nuclease (ZFN), and an endonuclease. In some embodiments, the CRISPR/Cas protein comprises a nuclease-inactivated Cas (dCas) protein.

[0528] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell further comprises a gene editing composition. In some embodiments, the gene editing composition comprises a sequence encoding a DNA binding domain and a sequence encoding a nuclease protein or a nuclease domain thereof. In some embodiments, the nuclease or the nuclease domain thereof comprises a nuclease-inactivated Cas (dCas) protein and an endonuclease. In some embodiments, the endonuclease comprises a Clo051 nuclease or a nuclease domain thereof. In some embodiments, the gene editing composition comprises a fusion protein. In some embodiments, the fusion protein comprises a nuclease-inactivated Cas9 (dCas9) protein and a Clo051 nuclease or a Clo051 nuclease domain. In some embodiments, the gene editing composition further comprises a guide sequence. In some embodiments, the guide sequence comprises an RNA sequence. In some embodiments, the fusion protein comprises or consists of the amino acid sequence:

MAPKKKRKVEGIKSNISLLKDELRGQISHISHEYLSLIDLAFDSKQNRLFEMKVLELLVNEYGFKGRHLGGSRKP
DGIVYSTTLEDNFGIIVDTKAYSEGYSLPISQADEMERYVRENSNRDEEVNPNKWWENFSEEVKKYYFVFISGSF
KGKFEEQLRRLSMTTGVNGSAVNVVNLLLGAEKIRSGEMTIEELERAMFNNSEFILKYGGGGSDKKYSIGLAIGT

NSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSN
EMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK
FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLF
GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEIT
KAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFA
WMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPA
FLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE
DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGF
ANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEM
ARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDV
DAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDK
AGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAY
LNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLI
ETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT
VAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRM
LASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLD
KVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLS
QLGGDGSPKKKRKVSS (SEQ ID NO: 17013)or a nucleic acid comprising or consisting of the sequence:

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   1 atggcaccaa agaagaaaag aaaagtggag ggcatcaagt caaacatcag cctgctgaaa
  61 gacgaactgc ggggacagat tagtcacatc agtcacgagt acctgtcact gattgatctg
 121 gccttcgaca gcaagcagaa tagactgttt gagatgaaag tgctggaact gctggtcaac
 181 gagtatggct tcaagggcag acatctgggc gggtctagga aacctgacgg catcgtgtac
 241 agtaccacac tggaagacaa cttcggaatc attgtcgata ccaaggctta ttccgagggc
 301 tactctctgc caattagtca ggcagatgag atggaaaggt acgtgcgcga aaactcaaat
 361 agggacgagg aagtcaaccc caataagtgg tgggagaatt tcagcgagga agtgaagaaa
 421 tactacttcg tctttatctc aggcagcttc aaagggaagt ttgaggaaca gctgcggaga
 481 ctgtccatga ctaccggggt gaacggatct gctgtcaacg tggtcaatct gctgctgggc
 541 gcagaaaaga tcaggtccgg ggagatgaca attgaggaac tggaacgcgc catgttcaac
 601 aattctgagt ttatcctgaa gtatggaggc gggggaagcg ataagaaata ctccatcgga
 661 ctggccattg gcaccaattc cgtgggctgg gctgtcatca cagacgagta caaggtgcca
 721 agcaagaagt tcaaggtcct ggggaacacc gatcgccaca gtatcaagaa aaatctgatt
 781 ggagccctgc tgttcgactc aggcgagact gctgaagcaa cccgactgaa gcggactgct
 841 aggcgccgat atacccggag aaaaaatcgg atctgctacc tgcaggaaat tttcagcaac
 901 gagatggcca aggtggacga tagtttcttt caccgcctgg aggaatcatt cctggtggag
 961 gaagataaga aacacgagcg gcatcccatc tttggcaaca ttgtggacga agtcgcttat
1021 cacgagaagt accctactat ctatcatctg aggaagaaac tggtggactc caccgataag
1081 gcagacctgc gcctgatcta tctggccctg gctcacatga tcaagttccg ggggcatttt
1141 ctgatcgagg gagatctgaa ccctgacaat tctgatgtgg acaagctgtt catccagctg
1201 gtccagacat acaatcagct gtttgaggaa aacccaatta atgcctcagg cgtggacgca
1261 aaggccatcc tgagcgccag actgtccaaa tctaggcgcc tggaaaacct gatcgctcag
1321 ctgccaggag agaagaaaaa cggcctgttt gggaatctga ttgcactgtc cctgggcctg
1381 acacccaact tcaagtctaa ttttgatctg gccgaggacg ctaagctgca gctgtccaaa
1441 gacacttatg acgatgacct ggataacctg ctggctcaga tcggcgatca gtacgcagac
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1501 ctgttcctgg ccgctaagaa tctgagtgac gccatcctgc tgtcagatat tctgcgcgtg
1561 aacacagaga ttactaaggc cccactgagt gcttcaatga tcaaaagata tgacgagcac
1621 catcaggatc tgaccctgct gaaggctctg gtgaggcagc agctgcccga gaaatacaag
1681 gaaatcttct ttgatcagag caagaatgga tacgccggct atattgacgg cggggcttcc
1741 caggaggagt tctacaagtt catcaagccc attctggaaa agatggacgg caccgaggaa
1801 ctgctggtga agctgaatcg ggaggacctg ctgagaaaac agaggacatt tgataacgga
1861 agcatccctc accagattca tctgggcgaa ctgcacgcca tcctgcgacg gcaggaggac
1921 ttctacccat ttctgaagga taaccgcgag aaaatcgaaa agatcctgac cttcagaatc
1981 ccctactatg tggggcctct ggcacgggga aatagtagat ttgcctggat gacaagaaag
2041 tcagaggaaa ctatcacccc ctggaacttc gaggaagtgg tcgataaagg cgctagcgca
2101 cagtccttca ttgaaaggat gacaaatttt gacaagaacc tgccaaatga gaaggtgctg
2161 cccaaacaca gcctgctgta cgaatatttc acagtgtata acgagctgac taaagtgaag
2221 tacgtcaccg aagggatgcg caagcccgca ttcctgtccg gagagcagaa gaaagccatc
2281 gtggacctgc tgtttaagac aaatcggaaa gtgactgtca aacagctgaa ggaagactat
2341 ttcaagaaaa ttgagtgttt cgattcagtg gaaatcagcg gcgtcgagga caggtttaac
2401 gcctccctgg ggacctacca cgatctgctg aagatcatca aggataagga cttcctggac
2461 aacgaggaaa atgaggacat cctggaggac attgtgctga cactgactct gtttgaggat
2521 cgcgaaatga tcgaggaacg actgaagact tatgcccatc tgttcgatga caaagtgatg
2581 aagcagctga aaagaaggcg ctacaccgga tggggacgcc tgagccgaaa actgatcaat
2641 gggattagag acaagcagag cggaaaaact atcctggact ttctgaagtc cgatggcttc
2701 gccaacagga acttcatgca gctgattcac gatgactctc tgaccttcaa ggaggacatc
2761 cagaaagcac aggtgtctgg ccagggggac agtctgcacg agcatatcgc aaacctggcc
2821 ggcagccccg ccatcaagaa agggattctg cagaccgtga aggtggtgga cgaactggtc
2881 aaggtcatgg gacgacacaa acctgagaac atcgtgattg agatggcccg cgaaaatcag
2941 acaactcaga agggccagaa aaacagtcga gaacggatga agagaatcga ggaaggcatc
3001 aaggagctgg ggtcacagat cctgaaggag catcctgtgg aaaacactca gctgcagaat
3061 gagaaactgt atctgtacta tctgcagaat ggacgggata tgtacgtgga ccaggagctg
3121 gatattaaca gactgagtga ttatgacgtg gatgccatcg tccctcagag cttcctgaag
3181 gatgactcca ttgacaacaa ggtgctgacc aggtccgaca agaaccgcgg caaatcagat
3241 aatgtgccaa gcgaggaagt ggtcaagaaa atgaagaact actggaggca gctgctgaat
3301 gccaagctga tcacacagcg gaaatttgat aacctgacta aggcagaaag aggaggcctg
3361 tctgagctgg acaaggccgg cttcatcaag cggcagctgg tggagacaag acagatcact
3421 aagcacgtcg ctcagattct ggatagcaga atgaacacaa agtacgatga aaacgacaag
3481 ctgatcaggg aggtgaaagt cattactctg aaatccaagc tggtgtctga ctttagaaag
3541 gatttccagt tttataaagt cagggagatc aacaactacc accatgctca tgacgcatac
3601 ctgaacgcag tggtcgggac cgccctgatt aagaaatacc ccaagctgga gtccgagttc
3661 gtgtacggag actataaagt gtacgatgtc cggaagatga tcgccaaatc tgagcaggaa
3721 attggcaagg ccaccgctaa gtatttcttt tacagtaaca tcatgaattt ctttaagacc
3781 gaaatcacac tggcaaatgg ggagatcaga aaaaggcctc tgattgagac caacggggag
3841 acaggagaaa tcgtgtggga caagggaagg gattttgcta ccgtgcgcaa agtcctgtcc
3901 atgccccaag tgaatattgt caagaaaact gaagtgcaga ccgggggatt ctctaaggag
3961 agtattctgc ctaagcgaaa ctctgataaa ctgatcgccc ggaagaaaga ctgggacccc
4021 aagaagtatg gcgggttcga ctctccaaca gtggcttaca gtgtcctggt ggtcgcaaag
4081 gtggaaaagg ggaagtccaa gaaactgaag tctgtcaaag agctgctggg aatcactatt
4141 atggaacgca gctccttcga gaagaatcct atcgattttc tggaagccaa gggctataaa
4201 gaggtgaaga aagacctgat cattaagctg ccaaaatact cactgtttga gctggaaaac
4261 ggacgaaagc gaatgctggc aagcgccgga gaactgcaga agggcaatga gctggccctg
4321 ccctccaaat acgtgaactt cctgtatctg gctagccact acgagaaact gaaggggtcc
4381 cctgaggata acgaacagaa gcagctgttt gtggagcagc acaaacatta tctggacgag
4441 atcattgaac agatttcaga gttcagcaag agagtgatcc tggctgacgc aaatctggat
4501 aaagtcctga gcgcatacaa caagcaccga gacaaaccaa tccgggagca ggccgaaaat
4561 atcattcatc tgttcaccct gacaaacctg ggcgcccctg cagccttcaa gtattttgac
4621 accacaatcg atcggaagag atacacttct accaaagagg tgctggatgc taccctgatc
4681 caccagagta ttaccggcct gtatgagaca cgcatcgacc tgtcacagct gggaggcgat
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4741 gggagcccca agaaaaagcg gaaggtgtct agttaa (SEQ ID NO: 17014).In some embodiments, the fusion protein comprises or consists of the amino acid sequence:

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   1 MPKKKRKVEG IKSNISLLKD ELRGQISHIS HEYLSLIDLA FDSKQNRLFE MKVLELLVNE
  61 YGFKGRHLGG SRKPDGIVYS TTLEDNFGII VDTKAYSEGY SLPISQADEM ERYVRENSNR
 121 DEEVNPNKWW ENFSEEVKKY YFVFISGSFK GKFEEQLRRL SMTTGVNGSA VNVVNLLLGA
 181 EKIRSGEMTI EELERAMFNN SEFILKYGGG GSDKKYSIGL AIGTNSVGWA VITDEYKVPS
 241 KKFKVLGNTD RHSIKKNLIG ALLFDSGETA EATRLKRTAR RRYTRRKNRI CYLQEIFSNE
 301 MAKVDDSFFH 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 QDLTLLKALV RQQLPEKYKE IFFDQSKNGY AGYIDGGASQ EEFYKFIKPI LEKMDGTEEL
 601 LVKLNREDLL RKQRTFDNGS IPHQIHLGEL HAILRRQEDF YPFLKDNREK IEKILTFRIP
 661 YYVGPLARGN SRFAWMTRKS EETITPWNFE EVVDKGASAQ SFIERMTNFD KNLPNEKVLP
 721 KHSLLYEYFT VYNELTKVKY VTEGMRKPAF LSGEQKKAIV DLLFKTNRKV TVKQLKEDYF
 781 KKIECFDSVE ISGVEDRFNA SLGTYHDLLK IIKDKDFLDN EENEDILEDI VLTLTLFEDR
 841 EMIEERLKTY AHLFDDKVMK QLKRRRYTGW GRLSRKLING IRDKQSGKTI LDFLKSDGFA
 901 NRNFMQLIHD DSLTFKEDIQ KAQVSGQGDS LHEHIANLAG SPAIKKGILQ TVKVVDELVK
 961 VMGRHKPENI VIEMARENQT TQKGQKNSRE RMKRIEEGIK ELGSQILKEH PVENTQLQNE
1021 KLYLYYLQNG RDMYVDQELD INRLSDYDVD AIVPQSFLKD DSIDNKVLTR SDKNRGKSDN
1081 VPSEEVVKKM KNYWRQLLNA KLITQRKFDN LTKAERGGLS ELDKAGFIKR QLVETRQITK
1141 HVAQILDSRM NTKYDENDKL IREVKVITLK SKLVSDFRKD FQFYKVREIN NYHHAHDAYL
1201 NAVVGTALIK KYPKLESEFV YGDYKVYDVR KMIAKSEQEI GKATAKYFFY SNIMNFFKTE
1261 ITLANGEIRK RPLIETNGET GEIVWDKGRD FATVRKVLSM PQVNIVKKTE VQTGGFSKES
1321 ILPKRNSDKL IARKKDWDPK KYGGFDSPTV AYSVLVVAKV EKGKSKKLKS VKELLGITIM
1381 ERSSFEKNPI DFLEAKGYKE VKKDLIIKLP KYSLFELENG RKRMLASAGE LQKGNELALP
1441 SKYVNFLYLA SHYEKLKGSP EDNEQKQLFV EQHKHYLDEI IEQISEFSKR VILADANLDK
1501 VLSAYNKHRD KPIREQAENI IHLFTLTNLG APAAFKYFDT TIDRKRYTST KEVLDATLIH
1561 QSITGLYETR IDLSQLGGDG SPKKKRKV ((SEQ ID NO: 17058) or a nucleic acid
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comprising or consisting of the sequence:

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   1 atgcctaaga agaagcggaa ggtggaaggc atcaaaagca acatctccct cctgaaagac
  61 gaactccggg ggcagattag ccacattagt cacgaatacc tctccctcat cgacctggct
 121 ttcgatagca agcagaacag gctctttgag atgaaagtgc tggaactgct cgtcaatgag
 181 tacgggttca agggtcgaca cctcggcgga tctaggaaac cagacggcat cgtgtatagt
 241 accacactgg aagacaactt tgggatcatt gtggatacca aggcatactc tgagggttat
 301 agtctgccca tttcacaggc cgacgagatg gaacggtacg tgcgcgagaa ctcaaataga
 361 gatgaggaag tcaaccctaa caagtggtgg gagaacttct ctgaggaagt gaagaaatac
 421 tacttcgtct ttatcagcgg gtccttcaag ggtaaatttg aggaacagct caggagactg
 481 agcatgacta ccggcgtgaa tggcagcgcc gtcaacgtgg tcaatctgct cctgggcgct
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 541 gaaaagattc ggagcggaga gatgaccatc gaagagctgg agagggcaat gtttaataat
 601 agcgagttta tcctgaaata cggtggcggt ggatccgata aaaagtattc tattggttta
 661 gccatcggca ctaattccgt tggatgggct gtcataaccg atgaatacaa agtaccttca
 721 aagaaattta aggtgttggg gaacacagac cgtcattcga ttaaaaagaa tcttatcggt
 781 gcctcctat tcgatagtgg cgaaacggca gaggcgactc gcctgaaacg aaccgctcgg
 841 agaaggtata cacgtcgcaa gaaccgaata tgttacttac aagaaatttt tagcaatgag
 901 atggccaaag ttgacgattc tttctttcac cgtttggaag agtccttcct tgtcgaagag
 961 gacaagaaac atgaacggca ccccatcttt ggaaacatag tagatgaggt ggcatatcat
1021 gaaaagtacc caacgattta tcacctcaga aaaaagctag ttgactcaac tgataaagcg
1081 gacctgaggt taatctactt ggctcttgcc catatgataa agttccgtgg gcactttctc
1141 attgagggtg atctaaatcc ggacaactcg gatgtcgaca aactgttcat ccagttagta
1201 caaacctata atcagttgtt tgaagagaac cctataaatg caagtggcgt ggatgcgaag
1261 gctattctta gcgcccgcct ctctaaatcc cgacggctag aaaacctgat cgcacaatta
1321 cccggagaga agaaaaatgg gttgttcggt aaccttatag cgctctcact aggcctgaca
1381 ccaaatttta agtcgaactt cgacttagct gaagatgcca aattgcagct tagtaaggac
1441 acgtacgatg acgatctcga caatctactg gcacaaattg gagatcagta tgcggactta
1501 tttttggctg ccaaaaacct tagcgatgca atcctcctat ctgacatact gagagttaat
1561 actgagatta ccaaggcgcc gttatccgct tcaatgatca aaaggtacga tgaacatcac
1621 caagacttga cacttctcaa ggccctagtc cgtcagcaac tgcctgagaa atataaggaa
1681 atattctttg atcagtcgaa aaacgggtac gcaggttata ttgacggcgg agcgagtcaa
1741 gaggaattct acaagtttat caaacccata ttagagaaga tggatgggac ggaagagttg
1801 cttgtaaaac tcaatcgcga agatctactg cgaaagcagc ggactttcga caacggtagc
1861 attccacatc aaatccactt aggcgaattg catgctatac ttagaaggca ggaggatttt
1921 tatccgttcc tcaaagacaa tcgtgaaaag attgagaaaa tcctaacctt tcgcatacct
1981 tactatgtgg gacccctggc ccgagggaac tctcggttcg catggatgac aagaaagtcc
2041 gaagaaacga ttactccatg gaattttgag gaagttgtcg ataaaggtgc gtcagctcaa
2101 tcgttcatcg agaggatgac caactttgac aagaatttac cgaacgaaaa agtattgcct
2161 aagcacagtt tactttacga gtatttcaca gtgtacaatg aactcacgaa agttaagtat
2221 gtcactgagg gcatgcgtaa acccgccttt ctaagcggag aacagaagaa agcaatagta
2281 gatctgttat tcaagaccaa ccgcaaagtg acagttaagc aattgaaaga ggactacttt
2341 aagaaaattg aatgcttcga ttctgtcgag atctccgggg tagaagatcg atttaatgcg
2401 tcacttggta cgtatcatga cctcctaaag ataattaaag ataaggactt cctggataac
2461 gaagagaatg aagatatctt agaagatata gtgttgactc ttaccctctt tgaagatcgg
2521 gaaatgattg aggaaagact aaaaacatac gctcacctgt tcgacgataa ggttatgaaa
2581 cagttaaaga ggcgtcgcta tacgggctgg ggacgattgt cgcggaaact tatcaacggg
2641 ataagagaca agcaaagtgg taaaactatt ctcgattttc taaagagcga cggcttcgcc
2701 aataggaact ttatgcagct gatccatgat gactctttaa ccttcaaaga ggatatacaa
2761 aaggcacagg tttccggaca aggggactca ttgcacgaac atattgcgaa tcttgctggt
2821 tcgccagcca tcaaaaaggg catactccag acagtcaaag tagtggatga gctagttaag
2881 gtcatgggac gtcacaaacc ggaaaacatt gtaatcgaga tggcacgcga aaatcaaacg
2941 actcagaagg ggcaaaaaaa cagtcgagag cggatgaaga gaatagaaga gggtattaaa
3001 gaactgggca gccagatctt aaaggagcat cctgtggaaa atacccaatt gcagaacgag
3061 aaactttacc tctattacct acaaaatgga agggacatgt atgttgatca ggaactggac
3121 ataaaccgtt tatctgatta cgacgtcgat gccattgtac cccaatcctt tttgaaggac
3181 gattcaatcg acaataaagt gcttacacgc tcggataaga accgagggaa aagtgacaat
3241 gttccaagcg aggaagtcgt aaagaaaatg aagaactatt ggcggcagct cctaaatgcg
3301 aaactgataa cgcaaagaaa gttcgataac ttaactaaag ctgagagggg tggcttgtct
3361 gaacttgaca aggccggatt tattaaacgt cagctcgtgg aaacccgcca aatcacaaag
3421 catgttgcac agatactaga ttcccgaatg aatacgaaat acgacgagaa cgataagctg
3481 attcgggaag tcaaagtaat cactttaaag tcaaaattgg tgtcggactt cagaaaggat
3541 tttcaattct ataaagttag ggagataaat aactaccacc atgcgcacga cgcttatctt
3601 aatgccgtcg tagggaccgc actcattaag aaatacccga agctagaaag tgagtttgtg
3661 tatggtgatt acaaagttta tgacgtccgt aagatgatcg cgaaaagcga acaggagata
3721 ggcaaggcta cagccaaata cttcttttat tctaacatta tgaatttctt taagacggaa
3781 atcactctgg caaacggaga gatacgcaaa cgacctttaa ttgaaaccaa tggggagaca
3841 ggtgaaatcg tatgggataa gggccgggac ttcgcgacgg tgagaaaagt tttgtccatg
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3901 ccccaagtca acatagtaaa gaaaactgag gtgcagaccg gagggttttc aaaggaatcg
3961 attcttccaa aaaggaatag tgataagctc atcgctcgta aaaaggactg ggacccgaaa
4021 aagtacggtg gcttcgatag ccctacagtt gcctattctg tcctagtagt ggcaaaagtt
4081 gagaagggaa aatccaagaa actgaagtca gtcaaagaat tattggggat aacgattatg
4141 gagcgctcgt cttttgaaaa gaaccccatc gacttccttg aggcgaaagg ttacaaggaa
4201 gtaaaaaagg atctcataat taaactacca aagtatagtc tgtttgagtt agaaaatggc
4261 cgaaaacgga tgttggctag cgccggagag cttcaaaagg ggaacgaact cgcactaccg
4321 tctaaatacg tgaatttcct gtatttagcg tcccattacg agaagttgaa aggttcacct
4381 gaagataacg aacagaagca acttttttgtt gagcagcaca aacattatct cgacgaaatc
4441 atagagcaaa tttcggaatt cagtaagaga gtcatcctag ctgatgccaa tctggacaaa
4501 gtattaagcg catacaacaa gcacagggat aaacccatac gtgagcaggc ggaaaatatt
4561 atccatttgt ttactcttac caacctcggc gctccagccg cattcaagta ttttgacaca
4621 acgatagatc gcaaacgata cacttctacc aaggaggtgc tagacgcgac actgattcac
4681 caatccatca cgggattata tgaaactcgg atagatttgt cacagcttgg gggtgacgga
4741 tcccccaaga agaagaggaa agtctga (SEQ ID NO: 17059).
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[0529] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, a nanotransposon comprises the gene editing composition comprising a guide sequence and a sequence encoding a fusion protein comprising a sequence encoding an inactivated Cas9 (dCas9) and a sequence encoding a Clo051 nuclease or a nuclease domain thereof.

[0530] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell expresses the gene editing composition transiently.

[0531] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the cell is a T cell and the guide RNA comprises a sequence complementary to a target sequence encoding an endogenous TCR. In some embodiments, the guide RNA comprises a sequence complementary to a target sequence encoding a B2M polypeptide.

[0532] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the guide RNA comprises a sequence complementary to a target sequence within a safe harbor site of a genomic DNA sequence.

[0533] In some embodiments of the cells, unmodified cells and modified cells of the disclosure, the Clo051 nuclease or a nuclease domain thereof induces a single or double strand break in a target sequence. In some embodiments, a donor sequence, a donor plasmid, or a donor nanotransposon intra-ITR sequence integrated at a position of single or double strand break and/or at a position of cellular repair within a target sequence.

[0534] The disclosure provides a composition comprising a modified cell according to the disclosure. In some embodiments, the composition further comprises a pharmaceutically-acceptable carrier.

[0535] The disclosure provides a composition comprising a plurality of modified cells according to the disclosure. In some embodiments, the composition further comprises a pharmaceutically-acceptable carrier.

[0536] The disclosure provides a composition of the disclosure for use in the treatment of a disease or disorder.

[0537] The disclosure provides the use of a composition of the disclosure for the treatment of a disease or disorder.

[0538] The disclosure provides a method of treating a disease or disorder comprising administering to a subject in need thereof a therapeutically-effective amount of a composition of the disclosure. In some embodiments, the subject does not develop graft vs. host (GvH) and/or host vs. graft (HvG) following administration of the composition. In some embodiments, the administration is systemic. In some embodiments, the composition is administered by an intravenous route. In some embodiments, the composition is administered by an intravenous injection or an intravenous infusion.

[0539] The disclosure provides a method of treating a disease or disorder comprising administering to a subject in need thereof a therapeutically-effective amount of a composition of the disclosure. In some embodiments, the subject does not develop graft vs. host (GvH) and/or host vs. graft (HvG) following administration of the composition. In some embodiments, the administration is local. In some embodiments, the composition is administered by an intra-tumoral route, an intraspinal route, an intracerebroventricular route, an intraocular route or an intraosseous route. In some embodiments, the composition is administered by an intra-tumoral injection or infusion, an intraspinal injection or infusion, an intracerebroventricular injection or infusion, an intraocular injection or infusion or an intraosseous injection or infusion.

[0540] In some embodiments of the methods of treating a disease or disorder of the disclosure, the therapeutically effective dose is a single dose and wherein the allogeneic cells of the composition engraft and/or persist for a sufficient time to treat the disease or disorder. In some embodiments, the single dose is one of at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of doses in between that are manufactured simultaneously.

[0541] In some embodiments of the methods of treating a disease or disorder of the disclosure, the therapeutically effective dose is a single dose and wherein the autologous cells of the composition engraft and/or persist for a sufficient time to treat the disease or disorder. In some embodiments, the single dose is one of at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of doses in between that are manufactured simultaneously.

Vectors and Host Cells

[0542] 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 Centyrin or CARTyrin 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.

[0543] For example, the PB-EF1a vector may be used. The vector comprises the following nucleotide sequence:

tgtacatagattaaccctagaaagataatcatattgtgacgtacgttaaagataatcatgcgtaaaattgacgcatgtgttttatcggtctgt
atatcgaggtttatttattaatttgaatagatattaagttttattatatttacacttacatactaataataaattcaacaaacaatttatttatgtttatt
tatttattaaaaaaaaacaaaaactcaaaatttcttctataaagtaacaaaacttttatcgaatacctgcagcccgggggatgcagaggga
cagccccccccccaaagccccccagggatgtaattacgtccctcccccgctaggggggcagcagcgagccgcccgggggctccgctcc
ggtccggcgctcccccccgcatccccgagccggcagcgtgcggggacagcccgggcacggggaaggtggcacgggatcgctttc
ctctgaacgcttctcgctgctctttgagcctgcagacacctgggggggatacggggaaaagttgactgtgcctttcgatcgaaccatgga
cagttagctttgcaaagatggataaagttttaaacagagaggaatctttgcagctaatggaccttctaggtcttgaaaggagtgggaattg
gctccggtgcccgtcagtgggcagagcgcacatcgcccacagtccccgagaagttgggggggaggggtcggcaattgaaccggtg
cctagagaaggtggcgcggggtaaactgggaaagtgatgtcgtgtactggctccgccttttcccgagggtgggggagaaccgtata
taagtgcagtagtcgccgtgaacgttcttttcgcaacgggtttgccgccagaacacaggtaagtgccgtgtgtggttcccgcgggcct
ggcctctttacgggttatggcccttgcgtgccttgaattacttccacctggctgcagtacgtgattcttgatcccgagcttcgggttggaag
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cgtcccagcgcacatgttcggcgaggcggggcctgcgagcgcggccaccgagaatcggacgggggtagtctcaagctggccggc
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acacaaaggaaaagggcctttccgtcctcagccgtcgcttcatgtgactccacggagtaccgggcgccgtccaggcacctcgattagt
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ttaggccagcttggcacttgatgtaattctccttggaatttgccctttttgagtttggatcttggttcattctcaagcctcagacagtggttcaa
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gcttgtcctgcaggagggtcgacgcctctagacgggcggccgctccggatccacgggtaccgatcacatatgcctttaattaaacact
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catgcgcttggcgtaatcatggtcatagctgtttcctgttttccccgtatccccccaggtgtctgcaggctcaaagagcagcgagaagcg
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gcgtcattttgactcacgcggtcgttatagttcaaaatcagtgacacttaccgcattgacaagcacgcctcacgggagctccaagcggc
gactgagatgtcctaaatgcacagcgacggattcgcgctatttagaaagagagagcaatatttcaagaatgcatgcgtcaattttacgca
gactatctttctagggttaatctagctagccttaagggcgcctattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgc
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gctcggtcgttcggctgcggcgagcggtatcagctcactcaaaggcggtaatacggttatccacagaatcaggggataacgcaggaa
agaacatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatccttt
ttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttc
cgaaggtaactggcttcagcagagcgcagataccaaatactgttcttctagtgtagccgtagttaggccaccacttcaagaactctgtag
caccgcctacatacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagac
gatagttaccggataaggcgcagcggtcgggctgaacgggggttcgtgcacacagcccagcttggagcgaacgacctacaccga
actgagatacctacagcgtgagctatgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagg
gtcggaacaggagagcgcacgagggagcttccagggggaaacgcctggtatctttatagtcctgtcgggtttcgccacctctgacttg
agcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgct
ggccttttgctcacatgagattatcaaaaaggatcttcacctagatcctttaaattaaaaatgaagttttaaatcaatctaaagtatatatga
gtaaacttggtctgacagtcagaagaactcgtcaagaaggcgatagaaggcgatgcgctgcgaatcgggagcggcgataccgtaaa
gcacgaggaagcggtcagcccattcgccgccaagctcttcagcaatatcacgggtagccaacgctatgtcctgatagcggtccgcca
cacccagccggccacagtcgatgaatccagaaaagcggccattttccaccatgatattcggcaagcaggcatcgccatgggtcacga
cgagatcctcgccgtcgggcatgctcgccttgagcctggcgaacagttcggctggcgcgagcccctgatgctcttcgtccagatcatc

ctgatcgacaagaccggcttccatccgagtacgtgctcgctcgatgcgatgtttcgcttggtggtcgaatgggcaggtagccggatca agcgtatgcagccgccgcattgcatcagccatgatggatactttctcggcaggagcaaggtgagatgacaggagatcctgccccggc acttcgcccaatagcagccagtcccttcccgcttcagtgacaacgtcgagcacagctgcgcaaggaacgcccgtcgtggccagcca cgatagccgcgctgcctcgtcttgcagttcattcagggcaccggacaggtcggtcttgacaaaaagaaccgggcgcccctgcgctga cagccggaacacggcggcatcagagcagccgattgtctgttgtgcccagtcatagccgaatagcctctccacccaagcggccggag aacctgcgtgcaatccatcttgttcaatcataatattattgaagcatttatcagggttcgtctcgtcccggtctcctcccaatgcatgtcaata ttggccattagccatattattcattggttatatagcataaatcaatattggctattggccattgcatacgttgtatctatatcataata (SEQ ID NO: 18051)

[0544] The polynucleotides can optionally be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid 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.

[0545] 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.

[0546] 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 (*hygB* 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.

[0547] 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).

[0548] 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, TYMS, FRANCF, RAD51C, GCS, MDR1, ALDH1, NKX2.2, or any combination thereof.

[0549] At least one Centyrin or CARTyrin 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 additional amino acids, particularly charged amino acids, can be added to the N-terminus of a CARTyrin to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties can be added to a CARTyrin of the disclosure to facilitate purification. Such regions can be removed prior to final preparation of a CARTyrin or at least one fragment thereof. Such methods are described in many standard laboratory manuals, such as Sambrook, supra, Chapters 17.29-17.42 and 18.1-18.74; Ausubel, supra, Chapters 16, 17 and 18.

[0550] 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 Centyrin or CARTyrin 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, and 5,733,761, entirely incorporated herein by reference.

[0551] Illustrative of cell cultures useful for the production of the CARTyrins, 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), 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 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.

[0552] 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 (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.

[0553] When eukaryotic host cells are employed, polyadenlyation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenlyation 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.

Purification of a CARTyrin

[0554] A Centyrin or CARTyrin can be recovered and purified from recombinant cell cultures by well-known methods including, but not limited to, protein A purification, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. High performance liquid chromatography ("HPLC") can also be employed for purification. See, e.g., Colligan, Current Protocols in Immunology, or Current Protocols in Protein Science, John Wiley & Sons, NY, N.Y., (1997-2001), e.g., Chapters 1, 4, 6, 8, 9, 10, each entirely incorporated herein by reference.

[0555] Centyrins or CARTyrins of the disclosure include purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, E. coli, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the CARTyrin of the disclosure can be glycosylated or can be non-glycosylated. Such methods are described in many standard laboratory manuals, such as Sambrook, supra, Sections 17.37-17.42; Ausubel, supra, Chapters 10, 12, 13, 16, 18 and 20, Colligan, Protein Science, supra, Chapters 12-14, all entirely incorporated herein by reference.

Amino Acid Codes

[0556] The amino acids that make up CARtyrins 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 CARTyrin of the disclosure can include one or more amino acid substitutions, deletions or additions, from spontaneous or mutations and/or human manipulation, as specified herein. Amino acids in a CARTyrin 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 CARTyrin 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)).

[0557] As those of skill will appreciate, the invention includes at least one biologically active CARTyrin of the disclosure. Biologically active CARTyrins 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 CARTyrin. Methods of assaying and quantifying measures of enzymatic activity and substrate specificity are well known to those of skill in the art.

[0558] In another aspect, the disclosure relates to Centyrins and fragments, as described herein, which are modified by the covalent attachment of an organic moiety. Such modification can produce a CARTyrin 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 (PPG)), carbohydrate polymer, amino acid polymer or polyvinyl pyrolidone, and the fatty acid or fatty acid ester group can comprise from about eight to about forty carbon atoms.

[0559] The modified CARTyrin and fragments of the disclosure can comprise one or more organic moieties that are covalently bonded, directly or indirectly, to the antibody. Each organic moiety that is bonded to a CARTyrin or fragment thereof of the disclosure can

independently be a hydrophilic polymeric group, a fatty acid group or a fatty acid ester group. As used herein, the term "fatty acid" encompasses mono-carboxylic acids and di-carboxylic acids. A "hydrophilic polymeric group," as the term is used herein, refers to an organic polymer that is more soluble in water than in octane. For example, polylysine is more soluble in water than in octane. Thus, a Centyrin or CARTyrin modified by the covalent attachment of polylysine is encompassed by the disclosure. Hydrophilic polymers suitable for modifying Centyrins or CARTyrins of the disclosure can be linear or branched and include, for example, polyalkane glycols (e.g., PEG, monomethoxy-polyethylene glycol (mPEG), PPG and the like), carbohydrates (e.g., dextran, cellulose, oligosaccharides, polysaccharides and the like), polymers of hydrophilic amino acids (e.g., polylysine, polyarginine, polyaspartate and the like), polyalkane oxides (e.g., polyethylene oxide, polypropylene oxide and the like) and polyvinyl pyrolidone. Preferably, the hydrophilic polymer that modifies the CARTyrin of the disclosure has a molecular weight of about 800 to about 150,000 Daltons as a separate molecular entity. For example, PEG5000 and PEG 20,000, wherein the subscript is the average molecular weight of the polymer in Daltons, can be used. The hydrophilic polymeric group can be substituted with one to about six alkyl, fatty acid or fatty acid ester groups. Hydrophilic polymers that are substituted with a fatty acid or fatty acid ester group can be prepared by employing suitable methods. For example, a polymer comprising an amine group can be coupled to a carboxylate of the fatty acid or fatty acid ester, and an activated carboxylate (e.g., activated with N,N-carbonyl diimidazole) on a fatty acid or fatty acid ester can be coupled to a hydroxyl group on a polymer.

[0560] Fatty acids and fatty acid esters suitable for modifying CARTyrins of the disclosure can be saturated or can contain one or more units of unsaturation. Fatty acids that are suitable for modifying CARtyrins of the disclosure include, for example, n-dodecanoate (C12, laurate), n-tetradecanoate (C14, myristate), n-octadecanoate (C18, stearate), n-eicosanoate (C20, arachidate), n-docosanoate (C22, behenate), n-triacontanoate (C30), n-tetracontanoate (C40), cis-Δ9-octadecanoate (C18, oleate), all cis-Δ5,8,11,14-eicosatetraenoate (C20, arachidonate), octanedioic acid, tetradecanedioic acid, octadecanedioic acid, docosanedioic acid, and the like. Suitable fatty acid esters include mono-esters of dicarboxylic acids that comprise a linear or branched lower alkyl group. The lower alkyl group can comprise from one to about twelve, preferably, one to about six, carbon atoms.

[0561] The modified CARTyrins and fragments can be prepared using suitable methods, such as by reaction with one or more modifying agents. A "modifying agent" as the term is used herein, refers to a suitable organic group (e.g., hydrophilic polymer, a fatty acid, a fatty acid ester) that comprises an activating group. An "activating group" is a chemical moiety or functional group that can, under appropriate conditions, react with a second chemical group thereby forming a covalent bond between the modifying agent and the second chemical group. For example, amine-reactive activating groups include electrophilic groups, such as tosylate, mesylate, halo (chloro, bromo, fluoro, iodo), N-hydroxysuccinimidyl esters (NHS), and the like. Activating groups that can react with thiols include, for example, maleimide, iodoacetyl, acrylolyl, pyridyl disulfides, 5-thiol-2-nitrobenzoic acid thiol (TNB-thiol), and the like. An aldehyde functional group can be coupled to amine- or hydrazide-containing molecules, and an azide group can react with a trivalent phosphorous group to form phosphoramidate or phosphorimide linkages. Suitable methods to introduce activating groups into molecules are known in the art (see for example, Hermanson, G. T., Bioconjugate Techniques, Academic Press: San Diego, Calif. (1996)). An activating group can be bonded directly to the organic group (e.g., hydrophilic polymer, fatty acid, fatty acid ester), or through a linker moiety, for example, a divalent C1-C12 group wherein one or more carbon atoms can be replaced by a heteroatom, such as oxygen, nitrogen or sulfur. Suitable linker moieties include, for example, tetraethylene glycol, —(CH2)3—, —NH—(CH2)6—NH—, —(CH2)2—NH— and —CH2—O—CH2—CH2—O—CH2—CH2—O—CH—NH—. Modifying agents that comprise a linker moiety can be produced, for example, by reacting a mono-Boc-alkyldiamine (e.g., mono-Boc-ethylenediamine, mono-Boc-diaminohexane) with a fatty acid in the presence of 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC) to form an amide bond between the free amine and the fatty acid carboxylate. The Boc protecting group can be removed from the product by treatment with trifluoroacetic acid (TFA) to expose a primary amine that can be coupled to another carboxylate, as described, or can be reacted with maleic anhydride and the resulting product cyclized to produce an activated maleimido derivative of the fatty acid. (See, for example, Thompson, et al., WO 92/16221, the entire teachings of which are incorporated herein by reference.)

[0562] The modified CARTyrins and fragments of the disclosure can be produced by reacting CARTyrin proteins or fragments with a modifying agent. For example, the organic

moieties can be bonded to the CARTyrin protein in a non-site specific manner by employing an amine-reactive modifying agent, for example, an NHS ester of PEG. Modified CARTyrin proteins and fragments comprising an organic moiety that is bonded to specific sites of a CARTyrin of the disclosure can be prepared using suitable methods, such as reverse proteolysis (Fisch et al., Bioconjugate Chem., 3:147-153 (1992); Werlen et al., Bioconjugate Chem., 5:411-417 (1994); Kumaran et al., Protein Sci. 6(10):2233-2241 (1997); Itoh et al., Bioorg. Chem., 24(1): 59-68 (1996); Capellas et al., Biotechnol. Bioeng., 56(4):456-463 (1997)), and the methods described in Hermanson, G. T., Bioconjugate Techniques, Academic Press: San Diego, Calif. (1996).

CARTyrin Compositions Comprising Further Therapeutically Active Ingredients

[0563] Centyrin or CARTyrin compounds, compositions or combinations of the present disclosure can further comprise at least one of any suitable auxiliary, such as, but not limited to, diluent, binder, stabilizer, buffers, salts, lipophilic solvents, preservative, adjuvant or the like. Pharmaceutically acceptable auxiliaries are preferred. Non-limiting examples of, and methods of preparing such sterile solutions are well known in the art, such as, but limited to, Gennaro, Ed., Remington's Pharmaceutical Sciences, 18th Edition, Mack Publishing Co. (Easton, Pa.) 1990. Pharmaceutically acceptable carriers can be routinely selected that are suitable for the mode of administration, solubility and/or stability of the Centyrin or CARTyrin, fragment or variant composition as well known in the art or as described herein.

[0564] Pharmaceutical excipients and additives useful in the present composition include, but are not limited to, proteins, peptides, amino acids, lipids, and carbohydrates (e.g., sugars, including monosaccharides, di-, tri-, tetra-, and oligosaccharides; derivatized sugars, such as alditols, aldonic acids, esterified sugars and the like; and polysaccharides or sugar polymers), which can be present singly or in combination, comprising alone or in combination 1-99.99% by weight or volume. Exemplary protein excipients include serum albumin, such as human serum albumin (HSA), recombinant human albumin (rHA), gelatin, casein, and the like. Representative amino acid/protein components, which can also function in a buffering capacity, include alanine, glycine, arginine, betaine, histidine, glutamic acid, aspartic acid, cysteine, lysine, leucine, isoleucine, valine, methionine, phenylalanine, aspartame, and the like. One preferred amino acid is glycine.

[0565] Carbohydrate excipients suitable for use in the invention include, for example, monosaccharides, such as fructose, maltose, galactose, glucose, D-mannose, sorbose, and the like; disaccharides, such as lactose, sucrose, trehalose, cellobiose, and the like; polysaccharides, such as raffinose, melezitose, maltodextrins, dextrans, starches, and the like; and alditols, such as mannitol, xylitol, maltitol, lactitol, xylitol sorbitol (glucitol), myoinositol and the like. Preferred carbohydrate excipients for use in the present invention are mannitol, trehalose, and raffinose.

[0566] CARTyrin compositions can also include a buffer or a pH-adjusting agent; typically, the buffer is a salt prepared from an organic acid or base. Representative buffers include organic acid salts, such as salts of citric acid, ascorbic acid, gluconic acid, carbonic acid, tartaric acid, succinic acid, acetic acid, or phthalic acid; Tris, tromethamine hydrochloride, or phosphate buffers. Preferred buffers for use in the present compositions are organic acid salts, such as citrate.

[0567] Additionally, CARTyrin compositions of the invention can include polymeric excipients/additives, such as polyvinylpyrrolidones, ficolls (a polymeric sugar), dextrates (e.g., cyclodextrins, such as 2-hydroxypropyl-β-cyclodextrin), polyethylene glycols, flavoring agents, antimicrobial agents, sweeteners, antioxidants, antistatic agents, surfactants (e.g., polysorbates, such as "TWEEN 20" and "TWEEN 80"), lipids (e.g., phospholipids, fatty acids), steroids (e.g., cholesterol), and chelating agents (e.g., EDTA).

[0568] These and additional known pharmaceutical excipients and/or additives suitable for use in the Centyrin or CARTyrin, portion or variant compositions according to the invention are known in the art, e.g., as listed in "Remington: The Science & Practice of Pharmacy", 19th ed., Williams & Williams, (1995), and in the "Physician's Desk Reference", 52nd ed., Medical Economics, Montvale, N.J. (1998), the disclosures of which are entirely incorporated herein by reference. Preferred carrier or excipient materials are carbohydrates (e.g., saccharides and alditols) and buffers (e.g., citrate) or polymeric agents. An exemplary carrier molecule is the mucopolysaccharide, hyaluronic acid, which may be useful for intraarticular delivery.

T Cell Isolation from a Leukapheresis Product

[0569] 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.

[0570] Alternatively, white blood cells (WBC)/Peripheral Blood 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 be significantly lower when isolated from whole blood than when isolated by leukapheresis.

[0571] Either the leukapheresis procedure and/or the direct cell isolation procedure may be used for any subject of the disclosure.

[0572] 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 of 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.

[0573] The cell concentration leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should not exceed $0.2x10^9$ cells per mL during transportation. Intense mixing of the leukapheresis product, blood, WBC/PBMC composition and/or T-cell composition should be avoided.

[0574] 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 $0.2x10^9$ cell per mL.

[0575] 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 $0.2x10^9$ cell per mL, the product should be diluted with autologous plasma.

[0576] 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).

[0577] 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).

[0578] 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).

[0579] 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 CARTyrin+ cells that is mediated via CARTyrin 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 CARTyrin+ 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.

[0580] 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).

[0581] 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.

[0582] 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.

[0583] 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

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.

[0584] The particular ratio at which CD4+ T cells and CD8+ T 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%:60% 75%:25% and 25%:75%.

[0585] 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 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 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.

[0586] 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.

[0587] 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 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.

[0588] T cell compositions and T cell product compositions may be prepared for cryopreservation, storage in standard T Cell Culture Medium, and/or genetic modification.

[0589] 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 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 Cryopreservation Medium) reduce freezing-related toxicity.

[0590] 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 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 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.

[0591] 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 form 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.

[0592] 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 OpTimizer T Cell Expansion SFM, TexMACS Medium, PRIME-XV T Cell Expansion Medium, ImmunoCult-XF T Cell Expansion Medium, or any combination thereof.

[0593] 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

[0594] 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.

[0595] Nucleofection and/or electroporation may be accomplished using, for example, Lonza Amaxa, MaxCyte PulseAgile, Harvard Apparatus BTX, and/or Invitrogen Neon. Non-metal electrode systems, including, but not limited to, plastic polymer electrodes, may be preferred for nucleofection.

[0596] 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. 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, 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.

[0597] 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, 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 comprised 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.

[0598] 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 CARTyrin, an anti-PSMA CARTyrin, a Centyrin, a PSMA-specific Centryin, a hinge, a transmembrane domain, a costimulatory domain, a chimeric antigen receptor (CAR), a chimeric T-cell

receptor (CAR-T, a CARTyrin or an anti-PSMA CARTyrin), 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 mutein or any combination thereof.

[0599] Transposons of the disclosure may be prepared in water, TAE, TBE, PBS, HBSS, media, a supplemental factor of the disclosure or any combination thereof.

[0600] 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.

[0601] Transposase enzymes of the disclosure may be encoded by one or more sequences of plasmid DNA, mRNA, protein, protein-nucleic acid combination or any combination thereof.

[0602] 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.

[0603] Transposons and transposase enzymes of the disclosure may be delivered to a cell by any means.

[0604] 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), the use of a plasmid 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.

[0605] 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.

[0606] 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.

[0607] 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-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, Manitol, Sodium succinate, Sodium Chloride, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, 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.

[0608] 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.

[0609] 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 may be kept still, or, alternatively, they may be perturbed (e.g. rocked, swirled, or shaken).

[0610] Post-nucleofection cell cultures may comprise genetically-modified cells. Post-nucleofection T cell cultures may 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.

[0611] 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).

[0612] As early as 24-hours post-nucleofection, expression of a Centyrin or 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).

[0613] 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 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.

[0614] Genetically modified cells of the disclosure may be selective expanded following a nucleofection reaction. In certain embodiments, modified T cells comprising a CARTyrin may be selectively expanded by CARTyrin stimulation. Modified T cells comprising a CARTyrin 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 CARTyrin 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 CARTyrin target protein. Selective expansion of modified T cells comprising a CARTyrin by CARTyrin stimulation may be optimized to avoid functionally-exhausting the modified T-cells.

[0615] 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.

[0616] Selected genetically-modified cells (including selected genetically-modified T cells of the disclosure) may be cryopreserved 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.

[0617] 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 CARTyrin). Alternatively, or in addition, a purity of T cells, a Mean Fluorescence Intensity (MFI) of the transposon expression (e.g. CARTyrin expression), an ability of a CARTyrin (delivered in the transposon) to mediate degranulation and/or killing of a target cell expressing the CARTyrin 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.

[0618] 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 CARTyrin on the cell surface.

Genetic modification of an autologous T cell product composition

[0619] 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.

[0620] 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.

[0621] 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 CARTyrin 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, 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.

[0622] 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 CARTyrin 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 CARTyrin of the disclosure.

[0623] 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 CARTyrin of the disclosure.

[0624] 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 CARTyrin of the disclosure. Alternatively, or in addition, expander beads coated with a CARTyrin target protein may be used to stimulate a cell or T-cell of the disclosure through a TCR and/or CARTyrin of the disclosure.

[0625] Expansion methods drawn to stimulation of a cell or T-cell of the disclosure through the TCR or CARTyrin and via surface-expressed CD2, CD3, CD28, 4-1BB, and/or other markers on genetically-modified T cells.

[0626] 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.

[0627] 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 CARTyrin-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), Lymphotoxin-alpha/TNF-beta, TGF-beta, TNF-alpha, TRANCE/TNFSF11/RANK L, 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, 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, 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.

[0628] 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.

[0629] 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), Becenum (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 (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.

[0630] 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.

[0631] A cell or T-cell culture of the disclosure may be kept steady, rocked, swirled, or shaken.

[0632] 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.

[0633] 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

[0634] 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 CARTyrin of the disclosure. Alternatively, or in addition, a purity of genetically-modified cells or T cells, the Mean Fluorescence Intensity (MFI) of a CARTyrin expressed by a genetically-modified cell or T cell of the disclosure, an ability of the CARTyrin to mediate degranulation and/or killing of a target cell expressing the CARTyrin ligand, and/or a phenotype of CARTyrin + T cells may be assessed.

[0635] 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 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 CARTyrin of the disclosure on their cell surface.

[0636] 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).

[0637] 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 300fL (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.

[0638] 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

[0639] A pharmaceutical formulation of the disclosure may be distributed into bags for infusion, cryopreservation, and/or storage.

[0640] 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.

[0641] 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.

[0642] 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.

Formulations

[0643] 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 CARTyrin 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.

[0644] 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 CARTyrin 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 CARTyrin, 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 CARTyrin in the aqueous diluent to form a solution that can be held over a period of twenty-four hours or greater.

[0645] The at least one CARTyrin 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.

[0646] The range of at least one CARTyrin 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.

[0647] 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-microbial effect. Such concentrations are dependent on the preservative selected and are readily determined by the skilled artisan.

[0648] 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).

[0649] 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® polyls, other block co-polymers, 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.

[0650] The formulations of the present invention can be prepared by a process which comprises mixing at least one CARTyrin 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 CARTyrin 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 CARTyrin 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.

[0651] The claimed formulations can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized at least one CARTyrin 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.

[0652] 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 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.

[0653] The solutions of at least one CARTyrin of the invention can be prepared by a process that comprises mixing at least one CARTyrin 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 CARTyrin 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.

[0654] The claimed products can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized at least one CARTyrin 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.

[0655] 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 CARTyrin 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 CARTyrin 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.

[0656] 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.bectondickenson.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.

[0657] 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 CARTyrin 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, 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.

[0658] The formulations of the present invention can be prepared by a process that comprises mixing at least one CARTyrin and a selected buffer, preferably, a phosphate buffer containing saline or a chosen salt. Mixing at least one CARTyrin and buffer 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 CARTyrin in water or buffer is combined with the desired buffering agent in water in 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 for the concentration and means of administration used.

[0659] The claimed stable or preserved formulations can be provided to patients as clear solutions or as dual vials comprising a vial of lyophilized CARTyrin that is reconstituted with a second vial containing a preservative or 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.

[0660] Other formulations or methods of stabilizing the CARTyrin may result in other than a clear solution of lyophilized powder comprising the CARTyrin. Among non-clear solutions are formulations comprising particulate suspensions, said particulates being a composition containing the CARTyrin in a structure of variable dimension and known variously as a microsphere, microparticle, nanoparticle, nanosphere, or liposome. Such relatively homogenous, essentially spherical, particulate formulations containing an active agent can be formed by contacting an 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 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 polymers selected from the group consisting of gelatin agar, starch, arabinogalactan, albumin, collagen, polyglycolic

acid, polylactic aced, glycolide-L(−) lactide poly(episilon-caprolactone, poly(epsilon-caprolactone-CO-lactic acid), poly(epsilon-caprolactone-CO-glycolic acid), poly(β-hydroxy butyric acid), polyethylene oxide, polyethylene, poly(alkyl-2-cyanoacrylate), poly(hydroxyethyl methacrylate), 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 aced, glycolide-L(−) lactide poly(episilon-caprolactone, poly(epsilon-caprolactone-CO-lactic acid), and poly(epsilon-caprolactone-CO-glycolic acid. Solvents useful for dissolving the polymer and/or the active include: water, hexafluoroisopropanol, methylenechloride, tetrahydrofuran, hexane, benzene, or hexafluoroacetone sesquihydrate. The process of dispersing 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.

[0661] 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 CARTyrin preparation is taught in U.S. Pat. No. 6,019,968. The CARTyrin-based dry powder compositions may be produced by spray drying solutions or slurries of the CARTyrin and, optionally, excipients, in a solvent under conditions to provide a respirable dry powder. Solvents may include polar compounds, such as water and ethanol, which may be readily dried. CARTyrin 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.

[0662] At least one CARTyrin 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

[0663] 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 CARTyrin of the present invention, e.g., administering or contacting the cell, tissue, organ, animal, or patient with a therapeutic effective amount of CARTyrin. The present invention also provides a method for modulating or treating a disease, in a cell, tissue, organ, animal, or patient including, but not limited to, a malignant disease.

[0664] The present invention also provides a method for modulating or treating at least one malignant disease in a cell, tissue, organ, animal or patient, including, but not limited to, at least one of: leukemia, acute leukemia, acute lymphoblastic leukemia (ALL), acute lymphocytic leukemia, B-cell, T-cell or FAB ALL, acute myeloid leukemia (AML), acute myelogenous leukemia, chronic myelocytic leukemia (CML), chronic lymphocytic leukemia (CLL), hairy cell leukemia, myelodyplastic syndrome (MDS), a lymphoma, Hodgkin's disease, a malignant lymphoma, non-Hodgkin's lymphoma, Burkitt's lymphoma, multiple myeloma, Kaposi's sarcoma, colorectal carcinoma, pancreatic carcinoma, nasopharyngeal carcinoma, malignant histiocytosis, paraneoplastic syndrome/hypercalcemia of malignancy, solid tumors, bladder cancer, breast cancer, colorectal cancer, endometrial cancer, head cancer, neck cancer, hereditary nonpolyposis cancer, Hodgkin's lymphoma, liver cancer, lung cancer, non-small cell lung cancer, ovarian cancer, pancreatic cancer, prostate cancer, renal cell carcinoma, testicular cancer, adenocarcinomas, sarcomas, malignant melanoma, hemangioma, metastatic disease, cancer related bone resorption, cancer related bone pain, and the like.

[0665] Any method of the present invention can comprise administering an effective amount of a composition or pharmaceutical composition comprising at least one CARTyrin 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 CARTyrin, 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 a 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.

[0666] 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 CARTyrin 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.

[0667] 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.

[0668] As a non-limiting example, treatment of humans or animals can be provided as a one-time or periodic dosage of at least one CARTyrin 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.

[0669] 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 0.5-99.999% by weight based on the total weight of the composition.

[0670] For parenteral administration, the CARTyrin 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.

[0671] 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

[0672] Many known and developed modes can be used according to the present invention for administering pharmaceutically effective amounts of at least one CARTyrin 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. CARTyrins 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

[0673] 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 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 semisynthtetic 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 needle-less 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

[0674] The invention further relates to the administration of at least one CARTyrin by parenteral, subcutaneous, intramuscular, intravenous, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravesical, intralesional, bolus, vaginal, rectal, buccal, sublingual, intranasal, or transdermal means. At least one CARTyrin 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

[0675] The disclosure provides modified cells that express one or more CARs and/or CARTyrins 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 viability and/or CAR/CARTyrin expression level to ensure a minimal level of cell function and CAR/CARTyrin 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.

Inducible Proapoptotic Polypeptides

[0676] 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.

[0677] 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 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 embodiments, the caspase 9 polypeptide is a truncated caspase 9 polypeptide. Inducible proapoptotic polypeptides of the disclosure may be non-naturally occurring.

[0678] 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 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.

[0679] 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 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 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 polypeptide of the disclosure compared to a wild type amino acid or a nucleic acid sequence.

[0680] 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 sequence encoding a Caspase Activation and Recruitment Domain (CARD) to eliminate or minimize the possibility of activating a local inflammatory response in addition to 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 polypeptides 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.

[0681] 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.

[0682] 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 FKBPs 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.

[0683] 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.

[0684] 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.

[0685] 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, 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 haptenic molecules, which are physiologically acceptable, and the individual antibody subunits screened for binding affinity. The cDNA encoding the subunits 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 way, almost any physiologically acceptable haptenic 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 binding.

[0686] 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 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 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 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, 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.

[0687] 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.

[0688] 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 polypeptide 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[(1R)-3-(3,4-dimethoxyphenyl)propylidene]]ester, [2S-[1(R*),2R*[S*[S*[1(R*),2R*]]]]]-(9Cl) 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.

[0689] 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.

[0690] 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.

[0691] 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.

[0692] 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: 18028). In preferred embodiments, the linker is a polypeptide and the nucleic acid encoding the polypeptide does not contain a restriction site for a restriction endonuclease. Linkers of the disclosure may be non-naturally occurring.

[0693] 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 polypeptide 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.

[0694] 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-Off™ or Tet-On™ 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-On™ system, gene expression is turned on in the presence of doxycycline, whereas in the Tet-Off™ 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-Off™ 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-On™ system, the tetracycline repressor is not wild type and in the presence of doxycycline activates transcription. For gene therapy vector production, the Tet-Off™ 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.

[0695] 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.

[0696] 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.

[0697] 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.

[0698] 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).

[0699] 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.

[0700] 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

[0701] 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.

[0702] 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 CARTyrin (a CAR comprising a Centyrin), 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 polypeptide, 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).

[0703] 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 TGFβ cytokine binding to a TGFβRII 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 1. 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 TGFβRII.

[0704] Table 1. Exemplary Inhibitory Checkpoint Signals (and proteins that induce immunosuppression). A CSR of the disclosure may comprise an endodomain of any one of the proteins of this table.

Full Name	**Abbreviation**	**SEQ ID NO:**
Programmed cell death protein 1	PD1	14643-14644
transforming growth factor β Receptor 1	TGFβR1	14645
transforming growth factor β Receptor 2	TGFβR2	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	BTLA	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
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

[0705] 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 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 2.

[0706] **Table 2.** 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

[0707] 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 a 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 3. 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.

[0708] **Table 3.** 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
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 (Drosophila)	ASH1L	14764
ash2 (absent, small, or homeotic)-like (Drosophila)	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,	Batf	14786
basic leucine zipper transcription factor, ATF-like	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 (Drosophila)	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 Binding Factor	Blimp-1	14803
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
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	CEBPD	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	CREBZF	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	DDB2	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
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)	ELK4	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
eomesodermin	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	ESRRA	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
folliculogenesis specific bHLH transcription factor	FIGLA	14966
FLT3-interacting zinc finger 1	FIZ1	14967
Fli-1 proto-oncogene, ETS transcription factor	FLI1	14968
FBJ murine osteosarcoma viral oncogene homolog	FOS	14969
FBJ 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
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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
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
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zinc finger protein 334	ZNF334	16104
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zinc finger protein 337	ZNF337	16106
zinc finger protein 33A	ZNF33A	16107
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
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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
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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
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
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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
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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

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zinc finger protein 530	ZNF530	16227
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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
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zinc finger protein 564	ZNF564	16253
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zinc finger protein 566	ZNF566	16255
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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
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
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zinc finger protein 585B	ZNF585B	16277
zinc finger protein 586	ZNF586	16278
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zinc finger protein 589	ZNF589	16280
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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
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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
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
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

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

[0709] 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 4.

[0710] **Table 4.** 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/APO-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
Bcl-2-associated X protein	Bax	16518
Bcl-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

[0711] 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, more tumor cells killed per armored T 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 5.

[0712] **Table 5.** 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

[0713] In some embodiments, a T-cell of the disclosure is modified to silence or reduce expression of one or more gene(s) encoding proteins that that confer sensitivity to a cancer 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 6.

[0714] **Table 6.** 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

[0715] 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 a non-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 7.

[0716] **Table 7.** 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
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
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

Armored T-Cells "Null or Switch Receptor" Strategy

[0717] 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.

[0718] 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 receptor, 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.

[0719] 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.

[0720] In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is a transmembrane receptor.

[0721] In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is a membrane-associated or membrane-linked receptor/protein.

[0722] In some embodiments, the modified/chimeric checkpoint receptor comprises a null receptor, decoy receptor or dominant negative receptor that is an intracellular receptor/protein.

[0723] 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 1 and 2), a transcription factor (as provided, for example, in Table 3), 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 4), a metabolic sensing molecule (as provided, for example, in Table 5), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 6), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 7). 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 8.

[0724] **Table 8.** 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
Bcl2-associated agonist of cell death	Bcl-xL or BAD	16619
Tumor necrosis factor receptor superfamily member 17	BCMA or TNFRSF17	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
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 TNFRSF8	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	CDw121b 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 IL10R	16690
Interleukin-17 receptor A	CDw217 or IL17RA	16691
C-X3-C motif chemokine 1	CX3CL1	16692
CX3C 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
Erythropoietin	Epo	16717
Erythropoietin receptor	EpoR	16718
Receptor-type tyrosine-protein kinase FLT3	Flt-3	16719
FLT3 Ligand	Flt-3L	16720
Granulocyte colony-stimulating factor receptor	G-CSF or GSF3R	16721
Tumor necrosis factor receptor superfamily member 18	GITR or TNFRSF18	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	IFNγ	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-1α	16747
Interleukin-1beta	IL-1β	16748
Interleukin-2	IL2	16749
Interleukin-20	IL-20	16750
Interleukin-20 receptor alpha	IL-20Rα	16751
Interleukin-20 receptor beta	IL-20Rβ	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	LTβR or TNFRSF3	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 Ligand	SCF or KITLG	16776
Tumor necrosis factor receptor superfamily member 13B	TACI or TNFRSF13B	16777

Tumor necrosis factor ligand superfamily member 13B	TALL-1 or TNFSF13B	16778
TGF-beta receptor type-1	TGF-βR1	16779
TGF-beta receptor type-2	TGF-βR2	16780
TGF-beta receptor type-3	TGF-βR3	16781
Transforming growth factor beta-1	TGF-β1	16782
Transforming growth factor beta-2	TGF-β2	16783
Transforming growth factor beta-3	TGF-β3	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

[0725] 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 blockage 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.

[0726] 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 1 and 2), a transcription factor (as provided, for example, in Table 3), 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 4), a metabolic sensing molecule (as provided, for example, in Table 5), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 6), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 7). 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 8.

Armored T-Cells "Synthetic Gene Expression" Strategy

[0727] 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

[0728] 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.

[0729] 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 gene expression chronically (e.g. the ligand irreversibly binds to the exogenous receptor).

[0730] 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.

[0731] 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.

[0732] 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).

[0733] 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.

[0734] In some embodiments of the CLR/CARs of the disclosure, the signal peptide comprises a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR signal peptide. In some embodiments, the signal peptide comprises a sequence encoding a human CD8α signal peptide. In some embodiments, the signal peptide comprises an amino acid sequence comprising MALPVTALLLPLALLLHAARP (SEQ ID NO: 18004). In some embodiments, the signal peptide is encoded by a nucleic acid sequence comprising atggcactgccagtcaccgccctgctgctgcctctggctctgctgctgcacgcagctagacca.

[0735] In some embodiments of the CLR/CARs of the disclosure, the transmembrane domain comprises a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR transmembrane domain. In some embodiments, the transmembrane domain comprises a sequence encoding a human CD8α transmembrane domain. In some embodiments, the transmembrane domain comprises an amino acid

sequence comprising IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006). In some embodiments, the transmembrane domain is encoded by a nucleic acid sequence comprising atctacatttgggcaccactggccgggacctgtggagtgctgctgctgagcctggtcatcacactgtactgc (SEQ ID NO: 18007).

[0736] In some embodiments of the CLR/CARs of the disclosure, the endodomain comprises a human CD3ζ endodomain. In some embodiments, the at least one costimulatory domain comprises a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof. In some embodiments, the at least one costimulatory domain comprises a human CD28 and/or a 4-1BB costimulatory domain. In some embodiments, the CD3ζ costimulatory domain comprises an amino acid sequence comprising RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR (SEQ ID NO: 18008). In some embodiments, the CD3ζ costimulatory domain is encoded by a nucleic acid sequence comprising cgcgtgaagtttagtcgatcagcagatgccccagcttacaaacagggacagaaccagctgtataacgagctgaatctgggccgccga gaggaatatgacgtgctggataagcggagaggacgcgaccccgaaatgggaggcaagcccaggcgcaaaaaccctcaggaagg cctgtataacgagctgcagaaggacaaaatggcagaagcctattctgagatcggcatgaaggggagcgacggagaggcaaagg gcacgatgggctgtaccagggactgagcaccgccacaaaggacacctatgatgctctgcatatgcaggcactgcctccaagg (SEQ ID NO: 18010). In some embodiments, the 4-1BB costimulatory domain comprises an amino acid sequence comprising KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 18011). In some embodiments, the 4-1BB costimulatory domain is encoded by a nucleic acid sequence comprising aagagaggcaggaagaaactgctgtatattttcaaacagcccttcatgcgccccgtgcagactacccaggaggaagacgggtgctcc tgtcgattccctgaggaagaggaaggcgggtgtgagctg (SEQ ID NO: 18013). In some embodiments, the 4-1BB costimulatory domain is located between the transmembrane domain and the CD28 costimulatory domain.

[0737] In some embodiments of the CLR/CARs of the disclosure, the hinge comprises a sequence derived from a human CD8α, IgG4, and/or CD4 sequence. In some embodiments, the hinge comprises a sequence derived from a human CD8α sequence. In some embodiments, the hinge comprises an amino acid sequence comprising

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18014). In some embodiments, the hinge is encoded by a nucleic acid sequence comprising ACCACAACCCCTGCCCCCAGACCTCCCACACCCGCCCCTACCATCGCGAGTCAGC CCCTGAGTCTGAGACCTGAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGTGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 18016) or ACCACAACCCCTGCCCCCAGACCTCCCACACCCGCCCCTACCATCGCGAGTCAGC CCCTGAGTCTGAGACCTGAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGTGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 18017). In some embodiments, the at least one protein scaffold specifically binds the ligand.

[0738] 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 afflilin, an affimer, an affitin, an alphabody, an anticalin, an avimer, a DARPin, a Fynomer, 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.

[0739] 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 LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDL TGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18018). In some embodiments, the consensus sequence comprises MLPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYD LTGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18019). 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 (SEQ ID NO:18020) at positions 13-16 of the consensus sequence; (b) a B-C loop comprising or consisting of the amino acid residues TAPDAAF (SEQ ID NO:18021) 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:18022) 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:18023) 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:18024) 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:18025) 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

[0740] In some embodiments of the compositions of the disclosure, the sequence encoding the inducible promoter of (a) comprises a sequence encoding an NFκB promoter. In some 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 some embodiments, the interferon (IFN) promoter is an IFNγ promoter. In some embodiments of the compositions of the disclosure, the inducible promoter is isolated or derived from the promoter of a cytokine or a chemokine. In some embodiments, the cytokine or chemokine comprises IL2, IL3, IL4, IL5, IL6, IL10, IL12, IL13, IL17A/F, IL21, IL22, IL23, transforming growth factor beta (TGFβ), colony stimulating factor 2 (GM-CSF), interferon gamma (IFNγ), Tumor necrosis factor (TNFα), LTα, 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).

[0741] In some 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 some embodiments, the gene comprises CD69, CD71, CTLA4, PD-1, TIGIT, LAG3, TIM-3, GITR, MHCII, COX-2, FASL and 4-1BB.

[0742] 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 from the promoter of Nr4a1, Nr4a3, Tnfrsf9 (4-1BB), Sema7a, Zfp36l2, Gadd45b, Dusp5, Dusp6 and Neto2.

Inducible transgene

[0743] In some embodiments, the inducible transgene construct comprises or drives expression of a signaling component downstream of an inhibitory checkpoint signal (as provided, for example, in Tables 1 and 2), a transcription factor (as provided, for example, in Table 3), 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 4), a metabolic sensing molecule (as provided, for example, in Table 5), a protein conferring sensitivity to a cancer therapy (as provided, for example, in Table 6 and/or 9), and an oncogene or a tumor suppressor gene (as provided, for example, in Table 7). 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 8.

[0744] Table 9. Exemplary therapeutic proteins (and proteins to enhance CAR-T efficacy).

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
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
AC008641.1		SEQ ID NO: 73
AC009133.22		SEQ ID NO: 76
AC009491.2		SEQ ID NO: 77
AC011513.3		SEQ ID NOS: 92 - 93
AC136352.5		SEQ ID NO: 88
AC145212.4	MaFF-interacting protein	SEQ ID NO: 90
AC233755.1		SEQ ID NO: 91
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	SEQ ID NOS: 152 - 158
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
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
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
ADCK1	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
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
AGRN	Agrin	SEQ ID NOS: 618 - 621
AGRP	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
AL356289.1		SEQ ID NO: 677
AL589743.1		SEQ ID NO: 678
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, chitobiosyldiphosphodolichol 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
ALKBH1	AlkB homolog 1, histone H2A dioxygenase	SEQ ID NOS: 746 - 748
ALKBH5	AlkB homolog 5, RNA demethylase	SEQ ID NOS: 749 - 750
ALPI	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-Mullerian hormone	SEQ ID NO: 771
AMICA1	Adhesion molecule, interacts with CXADR antigen 1	SEQ ID NOS: 7348 - 7356
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 (Drosophila)	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
ANK1	Ankyrin 1, erythrocytic	SEQ ID NOS: 833 - 843
ANKDD1A	Ankyrin repeat and death domain containing 1A	SEQ ID NOS: 844 - 850
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
ANO1	#N/A	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 1 (Fe65)	SEQ ID NOS: 891 - 907

APCDD1	Adenomatosis 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
APOA1BP	Apolipoprotein A-I binding protein	SEQ ID NOS: 9177 - 9179
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
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
ARHGAP6	Rho GTPase activating protein 6	SEQ ID NOS: 1043 - 1048
ARHGEF4	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
ART3	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
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	SEQ ID NOS: 1145 - 1195
ASAH2	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
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-glucuronyltransferase 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 - 1374
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	SEQ ID NO: 1375
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	SEQ ID NOS: 1376 - 1379
B4GAT1	Beta-1,4-glucuronyltransferase 1	SEQ ID NO: 1380
B9D1	B9 protein domain 1	SEQ ID NOS: 1381 - 1397
BACE2	Beta-site APP-cleaving enzyme 2	SEQ ID NOS: 1398 - 1400
BAGE5	B melanoma antigen family, member 5	SEQ ID NO: 1401
BCAM	Basal cell adhesion molecule (Lutheran blood group)	SEQ ID NOS: 1402 - 1405
BCAN	Brevican	SEQ ID NOS: 1406 - 1412
BCAP29	B-cell receptor-associated protein 29	SEQ ID NOS: 1413 - 1425
BCAR1	Breast cancer anti-estrogen resistance 1	SEQ ID NOS: 1426 - 1443
BCHE	Butyrylcholinesterase	SEQ ID NOS: 1444 - 1448
BCKDHB	Branched chain keto acid dehydrogenase E1, beta polypeptide	SEQ ID NOS: 1449 - 1451
BDNF	Brain-derived neurotrophic factor	SEQ ID NOS: 1452 - 1469
BGLAP	Bone gamma-carboxyglutamate (gla) protein	SEQ ID NO: 1470
BGN	Biglycan	SEQ ID NOS: 1471 - 1472
BLVRB	Biliverdin reductase B	SEQ ID NOS: 1473 - 1477
BMP1	Bone morphogenetic protein 1	SEQ ID NOS: 1478 - 1489
BMP10	Bone morphogenetic protein 10	SEQ ID NO: 1490

BMP15	Bone morphogenetic protein 15	SEQ ID NO: 1491
BMP2	Bone morphogenetic protein 2	SEQ ID NO: 1492
BMP3	Bone morphogenetic protein 3	SEQ ID NO: 1493
BMP4	Bone morphogenetic protein 4	SEQ ID NOS: 1494 - 1501
BMP6	Bone morphogenetic protein 6	SEQ ID NO: 1502
BMP7	Bone morphogenetic protein 7	SEQ ID NOS: 1503 - 1506
BMP8A	Bone morphogenetic protein 8a	SEQ ID NO: 1507
BMP8B	Bone morphogenetic protein 8b	SEQ ID NO: 1508
BMPER	BMP binding endothelial regulator	SEQ ID NOS: 1509 - 1512
BNC1	Basonuclin 1	SEQ ID NOS: 1513 - 1514
BOC	BOC cell adhesion associated, oncogene regulated	SEQ ID NOS: 1515 - 1525
BOD1	Biorientation of chromosomes in cell division 1	SEQ ID NOS: 1526 - 1530
BOLA1	BolA family member 1	SEQ ID NOS: 1531 - 1533
BPI	Bactericidal/permeability-increasing protein	SEQ ID NOS: 1534 - 1537
BPIFA1	BPI fold containing family A, member 1	SEQ ID NOS: 1538 - 1541
BPIFA2	BPI fold containing family A, member 2	SEQ ID NOS: 1542 - 1543
BPIFA3	BPI fold containing family A, member 3	SEQ ID NOS: 1544 - 1545
BPIFB1	BPI fold containing family B, member 1	SEQ ID NOS: 1546 - 1547
BPIFB2	BPI fold containing family B, member 2	SEQ ID NO: 1548
BPIFB3	BPI fold containing family B, member 3	SEQ ID NO: 1549
BPIFB4	BPI fold containing family B, member 4	SEQ ID NOS: 1550 - 1551
BPIFB6	BPI fold containing family B, member 6	SEQ ID NOS: 1552 - 1553
BPIFC	BPI fold containing family C	SEQ ID NOS: 1554 - 1557
BRF1	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	SEQ ID NOS: 1558 - 1573
BRINP1	Bone morphogenetic protein/retinoic acid inducible neural-specific 1	SEQ ID NOS: 1574 - 1575
BRINP2	Bone morphogenetic protein/retinoic acid inducible neural-specific 2	SEQ ID NO: 1576

BRINP3	Bone morphogenetic protein/retinoic acid inducible neural-specific 3	SEQ ID NOS: 1577 - 1579
BSG	Basigin (Ok blood group)	SEQ ID NOS: 1580 - 1590
BSPH1	Binder of sperm protein homolog 1	SEQ ID NO: 1591
BST1	Bone marrow stromal cell antigen 1	SEQ ID NOS: 1592 - 1596
BTBD17	BTB (POZ) domain containing 17	SEQ ID NO: 1597
BTD	Biotinidase	SEQ ID NOS: 1598 - 1607
BTN2A2	Butyrophilin, subfamily 2, member A2	SEQ ID NOS: 1608 - 1621
BTN3A1	Butyrophilin, subfamily 3, member A1	SEQ ID NOS: 1622 - 1628
BTN3A2	Butyrophilin, subfamily 3, member A2	SEQ ID NOS: 1629 - 1639
BTN3A3	Butyrophilin, subfamily 3, member A3	SEQ ID NOS: 1640 - 1648
C10orf10	Chromosome 10 open reading frame 10	SEQ ID NOS: 4169 - 4170
C10orf99	Chromosome 10 open reading frame 99	SEQ ID NO: 1650
C11orf1	Chromosome 11 open reading frame 1	SEQ ID NOS: 1651 - 1655
C11orf24	Chromosome 11 open reading frame 24	SEQ ID NOS: 1656 - 1658
C11orf45	Chromosome 11 open reading frame 45	SEQ ID NOS: 1659 - 1660
C11orf94	Chromosome 11 open reading frame 94	SEQ ID NO: 1661
C12orf10	Chromosome 12 open reading frame 10	SEQ ID NOS: 1662 - 1665
C12orf49	Chromosome 12 open reading frame 49	SEQ ID NOS: 1666 - 1669
C12orf73	Chromosome 12 open reading frame 73	SEQ ID NOS: 1670 - 1679
C12orf76	Chromosome 12 open reading frame 76	SEQ ID NOS: 1680 - 1687
C14orf80	Chromosome 14 open reading frame 80	SEQ ID NOS: 13083 - 13096
C14orf93	Chromosome 14 open reading frame 93	SEQ ID NOS: 1688 - 1703
C16orf89	Chromosome 16 open reading frame 89	SEQ ID NOS: 1704 - 1706
C16orf90	Chromosome 16 open reading frame 90	SEQ ID NOS: 1707 - 1708
C17orf67	Chromosome 17 open reading frame 67	SEQ ID NO: 1709

C17orf75	Chromosome 17 open reading frame 75	SEQ ID NOS: 1710 - 1718
C17orf99	Chromosome 17 open reading frame 99	SEQ ID NOS: 1719 - 1721
C18orf54	Chromosome 18 open reading frame 54	SEQ ID NOS: 1722 - 1726
C19orf47	Chromosome 19 open reading frame 47	SEQ ID NOS: 1727 - 1734
C19orf70	Chromosome 19 open reading frame 70	SEQ ID NOS: 1735 - 1738
C19orf80	Chromosome 19 open reading frame 80	SEQ ID NOS: 829 - 832
C1GALT1	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1	SEQ ID NOS: 1739 - 1743
C1orf127	Chromosome 1 open reading frame 127	SEQ ID NOS: 1744 - 1747
C1orf159	Chromosome 1 open reading frame 159	SEQ ID NOS: 1748 - 1760
C1orf198	Chromosome 1 open reading frame 198	SEQ ID NOS: 1761 - 1765
C1orf234	Chromosome 1 open reading frame 234	SEQ ID NOS: 13118 - 13120
C1orf54	Chromosome 1 open reading frame 54	SEQ ID NOS: 1766 - 1768
C1orf56	Chromosome 1 open reading frame 56	SEQ ID NO: 1769
C1QA	Complement component 1, q subcomponent, A chain	SEQ ID NOS: 1770 - 1772
C1QB	Complement component 1, q subcomponent, B chain	SEQ ID NOS: 1773 - 1776
C1QC	Complement component 1, q subcomponent, C chain	SEQ ID NOS: 1777 - 1779
C1QL1	Complement component 1, q subcomponent-like 1	SEQ ID NO: 1780
C1QL2	Complement component 1, q subcomponent-like 2	SEQ ID NO: 1781
C1QL3	Complement component 1, q subcomponent-like 3	SEQ ID NOS: 1782 - 1783
C1QL4	Complement component 1, q subcomponent-like 4	SEQ ID NO: 1784
C1QTNF1	C1q and tumor necrosis factor related protein 1	SEQ ID NOS: 1785 - 1794
C1QTNF2	C1q and tumor necrosis factor related protein 2	SEQ ID NO: 1796
C1QTNF3	C1q and tumor necrosis factor related protein 3	SEQ ID NOS: 1797 - 1798

C1QTNF4	C1q and tumor necrosis factor related protein 4	SEQ ID NOS: 1799 - 1800
C1QTNF5	C1q and tumor necrosis factor related protein 5	SEQ ID NOS: 1801 - 1803
C1QTNF7	C1q and tumor necrosis factor related protein 7	SEQ ID NOS: 1804 - 1808
C1QTNF8	C1q and tumor necrosis factor related protein 8	SEQ ID NOS: 1809 - 1810
C1QTNF9	C1q and tumor necrosis factor related protein 9	SEQ ID NOS: 1811 - 1812
C1QTNF9B	C1q and tumor necrosis factor related protein 9B	SEQ ID NOS: 1813 - 1815
C1R	Complement component 1, r subcomponent	SEQ ID NOS: 1816 - 1824
C1RL	Complement component 1, r subcomponent-like	SEQ ID NOS: 1825 - 1833
C1S	Complement component 1, s subcomponent	SEQ ID NOS: 1834 - 1843
C2	Complement component 2	SEQ ID NOS: 1844 - 1858
C21orf33	Chromosome 21 open reading frame 33	SEQ ID NOS: 1859 - 1867
C21orf62	Chromosome 21 open reading frame 62	SEQ ID NOS: 1868 - 1871
C22orf15	Chromosome 22 open reading frame 15	SEQ ID NOS: 1872 - 1874
C22orf46	Chromosome 22 open reading frame 46	SEQ ID NO: 1875
C2CD2	C2 calcium-dependent domain containing 2	SEQ ID NOS: 1876 - 1878
C2orf40	Chromosome 2 open reading frame 40	SEQ ID NOS: 1879 - 1881
C2orf66	Chromosome 2 open reading frame 66	SEQ ID NO: 1882
C2orf69	Chromosome 2 open reading frame 69	SEQ ID NO: 1883
C2orf78	Chromosome 2 open reading frame 78	SEQ ID NO: 1884
C3	Complement component 3	SEQ ID NOS: 1885 - 1889
C3orf33	Chromosome 3 open reading frame 33	SEQ ID NOS: 1890 - 1894
C3orf58	Chromosome 3 open reading frame 58	SEQ ID NOS: 1895 - 1898
C4A	Complement component 4A (Rodgers blood group)	SEQ ID NOS: 1899 - 1900
C4B	Complement component 4B (Chido blood group)	SEQ ID NOS: 1901 - 1902

C4BPA	Complement component 4 binding protein, alpha	SEQ ID NOS: 1903 - 1905
C4BPB	Complement component 4 binding protein, beta	SEQ ID NOS: 1906 - 1910
C4orf26	Chromosome 4 open reading frame 26	SEQ ID NOS: 9751 - 9754
C4orf48	Chromosome 4 open reading frame 48	SEQ ID NOS: 1911 - 1912
C5	Complement component 5	SEQ ID NO: 1913
C5orf46	Chromosome 5 open reading frame 46	SEQ ID NOS: 1914 - 1915
C6	Complement component 6	SEQ ID NOS: 1916 - 1919
C6orf120	Chromosome 6 open reading frame 120	SEQ ID NO: 1920
C6orf15	Chromosome 6 open reading frame 15	SEQ ID NO: 1921
C6orf25	Chromosome 6 open reading frame 25	SEQ ID NOS: 8832 - 8839
C6orf58	Chromosome 6 open reading frame 58	SEQ ID NO: 1922
C7	Complement component 7	SEQ ID NO: 1923
C7orf57	Chromosome 7 open reading frame 57	SEQ ID NOS: 1924 - 1928
C7orf73	Chromosome 7 open reading frame 73	SEQ ID NOS: 12924 - 12925
C8A	Complement component 8, alpha polypeptide	SEQ ID NO: 1929
C8B	Complement component 8, beta polypeptide	SEQ ID NOS: 1930 - 1932
C8G	Complement component 8, gamma polypeptide	SEQ ID NOS: 1933 - 1934
C9	Complement component 9	SEQ ID NO: 1935
C9orf47	Chromosome 9 open reading frame 47	SEQ ID NOS: 1936 - 1938
CA10	Carbonic anhydrase X	SEQ ID NOS: 1939 - 1945
CA11	Carbonic anhydrase XI	SEQ ID NOS: 1946 - 1947
CA6	Carbonic anhydrase VI	SEQ ID NOS: 1948 - 1952
CA9	Carbonic anhydrase IX	SEQ ID NOS: 1953 - 1954
CABLES1	Cdk5 and Abl enzyme substrate 1	SEQ ID NOS: 1955 - 1960
CABP1	Calcium binding protein 1	SEQ ID NOS: 1961 - 1964

CACNA2D1	Calcium channel, voltage-dependent, alpha 2/delta subunit 1	SEQ ID NOS: 1965 - 1968
CACNA2D4	Calcium channel, voltage-dependent, alpha 2/delta subunit 4	SEQ ID NOS: 1969 - 1982
CADM3	Cell adhesion molecule 3	SEQ ID NOS: 1983 - 1985
CALCA	Calcitonin-related polypeptide alpha	SEQ ID NOS: 1986 - 1990
CALCB	Calcitonin-related polypeptide beta	SEQ ID NOS: 1991 - 1993
CALCR	Calcitonin receptor	SEQ ID NOS: 1994 - 2000
CALCRL	Calcitonin receptor-like	SEQ ID NOS: 2001 - 2005
CALR	Calreticulin	SEQ ID NOS: 2011 - 2014
CALR3	Calreticulin 3	SEQ ID NOS: 2015 - 2016
CALU	Calumenin	SEQ ID NOS: 2017 - 2022
CAMK2D	Calcium/calmodulin-dependent protein kinase II delta	SEQ ID NOS: 2023 - 2034
CAMP	Cathelicidin antimicrobial peptide	SEQ ID NO: 2035
CANX	Calnexin	SEQ ID NOS: 2036 - 2050
CARKD	Carbohydrate kinase domain containing	SEQ ID NOS: 9175 - 9176
CARM1	Coactivator-associated arginine methyltransferase 1	SEQ ID NOS: 2051 - 2058
CARNS1	Carnosine synthase 1	SEQ ID NOS: 2059 - 2061
CARTPT	CART prepropeptide	SEQ ID NO: 2062
CASQ1	Calsequestrin 1 (fast-twitch, skeletal muscle)	SEQ ID NOS: 2063 - 2064
CASQ2	Calsequestrin 2 (cardiac muscle)	SEQ ID NO: 2065
CATSPERG	Catsper channel auxiliary subunit gamma	SEQ ID NOS: 2066 - 2073
CBLN1	Cerebellin 1 precursor	SEQ ID NOS: 2074 - 2076
CBLN2	Cerebellin 2 precursor	SEQ ID NOS: 2077 - 2080
CBLN3	Cerebellin 3 precursor	SEQ ID NOS: 2081 - 2082
CBLN4	Cerebellin 4 precursor	SEQ ID NO: 2083

CCBE1	Collagen and calcium binding EGF domains 1	SEQ ID NOS: 2084 - 2086
CCDC108	Coiled-coil domain containing 108	SEQ ID NOS: 2659 - 2668
CCDC112	Coiled-coil domain containing 112	SEQ ID NOS: 2087 - 2090
CCDC129	Coiled-coil domain containing 129	SEQ ID NOS: 2091 - 2098
CCDC134	Coiled-coil domain containing 134	SEQ ID NOS: 2099 - 2100
CCDC149	Coiled-coil domain containing 149	SEQ ID NOS: 2101 - 2104
CCDC3	Coiled-coil domain containing 3	SEQ ID NOS: 2105 - 2106
CCDC80	Coiled-coil domain containing 80	SEQ ID NOS: 2107 - 2110
CCDC85A	Coiled-coil domain containing 85A	SEQ ID NO: 2111
CCDC88B	Coiled-coil domain containing 88B	SEQ ID NOS: 2112 - 2114
CCER2	Coiled-coil glutamate-rich protein 2	SEQ ID NOS: 2115 - 2116
CCK	Cholecystokinin	SEQ ID NOS: 2117 - 2119
CCL1	Chemokine (C-C motif) ligand 1	SEQ ID NO: 2120
CCL11	Chemokine (C-C motif) ligand 11	SEQ ID NO: 2121
CCL13	Chemokine (C-C motif) ligand 13	SEQ ID NOS: 2122 - 2123
CCL14	Chemokine (C-C motif) ligand 14	SEQ ID NOS: 2124 - 2127
CCL15	Chemokine (C-C motif) ligand 15	SEQ ID NOS: 2128 - 2129
CCL16	Chemokine (C-C motif) ligand 16	SEQ ID NOS: 2130 - 2132
CCL17	Chemokine (C-C motif) ligand 17	SEQ ID NOS: 2133 - 2134
CCL18	Chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	SEQ ID NO: 2135
CCL19	Chemokine (C-C motif) ligand 19	SEQ ID NOS: 2136 - 2137
CCL2	Chemokine (C-C motif) ligand 2	SEQ ID NOS: 2138 - 2139
CCL20	Chemokine (C-C motif) ligand 20	SEQ ID NOS: 2140 - 2142
CCL21	Chemokine (C-C motif) ligand 21	SEQ ID NOS: 2143 - 2144

CCL22	Chemokine (C-C motif) ligand 22	SEQ ID NO: 2145
CCL23	Chemokine (C-C motif) ligand 23	SEQ ID NOS: 2146 - 2148
CCL24	Chemokine (C-C motif) ligand 24	SEQ ID NOS: 2149 - 2150
CCL25	Chemokine (C-C motif) ligand 25	SEQ ID NOS: 2151 - 2154
CCL26	Chemokine (C-C motif) ligand 26	SEQ ID NOS: 2155 - 2156
CCL27	Chemokine (C-C motif) ligand 27	SEQ ID NO: 2157
CCL28	Chemokine (C-C motif) ligand 28	SEQ ID NOS: 2158 - 2160
CCL3	Chemokine (C-C motif) ligand 3	SEQ ID NO: 2161
CCL3L3	Chemokine (C-C motif) ligand 3-like 3	SEQ ID NO: 2162
CCL4	Chemokine (C-C motif) ligand 4	SEQ ID NOS: 2163 - 2164
CCL4L2	Chemokine (C-C motif) ligand 4-like 2	SEQ ID NOS: 2165 - 2174
CCL5	Chemokine (C-C motif) ligand 5	SEQ ID NOS: 2175 - 2177
CCL7	Chemokine (C-C motif) ligand 7	SEQ ID NOS: 2178 - 2180
CCL8	Chemokine (C-C motif) ligand 8	SEQ ID NO: 2181
CCNB1IP1	Cyclin B1 interacting protein 1, E3 ubiquitin protein ligase	SEQ ID NOS: 2182 - 2193
CCNL1	Cyclin L1	SEQ ID NOS: 2194 - 2202
CCNL2	Cyclin L2	SEQ ID NOS: 2203 - 2210
CD14	CD14 molecule	SEQ ID NOS: 2211 - 2215
CD160	CD160 molecule	SEQ ID NOS: 2216 - 2220
CD164	CD164 molecule, sialomucin	SEQ ID NOS: 2221 - 2226
CD177	CD177 molecule	SEQ ID NOS: 2227 - 2229
CD1E	CD1e molecule	SEQ ID NOS: 2230 - 2243
CD2	CD2 molecule	SEQ ID NOS: 2244 - 2245
CD200	CD200 molecule	SEQ ID NOS: 2246 - 2252
CD200R1	CD200 receptor 1	SEQ ID NOS: 2253 - 2257

CD22	CD22 molecule	SEQ ID NOS: 2258 - 2275
CD226	CD226 molecule	SEQ ID NOS: 2276 - 2283
CD24	CD24 molecule	SEQ ID NOS: 2284 - 2290
CD276	CD276 molecule	SEQ ID NOS: 2291 - 2306
CD300A	CD300a molecule	SEQ ID NOS: 2307 - 2311
CD300LB	CD300 molecule-like family member b	SEQ ID NOS: 2312 - 2313
CD300LF	CD300 molecule-like family member f	SEQ ID NOS: 2314 - 2322
CD300LG	CD300 molecule-like family member g	SEQ ID NOS: 2323 - 2328
CD3D	CD3d molecule, delta (CD3-TCR complex)	SEQ ID NOS: 2329 - 2332
CD4	CD4 molecule	SEQ ID NOS: 2333 - 2335
CD40	CD40 molecule, TNF receptor superfamily member 5	SEQ ID NOS: 2336 - 2339
CD44	CD44 molecule (Indian blood group)	SEQ ID NOS: 2340 - 2366
CD48	CD48 molecule	SEQ ID NOS: 2367 - 2369
CD5	CD5 molecule	SEQ ID NOS: 2370 - 2371
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	SEQ ID NOS: 2372 - 2382
CD59	CD59 molecule, complement regulatory protein	SEQ ID NOS: 2383 - 2393
CD5L	CD5 molecule-like	SEQ ID NO: 2394
CD6	CD6 molecule	SEQ ID NOS: 2395 - 2402
CD68	CD68 molecule	SEQ ID NOS: 2403 - 2406
CD7	CD7 molecule	SEQ ID NOS: 2407 - 2412
CD79A	CD79a molecule, immunoglobulin-associated alpha	SEQ ID NOS: 2413 - 2415
CD80	CD80 molecule	SEQ ID NOS: 2416 - 2418
CD86	CD86 molecule	SEQ ID NOS: 2419 - 2425

CD8A	CD8a molecule	SEQ ID NOS: 2426 - 2429
CD8B	CD8b molecule	SEQ ID NOS: 2430 - 2435
CD99	CD99 molecule	SEQ ID NOS: 2436 - 2444
CDC23	Cell division cycle 23	SEQ ID NOS: 2445 - 2449
CDC40	Cell division cycle 40	SEQ ID NOS: 2450 - 2452
CDC45	Cell division cycle 45	SEQ ID NOS: 2453 - 2459
CDCP1	CUB domain containing protein 1	SEQ ID NOS: 2460 - 2461
CDCP2	CUB domain containing protein 2	SEQ ID NOS: 2462 - 2463
CDH1	Cadherin 1, type 1	SEQ ID NOS: 2464 - 2471
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)	SEQ ID NOS: 2472 - 2481
CDH13	Cadherin 13	SEQ ID NOS: 2482 - 2491
CDH17	Cadherin 17, LI cadherin (liver-intestine)	SEQ ID NOS: 2492 - 2496
CDH18	Cadherin 18, type 2	SEQ ID NOS: 2497 - 2503
CDH19	Cadherin 19, type 2	SEQ ID NOS: 2504 - 2508
CDH23	Cadherin-related 23	SEQ ID NOS: 2509 - 2524
CDH5	Cadherin 5, type 2 (vascular endothelium)	SEQ ID NOS: 2525 - 2532
CDHR1	Cadherin-related family member 1	SEQ ID NOS: 2533 - 2538
CDHR4	Cadherin-related family member 4	SEQ ID NOS: 2539 - 2543
CDHR5	Cadherin-related family member 5	SEQ ID NOS: 2544 - 2550
CDKN2A	Cyclin-dependent kinase inhibitor 2A	SEQ ID NOS: 2551 - 2561
CDNF	Cerebral dopamine neurotrophic factor	SEQ ID NOS: 2562 - 2563
CDON	Cell adhesion associated, oncogene regulated	SEQ ID NOS: 2564 - 2571
CDSN	Corneodesmosin	SEQ ID NO: 2572

CEACAM16	Carcinoembryonic antigen-related cell adhesion molecule 16	SEQ ID NOS: 2573 - 2574
CEACAM18	Carcinoembryonic antigen-related cell adhesion molecule 18	SEQ ID NO: 2575
CEACAM19	Carcinoembryonic antigen-related cell adhesion molecule 19	SEQ ID NOS: 2576 - 2582
CEACAM5	Carcinoembryonic antigen-related cell adhesion molecule 5	SEQ ID NOS: 2583 - 2590
CEACAM7	Carcinoembryonic antigen-related cell adhesion molecule 7	SEQ ID NOS: 2591 - 2593
CEACAM8	Carcinoembryonic antigen-related cell adhesion molecule 8	SEQ ID NOS: 2594 - 2595
CECR1	Cat eye syndrome chromosome region, candidate 1	SEQ ID NOS: 222 - 229
CECR5	Cat eye syndrome chromosome region, candidate 5	SEQ ID NOS: 6411 - 6413
CEL	Carboxyl ester lipase	SEQ ID NO: 2596
CELA2A	Chymotrypsin-like elastase family, member 2A	SEQ ID NO: 2597
CELA2B	Chymotrypsin-like elastase family, member 2B	SEQ ID NOS: 2598 - 2599
CELA3A	Chymotrypsin-like elastase family, member 3A	SEQ ID NOS: 2600 - 2602
CELA3B	Chymotrypsin-like elastase family, member 3B	SEQ ID NOS: 2603 - 2605
CEMIP	Cell migration inducing protein, hyaluronan binding	SEQ ID NOS: 2606 - 2610
CEP89	Centrosomal protein 89kDa	SEQ ID NOS: 2611 - 2616
CER1	Cerberus 1, DAN family BMP antagonist	SEQ ID NO: 2617
CERCAM	Cerebral endothelial cell adhesion molecule	SEQ ID NOS: 2618 - 2625
CERS1	Ceramide synthase 1	SEQ ID NOS: 2626 - 2630
CES1	Carboxylesterase 1	SEQ ID NOS: 2631 - 2636
CES3	Carboxylesterase 3	SEQ ID NOS: 2637 - 2641
CES4A	Carboxylesterase 4A	SEQ ID NOS: 2642 - 2647
CES5A	Carboxylesterase 5A	SEQ ID NOS: 2648 - 2655
CETP	Cholesteryl ester transfer protein, plasma	SEQ ID NOS: 2656 - 2658

CFB	Complement factor B	SEQ ID NOS: 2669 - 2673
CFC1	Cripto, FRL-1, cryptic family 1	SEQ ID NOS: 2674 - 2676
CFC1B	Cripto, FRL-1, cryptic family 1B	SEQ ID NOS: 2677 - 2679
CFD	Complement factor D (adipsin)	SEQ ID NOS: 2680 - 2681
CFDP1	Craniofacial development protein 1	SEQ ID NOS: 2682 - 2685
CFH	Complement factor H	SEQ ID NOS: 2686 - 2688
CFHR1	Complement factor H-related 1	SEQ ID NOS: 2689 - 2690
CFHR2	Complement factor H-related 2	SEQ ID NOS: 2691 - 2692
CFHR3	Complement factor H-related 3	SEQ ID NOS: 2693 - 2697
CFHR4	Complement factor H-related 4	SEQ ID NOS: 2698 - 2701
CFHR5	Complement factor H-related 5	SEQ ID NO: 2702
CFI	Complement factor I	SEQ ID NOS: 2703 - 2707
CFP	Complement factor properdin	SEQ ID NOS: 2708 - 2711
CGA	Glycoprotein hormones, alpha polypeptide	SEQ ID NOS: 2712 - 2716
CGB	Chorionic gonadotropin, beta polypeptide	SEQ ID NO: 2721
CGB1	Chorionic gonadotropin, beta polypeptide 1	SEQ ID NOS: 2717 - 2718
CGB2	Chorionic gonadotropin, beta polypeptide 2	SEQ ID NOS: 2719 - 2720
CGB5	Chorionic gonadotropin, beta polypeptide 5	SEQ ID NO: 2722
CGB7	Chorionic gonadotropin, beta polypeptide 7	SEQ ID NOS: 2723 - 2725
CGB8	Chorionic gonadotropin, beta polypeptide 8	SEQ ID NO: 2726
CGREF1	Cell growth regulator with EF-hand domain 1	SEQ ID NOS: 2727 - 2734
CH507-9B2.3		SEQ ID NOS: 5532 - 5538
CHAD	Chondroadherin	SEQ ID NOS: 2735 - 2737
CHADL	Chondroadherin-like	SEQ ID NOS: 2738 - 2740

CHEK2	Checkpoint kinase 2	SEQ ID NOS: 2741 - 2762
CHGA	Chromogranin A	SEQ ID NOS: 2763 - 2765
CHGB	Chromogranin B	SEQ ID NOS: 2766 - 2767
CHI3L1	Chitinase 3-like 1 (cartilage glycoprotein-39)	SEQ ID NOS: 2768 - 2769
CHI3L2	Chitinase 3-like 2	SEQ ID NOS: 2770 - 2783
CHIA	Chitinase, acidic	SEQ ID NOS: 2784 - 2792
CHID1	Chitinase domain containing 1	SEQ ID NOS: 2793 - 2811
CHIT1	Chitinase 1 (chitotriosidase)	SEQ ID NOS: 2812 - 2815
CHL1	Cell adhesion molecule L1-like	SEQ ID NOS: 2816 - 2824
CHN1	Chimerin 1	SEQ ID NOS: 2825 - 2835
CHPF	Chondroitin polymerizing factor	SEQ ID NOS: 2836 - 2838
CHPF2	Chondroitin polymerizing factor 2	SEQ ID NOS: 2839 - 2842
CHRD	Chordin	SEQ ID NOS: 2843 - 2848
CHRDL1	Chordin-like 1	SEQ ID NOS: 2849 - 2853
CHRDL2	Chordin-like 2	SEQ ID NOS: 2854 - 2862
CHRNA2	Cholinergic receptor, nicotinic, alpha 2 (neuronal)	SEQ ID NOS: 2863 - 2871
CHRNA5	Cholinergic receptor, nicotinic, alpha 5 (neuronal)	SEQ ID NOS: 2872 - 2875
CHRNB1	Cholinergic receptor, nicotinic, beta 1 (muscle)	SEQ ID NOS: 2876 - 2881
CHRND	Cholinergic receptor, nicotinic, delta (muscle)	SEQ ID NOS: 2882 - 2887
CHST1	Carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	SEQ ID NO: 2888
CHST10	Carbohydrate sulfotransferase 10	SEQ ID NOS: 2889 - 2896
CHST11	Carbohydrate (chondroitin 4) sulfotransferase 11	SEQ ID NOS: 2897 - 2901

CHST13	Carbohydrate (chondroitin 4) sulfotransferase 13	SEQ ID NOS: 2902 - 2903
CHST4	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	SEQ ID NOS: 2904 - 2905
CHST5	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	SEQ ID NOS: 2906 - 2907
CHST6	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	SEQ ID NOS: 2908 - 2909
CHST7	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	SEQ ID NO: 2910
CHST8	Carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	SEQ ID NOS: 2911 - 2914
CHSY1	Chondroitin sulfate synthase 1	SEQ ID NOS: 2915 - 2916
CHSY3	Chondroitin sulfate synthase 3	SEQ ID NO: 2917
CHTF8	Chromosome transmission fidelity factor 8	SEQ ID NOS: 2918 - 2928
CILP	Cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	SEQ ID NO: 2929
CILP2	Cartilage intermediate layer protein 2	SEQ ID NOS: 2930 - 2931
CIRH1A	Cirrhosis, autosomal recessive 1A (cirhin)	SEQ ID NOS: 13974 - 13983
CKLF	Chemokine-like factor	SEQ ID NOS: 2932 - 2937
CKMT1A	Creatine kinase, mitochondrial 1A	SEQ ID NOS: 2938 - 2943
CKMT1B	Creatine kinase, mitochondrial 1B	SEQ ID NOS: 2944 - 2953
CLCA1	Chloride channel accessory 1	SEQ ID NOS: 2954 - 2955
CLCF1	Cardiotrophin-like cytokine factor 1	SEQ ID NOS: 2956 - 2957
CLDN15	Claudin 15	SEQ ID NOS: 2958 - 2963
CLDN7	Claudin 7	SEQ ID NOS: 2964 - 2970
CLDND1	Claudin domain containing 1	SEQ ID NOS: 2971 - 2996
CLEC11A	C-type lectin domain family 11, member A	SEQ ID NOS: 2997 - 2999
CLEC16A	C-type lectin domain family 16, member A	SEQ ID NOS: 3000 - 3005
CLEC18A	C-type lectin domain family 18, member A	SEQ ID NOS: 3006 - 3011

CLEC18B	C-type lectin domain family 18, member B	SEQ ID NOS: 3012 - 3015
CLEC18C	C-type lectin domain family 18, member C	SEQ ID NOS: 3016 - 3022
CLEC19A	C-type lectin domain family 19, member A	SEQ ID NOS: 3023 - 3026
CLEC2B	C-type lectin domain family 2, member B	SEQ ID NOS: 3027 - 3028
CLEC3A	C-type lectin domain family 3, member A	SEQ ID NOS: 3029 - 3030
CLEC3B	C-type lectin domain family 3, member B	SEQ ID NOS: 3031 - 3032
CLGN	Calmegin	SEQ ID NOS: 3033 - 3035
CLN5	Ceroid-lipofuscinosis, neuronal 5	SEQ ID NOS: 3036 - 3047
CLPS	Colipase, pancreatic	SEQ ID NOS: 3048 - 3050
CLPSL1	Colipase-like 1	SEQ ID NOS: 3051 - 3052
CLPSL2	Colipase-like 2	SEQ ID NOS: 3053 - 3054
CLPX	Caseinolytic mitochondrial matrix peptidase chaperone subunit	SEQ ID NOS: 3055 - 3057
CLSTN3	Calsyntenin 3	SEQ ID NOS: 3058 - 3064
CLU	Clusterin	SEQ ID NOS: 3065 - 3078
CLUL1	Clusterin-like 1 (retinal)	SEQ ID NOS: 3079 - 3086
CMA1	Chymase 1, mast cell	SEQ ID NOS: 3087 - 3088
CMPK1	Cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	SEQ ID NOS: 3089 - 3092
CNBD1	Cyclic nucleotide binding domain containing 1	SEQ ID NOS: 3093 - 3096
CNDP1	Carnosine dipeptidase 1 (metallopeptidase M20 family)	SEQ ID NOS: 3097 - 3099
CNPY2	Canopy FGF signaling regulator 2	SEQ ID NOS: 3107 - 3111
CNPY3	Canopy FGF signaling regulator 3	SEQ ID NOS: 3112 - 3113
CNPY4	Canopy FGF signaling regulator 4	SEQ ID NOS: 3114 - 3116

CNTFR	Ciliary neurotrophic factor receptor	SEQ ID NOS: 3117 - 3120
CNTN1	Contactin 1	SEQ ID NOS: 3121 - 3130
CNTN2	Contactin 2 (axonal)	SEQ ID NOS: 3131 - 3142
CNTN3	Contactin 3 (plasmacytoma associated)	SEQ ID NO: 3143
CNTN4	Contactin 4	SEQ ID NOS: 3144 - 3152
CNTN5	Contactin 5	SEQ ID NOS: 3153 - 3158
CNTNAP2	Contactin associated protein-like 2	SEQ ID NOS: 3159 - 3162
CNTNAP3	Contactin associated protein-like 3	SEQ ID NOS: 3163 - 3167
CNTNAP3B	Contactin associated protein-like 3B	SEQ ID NOS: 3168 - 3176
COASY	CoA synthase	SEQ ID NOS: 3177 - 3186
COCH	Cochlin	SEQ ID NOS: 3187 - 3198
COG3	Component of oligomeric golgi complex 3	SEQ ID NOS: 3199 - 3202
COL10A1	Collagen, type X, alpha 1	SEQ ID NOS: 3203 - 3206
COL11A1	Collagen, type XI, alpha 1	SEQ ID NOS: 3207 - 3217
COL11A2	Collagen, type XI, alpha 2	SEQ ID NOS: 3218 - 3222
COL12A1	Collagen, type XII, alpha 1	SEQ ID NOS: 3223 - 3230
COL14A1	Collagen, type XIV, alpha 1	SEQ ID NOS: 3231 - 3238
COL15A1	Collagen, type XV, alpha 1	SEQ ID NOS: 3239 - 3240
COL16A1	Collagen, type XVI, alpha 1	SEQ ID NOS: 3241 - 3245
COL18A1	Collagen, type XVIII, alpha 1	SEQ ID NOS: 3246 - 3250
COL19A1	Collagen, type XIX, alpha 1	SEQ ID NOS: 3251 - 3253
COL1A1	Collagen, type I, alpha 1	SEQ ID NOS: 3254 - 3255
COL1A2	Collagen, type I, alpha 2	SEQ ID NOS: 3256 - 3257

COL20A1	Collagen, type XX, alpha 1	SEQ ID NOS: 3258 - 3261
COL21A1	Collagen, type XXI, alpha 1	SEQ ID NOS: 3262 - 3267
COL22A1	Collagen, type XXII, alpha 1	SEQ ID NOS: 3268 - 3270
COL24A1	Collagen, type XXIV, alpha 1	SEQ ID NOS: 3271 - 3274
COL26A1	Collagen, type XXVI, alpha 1	SEQ ID NOS: 3275 - 3276
COL27A1	Collagen, type XXVII, alpha 1	SEQ ID NOS: 3277 - 3279
COL28A1	Collagen, type XXVIII, alpha 1	SEQ ID NOS: 3280 - 3284
COL2A1	Collagen, type II, alpha 1	SEQ ID NOS: 3285 - 3286
COL3A1	Collagen, type III, alpha 1	SEQ ID NOS: 3287 - 3289
COL4A1	Collagen, type IV, alpha 1	SEQ ID NOS: 3290 - 3292
COL4A2	Collagen, type IV, alpha 2	SEQ ID NOS: 3293 - 3295
COL4A3	Collagen, type IV, alpha 3 (Goodpasture antigen)	SEQ ID NOS: 3296 - 3299
COL4A4	Collagen, type IV, alpha 4	SEQ ID NOS: 3300 - 3301
COL4A5	Collagen, type IV, alpha 5	SEQ ID NOS: 3302 - 3308
COL4A6	Collagen, type IV, alpha 6	SEQ ID NOS: 3309 - 3314
COL5A1	Collagen, type V, alpha 1	SEQ ID NOS: 3315 - 3317
COL5A2	Collagen, type V, alpha 2	SEQ ID NOS: 3318 - 3319
COL5A3	Collagen, type V, alpha 3	SEQ ID NO: 3320
COL6A1	Collagen, type VI, alpha 1	SEQ ID NOS: 3321 - 3322
COL6A2	Collagen, type VI, alpha 2	SEQ ID NOS: 3323 - 3328
COL6A3	Collagen, type VI, alpha 3	SEQ ID NOS: 3329 - 3337
COL6A5	Collagen, type VI, alpha 5	SEQ ID NOS: 3338 - 3342
COL6A6	Collagen, type VI, alpha 6	SEQ ID NOS: 3343 - 3345

COL7A1	Collagen, type VII, alpha 1	SEQ ID NOS: 3346 - 3347
COL8A1	Collagen, type VIII, alpha 1	SEQ ID NOS: 3348 - 3351
COL8A2	Collagen, type VIII, alpha 2	SEQ ID NOS: 3352 - 3354
COL9A1	Collagen, type IX, alpha 1	SEQ ID NOS: 3355 - 3358
COL9A2	Collagen, type IX, alpha 2	SEQ ID NOS: 3359 - 3362
COL9A3	Collagen, type IX, alpha 3	SEQ ID NOS: 3363 - 3364
COLEC10	Collectin sub-family member 10 (C-type lectin)	SEQ ID NO: 3365
COLEC11	Collectin sub-family member 11	SEQ ID NOS: 3366 - 3375
COLGALT1	Collagen beta(1-O)galactosyltransferase 1	SEQ ID NOS: 3376 - 3378
COLGALT2	Collagen beta(1-O)galactosyltransferase 2	SEQ ID NOS: 3379 - 3381
COLQ	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	SEQ ID NOS: 3382 - 3386
COMP	Cartilage oligomeric matrix protein	SEQ ID NOS: 3387 - 3389
COPS6	COP9 signalosome subunit 6	SEQ ID NOS: 3390 - 3393
COQ6	Coenzyme Q6 monooxygenase	SEQ ID NOS: 3394 - 3401
CORT	Cortistatin	SEQ ID NO: 3402
CP	Ceruloplasmin (ferroxidase)	SEQ ID NOS: 3403 - 3407
CPA1	Carboxypeptidase A1 (pancreatic)	SEQ ID NOS: 3408 - 3412
CPA2	Carboxypeptidase A2 (pancreatic)	SEQ ID NOS: 3413 - 3414
CPA3	Carboxypeptidase A3 (mast cell)	SEQ ID NO: 3415
CPA4	Carboxypeptidase A4	SEQ ID NOS: 3416 - 3421
CPA6	Carboxypeptidase A6	SEQ ID NOS: 3422 - 3424
CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	SEQ ID NOS: 3425 - 3430
CPB1	Carboxypeptidase B1 (tissue)	SEQ ID NOS: 3431 - 3435

CPB2	Carboxypeptidase B2 (plasma)	SEQ ID NOS: 3436 - 3438
CPE	Carboxypeptidase E	SEQ ID NOS: 3439 - 3443
CPM	Carboxypeptidase M	SEQ ID NOS: 3444 - 3453
CPN1	Carboxypeptidase N, polypeptide 1	SEQ ID NOS: 3454 - 3455
CPN2	Carboxypeptidase N, polypeptide 2	SEQ ID NOS: 3456 - 3457
CPO	Carboxypeptidase O	SEQ ID NO: 3458
CPQ	Carboxypeptidase Q	SEQ ID NOS: 3459 - 3464
CPVL	Carboxypeptidase, vitellogenic-like	SEQ ID NOS: 3465 - 3475
CPXM1	Carboxypeptidase X (M14 family), member 1	SEQ ID NO: 3476
CPXM2	Carboxypeptidase X (M14 family), member 2	SEQ ID NOS: 3477 - 3478
CPZ	Carboxypeptidase Z	SEQ ID NOS: 3479 - 3482
CR1L	Complement component (3b/4b) receptor 1-like	SEQ ID NOS: 3483 - 3484
CRB2	Crumbs family member 2	SEQ ID NOS: 3485 - 3487
CREG1	Cellular repressor of E1A-stimulated genes 1	SEQ ID NO: 3488
CREG2	Cellular repressor of E1A-stimulated genes 2	SEQ ID NO: 3489
CRELD1	Cysteine-rich with EGF-like domains 1	SEQ ID NOS: 3490 - 3495
CRELD2	Cysteine-rich with EGF-like domains 2	SEQ ID NOS: 3496 - 3500
CRH	Corticotropin releasing hormone	SEQ ID NO: 3501
CRHBP	Corticotropin releasing hormone binding protein	SEQ ID NOS: 3502 - 3503
CRHR1	Corticotropin releasing hormone receptor 1	SEQ ID NOS: 3504 - 3515
CRHR2	Corticotropin releasing hormone receptor 2	SEQ ID NOS: 3516 - 3522
CRISP1	Cysteine-rich secretory protein 1	SEQ ID NOS: 3523 - 3526
CRISP2	Cysteine-rich secretory protein 2	SEQ ID NOS: 3527 - 3529

CRISP3	Cysteine-rich secretory protein 3	SEQ ID NOS: 3530 - 3533
CRISPLD2	Cysteine-rich secretory protein LCCL domain containing 2	SEQ ID NOS: 3534 - 3541
CRLF1	Cytokine receptor-like factor 1	SEQ ID NOS: 3542 - 3543
CRP	C-reactive protein, pentraxin-related	SEQ ID NOS: 3544 - 3548
CRTAC1	Cartilage acidic protein 1	SEQ ID NOS: 3549 - 3553
CRTAP	Cartilage associated protein	SEQ ID NOS: 3554 - 3555
CRY2	Cryptochrome circadian clock 2	SEQ ID NOS: 3556 - 3559
CSAD	Cysteine sulfinic acid decarboxylase	SEQ ID NOS: 3560 - 3572
CSF1	Colony stimulating factor 1 (macrophage)	SEQ ID NOS: 3573 - 3580
CSF1R	Colony stimulating factor 1 receptor	SEQ ID NOS: 3581 - 3585
CSF2	Colony stimulating factor 2 (granulocyte-macrophage)	SEQ ID NO: 3586
CSF2RA	Colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	SEQ ID NOS: 3587 - 3598
CSF3	Colony stimulating factor 3 (granulocyte)	SEQ ID NOS: 3599 - 3605
CSGALNACT 1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	SEQ ID NOS: 3606 - 3614
CSH1	Chorionic somatomammotropin hormone 1 (placental lactogen)	SEQ ID NOS: 3615 - 3618
CSH2	Chorionic somatomammotropin hormone 2	SEQ ID NOS: 3619 - 3623
CSHL1	Chorionic somatomammotropin hormone-like 1	SEQ ID NOS: 3624 - 3630
CSN1S1	Casein alpha s1	SEQ ID NOS: 3631 - 3636
CSN2	Casein beta	SEQ ID NO: 3637
CSN3	Casein kappa	SEQ ID NO: 3638
CST1	Cystatin SN	SEQ ID NOS: 3639 - 3640
CST11	Cystatin 11	SEQ ID NOS: 3641 - 3642
CST2	Cystatin SA	SEQ ID NO: 3643
CST3	Cystatin C	SEQ ID NOS: 3644 - 3646

CST4	Cystatin S	SEQ ID NO: 3647
CST5	Cystatin D	SEQ ID NO: 3648
CST6	Cystatin E/M	SEQ ID NO: 3649
CST7	Cystatin F (leukocystatin)	SEQ ID NO: 3650
CST8	Cystatin 8 (cystatin-related epididymal specific)	SEQ ID NOS: 3651 - 3652
CST9	Cystatin 9 (testatin)	SEQ ID NO: 3653
CST9L	Cystatin 9-like	SEQ ID NO: 3654
CSTL1	Cystatin-like 1	SEQ ID NOS: 3655 - 3657
CT55	Cancer/testis antigen 55	SEQ ID NOS: 3658 - 3659
CTB-60B18.6		SEQ ID NOS: 74 - 75
CTBS	Chitobiase, di-N-acetyl-	SEQ ID NOS: 3660 - 3662
CTD-2313N18.7		SEQ ID NO: 4160
CTD-2370N5.3		SEQ ID NOS: 81 - 84
CTGF	Connective tissue growth factor	SEQ ID NO: 3663
CTHRC1	Collagen triple helix repeat containing 1	SEQ ID NOS: 3664 - 3667
CTLA4	Cytotoxic T-lymphocyte-associated protein 4	SEQ ID NOS: 3668 - 3671
CTNS	Cystinosin, lysosomal cystine transporter	SEQ ID NOS: 3672 - 3679
CTRB1	Chymotrypsinogen B1	SEQ ID NOS: 3680 - 3682
CTRB2	Chymotrypsinogen B2	SEQ ID NOS: 3683 - 3686
CTRC	Chymotrypsin C (caldecrin)	SEQ ID NOS: 3687 - 3688
CTRL	Chymotrypsin-like	SEQ ID NOS: 3689 - 3691
CTSA	Cathepsin A	SEQ ID NOS: 3692 - 3700
CTSB	Cathepsin B	SEQ ID NOS: 3701 - 3725
CTSC	Cathepsin C	SEQ ID NOS: 3726 - 3730
CTSD	Cathepsin D	SEQ ID NOS: 3731 - 3741
CTSE	Cathepsin E	SEQ ID NOS: 3742 - 3743

CTSF	Cathepsin F	SEQ ID NOS: 3744 - 3747
CTSG	Cathepsin G	SEQ ID NO: 3748
CTSH	Cathepsin H	SEQ ID NOS: 3749 - 3754
CTSK	Cathepsin K	SEQ ID NOS: 3755 - 3756
CTSL	Cathepsin L	SEQ ID NOS: 3757 - 3759
CTSO	Cathepsin O	SEQ ID NO: 3760
CTSS	Cathepsin S	SEQ ID NOS: 3761 - 3765
CTSV	Cathepsin V	SEQ ID NOS: 3766 - 3767
CTSW	Cathepsin W	SEQ ID NOS: 3768 - 3770
CTSZ	Cathepsin Z	SEQ ID NO: 3771
CUBN	Cubilin (intrinsic factor-cobalamin receptor)	SEQ ID NOS: 3772 - 3775
CUTA	CutA divalent cation tolerance homolog (E. coli)	SEQ ID NOS: 3776 - 3785
CX3CL1	Chemokine (C-X3-C motif) ligand 1	SEQ ID NOS: 3786 - 3789
CXADR	Coxsackie virus and adenovirus receptor	SEQ ID NOS: 3790 - 3794
CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	SEQ ID NO: 3795
CXCL10	Chemokine (C-X-C motif) ligand 10	SEQ ID NO: 3796
CXCL11	Chemokine (C-X-C motif) ligand 11	SEQ ID NOS: 3797 - 3798
CXCL12	Chemokine (C-X-C motif) ligand 12	SEQ ID NOS: 3799 - 3804
CXCL13	Chemokine (C-X-C motif) ligand 13	SEQ ID NO: 3805
CXCL14	Chemokine (C-X-C motif) ligand 14	SEQ ID NOS: 3806 - 3807
CXCL17	Chemokine (C-X-C motif) ligand 17	SEQ ID NOS: 3808 - 3809
CXCL2	Chemokine (C-X-C motif) ligand 2	SEQ ID NO: 3810
CXCL3	Chemokine (C-X-C motif) ligand 3	SEQ ID NO: 3811
CXCL5	Chemokine (C-X-C motif) ligand 5	SEQ ID NO: 3812
CXCL6	Chemokine (C-X-C motif) ligand 6	SEQ ID NOS: 3813 - 3814

CXCL8	Chemokine (C-X-C motif) ligand 8	SEQ ID NOS: 3815 - 3816
CXCL9	Chemokine (C-X-C motif) ligand 9	SEQ ID NO: 3817
CXorf36	Chromosome X open reading frame 36	SEQ ID NOS: 3818 - 3819
CYB5D2	Cytochrome b5 domain containing 2	SEQ ID NOS: 3820 - 3823
CYHR1	Cysteine/histidine-rich 1	SEQ ID NOS: 3824 - 3831
CYP17A1	Cytochrome P450, family 17, subfamily A, polypeptide 1	SEQ ID NOS: 3832 - 3836
CYP20A1	Cytochrome P450, family 20, subfamily A, polypeptide 1	SEQ ID NOS: 3837 - 3843
CYP21A2	Cytochrome P450, family 21, subfamily A, polypeptide 2	SEQ ID NOS: 3844 - 3851
CYP26B1	Cytochrome P450, family 26, subfamily B, polypeptide 1	SEQ ID NOS: 3852 - 3856
CYP2A6	Cytochrome P450, family 2, subfamily A, polypeptide 6	SEQ ID NOS: 3857 - 3858
CYP2A7	Cytochrome P450, family 2, subfamily A, polypeptide 7	SEQ ID NOS: 3859 - 3861
CYP2B6	Cytochrome P450, family 2, subfamily B, polypeptide 6	SEQ ID NOS: 3862 - 3865
CYP2C18	Cytochrome P450, family 2, subfamily C, polypeptide 18	SEQ ID NOS: 3866 - 3867
CYP2C19	Cytochrome P450, family 2, subfamily C, polypeptide 19	SEQ ID NOS: 3868 - 3869
CYP2C8	Cytochrome P450, family 2, subfamily C, polypeptide 8	SEQ ID NOS: 3870 - 3877
CYP2C9	Cytochrome P450, family 2, subfamily C, polypeptide 9	SEQ ID NOS: 3878 - 3880
CYP2E1	Cytochrome P450, family 2, subfamily E, polypeptide 1	SEQ ID NOS: 3881 - 3886
CYP2F1	Cytochrome P450, family 2, subfamily F, polypeptide 1	SEQ ID NOS: 3887 - 3890
CYP2J2	Cytochrome P450, family 2, subfamily J, polypeptide 2	SEQ ID NO: 3891
CYP2R1	Cytochrome P450, family 2, subfamily R, polypeptide 1	SEQ ID NOS: 3892 - 3897
CYP2S1	Cytochrome P450, family 2, subfamily S, polypeptide 1	SEQ ID NOS: 3898 - 3903
CYP2W1	Cytochrome P450, family 2, subfamily W, polypeptide 1	SEQ ID NOS: 3904 - 3906
CYP46A1	Cytochrome P450, family 46, subfamily A, polypeptide 1	SEQ ID NOS: 3907 - 3911

CYP4F11	Cytochrome P450, family 4, subfamily F, polypeptide 11	SEQ ID NOS: 3912 - 3916
CYP4F2	Cytochrome P450, family 4, subfamily F, polypeptide 2	SEQ ID NOS: 3917 - 3921
CYR61	Cysteine-rich, angiogenic inducer, 61	SEQ ID NO: 3922
CYTL1	Cytokine-like 1	SEQ ID NOS: 3923 - 3925
D2HGDH	D-2-hydroxyglutarate dehydrogenase	SEQ ID NOS: 3926 - 3934
DAG1	Dystroglycan 1 (dystrophin-associated glycoprotein 1)	SEQ ID NOS: 3935 - 3949
DAND5	DAN domain family member 5, BMP antagonist	SEQ ID NOS: 3950 - 3951
DAO	D-amino-acid oxidase	SEQ ID NOS: 3952 - 3957
DAZAP2	DAZ associated protein 2	SEQ ID NOS: 3958 - 3966
DBH	Dopamine beta-hydroxylase (dopamine beta-monooxygenase)	SEQ ID NOS: 3967 - 3968
DBNL	Drebrin-like	SEQ ID NOS: 3969 - 3986
DCD	Dermcidin	SEQ ID NOS: 3987 - 3989
DCN	Decorin	SEQ ID NOS: 3990 - 4008
DDIAS	DNA damage-induced apoptosis suppressor	SEQ ID NOS: 4009 - 4018
DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit (non-catalytic)	SEQ ID NOS: 4019 - 4022
DDR1	Discoidin domain receptor tyrosine kinase 1	SEQ ID NOS: 4023 - 4068
DDR2	Discoidin domain receptor tyrosine kinase 2	SEQ ID NOS: 4069 - 4074
DDT	D-dopachrome tautomerase	SEQ ID NOS: 4075 - 4080
DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17	SEQ ID NOS: 4081 - 4085
DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	SEQ ID NOS: 4086 - 4088
DDX25	DEAD (Asp-Glu-Ala-Asp) box helicase 25	SEQ ID NOS: 4089 - 4095
DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	SEQ ID NO: 4096
DEAF1	DEAF1 transcription factor	SEQ ID NOS: 4097 - 4099

DEF8	Differentially expressed in FDCP 8 homolog (mouse)	SEQ ID NOS: 4100 - 4119
DEFA1	Defensin, alpha 1	SEQ ID NOS: 4120 - 4121
DEFA1B	Defensin, alpha 1B	SEQ ID NO: 4122
DEFA3	Defensin, alpha 3, neutrophil-specific	SEQ ID NO: 4123
DEFA4	Defensin, alpha 4, corticostatin	SEQ ID NO: 4124
DEFA5	Defensin, alpha 5, Paneth cell-specific	SEQ ID NO: 4125
DEFA6	Defensin, alpha 6, Paneth cell-specific	SEQ ID NO: 4126
DEFB1	Defensin, beta 1	SEQ ID NO: 4127
DEFB103A	Defensin, beta 103A	SEQ ID NO: 4128
DEFB103B	Defensin, beta 103B	SEQ ID NO: 4129
DEFB104A	Defensin, beta 104A	SEQ ID NO: 4130
DEFB104B	Defensin, beta 104B	SEQ ID NO: 4131
DEFB105A	Defensin, beta 105A	SEQ ID NO: 4132
DEFB105B	Defensin, beta 105B	SEQ ID NO: 4133
DEFB106A	Defensin, beta 106A	SEQ ID NO: 4134
DEFB106B	Defensin, beta 106B	SEQ ID NO: 4135
DEFB107A	Defensin, beta 107A	SEQ ID NO: 4136
DEFB107B	Defensin, beta 107B	SEQ ID NO: 4137
DEFB108B	Defensin, beta 108B	SEQ ID NO: 4138
DEFB110	Defensin, beta 110	SEQ ID NOS: 4139 - 4140
DEFB113	Defensin, beta 113	SEQ ID NO: 4141
DEFB114	Defensin, beta 114	SEQ ID NO: 4142
DEFB115	Defensin, beta 115	SEQ ID NO: 4143
DEFB116	Defensin, beta 116	SEQ ID NO: 4144
DEFB118	Defensin, beta 118	SEQ ID NO: 4145
DEFB119	Defensin, beta 119	SEQ ID NOS: 4146 - 4148
DEFB121	Defensin, beta 121	SEQ ID NO: 4149
DEFB123	Defensin, beta 123	SEQ ID NO: 4150
DEFB124	Defensin, beta 124	SEQ ID NO: 4151
DEFB125	Defensin, beta 125	SEQ ID NO: 4152
DEFB126	Defensin, beta 126	SEQ ID NO: 4153
DEFB127	Defensin, beta 127	SEQ ID NO: 4154
DEFB128	Defensin, beta 128	SEQ ID NO: 4155
DEFB129	Defensin, beta 129	SEQ ID NO: 4156
DEFB130	Defensin, beta 130	SEQ ID NO: 4157
DEFB131	Defensin, beta 131	SEQ ID NO: 4159
DEFB132	Defensin, beta 132	SEQ ID NO: 4161
DEFB133	Defensin, beta 133	SEQ ID NO: 4162

DEFB134	Defensin, beta 134	SEQ ID NOS: 4163 - 4164
DEFB135	Defensin, beta 135	SEQ ID NO: 4165
DEFB136	Defensin, beta 136	SEQ ID NO: 4166
DEFB4A	Defensin, beta 4A	SEQ ID NO: 4167
DEFB4B	Defensin, beta 4B	SEQ ID NO: 4168
DFNA5	Deafness, autosomal dominant 5	SEQ ID NOS: 6271 - 6279
DFNB31	Deafness, autosomal recessive 31	SEQ ID NOS: 14251 - 14254
DGCR2	DiGeorge syndrome critical region gene 2	SEQ ID NOS: 4171 - 4174
DHH	Desert hedgehog	SEQ ID NO: 4175
DHRS4	Dehydrogenase/reductase (SDR family) member 4	SEQ ID NOS: 4176 - 4183
DHRS4L2	Dehydrogenase/reductase (SDR family) member 4 like 2	SEQ ID NOS: 4184 - 4193
DHRS7	Dehydrogenase/reductase (SDR family) member 7	SEQ ID NOS: 4194 - 4201
DHRS7C	Dehydrogenase/reductase (SDR family) member 7C	SEQ ID NOS: 4202 - 4204
DHRS9	Dehydrogenase/reductase (SDR family) member 9	SEQ ID NOS: 4205 - 4212
DHRSX	Dehydrogenase/reductase (SDR family) X-linked	SEQ ID NOS: 4213 - 4217
DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	SEQ ID NOS: 4218 - 4220
DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30	SEQ ID NOS: 4221 - 4228
DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	SEQ ID NOS: 4229 - 4233
DIO2	Deiodinase, iodothyronine, type II	SEQ ID NOS: 4234 - 4243
DIXDC1	DIX domain containing 1	SEQ ID NOS: 4244 - 4247
DKK1	Dickkopf WNT signaling pathway inhibitor 1	SEQ ID NO: 4248
DKK2	Dickkopf WNT signaling pathway inhibitor 2	SEQ ID NOS: 4249 - 4251
DKK3	Dickkopf WNT signaling pathway inhibitor 3	SEQ ID NOS: 4252 - 4257
DKK4	Dickkopf WNT signaling pathway inhibitor 4	SEQ ID NO: 4258
DKKL1	Dickkopf-like 1	SEQ ID NOS: 4259 - 4264

DLG4	Discs, large homolog 4 (Drosophila)	SEQ ID NOS: 4265 - 4273
DLK1	Delta-like 1 homolog (Drosophila)	SEQ ID NOS: 4274 - 4277
DLL1	Delta-like 1 (Drosophila)	SEQ ID NOS: 4278 - 4279
DLL3	Delta-like 3 (Drosophila)	SEQ ID NOS: 4280 - 4282
DMBT1	Deleted in malignant brain tumors 1	SEQ ID NOS: 4283 - 4289
DMKN	Dermokine	SEQ ID NOS: 4290 - 4336
DMP1	Dentin matrix acidic phosphoprotein 1	SEQ ID NOS: 4337 - 4338
DMRTA2	DMRT-like family A2	SEQ ID NOS: 4339 - 4340
DNAAF5	Dynein, axonemal, assembly factor 5	SEQ ID NOS: 4341 - 4344
DNAH14	Dynein, axonemal, heavy chain 14	SEQ ID NOS: 4345 - 4359
DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	SEQ ID NOS: 4360 - 4361
DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	SEQ ID NO: 4362
DNAJC25-GNG10	DNAJC25-GNG10 readthrough	SEQ ID NO: 4363
DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	SEQ ID NOS: 4364 - 4365
DNASE1	Deoxyribonuclease I	SEQ ID NOS: 4366 - 4376
DNASE1L1	Deoxyribonuclease I-like 1	SEQ ID NOS: 4377 - 4387
DNASE1L2	Deoxyribonuclease I-like 2	SEQ ID NOS: 4388 - 4393
DNASE1L3	Deoxyribonuclease I-like 3	SEQ ID NOS: 4394 - 4399
DNASE2	Deoxyribonuclease II, lysosomal	SEQ ID NOS: 4400 - 4401
DNASE2B	Deoxyribonuclease II beta	SEQ ID NOS: 4402 - 4403
DPEP1	Dipeptidase 1 (renal)	SEQ ID NOS: 4404 - 4408
DPEP2	Dipeptidase 2	SEQ ID NOS: 4409 - 4415
DPEP3	Dipeptidase 3	SEQ ID NO: 4416

DPF3	D4, zinc and double PHD fingers, family 3	SEQ ID NOS: 4417 - 4423
DPP4	Dipeptidyl-peptidase 4	SEQ ID NOS: 4424 - 4428
DPP7	Dipeptidyl-peptidase 7	SEQ ID NOS: 4429 - 4434
DPT	Dermatopontin	SEQ ID NO: 4435
DRAXIN	Dorsal inhibitory axon guidance protein	SEQ ID NO: 4436
DSE	Dermatan sulfate epimerase	SEQ ID NOS: 4437 - 4445
DSG2	Desmoglein 2	SEQ ID NOS: 4446 - 4447
DSPP	Dentin sialophosphoprotein	SEQ ID NOS: 4448 - 4449
DST	Dystonin	SEQ ID NOS: 4450 - 4468
DUOX1	Dual oxidase 1	SEQ ID NOS: 4469 - 4473
DYNLT3	Dynein, light chain, Tctex-type 3	SEQ ID NOS: 4474 - 4476
E2F5	E2F transcription factor 5, p130-binding	SEQ ID NOS: 4477 - 4483
EBAG9	Estrogen receptor binding site associated, antigen, 9	SEQ ID NOS: 4484 - 4492
EBI3	Epstein-Barr virus induced 3	SEQ ID NO: 4493
ECHDC1	Ethylmalonyl-CoA decarboxylase 1	SEQ ID NOS: 4494 - 4512
ECM1	Extracellular matrix protein 1	SEQ ID NOS: 4513 - 4515
ECM2	Extracellular matrix protein 2, female organ and adipocyte specific	SEQ ID NOS: 4516 - 4519
ECSIT	ECSIT signalling integrator	SEQ ID NOS: 4520 - 4531
EDDM3A	Epididymal protein 3A	SEQ ID NO: 4532
EDDM3B	Epididymal protein 3B	SEQ ID NO: 4533
EDEM2	ER degradation enhancer, mannosidase alpha-like 2	SEQ ID NOS: 4534 - 4535
EDEM3	ER degradation enhancer, mannosidase alpha-like 3	SEQ ID NOS: 4536 - 4538
EDIL3	EGF-like repeats and discoidin I-like domains 3	SEQ ID NOS: 4539 - 4540
EDN1	Endothelin 1	SEQ ID NO: 4541
EDN2	Endothelin 2	SEQ ID NO: 4542

EDN3	Endothelin 3	SEQ ID NOS: 4543 - 4548
EDNRB	Endothelin receptor type B	SEQ ID NOS: 4549 - 4557
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	SEQ ID NOS: 4558 - 4568
EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	SEQ ID NOS: 4569 - 4580
EFNA1	Ephrin-A1	SEQ ID NOS: 4581 - 4582
EFNA2	Ephrin-A2	SEQ ID NO: 4583
EFNA4	Ephrin-A4	SEQ ID NOS: 4584 - 4586
EGFL6	EGF-like-domain, multiple 6	SEQ ID NOS: 4587 - 4588
EGFL7	EGF-like-domain, multiple 7	SEQ ID NOS: 4589 - 4593
EGFL8	EGF-like-domain, multiple 8	SEQ ID NOS: 4594 - 4596
EGFLAM	EGF-like, fibronectin type III and laminin G domains	SEQ ID NOS: 4597 - 4605
EGFR	Epidermal growth factor receptor	SEQ ID NOS: 4606 - 4613
EHBP1	EH domain binding protein 1	SEQ ID NOS: 4614 - 4625
EHF	Ets homologous factor	SEQ ID NOS: 4626 - 4635
EHMT1	Euchromatic histone-lysine N-methyltransferase 1	SEQ ID NOS: 4636 - 4661
EHMT2	Euchromatic histone-lysine N-methyltransferase 2	SEQ ID NOS: 4662 - 4666
EIF2AK1	Eukaryotic translation initiation factor 2-alpha kinase 1	SEQ ID NOS: 4667 - 4670
ELANE	Elastase, neutrophil expressed	SEQ ID NOS: 4671 - 4672
ELN	Elastin	SEQ ID NOS: 4673 - 4695
ELP2	Elongator acetyltransferase complex subunit 2	SEQ ID NOS: 4696 - 4708
ELSPBP1	Epididymal sperm binding protein 1	SEQ ID NOS: 4709 - 4714
EMC1	ER membrane protein complex subunit 1	SEQ ID NOS: 4715 - 4721
EMC10	ER membrane protein complex subunit 10	SEQ ID NOS: 4722 - 4728

EMC9	ER membrane protein complex subunit 9	SEQ ID NOS: 4729 - 4732
EMCN	Endomucin	SEQ ID NOS: 4733 - 4737
EMID1	EMI domain containing 1	SEQ ID NOS: 4738 - 4744
EMILIN1	Elastin microfibril interfacer 1	SEQ ID NOS: 4745 - 4746
EMILIN2	Elastin microfibril interfacer 2	SEQ ID NO: 4747
EMILIN3	Elastin microfibril interfacer 3	SEQ ID NO: 4748
ENAM	Enamelin	SEQ ID NO: 4749
ENDOG	Endonuclease G	SEQ ID NO: 4750
ENDOU	Endonuclease, polyU-specific	SEQ ID NOS: 4751 - 4753
ENHO	Energy homeostasis associated	SEQ ID NO: 4754
ENO4	Enolase family member 4	SEQ ID NOS: 4755 - 4759
ENPP6	Ectonucleotide pyrophosphatase/phosphodiesterase 6	SEQ ID NOS: 4760 - 4761
ENPP7	Ectonucleotide pyrophosphatase/phosphodiesterase 7	SEQ ID NOS: 4762 - 4763
ENTPD5	Ectonucleoside triphosphate diphosphohydrolase 5	SEQ ID NOS: 4764 - 4768
ENTPD8	Ectonucleoside triphosphate diphosphohydrolase 8	SEQ ID NOS: 4769 - 4772
EOGT	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	SEQ ID NOS: 4773 - 4780
EPCAM	Epithelial cell adhesion molecule	SEQ ID NOS: 4781 - 4784
EPDR1	Ependymin related 1	SEQ ID NOS: 4785 - 4788
EPGN	Epithelial mitogen	SEQ ID NOS: 4789 - 4797
EPHA10	EPH receptor A10	SEQ ID NOS: 4798 - 4805
EPHA3	EPH receptor A3	SEQ ID NOS: 4806 - 4808
EPHA4	EPH receptor A4	SEQ ID NOS: 4809 - 4818
EPHA7	EPH receptor A7	SEQ ID NOS: 4819 - 4820
EPHA8	EPH receptor A8	SEQ ID NOS: 4821 - 4822
EPHB2	EPH receptor B2	SEQ ID NOS: 4823 - 4827

EPHB4	EPH receptor B4	SEQ ID NOS: 4828 - 4830
EPHX3	Epoxide hydrolase 3	SEQ ID NOS: 4831 - 4834
EPO	Erythropoietin	SEQ ID NO: 4835
EPPIN	Epididymal peptidase inhibitor	SEQ ID NOS: 4836 - 4838
EPPIN-WFDC6	EPPIN-WFDC6 readthrough	SEQ ID NO: 4839
EPS15	Epidermal growth factor receptor pathway substrate 15	SEQ ID NOS: 4840 - 4842
EPS8L1	EPS8-like 1	SEQ ID NOS: 4843 - 4848
EPX	Eosinophil peroxidase	SEQ ID NO: 4849
EPYC	Epiphycan	SEQ ID NOS: 4850 - 4851
EQTN	Equatorin, sperm acrosome associated	SEQ ID NOS: 4852 - 4854
ERAP1	Endoplasmic reticulum aminopeptidase 1	SEQ ID NOS: 4855 - 4859
ERAP2	Endoplasmic reticulum aminopeptidase 2	SEQ ID NOS: 4860 - 4867
ERBB3	Erb-b2 receptor tyrosine kinase 3	SEQ ID NOS: 4868 - 4881
ERLIN1	ER lipid raft associated 1	SEQ ID NOS: 4885 - 4887
ERLIN2	ER lipid raft associated 2	SEQ ID NOS: 4888 - 4896
ERN1	Endoplasmic reticulum to nucleus signaling 1	SEQ ID NOS: 4897 - 4898
ERN2	Endoplasmic reticulum to nucleus signaling 2	SEQ ID NOS: 4899 - 4903
ERO1A	Endoplasmic reticulum oxidoreductase alpha	SEQ ID NOS: 4904 - 4910
ERO1B	Endoplasmic reticulum oxidoreductase beta	SEQ ID NOS: 4911 - 4913
ERP27	Endoplasmic reticulum protein 27	SEQ ID NOS: 4914 - 4915
ERP29	Endoplasmic reticulum protein 29	SEQ ID NOS: 4916 - 4919
ERP44	Endoplasmic reticulum protein 44	SEQ ID NO: 4920
ERV3-1	Endogenous retrovirus group 3, member 1	SEQ ID NO: 4921
ESM1	Endothelial cell-specific molecule 1	SEQ ID NOS: 4922 - 4924

ESRP1	Epithelial splicing regulatory protein 1	SEQ ID NOS: 4925 - 4933
EXOG	Endo/exonuclease (5'-3'), endonuclease G-like	SEQ ID NOS: 4934 - 4947
EXTL1	Exostosin-like glycosyltransferase 1	SEQ ID NO: 4948
EXTL2	Exostosin-like glycosyltransferase 2	SEQ ID NOS: 4949 - 4953
F10	Coagulation factor X	SEQ ID NOS: 4954 - 4957
F11	Coagulation factor XI	SEQ ID NOS: 4958 - 4962
F12	Coagulation factor XII (Hageman factor)	SEQ ID NO: 4963
F13B	Coagulation factor XIII, B polypeptide	SEQ ID NO: 4964
F2	Coagulation factor II (thrombin)	SEQ ID NOS: 4965 - 4967
F2R	Coagulation factor II (thrombin) receptor	SEQ ID NOS: 4968 - 4969
F2RL3	Coagulation factor II (thrombin) receptor-like 3	SEQ ID NOS: 4970 - 4971
F5	Coagulation factor V (proaccelerin, labile factor)	SEQ ID NOS: 4972 - 4973
F7	Coagulation factor VII (serum prothrombin conversion accelerator)	SEQ ID NOS: 4974 - 4977
F8	Coagulation factor VIII, procoagulant component	SEQ ID NOS: 4978 - 4983
F9	Coagulation factor IX	SEQ ID NOS: 4984 - 4985
FABP6	Fatty acid binding protein 6, ileal	SEQ ID NOS: 4986 - 4988
FAM107B	Family with sequence similarity 107, member B	SEQ ID NOS: 4989 - 5010
FAM131A	Family with sequence similarity 131, member A	SEQ ID NOS: 5011 - 5019
FAM132A	Family with sequence similarity 132, member A	SEQ ID NO: 1795
FAM132B	Family with sequence similarity 132, member B	SEQ ID NOS: 4882 - 4884
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
FAM171A1	Family with sequence similarity 171, member A1	SEQ ID NOS: 5020 - 5021
FAM171B	Family with sequence similarity 171, member B	SEQ ID NOS: 5022 - 5023

FAM172A	Family with sequence similarity 172, member A	SEQ ID NOS: 5024 - 5028
FAM175A	Family with sequence similarity 175, member A	SEQ ID NOS: 64 - 71
FAM177A1	Family with sequence similarity 177, member A1	SEQ ID NOS: 5029 - 5038
FAM179B	Family with sequence similarity 179, member B	SEQ ID NOS: 13628 - 13633
FAM180A	Family with sequence similarity 180, member A	SEQ ID NOS: 5039 - 5041
FAM189A1	Family with sequence similarity 189, member A1	SEQ ID NOS: 5042 - 5043
FAM198A	Family with sequence similarity 198, member A	SEQ ID NOS: 5044 - 5046
FAM19A1	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	SEQ ID NOS: 5047 - 5049
FAM19A2	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	SEQ ID NOS: 5050 - 5057
FAM19A3	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A3	SEQ ID NOS: 5058 - 5059
FAM19A4	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	SEQ ID NOS: 5060 - 5062
FAM19A5	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	SEQ ID NOS: 5063 - 5066
FAM20A	Family with sequence similarity 20, member A	SEQ ID NOS: 5067 - 5070
FAM20C	Family with sequence similarity 20, member C	SEQ ID NO: 5071
FAM213A	Family with sequence similarity 213, member A	SEQ ID NOS: 5072 - 5077
FAM26D	Family with sequence similarity 26, member D	SEQ ID NOS: 2006 - 2010
FAM46B	Family with sequence similarity 46, member B	SEQ ID NO: 5078
FAM57A	Family with sequence similarity 57, member A	SEQ ID NOS: 5079 - 5084
FAM78A	Family with sequence similarity 78, member A	SEQ ID NOS: 5085 - 5087
FAM96A	Family with sequence similarity 96, member A	SEQ ID NOS: 5088 - 5092
FAM9B	Family with sequence similarity 9, member B	SEQ ID NOS: 5093 - 5096
FAP	Fibroblast activation protein, alpha	SEQ ID NOS: 5097 - 5103

FAS	Fas cell surface death receptor	SEQ ID NOS: 5104 - 5113
FAT1	FAT atypical cadherin 1	SEQ ID NOS: 5114 - 5120
FBLN1	Fibulin 1	SEQ ID NOS: 5121 - 5133
FBLN2	Fibulin 2	SEQ ID NOS: 5134 - 5139
FBLN5	Fibulin 5	SEQ ID NOS: 5140 - 5145
FBLN7	Fibulin 7	SEQ ID NOS: 5146 - 5151
FBN1	Fibrillin 1	SEQ ID NOS: 5152 - 5155
FBN2	Fibrillin 2	SEQ ID NOS: 5156 - 5161
FBN3	Fibrillin 3	SEQ ID NOS: 5162 - 5166
FBXW7	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	SEQ ID NOS: 5167 - 5177
FCAR	Fc fragment of IgA receptor	SEQ ID NOS: 5178 - 5187
FCGBP	Fc fragment of IgG binding protein	SEQ ID NOS: 5188 - 5190
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	SEQ ID NOS: 5191 - 5196
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	SEQ ID NOS: 5197 - 5203
FCGRT	Fc fragment of IgG, receptor, transporter, alpha	SEQ ID NOS: 5204 - 5214
FCMR	Fc fragment of IgM receptor	SEQ ID NOS: 5215 - 5221
FCN1	Ficolin (collagen/fibrinogen domain containing) 1	SEQ ID NOS: 5222 - 5223
FCN2	Ficolin (collagen/fibrinogen domain containing lectin) 2	SEQ ID NOS: 5224 - 5225
FCN3	Ficolin (collagen/fibrinogen domain containing) 3	SEQ ID NOS: 5226 - 5227
FCRL1	Fc receptor-like 1	SEQ ID NOS: 5228 - 5230
FCRL3	Fc receptor-like 3	SEQ ID NOS: 5231 - 5236
FCRL5	Fc receptor-like 5	SEQ ID NOS: 5237 - 5239

FCRLA	Fc receptor-like A	SEQ ID NOS: 5240 - 5251
FCRLB	Fc receptor-like B	SEQ ID NOS: 5252 - 5256
FDCSP	Follicular dendritic cell secreted protein	SEQ ID NO: 5257
FETUB	Fetuin B	SEQ ID NOS: 5258 - 5264
FGA	Fibrinogen alpha chain	SEQ ID NOS: 5265 - 5267
FGB	Fibrinogen beta chain	SEQ ID NOS: 5268 - 5270
FGF10	Fibroblast growth factor 10	SEQ ID NOS: 5271 - 5272
FGF17	Fibroblast growth factor 17	SEQ ID NOS: 5273 - 5274
FGF18	Fibroblast growth factor 18	SEQ ID NO: 5275
FGF19	Fibroblast growth factor 19	SEQ ID NO: 5276
FGF21	Fibroblast growth factor 21	SEQ ID NOS: 5277 - 5278
FGF22	Fibroblast growth factor 22	SEQ ID NOS: 5279 - 5280
FGF23	Fibroblast growth factor 23	SEQ ID NO: 5281
FGF3	Fibroblast growth factor 3	SEQ ID NO: 5282
FGF4	Fibroblast growth factor 4	SEQ ID NO: 5283
FGF5	Fibroblast growth factor 5	SEQ ID NOS: 5284 - 5286
FGF7	Fibroblast growth factor 7	SEQ ID NOS: 5287 - 5291
FGF8	Fibroblast growth factor 8 (androgen-induced)	SEQ ID NOS: 5292 - 5297
FGFBP1	Fibroblast growth factor binding protein 1	SEQ ID NO: 5298
FGFBP2	Fibroblast growth factor binding protein 2	SEQ ID NO: 5299
FGFBP3	Fibroblast growth factor binding protein 3	SEQ ID NO: 5300
FGFR1	Fibroblast growth factor receptor 1	SEQ ID NOS: 5301 - 5322
FGFR2	Fibroblast growth factor receptor 2	SEQ ID NOS: 5323 - 5344
FGFR3	Fibroblast growth factor receptor 3	SEQ ID NOS: 5345 - 5352
FGFR4	Fibroblast growth factor receptor 4	SEQ ID NOS: 5353 - 5362
FGFRL1	Fibroblast growth factor receptor-like 1	SEQ ID NOS: 5363 - 5368

FGG	Fibrinogen gamma chain	SEQ ID NOS: 5369 - 5374
FGL1	Fibrinogen-like 1	SEQ ID NOS: 5375 - 5381
FGL2	Fibrinogen-like 2	SEQ ID NOS: 5382 - 5383
FHL1	Four and a half LIM domains 1	SEQ ID NOS: 5384 - 5411
FHOD3	Formin homology 2 domain containing 3	SEQ ID NOS: 5412 - 5418
FIBIN	Fin bud initiation factor homolog (zebrafish)	SEQ ID NO: 5419
FICD	FIC domain containing	SEQ ID NOS: 5420 - 5423
FIGF	C-fos induced growth factor (vascular endothelial growth factor D)	SEQ ID NO: 14054
FJX1	Four jointed box 1	SEQ ID NO: 5424
FKBP10	FK506 binding protein 10, 65 kDa	SEQ ID NOS: 5425 - 5430
FKBP11	FK506 binding protein 11, 19 kDa	SEQ ID NOS: 5431 - 5437
FKBP14	FK506 binding protein 14, 22 kDa	SEQ ID NOS: 5438 - 5440
FKBP2	FK506 binding protein 2, 13kDa	SEQ ID NOS: 5441 - 5444
FKBP7	FK506 binding protein 7	SEQ ID NOS: 5445 - 5450
FKBP9	FK506 binding protein 9, 63 kDa	SEQ ID NOS: 5451 - 5454
FLT1	Fms-related tyrosine kinase 1	SEQ ID NOS: 5455 - 5463
FLT4	Fms-related tyrosine kinase 4	SEQ ID NOS: 5464 - 5468
FMO1	Flavin containing monooxygenase 1	SEQ ID NOS: 5469 - 5473
FMO2	Flavin containing monooxygenase 2 (non-functional)	SEQ ID NOS: 5474 - 5476
FMO3	Flavin containing monooxygenase 3	SEQ ID NOS: 5477 - 5479
FMO5	Flavin containing monooxygenase 5	SEQ ID NOS: 5480 - 5486
FMOD	Fibromodulin	SEQ ID NO: 5487
FN1	Fibronectin 1	SEQ ID NOS: 5488 - 5500

FNDC1	Fibronectin type III domain containing 1	SEQ ID NOS: 5501 - 5502
FNDC7	Fibronectin type III domain containing 7	SEQ ID NOS: 5503 - 5504
FOCAD	Focadhesin	SEQ ID NOS: 5505 - 5511
FOLR2	Folate receptor 2 (fetal)	SEQ ID NOS: 5512 - 5521
FOLR3	Folate receptor 3 (gamma)	SEQ ID NOS: 5522 - 5526
FOXRED2	FAD-dependent oxidoreductase domain containing 2	SEQ ID NOS: 5527 - 5530
FP325331.1	Uncharacterized protein UNQ6126/PRO20091	SEQ ID NO: 5531
FPGS	Folylpolyglutamate synthase	SEQ ID NOS: 5539 - 5545
FRAS1	Fraser extracellular matrix complex subunit 1	SEQ ID NOS: 5546 - 5551
FREM1	FRAS1 related extracellular matrix 1	SEQ ID NOS: 5552 - 5556
FREM3	FRAS1 related extracellular matrix 3	SEQ ID NO: 5557
FRMPD2	FERM and PDZ domain containing 2	SEQ ID NOS: 5558 - 5561
FRZB	Frizzled-related protein	SEQ ID NO: 5562
FSHB	Follicle stimulating hormone, beta polypeptide	SEQ ID NOS: 5563 - 5565
FSHR	Follicle stimulating hormone receptor	SEQ ID NOS: 5566 - 5569
FST	Follistatin	SEQ ID NOS: 5570 - 5573
FSTL1	Follistatin-like 1	SEQ ID NOS: 5574 - 5577
FSTL3	Follistatin-like 3 (secreted glycoprotein)	SEQ ID NOS: 5578 - 5583
FSTL4	Follistatin-like 4	SEQ ID NOS: 5584 - 5586
FSTL5	Follistatin-like 5	SEQ ID NOS: 5587 - 5589
FTCDNL1	Formiminotransferase cyclodeaminase N-terminal like	SEQ ID NOS: 5590 - 5593
FUCA1	Fucosidase, alpha-L- 1, tissue	SEQ ID NO: 5594
FUCA2	Fucosidase, alpha-L- 2, plasma	SEQ ID NOS: 5595 - 5596
FURIN	Furin (paired basic amino acid cleaving enzyme)	SEQ ID NOS: 5597 - 5603

FUT10	Fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	SEQ ID NOS: 5604 - 5606
FUT11	Fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	SEQ ID NOS: 5607 - 5608
FXN	Frataxin	SEQ ID NOS: 5609 - 5616
FXR1	Fragile X mental retardation, autosomal homolog 1	SEQ ID NOS: 5617 - 5629
FXYD3	FXYD domain containing ion transport regulator 3	SEQ ID NOS: 5630 - 5642
GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1	SEQ ID NOS: 5643 - 5654
GABRA1	Gamma-aminobutyric acid (GABA) A receptor, alpha 1	SEQ ID NOS: 5655 - 5670
GABRA2	Gamma-aminobutyric acid (GABA) A receptor, alpha 2	SEQ ID NOS: 5671 - 5685
GABRA5	Gamma-aminobutyric acid (GABA) A receptor, alpha 5	SEQ ID NOS: 5686 - 5694
GABRG3	Gamma-aminobutyric acid (GABA) A receptor, gamma 3	SEQ ID NOS: 5695 - 5700
GABRP	Gamma-aminobutyric acid (GABA) A receptor, pi	SEQ ID NOS: 5701 - 5709
GAL	Galanin/GMAP prepropeptide	SEQ ID NO: 5710
GAL3ST1	Galactose-3-O-sulfotransferase 1	SEQ ID NOS: 5711 - 5732
GAL3ST2	Galactose-3-O-sulfotransferase 2	SEQ ID NO: 5733
GAL3ST3	Galactose-3-O-sulfotransferase 3	SEQ ID NOS: 5734 - 5735
GALC	Galactosylceramidase	SEQ ID NOS: 5736 - 5745
GALNS	Galactosamine (N-acetyl)-6-sulfatase	SEQ ID NOS: 5746 - 5751
GALNT10	Polypeptide N-acetylgalactosaminyltransferase 10	SEQ ID NOS: 5752 - 5755
GALNT12	Polypeptide N-acetylgalactosaminyltransferase 12	SEQ ID NOS: 5756 - 5757
GALNT15	Polypeptide N-acetylgalactosaminyltransferase 15	SEQ ID NOS: 5758 - 5761
GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	SEQ ID NO: 5762
GALNT6	Polypeptide N-acetylgalactosaminyltransferase 6	SEQ ID NOS: 5763 - 5774
GALNT8	Polypeptide N-acetylgalactosaminyltransferase 8	SEQ ID NOS: 5775 - 5778

GALNTL6	Polypeptide N-acetylgalactosaminyltransferase-like 6	SEQ ID NOS: 5779 - 5782
GALP	Galanin-like peptide	SEQ ID NOS: 5783 - 5785
GANAB	Glucosidase, alpha; neutral AB	SEQ ID NOS: 5786 - 5794
GARS	Glycyl-tRNA synthetase	SEQ ID NOS: 5795 - 5798
GAS1	Growth arrest-specific 1	SEQ ID NO: 5799
GAS6	Growth arrest-specific 6	SEQ ID NO: 5800
GAST	Gastrin	SEQ ID NO: 5801
GBA	Glucosidase, beta, acid	SEQ ID NOS: 5811 - 5814
GBGT1	Globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	SEQ ID NOS: 5815 - 5823
GC	Group-specific component (vitamin D binding protein)	SEQ ID NOS: 5824 - 5828
GCG	Glucagon	SEQ ID NOS: 5829 - 5830
GCGR	Glucagon receptor	SEQ ID NOS: 5831 - 5833
GCNT7	Glucosaminyl (N-acetyl) transferase family member 7	SEQ ID NOS: 5834 - 5835
GCSH	Glycine cleavage system protein H (aminomethyl carrier)	SEQ ID NOS: 5836 - 5844
GDF1	Growth differentiation factor 1	SEQ ID NO: 5845
GDF10	Growth differentiation factor 10	SEQ ID NO: 5846
GDF11	Growth differentiation factor 11	SEQ ID NOS: 5847 - 5848
GDF15	Growth differentiation factor 15	SEQ ID NOS: 5849 - 5851
GDF2	Growth differentiation factor 2	SEQ ID NO: 5852
GDF3	Growth differentiation factor 3	SEQ ID NO: 5853
GDF5	Growth differentiation factor 5	SEQ ID NOS: 5854 - 5855
GDF6	Growth differentiation factor 6	SEQ ID NOS: 5856 - 5858
GDF7	Growth differentiation factor 7	SEQ ID NO: 5859
GDF9	Growth differentiation factor 9	SEQ ID NOS: 5860 - 5864
GDNF	Glial cell derived neurotrophic factor	SEQ ID NOS: 5865 - 5872
GFOD2	Glucose-fructose oxidoreductase domain containing 2	SEQ ID NOS: 5873 - 5878

GFPT2	Glutamine-fructose-6-phosphate transaminase 2	SEQ ID NOS: 5879 - 5881
GFRA2	GDNF family receptor alpha 2	SEQ ID NOS: 5882 - 5888
GFRA4	GDNF family receptor alpha 4	SEQ ID NOS: 5889 - 5891
GGA2	Golgi-associated, gamma adaptin ear containing, ARF binding protein 2	SEQ ID NOS: 5892 - 5900
GGH	Gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	SEQ ID NO: 5901
GGT1	Gamma-glutamyltransferase 1	SEQ ID NOS: 5902 - 5924
GGT5	Gamma-glutamyltransferase 5	SEQ ID NOS: 5925 - 5929
GH1	Growth hormone 1	SEQ ID NOS: 5930 - 5934
GH2	Growth hormone 2	SEQ ID NOS: 5935 - 5939
GHDC	GH3 domain containing	SEQ ID NOS: 5940 - 5947
GHRH	Growth hormone releasing hormone	SEQ ID NOS: 5948 - 5950
GHRHR	Growth hormone releasing hormone receptor	SEQ ID NOS: 5951 - 5956
GHRL	Ghrelin/obestatin prepropeptide	SEQ ID NOS: 5957 - 5967
GIF	Gastric intrinsic factor (vitamin B synthesis)	SEQ ID NOS: 5968 - 5969
GIP	Gastric inhibitory polypeptide	SEQ ID NO: 5970
GKN1	Gastrokine 1	SEQ ID NO: 5971
GKN2	Gastrokine 2	SEQ ID NOS: 5972 - 5973
GLA	Galactosidase, alpha	SEQ ID NOS: 5974 - 5975
GLB1	Galactosidase, beta 1	SEQ ID NOS: 5976 - 5984
GLB1L	Galactosidase, beta 1-like	SEQ ID NOS: 5985 - 5992
GLB1L2	Galactosidase, beta 1-like 2	SEQ ID NOS: 5993 - 5994
GLCE	Glucuronic acid epimerase	SEQ ID NOS: 5995 - 5996
GLG1	Golgi glycoprotein 1	SEQ ID NOS: 5997 - 6004

GLIPR1	GLI pathogenesis-related 1	SEQ ID NOS: 6005 - 6008
GLIPR1L1	GLI pathogenesis-related 1 like 1	SEQ ID NOS: 6009 - 6012
GLIS3	GLIS family zinc finger 3	SEQ ID NOS: 6013 - 6021
GLMP	Glycosylated lysosomal membrane protein	SEQ ID NOS: 6022 - 6030
GLRB	Glycine receptor, beta	SEQ ID NOS: 6031 - 6036
GLS	Glutaminase	SEQ ID NOS: 6037 - 6044
GLT6D1	Glycosyltransferase 6 domain containing 1	SEQ ID NOS: 6045 - 6046
GLTPD2	Glycolipid transfer protein domain containing 2	SEQ ID NO: 6047
GLUD1	Glutamate dehydrogenase 1	SEQ ID NO: 6048
GM2A	GM2 ganglioside activator	SEQ ID NOS: 6049 - 6051
GML	Glycosylphosphatidylinositol anchored molecule like	SEQ ID NOS: 6052 - 6053
GNAS	GNAS complex locus	SEQ ID NOS: 6054 - 6075
GNLY	Granulysin	SEQ ID NOS: 6076 - 6079
GNPTG	N-acetylglucosamine-1-phosphate transferase, gamma subunit	SEQ ID NOS: 6080 - 6084
GNRH1	Gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	SEQ ID NOS: 6085 - 6086
GNRH2	Gonadotropin-releasing hormone 2	SEQ ID NOS: 6087 - 6090
GNS	Glucosamine (N-acetyl)-6-sulfatase	SEQ ID NOS: 6091 - 6096
GOLM1	Golgi membrane protein 1	SEQ ID NOS: 6097 - 6101
GORAB	Golgin, RAB6-interacting	SEQ ID NOS: 6102 - 6104
GOT2	Glutamic-oxaloacetic transaminase 2, mitochondrial	SEQ ID NOS: 6105 - 6107
GP2	Glycoprotein 2 (zymogen granule membrane)	SEQ ID NOS: 6108 - 6116
GP6	Glycoprotein VI (platelet)	SEQ ID NOS: 6117 - 6120
GPC2	Glypican 2	SEQ ID NOS: 6121 - 6122

GPC5	Glypican 5	SEQ ID NOS: 6123 - 6125
GPC6	Glypican 6	SEQ ID NOS: 6126 - 6127
GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	SEQ ID NOS: 6128 - 6136
GPER1	G protein-coupled estrogen receptor 1	SEQ ID NOS: 6137 - 6143
GPHA2	Glycoprotein hormone alpha 2	SEQ ID NOS: 6144 - 6146
GPHB5	Glycoprotein hormone beta 5	SEQ ID NOS: 6147 - 6148
GPIHBP1	Glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	SEQ ID NO: 6149
GPLD1	Glycosylphosphatidylinositol specific phospholipase D1	SEQ ID NO: 6150
GPNMB	Glycoprotein (transmembrane) nmb	SEQ ID NOS: 6151 - 6153
GPR162	G protein-coupled receptor 162	SEQ ID NOS: 6154 - 6157
GPX3	Glutathione peroxidase 3	SEQ ID NOS: 6158 - 6165
GPX4	Glutathione peroxidase 4	SEQ ID NOS: 6166 - 6176
GPX5	Glutathione peroxidase 5	SEQ ID NOS: 6177 - 6178
GPX6	Glutathione peroxidase 6	SEQ ID NOS: 6179 - 6181
GPX7	Glutathione peroxidase 7	SEQ ID NO: 6182
GREM1	Gremlin 1, DAN family BMP antagonist	SEQ ID NOS: 6183 - 6185
GREM2	Gremlin 2, DAN family BMP antagonist	SEQ ID NO: 6186
GRHL3	Grainyhead-like transcription factor 3	SEQ ID NOS: 6187 - 6192
GRIA2	Glutamate receptor, ionotropic, AMPA 2	SEQ ID NOS: 6193 - 6204
GRIA3	Glutamate receptor, ionotropic, AMPA 3	SEQ ID NOS: 6205 - 6210
GRIA4	Glutamate receptor, ionotropic, AMPA 4	SEQ ID NOS: 6211 - 6222
GRIK2	Glutamate receptor, ionotropic, kainate 2	SEQ ID NOS: 6223 - 6231
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	SEQ ID NOS: 6232 - 6235

GRM2	Glutamate receptor, metabotropic 2	SEQ ID NOS: 6236 - 6239
GRM3	Glutamate receptor, metabotropic 3	SEQ ID NOS: 6240 - 6244
GRM5	Glutamate receptor, metabotropic 5	SEQ ID NOS: 6245 - 6249
GRN	Granulin	SEQ ID NOS: 6250 - 6265
GRP	Gastrin-releasing peptide	SEQ ID NOS: 6266 - 6270
GSG1	Germ cell associated 1	SEQ ID NOS: 6280 - 6288
GSN	Gelsolin	SEQ ID NOS: 6289 - 6297
GTDC1	Glycosyltransferase-like domain containing 1	SEQ ID NOS: 6298 - 6311
GTPBP10	GTP-binding protein 10 (putative)	SEQ ID NOS: 6312 - 6320
GUCA2A	Guanylate cyclase activator 2A (guanylin)	SEQ ID NO: 6321
GUCA2B	Guanylate cyclase activator 2B (uroguanylin)	SEQ ID NO: 6322
GUSB	Glucuronidase, beta	SEQ ID NOS: 6323 - 6327
GVQW1	GVQW motif containing 1	SEQ ID NO: 6328
GXYLT1	Glucoside xylosyltransferase 1	SEQ ID NOS: 6329 - 6330
GXYLT2	Glucoside xylosyltransferase 2	SEQ ID NOS: 6331 - 6333
GYLTL1B	Glycosyltransferase-like 1B	SEQ ID NOS: 7702 - 7707
GYPB	Glycophorin B (MNS blood group)	SEQ ID NOS: 6334 - 6342
GZMA	Granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	SEQ ID NO: 6343
GZMB	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	SEQ ID NOS: 6344 - 6352
GZMH	Granzyme H (cathepsin G-like 2, protein h-CCPX)	SEQ ID NOS: 6353 - 6355
GZMK	Granzyme K (granzyme 3; tryptase II)	SEQ ID NO: 6356
GZMM	Granzyme M (lymphocyte met-ase 1)	SEQ ID NOS: 6357 - 6358
H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	SEQ ID NOS: 6359 - 6360
HABP2	Hyaluronan binding protein 2	SEQ ID NOS: 6361 - 6362

HADHB	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	SEQ ID NOS: 6363 - 6369
HAMP	Hepcidin antimicrobial peptide	SEQ ID NOS: 6370 - 6371
HAPLN1	Hyaluronan and proteoglycan link protein 1	SEQ ID NOS: 6372 - 6378
HAPLN2	Hyaluronan and proteoglycan link protein 2	SEQ ID NOS: 6379 - 6380
HAPLN3	Hyaluronan and proteoglycan link protein 3	SEQ ID NOS: 6381 - 6384
HAPLN4	Hyaluronan and proteoglycan link protein 4	SEQ ID NO: 6385
HARS2	Histidyl-tRNA synthetase 2, mitochondrial	SEQ ID NOS: 6386 - 6401
HAVCR1	Hepatitis A virus cellular receptor 1	SEQ ID NOS: 6402 - 6406
HCCS	Holocytochrome c synthase	SEQ ID NOS: 6407 - 6409
HCRT	Hypocretin (orexin) neuropeptide precursor	SEQ ID NO: 6410
HEATR5A	HEAT repeat containing 5A	SEQ ID NOS: 6414 - 6420
HEPH	Hephaestin	SEQ ID NOS: 6421 - 6428
HEXA	Hexosaminidase A (alpha polypeptide)	SEQ ID NOS: 6429 - 6438
HEXB	Hexosaminidase B (beta polypeptide)	SEQ ID NOS: 6439 - 6444
HFE2	Hemochromatosis type 2 (juvenile)	SEQ ID NOS: 6445 - 6451
HGF	Hepatocyte growth factor (hepapoietin A; scatter factor)	SEQ ID NOS: 6452 - 6462
HGFAC	HGF activator	SEQ ID NOS: 6463 - 6464
HHIP	Hedgehog interacting protein	SEQ ID NOS: 6465 - 6466
HHIPL1	HHIP-like 1	SEQ ID NOS: 6467 - 6468
HHIPL2	HHIP-like 2	SEQ ID NO: 6469
HHLA1	HERV-H LTR-associating 1	SEQ ID NOS: 6470 - 6471
HHLA2	HERV-H LTR-associating 2	SEQ ID NOS: 6472 - 6482
HIBADH	3-hydroxyisobutyrate dehydrogenase	SEQ ID NOS: 6483 - 6485
HINT2	Histidine triad nucleotide binding protein 2	SEQ ID NO: 6486

HLA-A	Major histocompatibility complex, class I, A	SEQ ID NOS: 6487 - 6491
HLA-C	Major histocompatibility complex, class I, C	SEQ ID NOS: 6492 - 6496
HLA-DOA	Major histocompatibility complex, class II, DO alpha	SEQ ID NOS: 6497 - 6498
HLA-DPA1	Major histocompatibility complex, class II, DP alpha 1	SEQ ID NOS: 6499 - 6502
HLA-DQA1	Major histocompatibility complex, class II, DQ alpha 1	SEQ ID NOS: 6503 - 6508
HLA-DQB1	Major histocompatibility complex, class II, DQ beta 1	SEQ ID NOS: 6509 - 6514
HLA-DQB2	Major histocompatibility complex, class II, DQ beta 2	SEQ ID NOS: 6515 - 6518
HMCN1	Hemicentin 1	SEQ ID NOS: 6519 - 6520
HMCN2	Hemicentin 2	SEQ ID NOS: 6521 - 6524
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	SEQ ID NOS: 6525 - 6528
HMHA1	Histocompatibility (minor) HA-1	SEQ ID NOS: 1034 - 1042
HMSD	Histocompatibility (minor) serpin domain containing	SEQ ID NOS: 6529 - 6530
HP	Haptoglobin	SEQ ID NOS: 6531 - 6544
HPR	Haptoglobin-related protein	SEQ ID NOS: 6545 - 6547
HPSE	Heparanase	SEQ ID NOS: 6548 - 6554
HPSE2	Heparanase 2 (inactive)	SEQ ID NOS: 6555 - 6560
HPX	Hemopexin	SEQ ID NOS: 6561 - 6562
HRC	Histidine rich calcium binding protein	SEQ ID NOS: 6563 - 6565
HRG	Histidine-rich glycoprotein	SEQ ID NO: 6566
HRSP12	Heat-responsive protein 12	SEQ ID NOS: 11389 - 11392
HS2ST1	Heparan sulfate 2-O-sulfotransferase 1	SEQ ID NOS: 6567 - 6569
HS3ST1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	SEQ ID NOS: 6570 - 6572
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	SEQ ID NO: 6573

HS6ST3	Heparan sulfate 6-O-sulfotransferase 3	SEQ ID NOS: 6574 - 6575
HSD11B1L	Hydroxysteroid (11-beta) dehydrogenase 1-like	SEQ ID NOS: 6576 - 6594
HSD17B11	Hydroxysteroid (17-beta) dehydrogenase 11	SEQ ID NOS: 6595 - 6596
HSD17B7	Hydroxysteroid (17-beta) dehydrogenase 7	SEQ ID NOS: 6597 - 6601
HSP90B1	Heat shock protein 90kDa beta (Grp94), member 1	SEQ ID NOS: 6602 - 6607
HSPA13	Heat shock protein 70kDa family, member 13	SEQ ID NO: 6608
HSPA5	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	SEQ ID NO: 6609
HSPG2	Heparan sulfate proteoglycan 2	SEQ ID NOS: 6610 - 6614
HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	SEQ ID NOS: 6615 - 6622
HTN1	Histatin 1	SEQ ID NOS: 6623 - 6625
HTN3	Histatin 3	SEQ ID NOS: 6626 - 6628
HTRA1	HtrA serine peptidase 1	SEQ ID NOS: 6629 - 6630
HTRA3	HtrA serine peptidase 3	SEQ ID NOS: 6631 - 6632
HTRA4	HtrA serine peptidase 4	SEQ ID NO: 6633
HYAL1	Hyaluronoglucosaminidase 1	SEQ ID NOS: 6634 - 6642
HYAL2	Hyaluronoglucosaminidase 2	SEQ ID NOS: 6643 - 6651
HYAL3	Hyaluronoglucosaminidase 3	SEQ ID NOS: 6652 - 6658
HYOU1	Hypoxia up-regulated 1	SEQ ID NOS: 6659 - 6673
IAPP	Islet amyloid polypeptide	SEQ ID NOS: 6674 - 6678
IBSP	Integrin-binding sialoprotein	SEQ ID NO: 6679
ICAM1	Intercellular adhesion molecule 1	SEQ ID NOS: 6680 - 6682
ICAM2	Intercellular adhesion molecule 2	SEQ ID NOS: 6683 - 6693
ICAM4	Intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	SEQ ID NOS: 6694 - 6696

ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	SEQ ID NOS: 6697 - 6698
IDE	Insulin-degrading enzyme	SEQ ID NOS: 6699 - 6702
IDNK	IdnK, gluconokinase homolog (E. coli)	SEQ ID NOS: 6703 - 6708
IDS	Iduronate 2-sulfatase	SEQ ID NOS: 6709 - 6714
IDUA	Iduronidase, alpha-L-	SEQ ID NOS: 6715 - 6720
IFI27L2	Interferon, alpha-inducible protein 27-like 2	SEQ ID NOS: 6721 - 6722
IFI30	Interferon, gamma-inducible protein 30	SEQ ID NOS: 6723 - 6724
IFNA1	Interferon, alpha 1	SEQ ID NO: 6725
IFNA10	Interferon, alpha 10	SEQ ID NO: 6726
IFNA13	Interferon, alpha 13	SEQ ID NOS: 6727 - 6728
IFNA14	Interferon, alpha 14	SEQ ID NO: 6729
IFNA16	Interferon, alpha 16	SEQ ID NO: 6730
IFNA17	Interferon, alpha 17	SEQ ID NO: 6731
IFNA2	Interferon, alpha 2	SEQ ID NO: 6732
IFNA21	Interferon, alpha 21	SEQ ID NO: 6733
IFNA4	Interferon, alpha 4	SEQ ID NO: 6734
IFNA5	Interferon, alpha 5	SEQ ID NO: 6735
IFNA6	Interferon, alpha 6	SEQ ID NOS: 6736 - 6737
IFNA7	Interferon, alpha 7	SEQ ID NO: 6738
IFNA8	Interferon, alpha 8	SEQ ID NO: 6739
IFNAR1	Interferon (alpha, beta and omega) receptor 1	SEQ ID NOS: 6740 - 6741
IFNB1	Interferon, beta 1, fibroblast	SEQ ID NO: 6742
IFNE	Interferon, epsilon	SEQ ID NO: 6743
IFNG	Interferon, gamma	SEQ ID NO: 6744
IFNGR1	Interferon gamma receptor 1	SEQ ID NOS: 6745 - 6755
IFNL1	Interferon, lambda 1	SEQ ID NO: 6756
IFNL2	Interferon, lambda 2	SEQ ID NO: 6757
IFNL3	Interferon, lambda 3	SEQ ID NOS: 6758 - 6759
IFNLR1	Interferon, lambda receptor 1	SEQ ID NOS: 6760 - 6764
IFNW1	Interferon, omega 1	SEQ ID NO: 6765

IGF1	Insulin-like growth factor 1 (somatomedin C)	SEQ ID NOS: 6766 - 6771
IGF2	Insulin-like growth factor 2	SEQ ID NOS: 6772 - 6779
IGFALS	Insulin-like growth factor binding protein, acid labile subunit	SEQ ID NOS: 6780 - 6782
IGFBP1	Insulin-like growth factor binding protein 1	SEQ ID NOS: 6783 - 6785
IGFBP2	Insulin-like growth factor binding protein 2, 36kDa	SEQ ID NOS: 6786 - 6789
IGFBP3	Insulin-like growth factor binding protein 3	SEQ ID NOS: 6790 - 6797
IGFBP4	Insulin-like growth factor binding protein 4	SEQ ID NO: 6798
IGFBP5	Insulin-like growth factor binding protein 5	SEQ ID NOS: 6799 - 6800
IGFBP6	Insulin-like growth factor binding protein 6	SEQ ID NOS: 6801 - 6803
IGFBP7	Insulin-like growth factor binding protein 7	SEQ ID NOS: 6804 - 6805
IGFBPL1	Insulin-like growth factor binding protein-like 1	SEQ ID NO: 6806
IGFL1	IGF-like family member 1	SEQ ID NO: 6807
IGFL2	IGF-like family member 2	SEQ ID NOS: 6808 - 6810
IGFL3	IGF-like family member 3	SEQ ID NO: 6811
IGFLR1	IGF-like family receptor 1	SEQ ID NOS: 6812 - 6820
IGIP	IgA-inducing protein	SEQ ID NO: 6821
IGLON5	IgLON family member 5	SEQ ID NO: 6822
IGSF1	Immunoglobulin superfamily, member 1	SEQ ID NOS: 6823 - 6828
IGSF10	Immunoglobulin superfamily, member 10	SEQ ID NOS: 6829 - 6830
IGSF11	Immunoglobulin superfamily, member 11	SEQ ID NOS: 6831 - 6838
IGSF21	Immunoglobin superfamily, member 21	SEQ ID NO: 6839
IGSF8	Immunoglobulin superfamily, member 8	SEQ ID NOS: 6840 - 6843
IGSF9	Immunoglobulin superfamily, member 9	SEQ ID NOS: 6844 - 6846
IHH	Indian hedgehog	SEQ ID NO: 6847
IL10	Interleukin 10	SEQ ID NOS: 6848 - 6849

IL11	Interleukin 11	SEQ ID NOS: 6850 - 6853
IL11RA	Interleukin 11 receptor, alpha	SEQ ID NOS: 6854 - 6864
IL12B	Interleukin 12B	SEQ ID NO: 6865
IL12RB1	Interleukin 12 receptor, beta 1	SEQ ID NOS: 6866 - 6871
IL12RB2	Interleukin 12 receptor, beta 2	SEQ ID NOS: 6872 - 6876
IL13	Interleukin 13	SEQ ID NOS: 6877 - 6878
IL13RA1	Interleukin 13 receptor, alpha 1	SEQ ID NOS: 6879 - 6880
IL15RA	Interleukin 15 receptor, alpha	SEQ ID NOS: 6881 - 6898
IL17A	Interleukin 17A	SEQ ID NO: 6899
IL17B	Interleukin 17B	SEQ ID NO: 6900
IL17C	Interleukin 17C	SEQ ID NO: 6901
IL17D	Interleukin 17D	SEQ ID NOS: 6902 - 6904
IL17F	Interleukin 17F	SEQ ID NO: 6905
IL17RA	Interleukin 17 receptor A	SEQ ID NOS: 6906 - 6907
IL17RC	Interleukin 17 receptor C	SEQ ID NOS: 6908 - 6923
IL17RE	Interleukin 17 receptor E	SEQ ID NOS: 6924 - 6930
IL18BP	Interleukin 18 binding protein	SEQ ID NOS: 6931 - 6941
IL18R1	Interleukin 18 receptor 1	SEQ ID NOS: 6942 - 6945
IL18RAP	Interleukin 18 receptor accessory protein	SEQ ID NOS: 6946 - 6948
IL19	Interleukin 19	SEQ ID NOS: 6949 - 6951
IL1R1	Interleukin 1 receptor, type I	SEQ ID NOS: 6952 - 6964
IL1R2	Interleukin 1 receptor, type II	SEQ ID NOS: 6965 - 6968
IL1RAP	Interleukin 1 receptor accessory protein	SEQ ID NOS: 6969 - 6982
IL1RL1	Interleukin 1 receptor-like 1	SEQ ID NOS: 6983 - 6988
IL1RL2	Interleukin 1 receptor-like 2	SEQ ID NOS: 6989 - 6991

IL1RN	Interleukin 1 receptor antagonist	SEQ ID NOS: 6992 - 6996
IL2	Interleukin 2	SEQ ID NO: 6997
IL20	Interleukin 20	SEQ ID NOS: 6998 - 7000
IL20RA	Interleukin 20 receptor, alpha	SEQ ID NOS: 7001 - 7007
IL21	Interleukin 21	SEQ ID NOS: 7008 - 7009
IL22	Interleukin 22	SEQ ID NOS: 7010 - 7011
IL22RA2	Interleukin 22 receptor, alpha 2	SEQ ID NOS: 7012 - 7014
IL23A	Interleukin 23, alpha subunit p19	SEQ ID NO: 7015
IL24	Interleukin 24	SEQ ID NOS: 7016 - 7021
IL25	Interleukin 25	SEQ ID NOS: 7022 - 7023
IL26	Interleukin 26	SEQ ID NO: 7024
IL27	Interleukin 27	SEQ ID NOS: 7025 - 7026
IL2RB	Interleukin 2 receptor, beta	SEQ ID NOS: 7027 - 7031
IL3	Interleukin 3	SEQ ID NO: 7032
IL31	Interleukin 31	SEQ ID NO: 7033
IL31RA	Interleukin 31 receptor A	SEQ ID NOS: 7034 - 7041
IL32	Interleukin 32	SEQ ID NOS: 7042 - 7071
IL34	Interleukin 34	SEQ ID NOS: 7072 - 7075
IL3RA	Interleukin 3 receptor, alpha (low affinity)	SEQ ID NOS: 7076 - 7078
IL4	Interleukin 4	SEQ ID NOS: 7079 - 7081
IL4I1	Interleukin 4 induced 1	SEQ ID NOS: 7082 - 7089
IL4R	Interleukin 4 receptor	SEQ ID NOS: 7090 - 7103
IL5	Interleukin 5	SEQ ID NOS: 7104 - 7105
IL5RA	Interleukin 5 receptor, alpha	SEQ ID NOS: 7106 - 7115
IL6	Interleukin 6	SEQ ID NOS: 7116 - 7122

IL6R	Interleukin 6 receptor	SEQ ID NOS: 7123 - 7128
IL6ST	Interleukin 6 signal transducer	SEQ ID NOS: 7129 - 7138
IL7	Interleukin 7	SEQ ID NOS: 7139 - 7146
IL7R	Interleukin 7 receptor	SEQ ID NOS: 7147 - 7153
IL9	Interleukin 9	SEQ ID NO: 7154
ILDR1	Immunoglobulin-like domain containing receptor 1	SEQ ID NOS: 7155 - 7159
ILDR2	Immunoglobulin-like domain containing receptor 2	SEQ ID NOS: 7160 - 7166
IMP4	IMP4, U3 small nucleolar ribonucleoprotein	SEQ ID NOS: 7167 - 7172
IMPG1	Interphotoreceptor matrix proteoglycan 1	SEQ ID NOS: 7173 - 7176
INHA	Inhibin, alpha	SEQ ID NO: 7177
INHBA	Inhibin, beta A	SEQ ID NOS: 7178 - 7180
INHBB	Inhibin, beta B	SEQ ID NO: 7181
INHBC	Inhibin, beta C	SEQ ID NO: 7182
INHBE	Inhibin, beta E	SEQ ID NOS: 7183 - 7184
INPP5A	Inositol polyphosphate-5-phosphatase A	SEQ ID NOS: 7185 - 7189
INS	Insulin	SEQ ID NOS: 7190 - 7194
INS-IGF2	INS-IGF2 readthrough	SEQ ID NOS: 7195 - 7196
INSL3	Insulin-like 3 (Leydig cell)	SEQ ID NOS: 7197 - 7199
INSL4	Insulin-like 4 (placenta)	SEQ ID NO: 7200
INSL5	Insulin-like 5	SEQ ID NO: 7201
INSL6	Insulin-like 6	SEQ ID NO: 7202
INTS3	Integrator complex subunit 3	SEQ ID NOS: 7203 - 7208
IPO11	Importin 11	SEQ ID NOS: 7209 - 7217
IPO9	Importin 9	SEQ ID NOS: 7218 - 7219
IQCF6	IQ motif containing F6	SEQ ID NOS: 7220 - 7221

IRAK3	Interleukin-1 receptor-associated kinase 3	SEQ ID NOS: 7222 - 7224
IRS4	Insulin receptor substrate 4	SEQ ID NO: 7225
ISLR	Immunoglobulin superfamily containing leucine-rich repeat	SEQ ID NOS: 7226 - 7229
ISLR2	Immunoglobulin superfamily containing leucine-rich repeat 2	SEQ ID NOS: 7230 - 7239
ISM1	Isthmin 1, angiogenesis inhibitor	SEQ ID NO: 7240
ISM2	Isthmin 2	SEQ ID NOS: 7241 - 7246
ITGA4	Integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	SEQ ID NOS: 7247 - 7249
ITGA9	Integrin, alpha 9	SEQ ID NOS: 7250 - 7252
ITGAL	Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	SEQ ID NOS: 7253 - 7262
ITGAX	Integrin, alpha X (complement component 3 receptor 4 subunit)	SEQ ID NOS: 7263 - 7265
ITGB1	Integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	SEQ ID NOS: 7266 - 7281
ITGB2	Integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	SEQ ID NOS: 7282 - 7298
ITGB3	Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	SEQ ID NOS: 7299 - 7301
ITGB7	Integrin, beta 7	SEQ ID NOS: 7302 - 7309
ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	SEQ ID NOS: 7310 - 7315
ITIH1	Inter-alpha-trypsin inhibitor heavy chain 1	SEQ ID NOS: 7316 - 7321
ITIH2	Inter-alpha-trypsin inhibitor heavy chain 2	SEQ ID NOS: 7322 - 7324
ITIH3	Inter-alpha-trypsin inhibitor heavy chain 3	SEQ ID NOS: 7325 - 7327
ITIH4	Inter-alpha-trypsin inhibitor heavy chain family, member 4	SEQ ID NOS: 7328 - 7331
ITIH5	Inter-alpha-trypsin inhibitor heavy chain family, member 5	SEQ ID NOS: 7332 - 7335
ITIH6	Inter-alpha-trypsin inhibitor heavy chain family, member 6	SEQ ID NO: 7336
ITLN1	Intelectin 1 (galactofuranose binding)	SEQ ID NO: 7337
ITLN2	Intelectin 2	SEQ ID NO: 7338

IZUMO1R	IZUMO1 receptor, JUNO	SEQ ID NOS: 7339 - 7340
IZUMO4	IZUMO family member 4	SEQ ID NOS: 7341 - 7347
JCHAIN	Joining chain of multimeric IgA and IgM	SEQ ID NOS: 7357 - 7362
JMJD8	Jumonji domain containing 8	SEQ ID NOS: 7363 - 7367
JSRP1	Junctional sarcoplasmic reticulum protein 1	SEQ ID NO: 7368
KANSL2	KAT8 regulatory NSL complex subunit 2	SEQ ID NOS: 7369 - 7379
KAZALD1	Kazal-type serine peptidase inhibitor domain 1	SEQ ID NO: 7380
KCNIP3	Kv channel interacting protein 3, calsenilin	SEQ ID NOS: 7381 - 7383
KCNK7	Potassium channel, two pore domain subfamily K, member 7	SEQ ID NOS: 7384 - 7389
KCNN4	Potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 4	SEQ ID NOS: 7390 - 7395
KCNU1	Potassium channel, subfamily U, member 1	SEQ ID NOS: 7396 - 7400
KCP	Kielin/chordin-like protein	SEQ ID NOS: 7401 - 7404
KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	SEQ ID NO: 7405
KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	SEQ ID NOS: 7406 - 7409
KDM1A	Lysine (K)-specific demethylase 1A	SEQ ID NOS: 7410 - 7413
KDM3B	Lysine (K)-specific demethylase 3B	SEQ ID NOS: 7414 - 7417
KDM6A	Lysine (K)-specific demethylase 6A	SEQ ID NOS: 7418 - 7427
KDM7A	Lysine (K)-specific demethylase 7A	SEQ ID NOS: 7428 - 7429
KDSR	3-ketodihydrosphingosine reductase	SEQ ID NOS: 7430 - 7436
KERA	Keratocan	SEQ ID NO: 7437
KIAA0100	KIAA0100	SEQ ID NOS: 7438 - 7443
KIAA0319	KIAA0319	SEQ ID NOS: 7444 - 7449
KIAA1324	KIAA1324	SEQ ID NOS: 7450 - 7458

KIFC2	Kinesin family member C2	SEQ ID NOS: 7459 - 7461
KIR2DL4	Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	SEQ ID NOS: 7462 - 7468
KIR3DX1	Killer cell immunoglobulin-like receptor, three domains, X1	SEQ ID NOS: 7469 - 7473
KIRREL2	Kin of IRRE like 2 (Drosophila)	SEQ ID NOS: 7474 - 7478
KISS1	KiSS-1 metastasis-suppressor	SEQ ID NOS: 7479 - 7480
KLHL11	Kelch-like family member 11	SEQ ID NO: 7481
KLHL22	Kelch-like family member 22	SEQ ID NOS: 7482 - 7488
KLK1	Kallikrein 1	SEQ ID NOS: 7489 - 7490
KLK10	Kallikrein-related peptidase 10	SEQ ID NOS: 7491 - 7495
KLK11	Kallikrein-related peptidase 11	SEQ ID NOS: 7496 - 7504
KLK12	Kallikrein-related peptidase 12	SEQ ID NOS: 7505 - 7511
KLK13	Kallikrein-related peptidase 13	SEQ ID NOS: 7512 - 7520
KLK14	Kallikrein-related peptidase 14	SEQ ID NOS: 7521 - 7522
KLK15	Kallikrein-related peptidase 15	SEQ ID NOS: 7523 - 7527
KLK2	Kallikrein-related peptidase 2	SEQ ID NOS: 7528 - 7540
KLK3	Kallikrein-related peptidase 3	SEQ ID NOS: 7541 - 7552
KLK4	Kallikrein-related peptidase 4	SEQ ID NOS: 7553 - 7557
KLK5	Kallikrein-related peptidase 5	SEQ ID NOS: 7558 - 7561
KLK6	Kallikrein-related peptidase 6	SEQ ID NOS: 7562 - 7568
KLK7	Kallikrein-related peptidase 7	SEQ ID NOS: 7569 - 7573
KLK8	Kallikrein-related peptidase 8	SEQ ID NOS: 7574 - 7581
KLK9	Kallikrein-related peptidase 9	SEQ ID NOS: 7582 - 7583
KLKB1	Kallikrein B, plasma (Fletcher factor) 1	SEQ ID NOS: 7584 - 7588

KNDC1	Kinase non-catalytic C-lobe domain (KIND) containing 1	SEQ ID NOS: 7593 - 7594
KNG1	Kininogen 1	SEQ ID NOS: 7595 - 7599
KRBA2	KRAB-A domain containing 2	SEQ ID NOS: 7600 - 7603
KREMEN2	Kringle containing transmembrane protein 2	SEQ ID NOS: 7604 - 7609
KRTDAP	Keratinocyte differentiation-associated protein	SEQ ID NOS: 7610 - 7611
L1CAM	L1 cell adhesion molecule	SEQ ID NOS: 7612 - 7621
L3MBTL2	L(3)mbt-like 2 (Drosophila)	SEQ ID NOS: 7622 - 7626
LA16c-380H5.3		SEQ ID NO: 72
LACE1	Lactation elevated 1	SEQ ID NOS: 580 - 583
LACRT	Lacritin	SEQ ID NOS: 7627 - 7629
LACTB	Lactamase, beta	SEQ ID NOS: 7630 - 7632
LAG3	Lymphocyte-activation gene 3	SEQ ID NOS: 7633 - 7634
LAIR2	Leukocyte-associated immunoglobulin-like receptor 2	SEQ ID NOS: 7635 - 7638
LALBA	Lactalbumin, alpha-	SEQ ID NOS: 7639 - 7640
LAMA1	Laminin, alpha 1	SEQ ID NOS: 7641 - 7642
LAMA2	Laminin, alpha 2	SEQ ID NOS: 7643 - 7646
LAMA3	Laminin, alpha 3	SEQ ID NOS: 7647 - 7656
LAMA4	Laminin, alpha 4	SEQ ID NOS: 7657 - 7671
LAMA5	Laminin, alpha 5	SEQ ID NOS: 7672 - 7674
LAMB1	Laminin, beta 1	SEQ ID NOS: 7675 - 7679
LAMB2	Laminin, beta 2 (laminin S)	SEQ ID NOS: 7680 - 7682
LAMB3	Laminin, beta 3	SEQ ID NOS: 7683 - 7687
LAMB4	Laminin, beta 4	SEQ ID NOS: 7688 - 7691

LAMC1	Laminin, gamma 1 (formerly LAMB2)	SEQ ID NOS: 7692 - 7693
LAMC2	Laminin, gamma 2	SEQ ID NOS: 7694 - 7695
LAMC3	Laminin, gamma 3	SEQ ID NOS: 7696 - 7697
LAMP3	Lysosomal-associated membrane protein 3	SEQ ID NOS: 7698 - 7701
LAT	Linker for activation of T cells	SEQ ID NOS: 7708 - 7717
LAT2	Linker for activation of T cells family, member 2	SEQ ID NOS: 7718 - 7726
LBP	Lipopolysaccharide binding protein	SEQ ID NO: 7727
LCAT	Lecithin-cholesterol acyltransferase	SEQ ID NOS: 7728 - 7734
LCN1	Lipocalin 1	SEQ ID NOS: 7735 - 7736
LCN10	Lipocalin 10	SEQ ID NOS: 7737 - 7742
LCN12	Lipocalin 12	SEQ ID NOS: 7743 - 7745
LCN15	Lipocalin 15	SEQ ID NO: 7746
LCN2	Lipocalin 2	SEQ ID NOS: 7747 - 7749
LCN6	Lipocalin 6	SEQ ID NOS: 7750 - 7751
LCN8	Lipocalin 8	SEQ ID NOS: 7752 - 7753
LCN9	Lipocalin 9	SEQ ID NOS: 7754 - 7755
LCORL	Ligand dependent nuclear receptor corepressor-like	SEQ ID NOS: 7756 - 7761
LDLR	Low density lipoprotein receptor	SEQ ID NOS: 7762 - 7770
LDLRAD2	Low density lipoprotein receptor class A domain containing 2	SEQ ID NOS: 7771 - 7772
LEAP2	Liver expressed antimicrobial peptide 2	SEQ ID NO: 7773
LECT2	Leukocyte cell-derived chemotaxin 2	SEQ ID NOS: 7774 - 7777
LEFTY1	Left-right determination factor 1	SEQ ID NOS: 7778 - 7779
LEFTY2	Left-right determination factor 2	SEQ ID NOS: 7780 - 7781
LEP	Leptin	SEQ ID NO: 7782

LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 7783 - 7788
LGALS3BP	Lectin, galactoside-binding, soluble, 3 binding protein	SEQ ID NOS: 7789 - 7803
LGI1	Leucine-rich, glioma inactivated 1	SEQ ID NOS: 7804 - 7822
LGI2	Leucine-rich repeat LGI family, member 2	SEQ ID NOS: 7823 - 7824
LGI3	Leucine-rich repeat LGI family, member 3	SEQ ID NOS: 7825 - 7828
LGI4	Leucine-rich repeat LGI family, member 4	SEQ ID NOS: 7829 - 7832
LGMN	Legumain	SEQ ID NOS: 7833 - 7846
LGR4	Leucine-rich repeat containing G protein-coupled receptor 4	SEQ ID NOS: 7847 - 7849
LHB	Luteinizing hormone beta polypeptide	SEQ ID NO: 7850
LHCGR	Luteinizing hormone/choriogonadotropin receptor	SEQ ID NOS: 7851 - 7855
LIF	Leukemia inhibitory factor	SEQ ID NOS: 7856 - 7857
LIFR	Leukemia inhibitory factor receptor alpha	SEQ ID NOS: 7858 - 7862
LILRA1	Leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	SEQ ID NOS: 7863 - 7864
LILRA2	Leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	SEQ ID NOS: 7865 - 7871
LILRB3	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	SEQ ID NOS: 7872 - 7876
LIME1	Lck interacting transmembrane adaptor 1	SEQ ID NOS: 7877 - 7882
LINGO1	Leucine rich repeat and Ig domain containing 1	SEQ ID NOS: 7883 - 7893
LIPA	Lipase A, lysosomal acid, cholesterol esterase	SEQ ID NOS: 7894 - 7898
LIPC	Lipase, hepatic	SEQ ID NOS: 7899 - 7902
LIPF	Lipase, gastric	SEQ ID NOS: 7903 - 7906
LIPG	Lipase, endothelial	SEQ ID NOS: 7907 - 7912
LIPH	Lipase, member H	SEQ ID NOS: 7913 - 7917
LIPK	Lipase, family member K	SEQ ID NO: 7918

LIPM	Lipase, family member M	SEQ ID NOS: 7919 - 7920
LIPN	Lipase, family member N	SEQ ID NO: 7921
LMAN2	Lectin, mannose-binding 2	SEQ ID NOS: 7922 - 7926
LMNTD1	Lamin tail domain containing 1	SEQ ID NOS: 7927 - 7937
LNX1	Ligand of numb-protein X 1, E3 ubiquitin protein ligase	SEQ ID NOS: 7938 - 7944
LOX	Lysyl oxidase	SEQ ID NOS: 7945 - 7947
LOXL1	Lysyl oxidase-like 1	SEQ ID NOS: 7948 - 7949
LOXL2	Lysyl oxidase-like 2	SEQ ID NOS: 7950 - 7958
LOXL3	Lysyl oxidase-like 3	SEQ ID NOS: 7959 - 7965
LOXL4	Lysyl oxidase-like 4	SEQ ID NO: 7966
LPA	Lipoprotein, Lp(a)	SEQ ID NOS: 7967 - 7969
LPL	Lipoprotein lipase	SEQ ID NOS: 7970 - 7974
LPO	Lactoperoxidase	SEQ ID NOS: 7975 - 7981
LRAT	Lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	SEQ ID NOS: 7982 - 7984
LRCH3	Leucine-rich repeats and calponin homology (CH) domain containing 3	SEQ ID NOS: 7985 - 7993
LRCOL1	Leucine rich colipase-like 1	SEQ ID NOS: 7994 - 7997
LRFN4	Leucine rich repeat and fibronectin type III domain containing 4	SEQ ID NOS: 7998 - 7999
LRFN5	Leucine rich repeat and fibronectin type III domain containing 5	SEQ ID NOS: 8000 - 8002
LRG1	Leucine-rich alpha-2-glycoprotein 1	SEQ ID NO: 8003
LRP1	Low density lipoprotein receptor-related protein 1	SEQ ID NOS: 8004 - 8009
LRP11	Low density lipoprotein receptor-related protein 11	SEQ ID NOS: 8010 - 8011
LRP1B	Low density lipoprotein receptor-related protein 1B	SEQ ID NOS: 8012 - 8015
LRP2	Low density lipoprotein receptor-related protein 2	SEQ ID NOS: 8016 - 8017

LRP4	Low density lipoprotein receptor-related protein 4	SEQ ID NOS: 8018 - 8019
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1	SEQ ID NOS: 8020 - 8021
LRRC17	Leucine rich repeat containing 17	SEQ ID NOS: 8022 - 8024
LRRC32	Leucine rich repeat containing 32	SEQ ID NOS: 8025 - 8028
LRRC3B	Leucine rich repeat containing 3B	SEQ ID NOS: 8029 - 8033
LRRC4B	Leucine rich repeat containing 4B	SEQ ID NOS: 8034 - 8036
LRRC70	Leucine rich repeat containing 70	SEQ ID NOS: 8037 - 8038
LRRN3	Leucine rich repeat neuronal 3	SEQ ID NOS: 8039 - 8042
LRRTM1	Leucine rich repeat transmembrane neuronal 1	SEQ ID NOS: 8043 - 8049
LRRTM2	Leucine rich repeat transmembrane neuronal 2	SEQ ID NOS: 8050 - 8052
LRRTM4	Leucine rich repeat transmembrane neuronal 4	SEQ ID NOS: 8053 - 8058
LRTM2	Leucine-rich repeats and transmembrane domains 2	SEQ ID NOS: 8059 - 8063
LSR	Lipolysis stimulated lipoprotein receptor	SEQ ID NOS: 8064 - 8074
LST1	Leukocyte specific transcript 1	SEQ ID NOS: 8075 - 8092
LTA	Lymphotoxin alpha	SEQ ID NOS: 8093 - 8094
LTBP1	Latent transforming growth factor beta binding protein 1	SEQ ID NOS: 8095 - 8104
LTBP2	Latent transforming growth factor beta binding protein 2	SEQ ID NOS: 8105 - 8108
LTBP3	Latent transforming growth factor beta binding protein 3	SEQ ID NOS: 8109 - 8121
LTBP4	Latent transforming growth factor beta binding protein 4	SEQ ID NOS: 8122 - 8137
LTBR	Lymphotoxin beta receptor (TNFR superfamily, member 3)	SEQ ID NOS: 8138 - 8143
LTF	Lactotransferrin	SEQ ID NOS: 8144 - 8148
LTK	Leukocyte receptor tyrosine kinase	SEQ ID NOS: 8149 - 8152
LUM	Lumican	SEQ ID NO: 8153

LUZP2	Leucine zipper protein 2	SEQ ID NOS: 8154 - 8157
LVRN	Laeverin	SEQ ID NOS: 8158 - 8163
LY6E	Lymphocyte antigen 6 complex, locus E	SEQ ID NOS: 8164 - 8177
LY6G5B	Lymphocyte antigen 6 complex, locus G5B	SEQ ID NOS: 8178 - 8179
LY6G6D	Lymphocyte antigen 6 complex, locus G6D	SEQ ID NOS: 8180 - 8181
LY6G6E	Lymphocyte antigen 6 complex, locus G6E (pseudogene)	SEQ ID NOS: 8182 - 8185
LY6H	Lymphocyte antigen 6 complex, locus H	SEQ ID NOS: 8186 - 8189
LY6K	Lymphocyte antigen 6 complex, locus K	SEQ ID NOS: 8190 - 8193
LY86	Lymphocyte antigen 86	SEQ ID NOS: 8195 - 8196
LY96	Lymphocyte antigen 96	SEQ ID NOS: 8197 - 8198
LYG1	Lysozyme G-like 1	SEQ ID NOS: 8199 - 8200
LYG2	Lysozyme G-like 2	SEQ ID NOS: 8201 - 8206
LYNX1	Ly6/neurotoxin 1	SEQ ID NOS: 8207 - 8211
LYPD1	LY6/PLAUR domain containing 1	SEQ ID NOS: 8212 - 8214
LYPD2	LY6/PLAUR domain containing 2	SEQ ID NO: 8215
LYPD4	LY6/PLAUR domain containing 4	SEQ ID NOS: 8216 - 8218
LYPD6	LY6/PLAUR domain containing 6	SEQ ID NOS: 8219 - 8223
LYPD6B	LY6/PLAUR domain containing 6B	SEQ ID NOS: 8224 - 8230
LYPD8	LY6/PLAUR domain containing 8	SEQ ID NOS: 8231 - 8232
LYZ	Lysozyme	SEQ ID NOS: 8233 - 8235
LYZL4	Lysozyme-like 4	SEQ ID NOS: 8236 - 8237
LYZL6	Lysozyme-like 6	SEQ ID NOS: 8238 - 8240
M6PR	Mannose-6-phosphate receptor (cation dependent)	SEQ ID NOS: 8241 - 8251

MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	SEQ ID NOS: 8252 - 8264
MAG	Myelin associated glycoprotein	SEQ ID NOS: 8265 - 8270
MAGT1	Magnesium transporter 1	SEQ ID NOS: 8271 - 8274
MALSU1	Mitochondrial assembly of ribosomal large subunit 1	SEQ ID NO: 8275
MAMDC2	MAM domain containing 2	SEQ ID NO: 8276
MAN2B1	Mannosidase, alpha, class 2B, member 1	SEQ ID NOS: 8277 - 8282
MAN2B2	Mannosidase, alpha, class 2B, member 2	SEQ ID NOS: 8283 - 8285
MANBA	Mannosidase, beta A, lysosomal	SEQ ID NOS: 8286 - 8299
MANEAL	Mannosidase, endo-alpha-like	SEQ ID NOS: 8300 - 8304
MANF	Mesencephalic astrocyte-derived neurotrophic factor	SEQ ID NOS: 8305 - 8306
MANSC1	MANSC domain containing 1	SEQ ID NOS: 8307 - 8310
MAP3K9	Mitogen-activated protein kinase 9	SEQ ID NOS: 8311 - 8316
MASP1	Mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	SEQ ID NOS: 8317 - 8324
MASP2	Mannan-binding lectin serine peptidase 2	SEQ ID NOS: 8325 - 8326
MATN1	Matrilin 1, cartilage matrix protein	SEQ ID NO: 8327
MATN2	Matrilin 2	SEQ ID NOS: 8328 - 8340
MATN3	Matrilin 3	SEQ ID NOS: 8341 - 8342
MATN4	Matrilin 4	SEQ ID NOS: 8343 - 8347
MATR3	Matrin 3	SEQ ID NOS: 8348 - 8375
MAU2	MAU2 sister chromatid cohesion factor	SEQ ID NOS: 8376 - 8378
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	SEQ ID NOS: 8379 - 8393
MBD6	Methyl-CpG binding domain protein 6	SEQ ID NOS: 8394 - 8405
MBL2	Mannose-binding lectin (protein C) 2, soluble	SEQ ID NO: 8406

MBNL1	Muscleblind-like splicing regulator 1	SEQ ID NOS: 8407 - 8425
MCCC1	Methylcrotonoyl-CoA carboxylase 1 (alpha)	SEQ ID NOS: 8426 - 8437
MCCD1	Mitochondrial coiled-coil domain 1	SEQ ID NO: 8438
MCEE	Methylmalonyl CoA epimerase	SEQ ID NOS: 8439 - 8442
MCF2L	MCF.2 cell line derived transforming sequence-like	SEQ ID NOS: 8443 - 8464
MCFD2	Multiple coagulation factor deficiency 2	SEQ ID NOS: 8465 - 8476
MDFIC	MyoD family inhibitor domain containing	SEQ ID NOS: 8477 - 8484
MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	SEQ ID NOS: 8485 - 8490
MDK	Midkine (neurite growth-promoting factor 2)	SEQ ID NOS: 8491 - 8500
MED20	Mediator complex subunit 20	SEQ ID NOS: 8501 - 8505
MEGF10	Multiple EGF-like-domains 10	SEQ ID NOS: 8506 - 8509
MEGF6	Multiple EGF-like-domains 6	SEQ ID NOS: 8510 - 8513
MEI1	Meiotic double-stranded break formation protein 1	SEQ ID NOS: 8514 - 8517
MEI4	Meiotic double-stranded break formation protein 4	SEQ ID NO: 8518
MEIS1	Meis homeobox 1	SEQ ID NOS: 8519 - 8524
MEIS3	Meis homeobox 3	SEQ ID NOS: 8525 - 8534
MEPE	Matrix extracellular phosphoglycoprotein	SEQ ID NOS: 8538 - 8544
MESDC2	Mesoderm development candidate 2	SEQ ID NOS: 8545 - 8549
MEST	Mesoderm specific transcript	SEQ ID NOS: 8550 - 8563
MET	MET proto-oncogene, receptor tyrosine kinase	SEQ ID NOS: 8564 - 8569
METRN	Meteorin, glial cell differentiation regulator	SEQ ID NOS: 8570 - 8574
METRNL	Meteorin, glial cell differentiation regulator-like	SEQ ID NOS: 8575 - 8578
METTL17	Methyltransferase like 17	SEQ ID NOS: 8579 - 8589

METTL24	Methyltransferase like 24	SEQ ID NO: 8590
METTL7B	Methyltransferase like 7B	SEQ ID NOS: 8591 - 8592
METTL9	Methyltransferase like 9	SEQ ID NOS: 8593 - 8601
MEX3C	Mex-3 RNA binding family member C	SEQ ID NOS: 8602 - 8604
MFAP2	Microfibrillar-associated protein 2	SEQ ID NOS: 8605 - 8606
MFAP3	Microfibrillar-associated protein 3	SEQ ID NOS: 8607 - 8611
MFAP3L	Microfibrillar-associated protein 3-like	SEQ ID NOS: 8612 - 8621
MFAP4	Microfibrillar-associated protein 4	SEQ ID NOS: 8622 - 8624
MFAP5	Microfibrillar associated protein 5	SEQ ID NOS: 8625 - 8635
MFGE8	Milk fat globule-EGF factor 8 protein	SEQ ID NOS: 8636 - 8642
MFI2	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	SEQ ID NOS: 8535 - 8537
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 8643 - 8650
MGA	MGA, MAX dimerization protein	SEQ ID NOS: 8651 - 8659
MGAT2	Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	SEQ ID NO: 8660
MGAT3	Mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	SEQ ID NOS: 8661 - 8663
MGAT4A	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	SEQ ID NOS: 8664 - 8668
MGAT4B	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	SEQ ID NOS: 8669 - 8679
MGAT4D	MGAT4 family, member D	SEQ ID NOS: 8680 - 8685
MGLL	Monoglyceride lipase	SEQ ID NOS: 8686 - 8695
MGP	Matrix Gla protein	SEQ ID NOS: 8696 - 8698
MGST2	Microsomal glutathione S-transferase 2	SEQ ID NOS: 8699 - 8702

MIA	Melanoma inhibitory activity	SEQ ID NOS: 8703 - 8708
MIA2	Melanoma inhibitory activity 2	SEQ ID NO: 8709
MIA3	Melanoma inhibitory activity family, member 3	SEQ ID NOS: 8710 - 8714
MICU1	Mitochondrial calcium uptake 1	SEQ ID NOS: 8715 - 8724
MIER1	Mesoderm induction early response 1, transcriptional regulator	SEQ ID NOS: 8725 - 8733
MINOS1-NBL1	MINOS1-NBL1 readthrough	SEQ ID NOS: 8734 - 8736
MINPP1	Multiple inositol-polyphosphate phosphatase 1	SEQ ID NOS: 8737 - 8739
MLEC	Malectin	SEQ ID NOS: 8740 - 8743
MLN	Motilin	SEQ ID NOS: 8744 - 8746
MLXIP	MLX interacting protein	SEQ ID NOS: 8747 - 8752
MLXIPL	MLX interacting protein-like	SEQ ID NOS: 8753 - 8760
MMP1	Matrix metallopeptidase 1	SEQ ID NO: 8761
MMP10	Matrix metallopeptidase 10	SEQ ID NOS: 8762 - 8763
MMP11	Matrix metallopeptidase 11	SEQ ID NOS: 8764 - 8767
MMP12	Matrix metallopeptidase 12	SEQ ID NO: 8768
MMP13	Matrix metallopeptidase 13	SEQ ID NOS: 8769 - 8771
MMP14	Matrix metallopeptidase 14 (membrane-inserted)	SEQ ID NOS: 8772 - 8774
MMP17	Matrix metallopeptidase 17 (membrane-inserted)	SEQ ID NOS: 8775 - 8782
MMP19	Matrix metallopeptidase 19	SEQ ID NOS: 8783 - 8788
MMP2	Matrix metallopeptidase 2	SEQ ID NOS: 8789 - 8796
MMP20	Matrix metallopeptidase 20	SEQ ID NO: 8797
MMP21	Matrix metallopeptidase 21	SEQ ID NO: 8798
MMP25	Matrix metallopeptidase 25	SEQ ID NOS: 8799 - 8800
MMP26	Matrix metallopeptidase 26	SEQ ID NOS: 8801 - 8802
MMP27	Matrix metallopeptidase 27	SEQ ID NO: 8803

MMP28	Matrix metallopeptidase 28	SEQ ID NOS: 8804 - 8809
MMP3	Matrix metallopeptidase 3	SEQ ID NOS: 8810 - 8812
MMP7	Matrix metallopeptidase 7	SEQ ID NO: 8813
MMP8	Matrix metallopeptidase 8	SEQ ID NOS: 8814 - 8819
MMP9	Matrix metallopeptidase 9	SEQ ID NO: 8820
MMRN1	Multimerin 1	SEQ ID NOS: 8821 - 8823
MMRN2	Multimerin 2	SEQ ID NOS: 8824 - 8828
MOXD1	Monooxygenase, DBH-like 1	SEQ ID NOS: 8829 - 8831
MPO	Myeloperoxidase	SEQ ID NOS: 8840 - 8841
MPPED1	Metallophosphoesterase domain containing 1	SEQ ID NOS: 8842 - 8845
MPZL1	Myelin protein zero-like 1	SEQ ID NOS: 8846 - 8850
MR1	Major histocompatibility complex, class I-related	SEQ ID NOS: 8851 - 8856
MRPL2	Mitochondrial ribosomal protein L2	SEQ ID NOS: 8857 - 8861
MRPL21	Mitochondrial ribosomal protein L21	SEQ ID NOS: 8862 - 8868
MRPL22	Mitochondrial ribosomal protein L22	SEQ ID NOS: 8869 - 8873
MRPL24	Mitochondrial ribosomal protein L24	SEQ ID NOS: 8874 - 8878
MRPL27	Mitochondrial ribosomal protein L27	SEQ ID NOS: 8879 - 8884
MRPL32	Mitochondrial ribosomal protein L32	SEQ ID NOS: 8885 - 8887
MRPL34	Mitochondrial ribosomal protein L34	SEQ ID NOS: 8888 - 8892
MRPL35	Mitochondrial ribosomal protein L35	SEQ ID NOS: 8893 - 8896
MRPL52	Mitochondrial ribosomal protein L52	SEQ ID NOS: 8897 - 8907
MRPL55	Mitochondrial ribosomal protein L55	SEQ ID NOS: 8908 - 8933
MRPS14	Mitochondrial ribosomal protein S14	SEQ ID NOS: 8934 - 8935

MRPS22	Mitochondrial ribosomal protein S22	SEQ ID NOS: 8936 - 8944
MRPS28	Mitochondrial ribosomal protein S28	SEQ ID NOS: 8945 - 8952
MS4A14	Membrane-spanning 4-domains, subfamily A, member 14	SEQ ID NOS: 8953 - 8963
MS4A3	Membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	SEQ ID NOS: 8964 - 8968
MSH3	MutS homolog 3	SEQ ID NO: 8969
MSH5	MutS homolog 5	SEQ ID NOS: 8970 - 8981
MSLN	Mesothelin	SEQ ID NOS: 8982 - 8989
MSMB	Microseminoprotein, beta-	SEQ ID NOS: 8990 - 8991
MSRA	Methionine sulfoxide reductase A	SEQ ID NOS: 8992 - 8999
MSRB2	Methionine sulfoxide reductase B2	SEQ ID NOS: 9000 - 9001
MSRB3	Methionine sulfoxide reductase B3	SEQ ID NOS: 9002 - 9015
MST1	Macrophage stimulating 1	SEQ ID NOS: 9016 - 9017
MSTN	Myostatin	SEQ ID NO: 9018
MT1G	Metallothionein 1G	SEQ ID NOS: 9019 - 9022
MTHFD2	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	SEQ ID NOS: 9023 - 9027
MTMR14	Myotubularin related protein 14	SEQ ID NOS: 9028 - 9038
MTRNR2L11	MT-RNR2-like 11 (pseudogene)	SEQ ID NO: 9039
MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	SEQ ID NOS: 9040 - 9052
MTTP	Microsomal triglyceride transfer protein	SEQ ID NOS: 9053 - 9063
MTX2	Metaxin 2	SEQ ID NOS: 9064 - 9068
MUC1	Mucin 1, cell surface associated	SEQ ID NOS: 9069 - 9094
MUC13	Mucin 13, cell surface associated	SEQ ID NOS: 9095 - 9096
MUC20	Mucin 20, cell surface associated	SEQ ID NOS: 9097 - 9101

MUC3A	Mucin 3A, cell surface associated	SEQ ID NOS: 9102 - 9104
MUC5AC	Mucin 5AC, oligomeric mucus/gel-forming	SEQ ID NO: 9105
MUC5B	Mucin 5B, oligomeric mucus/gel-forming	SEQ ID NOS: 9106 - 9107
MUC6	Mucin 6, oligomeric mucus/gel-forming	SEQ ID NOS: 9108 - 9111
MUC7	Mucin 7, secreted	SEQ ID NOS: 9112 - 9115
MUCL1	Mucin-like 1	SEQ ID NOS: 9116 - 9118
MXRA5	Matrix-remodelling associated 5	SEQ ID NO: 9119
MXRA7	Matrix-remodelling associated 7	SEQ ID NOS: 9120 - 9126
MYDGF	Myeloid-derived growth factor	SEQ ID NOS: 9127 - 9129
MYL1	Myosin, light chain 1, alkali; skeletal, fast	SEQ ID NOS: 9130 - 9131
MYOC	Myocilin, trabecular meshwork inducible glucocorticoid response	SEQ ID NOS: 9132 - 9133
MYRFL	Myelin regulatory factor-like	SEQ ID NOS: 9134 - 9138
MZB1	Marginal zone B and B1 cell-specific protein	SEQ ID NOS: 9139 - 9143
N4BP2L2	NEDD4 binding protein 2-like 2	SEQ ID NOS: 9144 - 9149
NAA38	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	SEQ ID NOS: 9150 - 9155
NAAA	N-acylethanolamine acid amidase	SEQ ID NOS: 9156 - 9161
NAGA	N-acetylgalactosaminidase, alpha-	SEQ ID NOS: 9162 - 9164
NAGLU	N-acetylglucosaminidase, alpha	SEQ ID NOS: 9165 - 9169
NAGS	N-acetylglutamate synthase	SEQ ID NOS: 9170 - 9171
NAPSA	Napsin A aspartic peptidase	SEQ ID NOS: 9172 - 9174
NBL1	Neuroblastoma 1, DAN family BMP antagonist	SEQ ID NOS: 9180 - 9193
NCAM1	Neural cell adhesion molecule 1	SEQ ID NOS: 9194 - 9213
NCAN	Neurocan	SEQ ID NOS: 9214 - 9215
NCBP2-AS2	NCBP2 antisense RNA 2 (head to head)	SEQ ID NO: 9216

NCSTN	Nicastrin	SEQ ID NOS: 9217 - 9226
NDNF	Neuron-derived neurotrophic factor	SEQ ID NOS: 9227 - 9229
NDP	Norrie disease (pseudoglioma)	SEQ ID NOS: 9230 - 9232
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	SEQ ID NOS: 9233 - 9242
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	SEQ ID NOS: 9243 - 9251
NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	SEQ ID NOS: 9252 - 9261
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	SEQ ID NOS: 9262 - 9275
NECAB3	N-terminal EF-hand calcium binding protein 3	SEQ ID NOS: 9276 - 9285
NELL1	Neural EGFL like 1	SEQ ID NOS: 9289 - 9292
NELL2	Neural EGFL like 2	SEQ ID NOS: 9293 - 9307
NENF	Neudesin neurotrophic factor	SEQ ID NO: 9308
NETO1	Neuropilin (NRP) and tolloid (TLL)-like 1	SEQ ID NOS: 9309 - 9312
NFASC	Neurofascin	SEQ ID NOS: 9313 - 9327
NFE2L1	Nuclear factor, erythroid 2-like 1	SEQ ID NOS: 9328 - 9346
NFE2L3	Nuclear factor, erythroid 2-like 3	SEQ ID NOS: 9347 - 9348
NGEF	Neuronal guanine nucleotide exchange factor	SEQ ID NOS: 9349 - 9354
NGF	Nerve growth factor (beta polypeptide)	SEQ ID NO: 9355
NGLY1	N-glycanase 1	SEQ ID NOS: 9356 - 9362
NGRN	Neugrin, neurite outgrowth associated	SEQ ID NOS: 9363 - 9364
NHLRC3	NHL repeat containing 3	SEQ ID NOS: 9365 - 9367
NID1	Nidogen 1	SEQ ID NOS: 9368 - 9369
NID2	Nidogen 2 (osteonidogen)	SEQ ID NOS: 9370 - 9372
NKG7	Natural killer cell granule protein 7	SEQ ID NOS: 9373 - 9377

NLGN3	Neuroligin 3	SEQ ID NOS: 9378 - 9382
NLGN4Y	Neuroligin 4, Y-linked	SEQ ID NOS: 9383 - 9389
NLRP5	NLR family, pyrin domain containing 5	SEQ ID NOS: 9390 - 9392
NMB	Neuromedin B	SEQ ID NOS: 9393 - 9394
NME1	NME/NM23 nucleoside diphosphate kinase 1	SEQ ID NOS: 9395 - 9401
NME1-NME2	NME1-NME2 readthrough	SEQ ID NOS: 9402 - 9404
NME3	NME/NM23 nucleoside diphosphate kinase 3	SEQ ID NOS: 9405 - 9409
NMS	Neuromedin S	SEQ ID NO: 9410
NMU	Neuromedin U	SEQ ID NOS: 9411 - 9414
NOA1	Nitric oxide associated 1	SEQ ID NO: 9415
NODAL	Nodal growth differentiation factor	SEQ ID NOS: 9416 - 9417
NOG	Noggin	SEQ ID NO: 9418
NOMO3	NODAL modulator 3	SEQ ID NOS: 9419 - 9425
NOS1AP	Nitric oxide synthase 1 (neuronal) adaptor protein	SEQ ID NOS: 9426 - 9430
NOTCH3	Notch 3	SEQ ID NOS: 9431 - 9434
NOTUM	Notum pectinacetylesterase homolog (Drosophila)	SEQ ID NOS: 9435 - 9437
NOV	Nephroblastoma overexpressed	SEQ ID NO: 9438
NPB	Neuropeptide B	SEQ ID NOS: 9439 - 9440
NPC2	Niemann-Pick disease, type C2	SEQ ID NOS: 9441 - 9449
NPFF	Neuropeptide FF-amide peptide precursor	SEQ ID NO: 9450
NPFFR2	Neuropeptide FF receptor 2	SEQ ID NOS: 9451 - 9454
NPHS1	Nephrosis 1, congenital, Finnish type (nephrin)	SEQ ID NOS: 9455 - 9456
NPNT	Nephronectin	SEQ ID NOS: 9457 - 9467
NPPA	Natriuretic peptide A	SEQ ID NOS: 9468 - 9470
NPPB	Natriuretic peptide B	SEQ ID NO: 9471

NPPC	Natriuretic peptide C	SEQ ID NOS: 9472 - 9473
NPS	Neuropeptide S	SEQ ID NO: 9474
NPTX1	Neuronal pentraxin I	SEQ ID NO: 9475
NPTX2	Neuronal pentraxin II	SEQ ID NO: 9476
NPTXR	Neuronal pentraxin receptor	SEQ ID NOS: 9477 - 9478
NPVF	Neuropeptide VF precursor	SEQ ID NO: 9479
NPW	Neuropeptide W	SEQ ID NOS: 9480 - 9482
NPY	Neuropeptide Y	SEQ ID NOS: 9483 - 9485
NQO2	NAD(P)H dehydrogenase, quinone 2	SEQ ID NOS: 9486 - 9494
NRCAM	Neuronal cell adhesion molecule	SEQ ID NOS: 9495 - 9507
NRG1	Neuregulin 1	SEQ ID NOS: 9508 - 9525
NRN1L	Neuritin 1-like	SEQ ID NOS: 9526 - 9528
NRP1	Neuropilin 1	SEQ ID NOS: 9529 - 9542
NRP2	Neuropilin 2	SEQ ID NOS: 9543 - 9549
NRTN	Neurturin	SEQ ID NO: 9550
NRXN1	Neurexin 1	SEQ ID NOS: 9551 - 9581
NRXN2	Neurexin 2	SEQ ID NOS: 9582 - 9590
NT5C3A	5'-nucleotidase, cytosolic IIIA	SEQ ID NOS: 9591 - 9601
NT5DC3	5'-nucleotidase domain containing 3	SEQ ID NOS: 9602 - 9604
NT5E	5'-nucleotidase, ecto (CD73)	SEQ ID NOS: 9605 - 9609
NTF3	Neurotrophin 3	SEQ ID NOS: 9610 - 9611
NTF4	Neurotrophin 4	SEQ ID NOS: 9612 - 9613
NTM	Neurotrimin	SEQ ID NOS: 9614 - 9623
NTN1	Netrin 1	SEQ ID NOS: 9624 - 9625
NTN3	Netrin 3	SEQ ID NO: 9626

NTN4	Netrin 4	SEQ ID NOS: 9627 - 9631
NTN5	Netrin 5	SEQ ID NOS: 9632 - 9633
NTNG1	Netrin G1	SEQ ID NOS: 9634 - 9640
NTNG2	Netrin G2	SEQ ID NOS: 9641 - 9642
NTS	Neurotensin	SEQ ID NOS: 9643 - 9644
NUBPL	Nucleotide binding protein-like	SEQ ID NOS: 9645 - 9651
NUCB1	Nucleobindin 1	SEQ ID NOS: 9652 - 9658
NUCB2	Nucleobindin 2	SEQ ID NOS: 9659 - 9674
NUDT19	Nudix (nucleoside diphosphate linked moiety X)-type motif 19	SEQ ID NO: 9675
NUDT9	Nudix (nucleoside diphosphate linked moiety X)-type motif 9	SEQ ID NOS: 9676 - 9680
NUP155	Nucleoporin 155kDa	SEQ ID NOS: 9681 - 9684
NUP214	Nucleoporin 214kDa	SEQ ID NOS: 9685 - 9696
NUP85	Nucleoporin 85kDa	SEQ ID NOS: 9697 - 9711
NXPE3	Neurexophilin and PC-esterase domain family, member 3	SEQ ID NOS: 9712 - 9716
NXPE4	Neurexophilin and PC-esterase domain family, member 4	SEQ ID NOS: 9717 - 9718
NXPH1	Neurexophilin 1	SEQ ID NOS: 9719 - 9722
NXPH2	Neurexophilin 2	SEQ ID NO: 9723
NXPH3	Neurexophilin 3	SEQ ID NOS: 9724 - 9725
NXPH4	Neurexophilin 4	SEQ ID NOS: 9726 - 9727
NYX	Nyctalopin	SEQ ID NOS: 9728 - 9729
OAF	Out at first homolog	SEQ ID NOS: 9730 - 9731
OBP2A	Odorant binding protein 2A	SEQ ID NOS: 9732 - 9738
OBP2B	Odorant binding protein 2B	SEQ ID NOS: 9739 - 9742

OC90	Otoconin 90	SEQ ID NO: 9743
OCLN	Occludin	SEQ ID NOS: 9744 - 9746
ODAM	Odontogenic, ameloblast asssociated	SEQ ID NOS: 9747 - 9750
OGG1	8-oxoguanine DNA glycosylase	SEQ ID NOS: 9755 - 9768
OGN	Osteoglycin	SEQ ID NOS: 9769 - 9771
OIT3	Oncoprotein induced transcript 3	SEQ ID NOS: 9772 - 9773
OLFM1	Olfactomedin 1	SEQ ID NOS: 9774 - 9784
OLFM2	Olfactomedin 2	SEQ ID NOS: 9785 - 9788
OLFM3	Olfactomedin 3	SEQ ID NOS: 9789 - 9791
OLFM4	Olfactomedin 4	SEQ ID NO: 9792
OLFML1	Olfactomedin-like 1	SEQ ID NOS: 9793 - 9796
OLFML2A	Olfactomedin-like 2A	SEQ ID NOS: 9797 - 9799
OLFML2B	Olfactomedin-like 2B	SEQ ID NOS: 9800 - 9804
OLFML3	Olfactomedin-like 3	SEQ ID NOS: 9805 - 9807
OMD	Osteomodulin	SEQ ID NO: 9808
OMG	Oligodendrocyte myelin glycoprotein	SEQ ID NO: 9809
OOSP2	Oocyte secreted protein 2	SEQ ID NOS: 9810 - 9811
OPCML	Opioid binding protein/cell adhesion molecule-like	SEQ ID NOS: 9812 - 9816
OPTC	Opticin	SEQ ID NOS: 9818 - 9819
ORAI1	ORAI calcium release-activated calcium modulator 1	SEQ ID NO: 9820
ORM1	Orosomucoid 1	SEQ ID NO: 9821
ORM2	Orosomucoid 2	SEQ ID NO: 9822
ORMDL2	ORMDL sphingolipid biosynthesis regulator 2	SEQ ID NOS: 9823 - 9826
OS9	Osteosarcoma amplified 9, endoplasmic reticulum lectin	SEQ ID NOS: 9827 - 9841
OSCAR	Osteoclast associated, immunoglobulin-like receptor	SEQ ID NOS: 9842 - 9852

OSM	Oncostatin M	SEQ ID NOS: 9853 - 9855
OSMR	Oncostatin M receptor	SEQ ID NOS: 9856 - 9860
OSTN	Osteocrin	SEQ ID NOS: 9861 - 9862
OTOA	Otoancorin	SEQ ID NOS: 9863 - 9868
OTOG	Otogelin	SEQ ID NOS: 9869 - 9871
OTOGL	Otogelin-like	SEQ ID NOS: 9872 - 9878
OTOL1	Otolin 1	SEQ ID NO: 9879
OTOR	Otoraplin	SEQ ID NO: 9880
OTOS	Otospiralin	SEQ ID NOS: 9881 - 9882
OVCH1	Ovochymase 1	SEQ ID NOS: 9883 - 9885
OVCH2	Ovochymase 2 (gene/pseudogene)	SEQ ID NOS: 9886 - 9887
OVGP1	Oviductal glycoprotein 1, 120kDa	SEQ ID NO: 9888
OXCT1	3-oxoacid CoA transferase 1	SEQ ID NOS: 9889 - 9892
OXCT2	3-oxoacid CoA transferase 2	SEQ ID NO: 9893
OXNAD1	Oxidoreductase NAD-binding domain containing 1	SEQ ID NOS: 9894 - 9900
OXT	Oxytocin/neurophysin I prepropeptide	SEQ ID NO: 9901
P3H1	Prolyl 3-hydroxylase 1	SEQ ID NOS: 9902 - 9906
P3H2	Prolyl 3-hydroxylase 2	SEQ ID NOS: 9907 - 9910
P3H3	Prolyl 3-hydroxylase 3	SEQ ID NO: 9911
P3H4	Prolyl 3-hydroxylase family member 4 (non-enzymatic)	SEQ ID NOS: 9912 - 9916
P4HA1	Prolyl 4-hydroxylase, alpha polypeptide I	SEQ ID NOS: 9917 - 9921
P4HA2	Prolyl 4-hydroxylase, alpha polypeptide II	SEQ ID NOS: 9922 - 9936
P4HA3	Prolyl 4-hydroxylase, alpha polypeptide III	SEQ ID NOS: 9937 - 9941
P4HB	Prolyl 4-hydroxylase, beta polypeptide	SEQ ID NOS: 9942 - 9953
PAEP	Progestagen-associated endometrial protein	SEQ ID NOS: 9954 - 9962

PAM	Peptidylglycine alpha-amidating monooxygenase	SEQ ID NOS: 9963 - 9976
PAMR1	Peptidase domain containing associated with muscle regeneration 1	SEQ ID NOS: 9977 - 9983
PAPL	Iron/zinc purple acid phosphatase-like protein	SEQ ID NOS: 159 - 162
PAPLN	Papilin, proteoglycan-like sulfated glycoprotein	SEQ ID NOS: 9984 - 9991
PAPPA	Pregnancy-associated plasma protein A, pappalysin 1	SEQ ID NO: 9992
PAPPA2	Pappalysin 2	SEQ ID NOS: 9993 - 9994
PARP15	Poly (ADP-ribose) polymerase family, member 15	SEQ ID NOS: 9995 - 9998
PARVB	Parvin, beta	SEQ ID NOS: 9999 - 10003
PATE1	Prostate and testis expressed 1	SEQ ID NOS: 10004 - 10005
PATE2	Prostate and testis expressed 2	SEQ ID NOS: 10006 - 10007
PATE3	Prostate and testis expressed 3	SEQ ID NO: 10008
PATE4	Prostate and testis expressed 4	SEQ ID NOS: 10009 - 10010
PATL2	Protein associated with topoisomerase II homolog 2 (yeast)	SEQ ID NOS: 10011 - 10016
PAX2	Paired box 2	SEQ ID NOS: 10017 - 10022
PAX4	Paired box 4	SEQ ID NOS: 10023 - 10029
PCCB	Propionyl CoA carboxylase, beta polypeptide	SEQ ID NOS: 10030 - 10044
PCDH1	Protocadherin 1	SEQ ID NOS: 10045 - 10050
PCDH12	Protocadherin 12	SEQ ID NOS: 10051 - 10052
PCDH15	Protocadherin-related 15	SEQ ID NOS: 10053 - 10086
PCDHA1	Protocadherin alpha 1	SEQ ID NOS: 10087 - 10089
PCDHA10	Protocadherin alpha 10	SEQ ID NOS: 10090 - 10092
PCDHA11	Protocadherin alpha 11	SEQ ID NOS: 10093 - 10095
PCDHA6	Protocadherin alpha 6	SEQ ID NOS: 10096 - 10098

PCDHB12	Protocadherin beta 12	SEQ ID NOS: 10099 - 10101
PCDHGA11	Protocadherin gamma subfamily A, 11	SEQ ID NOS: 10102 - 10104
PCF11	PCF11 cleavage and polyadenylation factor subunit	SEQ ID NOS: 10105 - 10109
PCOLCE	Procollagen C-endopeptidase enhancer	SEQ ID NO: 10110
PCOLCE2	Procollagen C-endopeptidase enhancer 2	SEQ ID NOS: 10111 - 10114
PCSK1	Proprotein convertase subtilisin/kexin type 1	SEQ ID NOS: 10115 - 10117
PCSK1N	Proprotein convertase subtilisin/kexin type 1 inhibitor	SEQ ID NO: 10118
PCSK2	Proprotein convertase subtilisin/kexin type 2	SEQ ID NOS: 10119 - 10121
PCSK4	Proprotein convertase subtilisin/kexin type 4	SEQ ID NOS: 10122 - 10124
PCSK5	Proprotein convertase subtilisin/kexin type 5	SEQ ID NOS: 10125 - 10129
PCSK9	Proprotein convertase subtilisin/kexin type 9	SEQ ID NO: 10130
PCYOX1	Prenylcysteine oxidase 1	SEQ ID NOS: 10131 - 10135
PCYOX1L	Prenylcysteine oxidase 1 like	SEQ ID NOS: 10136 - 10140
PDDC1	Parkinson disease 7 domain containing 1	SEQ ID NOS: 5802 - 5810
PDE11A	Phosphodiesterase 11A	SEQ ID NOS: 10141 - 10146
PDE2A	Phosphodiesterase 2A, cGMP-stimulated	SEQ ID NOS: 10147 - 10168
PDE7A	Phosphodiesterase 7A	SEQ ID NOS: 10169 - 10172
PDF	Peptide deformylase (mitochondrial)	SEQ ID NO: 10173
PDGFA	Platelet-derived growth factor alpha polypeptide	SEQ ID NOS: 10174 - 10177
PDGFB	Platelet-derived growth factor beta polypeptide	SEQ ID NOS: 10178 - 10181
PDGFC	Platelet derived growth factor C	SEQ ID NOS: 10182 - 10185
PDGFD	Platelet derived growth factor D	SEQ ID NOS: 10186 - 10188
PDGFRA	Platelet-derived growth factor receptor, alpha polypeptide	SEQ ID NOS: 10189 - 10195

PDGFRB	Platelet-derived growth factor receptor, beta polypeptide	SEQ ID NOS: 10196 - 10199
PDGFRL	Platelet-derived growth factor receptor-like	SEQ ID NOS: 10200 - 10201
PDHA1	Pyruvate dehydrogenase (lipoamide) alpha 1	SEQ ID NOS: 10202 - 10210
PDIA2	Protein disulfide isomerase family A, member 2	SEQ ID NOS: 10211 - 10214
PDIA3	Protein disulfide isomerase family A, member 3	SEQ ID NOS: 10215 - 10218
PDIA4	Protein disulfide isomerase family A, member 4	SEQ ID NOS: 10219 - 10220
PDIA5	Protein disulfide isomerase family A, member 5	SEQ ID NOS: 10221 - 10224
PDIA6	Protein disulfide isomerase family A, member 6	SEQ ID NOS: 10225 - 10231
PDILT	Protein disulfide isomerase-like, testis expressed	SEQ ID NOS: 10232 - 10233
PDYN	Prodynorphin	SEQ ID NOS: 10234 - 10236
PDZD8	PDZ domain containing 8	SEQ ID NO: 10237
PDZRN4	PDZ domain containing ring finger 4	SEQ ID NOS: 10238 - 10240
PEAR1	Platelet endothelial aggregation receptor 1	SEQ ID NOS: 10241 - 10244
PEBP4	Phosphatidylethanolamine-binding protein 4	SEQ ID NOS: 10245 - 10246
PECAM1	Platelet/endothelial cell adhesion molecule 1	SEQ ID NOS: 10247 - 10250
PENK	Proenkephalin	SEQ ID NOS: 10251 - 10256
PET117	PET117 homolog	SEQ ID NO: 10257
PF4	Platelet factor 4	SEQ ID NO: 10258
PF4V1	Platelet factor 4 variant 1	SEQ ID NO: 10259
PFKP	Phosphofructokinase, platelet	SEQ ID NOS: 10260 - 10268
PFN1	Profilin 1	SEQ ID NOS: 10269 - 10271
PGA3	Pepsinogen 3, group I (pepsinogen A)	SEQ ID NOS: 10272 - 10275
PGA4	Pepsinogen 4, group I (pepsinogen A)	SEQ ID NOS: 10276 - 10278
PGA5	Pepsinogen 5, group I (pepsinogen A)	SEQ ID NOS: 10279 - 10281

PGAM5	PGAM family member 5, serine/threonine protein phosphatase, mitochondrial	SEQ ID NOS: 10282 - 10285
PGAP3	Post-GPI attachment to proteins 3	SEQ ID NOS: 10286 - 10293
PGC	Progastricsin (pepsinogen C)	SEQ ID NOS: 10294 - 10297
PGF	Placental growth factor	SEQ ID NOS: 10298 - 10301
PGLYRP1	Peptidoglycan recognition protein 1	SEQ ID NO: 10302
PGLYRP2	Peptidoglycan recognition protein 2	SEQ ID NOS: 10303 - 10306
PGLYRP3	Peptidoglycan recognition protein 3	SEQ ID NO: 10307
PGLYRP4	Peptidoglycan recognition protein 4	SEQ ID NOS: 10308 - 10309
PHACTR1	Phosphatase and actin regulator 1	SEQ ID NOS: 10310 - 10316
PHB	Prohibitin	SEQ ID NOS: 10317 - 10325
PI15	Peptidase inhibitor 15	SEQ ID NOS: 10326 - 10327
PI3	Peptidase inhibitor 3, skin-derived	SEQ ID NO: 10328
PIANP	PILR alpha associated neural protein	SEQ ID NOS: 10329 - 10334
PIGK	Phosphatidylinositol glycan anchor biosynthesis, class K	SEQ ID NOS: 10335 - 10338
PIGL	Phosphatidylinositol glycan anchor biosynthesis, class L	SEQ ID NOS: 10339 - 10346
PIGT	Phosphatidylinositol glycan anchor biosynthesis, class T	SEQ ID NOS: 10347 - 10400
PIGZ	Phosphatidylinositol glycan anchor biosynthesis, class Z	SEQ ID NOS: 10401 - 10403
PIK3AP1	Phosphoinositide-3-kinase adaptor protein 1	SEQ ID NOS: 10404 - 10406
PIK3IP1	Phosphoinositide-3-kinase interacting protein 1	SEQ ID NOS: 10407 - 10410
PILRA	Paired immunoglobin-like type 2 receptor alpha	SEQ ID NOS: 10411 - 10415
PILRB	Paired immunoglobin-like type 2 receptor beta	SEQ ID NOS: 10416 - 10427
PINLYP	Phospholipase A2 inhibitor and LY6/PLAUR domain containing	SEQ ID NOS: 10428 - 10432
PIP	Prolactin-induced protein	SEQ ID NO: 10433
PIWIL4	Piwi-like RNA-mediated gene silencing 4	SEQ ID NOS: 10434 - 10438

PKDCC	Protein kinase domain containing, cytoplasmic	SEQ ID NOS: 10439 - 10440
PKHD1	Polycystic kidney and hepatic disease 1 (autosomal recessive)	SEQ ID NOS: 10441 - 10442
PLA1A	Phospholipase A1 member A	SEQ ID NOS: 10443 - 10447
PLA2G10	Phospholipase A2, group X	SEQ ID NOS: 10448 - 10449
PLA2G12A	Phospholipase A2, group XIIA	SEQ ID NOS: 10450 - 10452
PLA2G12B	Phospholipase A2, group XIIB	SEQ ID NO: 10453
PLA2G15	Phospholipase A2, group XV	SEQ ID NOS: 10454 - 10461
PLA2G1B	Phospholipase A2, group IB (pancreas)	SEQ ID NOS: 10462 - 10464
PLA2G2A	Phospholipase A2, group IIA (platelets, synovial fluid)	SEQ ID NOS: 10465 - 10466
PLA2G2C	Phospholipase A2, group IIC	SEQ ID NOS: 10467 - 10468
PLA2G2D	Phospholipase A2, group IID	SEQ ID NOS: 10469 - 10470
PLA2G2E	Phospholipase A2, group IIE	SEQ ID NO: 10471
PLA2G3	Phospholipase A2, group III	SEQ ID NO: 10472
PLA2G5	Phospholipase A2, group V	SEQ ID NO: 10473
PLA2G7	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	SEQ ID NOS: 10474 - 10475
PLA2R1	Phospholipase A2 receptor 1, 180kDa	SEQ ID NOS: 10476 - 10477
PLAC1	Placenta-specific 1	SEQ ID NO: 10478
PLAC9	Placenta-specific 9	SEQ ID NOS: 10479 - 10481
PLAT	Plasminogen activator, tissue	SEQ ID NOS: 10482 - 10490
PLAU	Plasminogen activator, urokinase	SEQ ID NOS: 10491 - 10493
PLAUR	Plasminogen activator, urokinase receptor	SEQ ID NOS: 10494 - 10505
PLBD1	Phospholipase B domain containing 1	SEQ ID NOS: 10506 - 10508
PLBD2	Phospholipase B domain containing 2	SEQ ID NOS: 10509 - 10511
PLG	Plasminogen	SEQ ID NOS: 10512 - 10514
PLGLB1	Plasminogen-like B1	SEQ ID NOS: 10515 - 10518

PLGLB2	Plasminogen-like B2	SEQ ID NOS: 10519 - 10520
PLOD1	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	SEQ ID NOS: 10521 - 10523
PLOD2	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	SEQ ID NOS: 10524 - 10529
PLOD3	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	SEQ ID NOS: 10530 - 10536
PLTP	Phospholipid transfer protein	SEQ ID NOS: 10537 - 10541
PLXNA4	Plexin A4	SEQ ID NOS: 10542 - 10545
PLXNB2	Plexin B2	SEQ ID NOS: 10546 - 10554
PM20D1	Peptidase M20 domain containing 1	SEQ ID NO: 10555
PMCH	Pro-melanin-concentrating hormone	SEQ ID NO: 10556
PMEL	Premelanosome protein	SEQ ID NOS: 10557 - 10568
PMEPA1	Prostate transmembrane protein, androgen induced 1	SEQ ID NOS: 10569 - 10575
PNLIP	Pancreatic lipase	SEQ ID NO: 10576
PNLIPRP1	Pancreatic lipase-related protein 1	SEQ ID NOS: 10577 - 10585
PNLIPRP3	Pancreatic lipase-related protein 3	SEQ ID NO: 10586
PNOC	Prepronociceptin	SEQ ID NOS: 10587 - 10589
PNP	Purine nucleoside phosphorylase	SEQ ID NOS: 10590 - 10593
PNPLA4	Patatin-like phospholipase domain containing 4	SEQ ID NOS: 10594 - 10597
PODNL1	Podocan-like 1	SEQ ID NOS: 10598 - 10609
POFUT1	Protein O-fucosyltransferase 1	SEQ ID NOS: 10610 - 10611
POFUT2	Protein O-fucosyltransferase 2	SEQ ID NOS: 10612 - 10617
POGLUT1	Protein O-glucosyltransferase 1	SEQ ID NOS: 10618 - 10622
POLL	Polymerase (DNA directed), lambda	SEQ ID NOS: 10623 - 10635
POMC	Proopiomelanocortin	SEQ ID NOS: 10636 - 10640
POMGNT2	Protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	SEQ ID NOS: 10641 - 10642

PON1	Paraoxonase 1	SEQ ID NOS: 10643 - 10644
PON2	Paraoxonase 2	SEQ ID NOS: 10645 - 10657
PON3	Paraoxonase 3	SEQ ID NOS: 10658 - 10663
POSTN	Periostin, osteoblast specific factor	SEQ ID NOS: 10664 - 10669
PPBP	Pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	SEQ ID NO: 10670
PPIB	Peptidylprolyl isomerase B (cyclophilin B)	SEQ ID NO: 10671
PPIC	Peptidylprolyl isomerase C (cyclophilin C)	SEQ ID NO: 10672
PPOX	Protoporphyrinogen oxidase	SEQ ID NOS: 10673 - 10683
PPP1CA	Protein phosphatase 1, catalytic subunit, alpha isozyme	SEQ ID NOS: 10684 - 10689
PPT1	Palmitoyl-protein thioesterase 1	SEQ ID NOS: 10690 - 10706
PPT2	Palmitoyl-protein thioesterase 2	SEQ ID NOS: 10707 - 10714
PPY	Pancreatic polypeptide	SEQ ID NOS: 10715 - 10719
PRAC2	Prostate cancer susceptibility candidate 2	SEQ ID NOS: 10720 - 10721
PRADC1	Protease-associated domain containing 1	SEQ ID NO: 10722
PRAP1	Proline-rich acidic protein 1	SEQ ID NOS: 10723 - 10724
PRB1	Proline-rich protein BstNI subfamily 1	SEQ ID NOS: 10725 - 10728
PRB2	Proline-rich protein BstNI subfamily 2	SEQ ID NOS: 10729 - 10730
PRB3	Proline-rich protein BstNI subfamily 3	SEQ ID NOS: 10731 - 10732
PRB4	Proline-rich protein BstNI subfamily 4	SEQ ID NOS: 10733 - 10736
PRCD	Progressive rod-cone degeneration	SEQ ID NOS: 10737 - 10738
PRCP	Prolylcarboxypeptidase (angiotensinase C)	SEQ ID NOS: 10739 - 10750
PRDM12	PR domain containing 12	SEQ ID NO: 10751
PRDX4	Peroxiredoxin 4	SEQ ID NOS: 10752 - 10755
PRELP	Proline/arginine-rich end leucine-rich repeat protein	SEQ ID NO: 10756

PRF1	Perforin 1 (pore forming protein)	SEQ ID NOS: 10757 - 10759
PRG2	Proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	SEQ ID NOS: 10760 - 10762
PRG3	Proteoglycan 3	SEQ ID NO: 10763
PRG4	Proteoglycan 4	SEQ ID NOS: 10764 - 10769
PRH1	Proline-rich protein HaeIII subfamily 1	SEQ ID NOS: 10770 - 10772
PRH2	Proline-rich protein HaeIII subfamily 2	SEQ ID NOS: 10773 - 10774
PRKAG1	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	SEQ ID NOS: 10775 - 10789
PRKCSH	Protein kinase C substrate 80K-H	SEQ ID NOS: 10790 - 10799
PRKD1	Protein kinase D1	SEQ ID NOS: 10800 - 10805
PRL	Prolactin	SEQ ID NOS: 10806 - 10808
PRLH	Prolactin releasing hormone	SEQ ID NO: 10809
PRLR	Prolactin receptor	SEQ ID NOS: 10810 - 10828
PRNP	Prion protein	SEQ ID NOS: 10829 - 10832
PRNT	Prion protein (testis specific)	SEQ ID NO: 10833
PROC	Protein C (inactivator of coagulation factors Va and VIIIa)	SEQ ID NOS: 10834 - 10841
PROK1	Prokineticin 1	SEQ ID NO: 10842
PROK2	Prokineticin 2	SEQ ID NOS: 10843 - 10844
PROL1	Proline rich, lacrimal 1	SEQ ID NO: 9817
PROM1	Prominin 1	SEQ ID NOS: 10845 - 10856
PROS1	Protein S (alpha)	SEQ ID NOS: 10857 - 10860
PROZ	Protein Z, vitamin K-dependent plasma glycoprotein	SEQ ID NOS: 10861 - 10862
PRR27	Proline rich 27	SEQ ID NOS: 10863 - 10866
PRR4	Proline rich 4 (lacrimal)	SEQ ID NOS: 10867 - 10869
PRRG2	Proline rich Gla (G-carboxyglutamic acid) 2	SEQ ID NOS: 10870 - 10872

PRRT3	Proline-rich transmembrane protein 3	SEQ ID NOS: 10873 - 10875
PRRT4	Proline-rich transmembrane protein 4	SEQ ID NOS: 10876 - 10882
PRSS1	Protease, serine, 1 (trypsin 1)	SEQ ID NOS: 10883 - 10886
PRSS12	Protease, serine, 12 (neurotrypsin, motopsin)	SEQ ID NO: 10887
PRSS16	Protease, serine, 16 (thymus)	SEQ ID NOS: 10888 - 10895
PRSS2	Protease, serine, 2 (trypsin 2)	SEQ ID NOS: 10896 - 10899
PRSS21	Protease, serine, 21 (testisin)	SEQ ID NOS: 10900 - 10905
PRSS22	Protease, serine, 22	SEQ ID NOS: 10906 - 10908
PRSS23	Protease, serine, 23	SEQ ID NOS: 10909 - 10912
PRSS27	Protease, serine 27	SEQ ID NOS: 10913 - 10915
PRSS3	Protease, serine, 3	SEQ ID NOS: 10916 - 10920
PRSS33	Protease, serine, 33	SEQ ID NOS: 10921 - 10924
PRSS35	Protease, serine, 35	SEQ ID NO: 10925
PRSS36	Protease, serine, 36	SEQ ID NOS: 10926 - 10929
PRSS37	Protease, serine, 37	SEQ ID NOS: 10930 - 10933
PRSS38	Protease, serine, 38	SEQ ID NO: 10934
PRSS42	Protease, serine, 42	SEQ ID NOS: 10935 - 10936
PRSS48	Protease, serine, 48	SEQ ID NOS: 10937 - 10938
PRSS50	Protease, serine, 50	SEQ ID NO: 10939
PRSS53	Protease, serine, 53	SEQ ID NO: 10940
PRSS54	Protease, serine, 54	SEQ ID NOS: 10941 - 10945
PRSS55	Protease, serine, 55	SEQ ID NOS: 10946 - 10948
PRSS56	Protease, serine, 56	SEQ ID NOS: 10949 - 10950
PRSS57	Protease, serine, 57	SEQ ID NOS: 10951 - 10952

PRSS58	Protease, serine, 58	SEQ ID NOS: 10953 - 10954
PRSS8	Protease, serine, 8	SEQ ID NOS: 10955 - 10958
PRTG	Protogenin	SEQ ID NOS: 10959 - 10962
PRTN3	Proteinase 3	SEQ ID NOS: 10963 - 10964
PSAP	Prosaposin	SEQ ID NOS: 10965 - 10968
PSAPL1	Prosaposin-like 1 (gene/pseudogene)	SEQ ID NO: 10969
PSG1	Pregnancy specific beta-1-glycoprotein 1	SEQ ID NOS: 10970 - 10977
PSG11	Pregnancy specific beta-1-glycoprotein 11	SEQ ID NOS: 10978 - 10982
PSG2	Pregnancy specific beta-1-glycoprotein 2	SEQ ID NOS: 10983 - 10984
PSG3	Pregnancy specific beta-1-glycoprotein 3	SEQ ID NOS: 10985 - 10988
PSG4	Pregnancy specific beta-1-glycoprotein 4	SEQ ID NOS: 10989 - 11000
PSG5	Pregnancy specific beta-1-glycoprotein 5	SEQ ID NOS: 11001 - 11006
PSG6	Pregnancy specific beta-1-glycoprotein 6	SEQ ID NOS: 11007 - 11012
PSG7	Pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	SEQ ID NOS: 11013 - 11015
PSG8	Pregnancy specific beta-1-glycoprotein 8	SEQ ID NOS: 11016 - 11020
PSG9	Pregnancy specific beta-1-glycoprotein 9	SEQ ID NOS: 11021 - 11028
PSMD1	Proteasome 26S subunit, non-ATPase 1	SEQ ID NOS: 11029 - 11036
PSORS1C2	Psoriasis susceptibility 1 candidate 2	SEQ ID NO: 11037
PSPN	Persephin	SEQ ID NOS: 11038 - 11039
PTGDS	Prostaglandin D2 synthase 21kDa (brain)	SEQ ID NOS: 11040 - 11044
PTGIR	Prostaglandin I2 (prostacyclin) receptor (IP)	SEQ ID NOS: 11045 - 11049
PTGS1	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	SEQ ID NOS: 11050 - 11058

PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	SEQ ID NOS: 11059 - 11060
PTH	Parathyroid hormone	SEQ ID NOS: 11061 - 11062
PTH2	Parathyroid hormone 2	SEQ ID NO: 11063
PTHLH	Parathyroid hormone-like hormone	SEQ ID NOS: 11064 - 11072
PTK7	Protein tyrosine kinase 7 (inactive)	SEQ ID NOS: 11073 - 11088
PTN	Pleiotrophin	SEQ ID NOS: 11089 - 11090
PTPRA	Protein tyrosine phosphatase, receptor type, A	SEQ ID NOS: 11091 - 11098
PTPRB	Protein tyrosine phosphatase, receptor type, B	SEQ ID NOS: 11099 - 11106
PTPRC	Protein tyrosine phosphatase, receptor type, C	SEQ ID NOS: 11107 - 11117
PTPRCAP	Protein tyrosine phosphatase, receptor type, C-associated protein	SEQ ID NO: 11118
PTPRD	Protein tyrosine phosphatase, receptor type, D	SEQ ID NOS: 11119 - 11130
PTPRF	Protein tyrosine phosphatase, receptor type, F	SEQ ID NOS: 11131 - 11138
PTPRJ	Protein tyrosine phosphatase, receptor type, J	SEQ ID NOS: 11139 - 11144
PTPRO	Protein tyrosine phosphatase, receptor type, O	SEQ ID NOS: 11145 - 11153
PTPRS	Protein tyrosine phosphatase, receptor type, S	SEQ ID NOS: 11154 - 11161
PTTG1IP	Pituitary tumor-transforming 1 interacting protein	SEQ ID NOS: 11162 - 11165
PTX3	Pentraxin 3, long	SEQ ID NO: 11166
PTX4	Pentraxin 4, long	SEQ ID NOS: 11167 - 11169
PVR	Poliovirus receptor	SEQ ID NOS: 11170 - 11175
PVRL1	Poliovirus receptor-related 1 (herpesvirus entry mediator C)	SEQ ID NOS: 9286 - 9288
PXDN	Peroxidasin	SEQ ID NOS: 11176 - 11180
PXDNL	Peroxidasin-like	SEQ ID NOS: 11181 - 11183
PXYLP1	2-phosphoxylose phosphatase 1	SEQ ID NOS: 11184 - 11196

PYY	Peptide YY	SEQ ID NOS: 11197 - 11198
PZP	Pregnancy-zone protein	SEQ ID NOS: 11199 - 11200
QPCT	Glutaminyl-peptide cyclotransferase	SEQ ID NOS: 11201 - 11203
QPRT	Quinolinate phosphoribosyltransferase	SEQ ID NOS: 11204 - 11205
QRFP	Pyroglutamylated RFamide peptide	SEQ ID NOS: 11206 - 11207
QSOX1	Quiescin Q6 sulfhydryl oxidase 1	SEQ ID NOS: 11208 - 11211
R3HDML	R3H domain containing-like	SEQ ID NO: 11212
RAB26	RAB26, member RAS oncogene family	SEQ ID NOS: 11213 - 11216
RAB36	RAB36, member RAS oncogene family	SEQ ID NOS: 11217 - 11219
RAB9B	RAB9B, member RAS oncogene family	SEQ ID NO: 11220
RAET1E	Retinoic acid early transcript 1E	SEQ ID NOS: 11221 - 11226
RAET1G	Retinoic acid early transcript 1G	SEQ ID NOS: 11227 - 11229
RAMP2	Receptor (G protein-coupled) activity modifying protein 2	SEQ ID NOS: 11230 - 11234
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	SEQ ID NOS: 11235 - 11241
RARRES1	Retinoic acid receptor responder (tazarotene induced) 1	SEQ ID NOS: 11242 - 11243
RARRES2	Retinoic acid receptor responder (tazarotene induced) 2	SEQ ID NOS: 11244 - 11247
RASA2	RAS p21 protein activator 2	SEQ ID NOS: 11248 - 11250
RBM3	RNA binding motif (RNP1, RRM) protein 3	SEQ ID NOS: 11251 - 11253
RBP3	Retinol binding protein 3, interstitial	SEQ ID NO: 11254
RBP4	Retinol binding protein 4, plasma	SEQ ID NOS: 11255 - 11258
RCN1	Reticulocalbin 1, EF-hand calcium binding domain	SEQ ID NOS: 11259 - 11262
RCN2	Reticulocalbin 2, EF-hand calcium binding domain	SEQ ID NOS: 11263 - 11266
RCN3	Reticulocalbin 3, EF-hand calcium binding domain	SEQ ID NOS: 11267 - 11270
RCOR1	REST corepressor 1	SEQ ID NOS: 11271 - 11272

RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	SEQ ID NOS: 11273 - 11280
RDH12	Retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	SEQ ID NOS: 11281 - 11282
RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	SEQ ID NOS: 11283 - 11291
RDH5	Retinol dehydrogenase 5 (11-cis/9-cis)	SEQ ID NOS: 11292 - 11296
RDH8	Retinol dehydrogenase 8 (all-trans)	SEQ ID NOS: 11297 - 11298
REG1A	Regenerating islet-derived 1 alpha	SEQ ID NO: 11299
REG1B	Regenerating islet-derived 1 beta	SEQ ID NOS: 11300 - 11301
REG3A	Regenerating islet-derived 3 alpha	SEQ ID NOS: 11302 - 11304
REG3G	Regenerating islet-derived 3 gamma	SEQ ID NOS: 11305 - 11307
REG4	Regenerating islet-derived family, member 4	SEQ ID NOS: 11308 - 11311
RELN	Reelin	SEQ ID NOS: 11312 - 11315
RELT	RELT tumor necrosis factor receptor	SEQ ID NOS: 11316 - 11319
REN	Renin	SEQ ID NOS: 11320 - 11321
REPIN1	Replication initiator 1	SEQ ID NOS: 11322 - 11335
REPS2	RALBP1 associated Eps domain containing 2	SEQ ID NOS: 11336 - 11337
RET	Ret proto-oncogene	SEQ ID NOS: 11338 - 11343
RETN	Resistin	SEQ ID NOS: 11344 - 11346
RETNLB	Resistin like beta	SEQ ID NO: 11347
RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)	SEQ ID NOS: 11348 - 11352
RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	SEQ ID NOS: 11353 - 11355
RGCC	Regulator of cell cycle	SEQ ID NO: 11356
RGL4	Ral guanine nucleotide dissociation stimulator-like 4	SEQ ID NOS: 11357 - 11363
RGMA	Repulsive guidance molecule family member a	SEQ ID NOS: 11364 - 11373
RGMB	Repulsive guidance molecule family member b	SEQ ID NOS: 11374 - 11375

RHOQ	Ras homolog family member Q	SEQ ID NOS: 11376 - 11380
RIC3	RIC3 acetylcholine receptor chaperone	SEQ ID NOS: 11381 - 11388
RIMS1	Regulating synaptic membrane exocytosis 1	SEQ ID NOS: 11393 - 11408
RIPPLY1	Ripply transcriptional repressor 1	SEQ ID NOS: 11409 - 11410
RLN1	Relaxin 1	SEQ ID NO: 11411
RLN2	Relaxin 2	SEQ ID NOS: 11412 - 11413
RLN3	Relaxin 3	SEQ ID NOS: 11414 - 11415
RMDN1	Regulator of microtubule dynamics 1	SEQ ID NOS: 11416 - 11429
RNASE1	Ribonuclease, RNase A family, 1 (pancreatic)	SEQ ID NOS: 11430 - 11434
RNASE10	Ribonuclease, RNase A family, 10 (non-active)	SEQ ID NOS: 11435 - 11436
RNASE11	Ribonuclease, RNase A family, 11 (non-active)	SEQ ID NOS: 11437 - 11447
RNASE12	Ribonuclease, RNase A family, 12 (non-active)	SEQ ID NO: 11448
RNASE13	Ribonuclease, RNase A family, 13 (non-active)	SEQ ID NO: 11449
RNASE2	Ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	SEQ ID NO: 11450
RNASE3	Ribonuclease, RNase A family, 3	SEQ ID NO: 11451
RNASE4	Ribonuclease, RNase A family, 4	SEQ ID NOS: 11452 - 11454
RNASE6	Ribonuclease, RNase A family, k6	SEQ ID NO: 11455
RNASE7	Ribonuclease, RNase A family, 7	SEQ ID NOS: 11456 - 11457
RNASE8	Ribonuclease, RNase A family, 8	SEQ ID NO: 11458
RNASE9	Ribonuclease, RNase A family, 9 (non-active)	SEQ ID NOS: 11459 - 11469
RNASEH1	Ribonuclease H1	SEQ ID NOS: 11470 - 11472
RNASET2	Ribonuclease T2	SEQ ID NOS: 11473 - 11480
RNF146	Ring finger protein 146	SEQ ID NOS: 11481 - 11492
RNF148	Ring finger protein 148	SEQ ID NOS: 11493 - 11494

RNF150	Ring finger protein 150	SEQ ID NOS: 11495 - 11499
RNF167	Ring finger protein 167	SEQ ID NOS: 11500 - 11510
RNF220	Ring finger protein 220	SEQ ID NOS: 11511 - 11517
RNF34	Ring finger protein 34, E3 ubiquitin protein ligase	SEQ ID NOS: 11518 - 11525
RNLS	Renalase, FAD-dependent amine oxidase	SEQ ID NOS: 11526 - 11528
RNPEP	Arginyl aminopeptidase (aminopeptidase B)	SEQ ID NOS: 11529 - 11534
ROR1	Receptor tyrosine kinase-like orphan receptor 1	SEQ ID NOS: 11535 - 11537
RP11-1236K1.1		SEQ ID NO: 4158
RP11-14J7.7		SEQ ID NOS: 674 - 675
RP11-196G11.1		SEQ ID NOS: 85 - 87
RP11-350O14.18		SEQ ID NO: 683
RP11-520P18.5		SEQ ID NO: 8194
RP11-812E19.9		SEQ ID NO: 89
RP11-903H12.5		SEQ ID NO: 676
RP11-977G19.10		SEQ ID NOS: 78 - 80
RP4-576H24.4		SEQ ID NOS: 670 - 672
RP4-608O15.3	Complement factor H-related protein 2	SEQ ID NO: 1649
RPL3	Ribosomal protein L3	SEQ ID NOS: 11538 - 11543
RPLP2	Ribosomal protein, large, P2	SEQ ID NOS: 11544 - 11546
RPN2	Ribophorin II	SEQ ID NOS: 11547 - 11553
RPS27L	Ribosomal protein S27-like	SEQ ID NOS: 11554 - 11559
RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	SEQ ID NOS: 3100 - 3106
RS1	Retinoschisin 1	SEQ ID NO: 11560
RSF1	Remodeling and spacing factor 1	SEQ ID NOS: 11561 - 11567

RSPO1	R-spondin 1	SEQ ID NOS: 11568 - 11571
RSPO2	R-spondin 2	SEQ ID NOS: 11572 - 11579
RSPO3	R-spondin 3	SEQ ID NOS: 11580 - 11581
RSPO4	R-spondin 4	SEQ ID NOS: 11582 - 11583
RSPRY1	Ring finger and SPRY domain containing 1	SEQ ID NOS: 11584 - 11590
RTBDN	Retbindin	SEQ ID NOS: 11591 - 11603
RTN4RL1	Reticulon 4 receptor-like 1	SEQ ID NO: 11604
RTN4RL2	Reticulon 4 receptor-like 2	SEQ ID NOS: 11605 - 11607
SAA1	Serum amyloid A1	SEQ ID NOS: 11608 - 11610
SAA2	Serum amyloid A2	SEQ ID NOS: 11611 - 11616
SAA4	Serum amyloid A4, constitutive	SEQ ID NO: 11617
SAP30	Sin3A-associated protein, 30kDa	SEQ ID NO: 11618
SAR1A	Secretion associated, Ras related GTPase 1A	SEQ ID NOS: 11619 - 11625
SARAF	Store-operated calcium entry-associated regulatory factor	SEQ ID NOS: 11626 - 11636
SARM1	Sterile alpha and TIR motif containing 1	SEQ ID NOS: 11637 - 11640
SATB1	SATB homeobox 1	SEQ ID NOS: 11641 - 11653
SAXO2	Stabilizer of axonemal microtubules 2	SEQ ID NOS: 11654 - 11658
SBSN	Suprabasin	SEQ ID NOS: 11659 - 11661
SBSPON	Somatomedin B and thrombospondin, type 1 domain containing	SEQ ID NO: 11662
SCARF1	Scavenger receptor class F, member 1	SEQ ID NOS: 11663 - 11667
SCG2	Secretogranin II	SEQ ID NOS: 11668 - 11670
SCG3	Secretogranin III	SEQ ID NOS: 11671 - 11673
SCG5	Secretogranin V	SEQ ID NOS: 11674 - 11678
SCGB1A1	Secretoglobin, family 1A, member 1 (uteroglobin)	SEQ ID NOS: 11679 - 11680

SCGB1C1	Secretoglobin, family 1C, member 1	SEQ ID NO: 11681
SCGB1C2	Secretoglobin, family 1C, member 2	SEQ ID NO: 11682
SCGB1D1	Secretoglobin, family 1D, member 1	SEQ ID NO: 11683
SCGB1D2	Secretoglobin, family 1D, member 2	SEQ ID NO: 11684
SCGB1D4	Secretoglobin, family 1D, member 4	SEQ ID NO: 11685
SCGB2A1	Secretoglobin, family 2A, member 1	SEQ ID NO: 11686
SCGB2A2	Secretoglobin, family 2A, member 2	SEQ ID NOS: 11687 - 11688
SCGB2B2	Secretoglobin, family 2B, member 2	SEQ ID NOS: 11689 - 11690
SCGB3A1	Secretoglobin, family 3A, member 1	SEQ ID NO: 11691
SCGB3A2	Secretoglobin, family 3A, member 2	SEQ ID NOS: 11692 - 11693
SCN1B	Sodium channel, voltage gated, type I beta subunit	SEQ ID NOS: 11694 - 11699
SCN3B	Sodium channel, voltage gated, type III beta subunit	SEQ ID NOS: 11700 - 11704
SCPEP1	Serine carboxypeptidase 1	SEQ ID NOS: 11705 - 11712
SCRG1	Stimulator of chondrogenesis 1	SEQ ID NOS: 11713 - 11714
SCT	Secretin	SEQ ID NO: 11715
SCUBE1	Signal peptide, CUB domain, EGF-like 1	SEQ ID NOS: 11716 - 11719
SCUBE2	Signal peptide, CUB domain, EGF-like 2	SEQ ID NOS: 11720 - 11726
SCUBE3	Signal peptide, CUB domain, EGF-like 3	SEQ ID NO: 11727
SDC1	Syndecan 1	SEQ ID NOS: 11728 - 11732
SDF2	Stromal cell-derived factor 2	SEQ ID NOS: 11733 - 11735
SDF2L1	Stromal cell-derived factor 2-like 1	SEQ ID NO: 11736
SDF4	Stromal cell derived factor 4	SEQ ID NOS: 11737 - 11740
SDHAF2	Succinate dehydrogenase complex assembly factor 2	SEQ ID NOS: 11741 - 11748
SDHAF4	Succinate dehydrogenase complex assembly factor 4	SEQ ID NO: 11749
SDHB	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	SEQ ID NOS: 11750 - 11752
SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein	SEQ ID NOS: 11753 - 11762
SEC14L3	SEC14-like lipid binding 3	SEQ ID NOS: 11763 - 11769

SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	SEQ ID NOS: 11770 - 11776
SEC16B	SEC16 homolog B, endoplasmic reticulum export factor	SEQ ID NOS: 11777 - 11780
SEC22C	SEC22 homolog C, vesicle trafficking protein	SEQ ID NOS: 11781 - 11793
SEC31A	SEC31 homolog A, COPII coat complex component	SEQ ID NOS: 11794 - 11823
SECISBP2	SECIS binding protein 2	SEQ ID NOS: 11824 - 11828
SECTM1	Secreted and transmembrane 1	SEQ ID NOS: 11829 - 11836
SEL1L	Sel-1 suppressor of lin-12-like (C. elegans)	SEQ ID NOS: 11837 - 11839
SELM	Selenoprotein M	SEQ ID NOS: 11847 - 11849
SELO	Selenoprotein O	SEQ ID NOS: 11854 - 11855
SEMA3A	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	SEQ ID NOS: 11862 - 11866
SEMA3B	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	SEQ ID NOS: 11867 - 11873
SEMA3C	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEQ ID NOS: 11874 - 11878
SEMA3E	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	SEQ ID NOS: 11879 - 11883
SEMA3F	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEQ ID NOS: 11884 - 11890
SEMA3G	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	SEQ ID NOS: 11891 - 11893
SEMA4A	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	SEQ ID NOS: 11894 - 11902
SEMA4B	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	SEQ ID NOS: 11903 - 11913
SEMA4C	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	SEQ ID NOS: 11914 - 11916

SEMA4D	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	SEQ ID NOS: 11917 - 11930
SEMA4F	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	SEQ ID NOS: 11931 - 11939
SEMA4G	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	SEQ ID NOS: 11940 - 11947
SEMA5A	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	SEQ ID NOS: 11948 - 11949
SEMA6A	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	SEQ ID NOS: 11950 - 11957
SEMA6C	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	SEQ ID NOS: 11958 - 11963
SEMA6D	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	SEQ ID NOS: 11964 - 11977
SEMG1	Semenogelin I	SEQ ID NO: 11978
SEMG2	Semenogelin II	SEQ ID NO: 11979
SEPN1	Selenoprotein N, 1	SEQ ID NOS: 11850 - 11853
SEPP1	Selenoprotein P, plasma, 1	SEQ ID NOS: 11856 - 11861
SEPT15	15 kDa selenoprotein	SEQ ID NOS: 11840 - 11846
SEPT9	Septin 9	SEQ ID NOS: 11980 - 12016
SERPINA1	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SEQ ID NOS: 12017 - 12033
SERPINA10	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	SEQ ID NOS: 12034 - 12037
SERPINA11	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11	SEQ ID NO: 12038
SERPINA12	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	SEQ ID NOS: 12039 - 12040
SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	SEQ ID NOS: 673 - 12047
SERPINA4	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4	SEQ ID NOS: 12048 - 12050

SERPINA5	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	SEQ ID NOS: 12051 - 12062
SERPINA6	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	SEQ ID NOS: 12063 - 12065
SERPINA7	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7	SEQ ID NOS: 12066 - 12067
SERPINA9	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	SEQ ID NOS: 12068 - 12074
SERPINB2	Serpin peptidase inhibitor, clade B (ovalbumin), member 2	SEQ ID NOS: 12075 - 12079
SERPINC1	Serpin peptidase inhibitor, clade C (antithrombin), member 1	SEQ ID NOS: 12080 - 12081
SERPIND1	Serpin peptidase inhibitor, clade D (heparin cofactor), member 1	SEQ ID NOS: 12082 - 12083
SERPINE1	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SEQ ID NO: 12084
SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	SEQ ID NOS: 12085 - 12091
SERPINE3	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3	SEQ ID NOS: 12092 - 12095
SERPINF1	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	SEQ ID NOS: 12096 - 12104
SERPINF2	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	SEQ ID NOS: 12105 - 12109
SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	SEQ ID NOS: 12110 - 12120
SERPINH1	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	SEQ ID NOS: 12121 - 12135
SERPINI1	Serpin peptidase inhibitor, clade I (neuroserpin), member 1	SEQ ID NOS: 12136 - 12140
SERPINI2	Serpin peptidase inhibitor, clade I (pancpin), member 2	SEQ ID NOS: 12141 - 12147
SETD8	SET domain containing (lysine methyltransferase) 8	SEQ ID NOS: 7589 - 7592
SEZ6L2	Seizure related 6 homolog (mouse)-like 2	SEQ ID NOS: 12148 - 12154
SFRP1	Secreted frizzled-related protein 1	SEQ ID NOS: 12155 - 12156
SFRP2	Secreted frizzled-related protein 2	SEQ ID NO: 12157

SFRP4	Secreted frizzled-related protein 4	SEQ ID NOS: 12158 - 12159
SFRP5	Secreted frizzled-related protein 5	SEQ ID NO: 12160
SFTA2	Surfactant associated 2	SEQ ID NOS: 12161 - 12162
SFTPA1	Surfactant protein A1	SEQ ID NOS: 12163 - 12167
SFTPA2	Surfactant protein A2	SEQ ID NOS: 12168 - 12172
SFTPB	Surfactant protein B	SEQ ID NOS: 12173 - 12177
SFTPD	Surfactant protein D	SEQ ID NOS: 12178 - 12179
SFXN5	Sideroflexin 5	SEQ ID NOS: 12180 - 12184
SGCA	Sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	SEQ ID NOS: 12185 - 12192
SGSH	N-sulfoglucosamine sulfohydrolase	SEQ ID NOS: 12193 - 12201
SH3RF3	SH3 domain containing ring finger 3	SEQ ID NO: 12202
SHBG	Sex hormone-binding globulin	SEQ ID NOS: 12203 - 12221
SHE	Src homology 2 domain containing E	SEQ ID NOS: 12222 - 12224
SHH	Sonic hedgehog	SEQ ID NOS: 12225 - 12228
SHKBP1	SH3KBP1 binding protein 1	SEQ ID NOS: 12229 - 12244
SIAE	Sialic acid acetylesterase	SEQ ID NOS: 12245 - 12247
SIDT2	SID1 transmembrane family, member 2	SEQ ID NOS: 12248 - 12257
SIGLEC10	Sialic acid binding Ig-like lectin 10	SEQ ID NOS: 12258 - 12266
SIGLEC6	Sialic acid binding Ig-like lectin 6	SEQ ID NOS: 12267 - 12272
SIGLEC7	Sialic acid binding Ig-like lectin 7	SEQ ID NOS: 12273 - 12277
SIGLECL1	SIGLEC family like 1	SEQ ID NOS: 12278 - 12283
SIGMAR1	Sigma non-opioid intracellular receptor 1	SEQ ID NOS: 12284 - 12287
SIL1	SIL1 nucleotide exchange factor	SEQ ID NOS: 12288 - 12296

SIRPB1	Signal-regulatory protein beta 1	SEQ ID NOS: 12297 - 12309
SIRPD	Signal-regulatory protein delta	SEQ ID NOS: 12310 - 12312
SLAMF1	Signaling lymphocytic activation molecule family member 1	SEQ ID NOS: 12313 - 12315
SLAMF7	SLAM family member 7	SEQ ID NOS: 12316 - 12324
SLC10A3	Solute carrier family 10, member 3	SEQ ID NOS: 12325 - 12329
SLC15A3	Solute carrier family 15 (oligopeptide transporter), member 3	SEQ ID NOS: 12330 - 12335
SLC25A14	Solute carrier family 25 (mitochondrial carrier, brain), member 14	SEQ ID NOS: 12336 - 12342
SLC25A25	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	SEQ ID NOS: 12343 - 12349
SLC2A5	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	SEQ ID NOS: 12350 - 12358
SLC35E3	Solute carrier family 35, member E3	SEQ ID NOS: 12359 - 12360
SLC39A10	Solute carrier family 39 (zinc transporter), member 10	SEQ ID NOS: 12361 - 12367
SLC39A14	Solute carrier family 39 (zinc transporter), member 14	SEQ ID NOS: 12368 - 12378
SLC39A4	Solute carrier family 39 (zinc transporter), member 4	SEQ ID NOS: 12379 - 12381
SLC39A5	Solute carrier family 39 (zinc transporter), member 5	SEQ ID NOS: 12382 - 12388
SLC3A1	Solute carrier family 3 (amino acid transporter heavy chain), member 1	SEQ ID NOS: 12389 - 12398
SLC51A	Solute carrier family 51, alpha subunit	SEQ ID NOS: 12399 - 12403
SLC52A2	Solute carrier family 52 (riboflavin transporter), member 2	SEQ ID NOS: 12404 - 12414
SLC5A6	Solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6	SEQ ID NOS: 12415 - 12425
SLC6A9	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9	SEQ ID NOS: 12426 - 12433
SLC8A1	Solute carrier family 8 (sodium/calcium exchanger), member 1	SEQ ID NOS: 12434 - 12445
SLC8B1	Solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	SEQ ID NOS: 12446 - 12456

SLC9A6	Solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6	SEQ ID NOS: 12457 - 12468
SLCO1A2	Solute carrier organic anion transporter family, member 1A2	SEQ ID NOS: 12469 - 12481
SLIT1	Slit guidance ligand 1	SEQ ID NOS: 12482 - 12485
SLIT2	Slit guidance ligand 2	SEQ ID NOS: 12486 - 12494
SLIT3	Slit guidance ligand 3	SEQ ID NOS: 12495 - 12497
SLITRK3	SLIT and NTRK-like family, member 3	SEQ ID NOS: 12498 - 12500
SLPI	Secretory leukocyte peptidase inhibitor	SEQ ID NO: 12501
SLTM	SAFB-like, transcription modulator	SEQ ID NOS: 12502 - 12515
SLURP1	Secreted LY6/PLAUR domain containing 1	SEQ ID NO: 12516
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID NOS: 12517 - 12562
SMG6	SMG6 nonsense mediated mRNA decay factor	SEQ ID NOS: 12563 - 12574
SMIM7	Small integral membrane protein 7	SEQ ID NOS: 12575 - 12591
SMOC1	SPARC related modular calcium binding 1	SEQ ID NOS: 12592 - 12593
SMOC2	SPARC related modular calcium binding 2	SEQ ID NOS: 12594 - 12598
SMPDL3A	Sphingomyelin phosphodiesterase, acid-like 3A	SEQ ID NOS: 12599 - 12600
SMPDL3B	Sphingomyelin phosphodiesterase, acid-like 3B	SEQ ID NOS: 12601 - 12605
SMR3A	Submaxillary gland androgen regulated protein 3A	SEQ ID NO: 12606
SMR3B	Submaxillary gland androgen regulated protein 3B	SEQ ID NOS: 12607 - 12609
SNED1	Sushi, nidogen and EGF-like domains 1	SEQ ID NOS: 12610 - 12616
SNTB1	Syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	SEQ ID NOS: 12617 - 12619
SNTB2	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	SEQ ID NOS: 12620 - 12624
SNX14	Sorting nexin 14	SEQ ID NOS: 12625 - 12636

SOD3	Superoxide dismutase 3, extracellular	SEQ ID NOS: 12637 - 12638
SOST	Sclerostin	SEQ ID NO: 12639
SOSTDC1	Sclerostin domain containing 1	SEQ ID NOS: 12640 - 12641
SOWAHA	Sosondowah ankyrin repeat domain family member A	SEQ ID NO: 12642
SPACA3	Sperm acrosome associated 3	SEQ ID NOS: 12643 - 12645
SPACA4	Sperm acrosome associated 4	SEQ ID NO: 12646
SPACA5	Sperm acrosome associated 5	SEQ ID NOS: 12647 - 12648
SPACA5B	Sperm acrosome associated 5B	SEQ ID NO: 12649
SPACA7	Sperm acrosome associated 7	SEQ ID NOS: 12650 - 12653
SPAG11A	Sperm associated antigen 11A	SEQ ID NOS: 12654 - 12662
SPAG11B	Sperm associated antigen 11B	SEQ ID NOS: 12663 - 12671
SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)	SEQ ID NOS: 12672 - 12676
SPARCL1	SPARC-like 1 (hevin)	SEQ ID NOS: 12677 - 12686
SPATA20	Spermatogenesis associated 20	SEQ ID NOS: 12687 - 12700
SPESP1	Sperm equatorial segment protein 1	SEQ ID NO: 12701
SPINK1	Serine peptidase inhibitor, Kazal type 1	SEQ ID NOS: 12702 - 12703
SPINK13	Serine peptidase inhibitor, Kazal type 13 (putative)	SEQ ID NOS: 12704 - 12706
SPINK14	Serine peptidase inhibitor, Kazal type 14 (putative)	SEQ ID NOS: 12707 - 12708
SPINK2	Serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	SEQ ID NOS: 12709 - 12714
SPINK4	Serine peptidase inhibitor, Kazal type 4	SEQ ID NOS: 12715 - 12716
SPINK5	Serine peptidase inhibitor, Kazal type 5	SEQ ID NOS: 12717 - 12722
SPINK6	Serine peptidase inhibitor, Kazal type 6	SEQ ID NOS: 12723 - 12725
SPINK7	Serine peptidase inhibitor, Kazal type 7 (putative)	SEQ ID NOS: 12726 - 12727
SPINK8	Serine peptidase inhibitor, Kazal type 8 (putative)	SEQ ID NO: 12728

SPINK9	Serine peptidase inhibitor, Kazal type 9	SEQ ID NOS: 12729 - 12730
SPINT1	Serine peptidase inhibitor, Kunitz type 1	SEQ ID NOS: 12731 - 12738
SPINT2	Serine peptidase inhibitor, Kunitz type, 2	SEQ ID NOS: 12739 - 12746
SPINT3	Serine peptidase inhibitor, Kunitz type, 3	SEQ ID NO: 12747
SPINT4	Serine peptidase inhibitor, Kunitz type 4	SEQ ID NO: 12748
SPOCK1	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	SEQ ID NOS: 12749 - 12752
SPOCK2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SEQ ID NOS: 12753 - 12756
SPOCK3	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	SEQ ID NOS: 12757 - 12782
SPON1	Spondin 1, extracellular matrix protein	SEQ ID NO: 12783
SPON2	Spondin 2, extracellular matrix protein	SEQ ID NOS: 12784 - 12793
SPP1	Secreted phosphoprotein 1	SEQ ID NOS: 12794 - 12798
SPP2	Secreted phosphoprotein 2, 24kDa	SEQ ID NOS: 12799 - 12801
SPRN	Shadow of prion protein homolog (zebrafish)	SEQ ID NO: 12802
SPRYD3	SPRY domain containing 3	SEQ ID NOS: 12803 - 12806
SPRYD4	SPRY domain containing 4	SEQ ID NO: 12807
SPTY2D1-AS1	SPTY2D1 antisense RNA 1	SEQ ID NOS: 12808 - 12813
SPX	Spexin hormone	SEQ ID NOS: 12814 - 12815
SRGN	Serglycin	SEQ ID NO: 12816
SRL	Sarcalumenin	SEQ ID NOS: 12817 - 12819
SRP14	Signal recognition particle 14kDa (homologous Alu RNA binding protein)	SEQ ID NOS: 12820 - 12823
SRPX	Sushi-repeat containing protein, X-linked	SEQ ID NOS: 12824 - 12827
SRPX2	Sushi-repeat containing protein, X-linked 2	SEQ ID NOS: 12828 - 12831
SSC4D	Scavenger receptor cysteine rich family, 4 domains	SEQ ID NO: 12832
SSC5D	Scavenger receptor cysteine rich family, 5 domains	SEQ ID NOS: 12833 - 12836
SSPO	SCO-spondin	SEQ ID NO: 12837

SSR2	Signal sequence receptor, beta (translocon-associated protein beta)	SEQ ID NOS: 12838 - 12847
SST	Somatostatin	SEQ ID NO: 12848
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	SEQ ID NOS: 12849 - 12856
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	SEQ ID NOS: 12857 - 12872
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	SEQ ID NOS: 12873 - 12888
ST6GALNAC 2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	SEQ ID NOS: 12889 - 12893
ST6GALNAC 5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	SEQ ID NOS: 12894 - 12895
ST6GALNAC 6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	SEQ ID NOS: 12896 - 12903
ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	SEQ ID NOS: 12904 - 12906
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	SEQ ID NOS: 12907 - 12909
ST8SIA6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	SEQ ID NOS: 12910 - 12911
STARD7	StAR-related lipid transfer (START) domain containing 7	SEQ ID NOS: 12912 - 12913
STATH	Statherin	SEQ ID NOS: 12914 - 12916
STC1	Stanniocalcin 1	SEQ ID NOS: 12917 - 12918
STC2	Stanniocalcin 2	SEQ ID NOS: 12919 - 12921
STMND1	Stathmin domain containing 1	SEQ ID NOS: 12922 - 12923
STOML2	Stomatin (EPB72)-like 2	SEQ ID NOS: 12926 - 12929
STOX1	Storkhead box 1	SEQ ID NOS: 12930 - 12934
STRC	Stereocilin	SEQ ID NOS: 12935 - 12940
SUCLG1	Succinate-CoA ligase, alpha subunit	SEQ ID NOS: 12941 - 12942
SUDS3	SDS3 homolog, SIN3A corepressor complex component	SEQ ID NO: 12943

SULF1	Sulfatase 1	SEQ ID NOS: 12944 - 12954
SULF2	Sulfatase 2	SEQ ID NOS: 12955 - 12959
SUMF1	Sulfatase modifying factor 1	SEQ ID NOS: 12960 - 12964
SUMF2	Sulfatase modifying factor 2	SEQ ID NOS: 12965 - 12978
SUSD1	Sushi domain containing 1	SEQ ID NOS: 12979 - 12984
SUSD5	Sushi domain containing 5	SEQ ID NOS: 12985 - 12986
SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	SEQ ID NOS: 12987 - 12989
SWSAP1	SWIM-type zinc finger 7 associated protein 1	SEQ ID NO: 12990
SYAP1	Synapse associated protein 1	SEQ ID NO: 12991
SYCN	Syncollin	SEQ ID NO: 12992
TAC1	Tachykinin, precursor 1	SEQ ID NOS: 12993 - 12995
TAC3	Tachykinin 3	SEQ ID NOS: 12996 - 13005
TAC4	Tachykinin 4 (hemokinin)	SEQ ID NOS: 13006 - 13011
TAGLN2	Transgelin 2	SEQ ID NOS: 13012 - 13015
TAPBP	TAP binding protein (tapasin)	SEQ ID NOS: 13016 - 13021
TAPBPL	TAP binding protein-like	SEQ ID NOS: 13022 - 13023
TBL2	Transducin (beta)-like 2	SEQ ID NOS: 13024 - 13036
TBX10	T-box 10	SEQ ID NO: 13037
TCF12	Transcription factor 12	SEQ ID NOS: 13038 - 13051
TCN1	Transcobalamin I (vitamin B12 binding protein, R binder family)	SEQ ID NO: 13052
TCN2	Transcobalamin II	SEQ ID NOS: 13053 - 13056
TCTN1	Tectonic family member 1	SEQ ID NOS: 13057 - 13075
TCTN3	Tectonic family member 3	SEQ ID NOS: 13076 - 13080
TDP2	Tyrosyl-DNA phosphodiesterase 2	SEQ ID NOS: 13081 - 13082

TEK	TEK tyrosine kinase, endothelial	SEQ ID NOS: 13097 - 13101
TEPP	Testis, prostate and placenta expressed	SEQ ID NOS: 13102 - 13103
TEX101	Testis expressed 101	SEQ ID NOS: 13104 - 13105
TEX264	Testis expressed 264	SEQ ID NOS: 13106 - 13117
TF	Transferrin	SEQ ID NOS: 13121 - 13127
TFAM	Transcription factor A, mitochondrial	SEQ ID NOS: 13128 - 13130
TFF1	Trefoil factor 1	SEQ ID NO: 13131
TFF2	Trefoil factor 2	SEQ ID NO: 13132
TFF3	Trefoil factor 3 (intestinal)	SEQ ID NOS: 13133 - 13135
TFPI	Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	SEQ ID NOS: 13136 - 13145
TFPI2	Tissue factor pathway inhibitor 2	SEQ ID NOS: 13146 - 13147
TG	Thyroglobulin	SEQ ID NOS: 13148 - 13157
TGFB1	Transforming growth factor, beta 1	SEQ ID NOS: 13158 - 13159
TGFB2	Transforming growth factor, beta 2	SEQ ID NOS: 13160 - 13161
TGFB3	Transforming growth factor, beta 3	SEQ ID NOS: 13162 - 13163
TGFBI	Transforming growth factor, beta-induced, 68kDa	SEQ ID NOS: 13164 - 13171
TGFBR1	Transforming growth factor, beta receptor 1	SEQ ID NOS: 13172 - 13181
TGFBR3	Transforming growth factor, beta receptor III	SEQ ID NOS: 13182 - 13188
THBS1	Thrombospondin 1	SEQ ID NOS: 13189 - 13190
THBS2	Thrombospondin 2	SEQ ID NOS: 13191 - 13193
THBS3	Thrombospondin 3	SEQ ID NOS: 13194 - 13198
THBS4	Thrombospondin 4	SEQ ID NOS: 13199 - 13200
THOC3	THO complex 3	SEQ ID NOS: 13201 - 13210

THPO	Thrombopoietin	SEQ ID NOS: 13211 - 13216
THSD4	Thrombospondin, type I, domain containing 4	SEQ ID NOS: 13217 - 13220
THY1	Thy-1 cell surface antigen	SEQ ID NOS: 13221 - 13226
TIE1	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1	SEQ ID NOS: 13227 - 13228
TIMMDC1	Translocase of inner mitochondrial membrane domain containing 1	SEQ ID NOS: 13229 - 13236
TIMP1	TIMP metallopeptidase inhibitor 1	SEQ ID NOS: 13237 - 13241
TIMP2	TIMP metallopeptidase inhibitor 2	SEQ ID NOS: 13242 - 13246
TIMP3	TIMP metallopeptidase inhibitor 3	SEQ ID NO: 13247
TIMP4	TIMP metallopeptidase inhibitor 4	SEQ ID NO: 13248
TINAGL1	Tubulointerstitial nephritis antigen-like 1	SEQ ID NOS: 13249 - 13251
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	SEQ ID NOS: 13252 - 13261
TLL2	Tolloid-like 2	SEQ ID NO: 13262
TLR1	Toll-like receptor 1	SEQ ID NOS: 13263 - 13268
TLR3	Toll-like receptor 3	SEQ ID NOS: 13269 - 13271
TM2D2	TM2 domain containing 2	SEQ ID NOS: 13272 - 13277
TM2D3	TM2 domain containing 3	SEQ ID NOS: 13278 - 13285
TM7SF3	Transmembrane 7 superfamily member 3	SEQ ID NOS: 13286 - 13300
TM9SF1	Transmembrane 9 superfamily member 1	SEQ ID NOS: 13301 - 13311
TMCO6	Transmembrane and coiled-coil domains 6	SEQ ID NOS: 13312 - 13319
TMED1	Transmembrane p24 trafficking protein 1	SEQ ID NOS: 13320 - 13326
TMED2	Transmembrane p24 trafficking protein 2	SEQ ID NOS: 13327 - 13329
TMED3	Transmembrane p24 trafficking protein 3	SEQ ID NOS: 13330 - 13333
TMED4	Transmembrane p24 trafficking protein 4	SEQ ID NOS: 13334 - 13336
TMED5	Transmembrane p24 trafficking protein 5	SEQ ID NOS: 13337 - 13340

TMED7	Transmembrane p24 trafficking protein 7	SEQ ID NOS: 13341 - 13342
TMED7-TICAM2	TMED7-TICAM2 readthrough	SEQ ID NOS: 13343 - 13344
TMEM108	Transmembrane protein 108	SEQ ID NOS: 13345 - 13353
TMEM116	Transmembrane protein 116	SEQ ID NOS: 13354 - 13365
TMEM119	Transmembrane protein 119	SEQ ID NOS: 13366 - 13369
TMEM155	Transmembrane protein 155	SEQ ID NOS: 13370 - 13373
TMEM168	Transmembrane protein 168	SEQ ID NOS: 13374 - 13379
TMEM178A	Transmembrane protein 178A	SEQ ID NOS: 13380 - 13381
TMEM179	Transmembrane protein 179	SEQ ID NOS: 13382 - 13387
TMEM196	Transmembrane protein 196	SEQ ID NOS: 13388 - 13392
TMEM199	Transmembrane protein 199	SEQ ID NOS: 13393 - 13396
TMEM205	Transmembrane protein 205	SEQ ID NOS: 13397 - 13410
TMEM213	Transmembrane protein 213	SEQ ID NOS: 13411 - 13414
TMEM25	Transmembrane protein 25	SEQ ID NOS: 13415 - 13431
TMEM30C	Transmembrane protein 30C	SEQ ID NO: 13432
TMEM38B	Transmembrane protein 38B	SEQ ID NOS: 13433 - 13437
TMEM44	Transmembrane protein 44	SEQ ID NOS: 13438 - 13447
TMEM52	Transmembrane protein 52	SEQ ID NOS: 13448 - 13452
TMEM52B	Transmembrane protein 52B	SEQ ID NOS: 13453 - 13455
TMEM59	Transmembrane protein 59	SEQ ID NOS: 13456 - 13463
TMEM67	Transmembrane protein 67	SEQ ID NOS: 13464 - 13475
TMEM70	Transmembrane protein 70	SEQ ID NOS: 13476 - 13478
TMEM87A	Transmembrane protein 87A	SEQ ID NOS: 13479 - 13488

TMEM94	Transmembrane protein 94	SEQ ID NOS: 13489 - 13504
TMEM95	Transmembrane protein 95	SEQ ID NOS: 13505 - 13507
TMIGD1	Transmembrane and immunoglobulin domain containing 1	SEQ ID NOS: 13508 - 13509
TMPRSS12	Transmembrane (C-terminal) protease, serine 12	SEQ ID NOS: 13510 - 13511
TMPRSS5	Transmembrane protease, serine 5	SEQ ID NOS: 13512 - 13523
TMUB1	Transmembrane and ubiquitin-like domain containing 1	SEQ ID NOS: 13524 - 13530
TMX2	Thioredoxin-related transmembrane protein 2	SEQ ID NOS: 13531 - 13538
TMX3	Thioredoxin-related transmembrane protein 3	SEQ ID NOS: 13539 - 13546
TNC	Tenascin C	SEQ ID NOS: 13547 - 13555
TNFAIP6	Tumor necrosis factor, alpha-induced protein 6	SEQ ID NO: 13556
TNFRSF11A	Tumor necrosis factor receptor superfamily, member 11a, NFKB activator	SEQ ID NOS: 13557 - 13561
TNFRSF11B	Tumor necrosis factor receptor superfamily, member 11b	SEQ ID NOS: 13562 - 13563
TNFRSF12A	Tumor necrosis factor receptor superfamily, member 12A	SEQ ID NOS: 13564 - 13569
TNFRSF14	Tumor necrosis factor receptor superfamily, member 14	SEQ ID NOS: 13570 - 13576
TNFRSF18	Tumor necrosis factor receptor superfamily, member 18	SEQ ID NOS: 13577 - 13580
TNFRSF1A	Tumor necrosis factor receptor superfamily, member 1A	SEQ ID NOS: 13581 - 13589
TNFRSF1B	Tumor necrosis factor receptor superfamily, member 1B	SEQ ID NOS: 13590 - 13591
TNFRSF25	Tumor necrosis factor receptor superfamily, member 25	SEQ ID NOS: 13592 - 13603
TNFRSF6B	Tumor necrosis factor receptor superfamily, member 6b, decoy	SEQ ID NO: 13604
TNFSF11	Tumor necrosis factor (ligand) superfamily, member 11	SEQ ID NOS: 13605 - 13609
TNFSF12	Tumor necrosis factor (ligand) superfamily, member 12	SEQ ID NOS: 13610 - 13611
TNFSF12-TNFSF13	TNFSF12-TNFSF13 readthrough	SEQ ID NO: 13612

TNFSF15	Tumor necrosis factor (ligand) superfamily, member 15	SEQ ID NOS: 13613 - 13614
TNN	Tenascin N	SEQ ID NOS: 13615 - 13617
TNR	Tenascin R	SEQ ID NOS: 13618 - 13620
TNXB	Tenascin XB	SEQ ID NOS: 13621 - 13627
TOMM7	Translocase of outer mitochondrial membrane 7 homolog (yeast)	SEQ ID NOS: 13634 - 13637
TOP1MT	Topoisomerase (DNA) I, mitochondrial	SEQ ID NOS: 13638 - 13652
TOR1A	Torsin family 1, member A (torsin A)	SEQ ID NO: 13653
TOR1B	Torsin family 1, member B (torsin B)	SEQ ID NOS: 13654 - 13655
TOR2A	Torsin family 2, member A	SEQ ID NOS: 13656 - 13662
TOR3A	Torsin family 3, member A	SEQ ID NOS: 13663 - 13667
TPD52	Tumor protein D52	SEQ ID NOS: 13668 - 13680
TPO	Thyroid peroxidase	SEQ ID NOS: 13681 - 13691
TPP1	Tripeptidyl peptidase I	SEQ ID NOS: 13692 - 13709
TPSAB1	Tryptase alpha/beta 1	SEQ ID NOS: 13710 - 13712
TPSB2	Tryptase beta 2 (gene/pseudogene)	SEQ ID NOS: 13713 - 13715
TPSD1	Tryptase delta 1	SEQ ID NOS: 13716 - 13717
TPST1	Tyrosylprotein sulfotransferase 1	SEQ ID NOS: 13718 - 13720
TPST2	Tyrosylprotein sulfotransferase 2	SEQ ID NOS: 13721 - 13729
TRABD2A	TraB domain containing 2A	SEQ ID NOS: 13730 - 13732
TRABD2B	TraB domain containing 2B	SEQ ID NO: 13733
TREH	Trehalase (brush-border membrane glycoprotein)	SEQ ID NOS: 13734 - 13736
TREM1	Triggering receptor expressed on myeloid cells 1	SEQ ID NOS: 13737 - 13740
TREM2	Triggering receptor expressed on myeloid cells 2	SEQ ID NOS: 13741 - 13743

TRH	Thyrotropin-releasing hormone	SEQ ID NOS: 13744 - 13745
TRIM24	Tripartite motif containing 24	SEQ ID NOS: 13746 - 13747
TRIM28	Tripartite motif containing 28	SEQ ID NOS: 13748 - 13753
TRIO	Trio Rho guanine nucleotide exchange factor	SEQ ID NOS: 13754 - 13760
TRNP1	TMF1-regulated nuclear protein 1	SEQ ID NOS: 13761 - 13762
TSC22D4	TSC22 domain family, member 4	SEQ ID NOS: 13763 - 13766
TSHB	Thyroid stimulating hormone, beta	SEQ ID NOS: 13767 - 13768
TSHR	Thyroid stimulating hormone receptor	SEQ ID NOS: 13769 - 13776
TSKU	Tsukushi, small leucine rich proteoglycan	SEQ ID NOS: 13777 - 13781
TSLP	Thymic stromal lymphopoietin	SEQ ID NOS: 13782 - 13784
TSPAN3	Tetraspanin 3	SEQ ID NOS: 13785 - 13790
TSPAN31	Tetraspanin 31	SEQ ID NOS: 13791 - 13797
TSPEAR	Thrombospondin-type laminin G domain and EAR repeats	SEQ ID NOS: 13798 - 13801
TTC13	Tetratricopeptide repeat domain 13	SEQ ID NOS: 13802 - 13808
TTC19	Tetratricopeptide repeat domain 19	SEQ ID NOS: 13809 - 13814
TTC9B	Tetratricopeptide repeat domain 9B	SEQ ID NO: 13815
TTLL11	Tubulin tyrosine ligase-like family member 11	SEQ ID NOS: 13816 - 13820
TTR	Transthyretin	SEQ ID NOS: 13821 - 13823
TWSG1	Twisted gastrulation BMP signaling modulator 1	SEQ ID NOS: 13824 - 13826
TXNDC12	Thioredoxin domain containing 12 (endoplasmic reticulum)	SEQ ID NOS: 13827 - 13829
TXNDC15	Thioredoxin domain containing 15	SEQ ID NOS: 13830 - 13836
TXNDC5	Thioredoxin domain containing 5 (endoplasmic reticulum)	SEQ ID NOS: 13837 - 13838
TXNRD2	Thioredoxin reductase 2	SEQ ID NOS: 13839 - 13851

TYRP1	Tyrosinase-related protein 1	SEQ ID NOS: 13852 - 13854
UBAC2	UBA domain containing 2	SEQ ID NOS: 13855 - 13859
UBALD1	UBA-like domain containing 1	SEQ ID NOS: 13860 - 13868
UBAP2	Ubiquitin associated protein 2	SEQ ID NOS: 13869 - 13875
UBXN8	UBX domain protein 8	SEQ ID NOS: 13876 - 13882
UCMA	Upper zone of growth plate and cartilage matrix associated	SEQ ID NOS: 13883 - 13884
UCN	Urocortin	SEQ ID NO: 13885
UCN2	Urocortin 2	SEQ ID NO: 13886
UCN3	Urocortin 3	SEQ ID NO: 13887
UGGT2	UDP-glucose glycoprotein glucosyltransferase 2	SEQ ID NOS: 13888 - 13893
UGT1A10	UDP glucuronosyltransferase 1 family, polypeptide A10	SEQ ID NOS: 13894 - 13895
UGT2A1	UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus	SEQ ID NOS: 13896 - 13900
UGT2B11	UDP glucuronosyltransferase 2 family, polypeptide B11	SEQ ID NO: 13901
UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	SEQ ID NOS: 13902 - 13903
UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	SEQ ID NOS: 13904 - 13907
UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	SEQ ID NOS: 13908 - 13911
UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1	SEQ ID NOS: 13912 - 13917
UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	SEQ ID NOS: 13918 - 13921
UGT8	UDP glycosyltransferase 8	SEQ ID NOS: 13922 - 13924
ULBP3	UL16 binding protein 3	SEQ ID NOS: 13925 - 13926
UMOD	Uromodulin	SEQ ID NOS: 13927 - 13938
UNC5C	Unc-5 netrin receptor C	SEQ ID NOS: 13939 - 13943
UPK3B	Uroplakin 3B	SEQ ID NOS: 13944 - 13946
USP11	Ubiquitin specific peptidase 11	SEQ ID NOS: 13947 - 13950

USP14	Ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	SEQ ID NOS: 13951 - 13957
USP3	Ubiquitin specific peptidase 3	SEQ ID NOS: 13958 - 13973
UTS2	Urotensin 2	SEQ ID NOS: 13984 - 13986
UTS2B	Urotensin 2B	SEQ ID NOS: 13987 - 13992
UTY	Ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	SEQ ID NOS: 13993 - 14005
UXS1	UDP-glucuronate decarboxylase 1	SEQ ID NOS: 14006 - 14013
VASH1	Vasohibin 1	SEQ ID NOS: 14014 - 14016
VCAN	Versican	SEQ ID NOS: 14017 - 14023
VEGFA	Vascular endothelial growth factor A	SEQ ID NOS: 14024 - 14049
VEGFB	Vascular endothelial growth factor B	SEQ ID NOS: 14050 - 14052
VEGFC	Vascular endothelial growth factor C	SEQ ID NO: 14053
VGF	VGF nerve growth factor inducible	SEQ ID NOS: 14055 - 14057
VIP	Vasoactive intestinal peptide	SEQ ID NOS: 14058 - 14060
VIPR2	Vasoactive intestinal peptide receptor 2	SEQ ID NOS: 14061 - 14064
VIT	Vitrin	SEQ ID NOS: 14065 - 14072
VKORC1	Vitamin K epoxide reductase complex, subunit 1	SEQ ID NOS: 14073 - 14080
VLDLR	Very low density lipoprotein receptor	SEQ ID NOS: 14081 - 14083
VMO1	Vitelline membrane outer layer 1 homolog (chicken)	SEQ ID NOS: 14084 - 14087
VNN1	Vanin 1	SEQ ID NO: 14088
VNN2	Vanin 2	SEQ ID NOS: 14089 - 14102
VNN3	Vanin 3	SEQ ID NOS: 14103 - 14114
VOPP1	Vesicular, overexpressed in cancer, prosurvival protein 1	SEQ ID NOS: 14115 - 14127
VPREB1	Pre-B lymphocyte 1	SEQ ID NOS: 14128 - 14129

VPREB3	Pre-B lymphocyte 3	SEQ ID NOS: 14130 - 14131
VPS37B	Vacuolar protein sorting 37 homolog B (S. cerevisiae)	SEQ ID NOS: 14132 - 14134
VPS51	Vacuolar protein sorting 51 homolog (S. cerevisiae)	SEQ ID NOS: 14135 - 14146
VSIG1	V-set and immunoglobulin domain containing 1	SEQ ID NOS: 14147 - 14149
VSIG10	V-set and immunoglobulin domain containing 10	SEQ ID NOS: 14150 - 14151
VSTM1	V-set and transmembrane domain containing 1	SEQ ID NOS: 14152 - 14158
VSTM2A	V-set and transmembrane domain containing 2A	SEQ ID NOS: 14159 - 14162
VSTM2B	V-set and transmembrane domain containing 2B	SEQ ID NO: 14163
VSTM2L	V-set and transmembrane domain containing 2 like	SEQ ID NOS: 14164 - 14166
VSTM4	V-set and transmembrane domain containing 4	SEQ ID NOS: 14167 - 14168
VTN	Vitronectin	SEQ ID NOS: 14169 - 14170
VWA1	Von Willebrand factor A domain containing 1	SEQ ID NOS: 14171 - 14174
VWA2	Von Willebrand factor A domain containing 2	SEQ ID NOS: 14175 - 14176
VWA5B2	Von Willebrand factor A domain containing 5B2	SEQ ID NOS: 14177 - 14178
VWA7	Von Willebrand factor A domain containing 7	SEQ ID NO: 14179
VWC2	Von Willebrand factor C domain containing 2	SEQ ID NO: 14180
VWC2L	Von Willebrand factor C domain containing protein 2-like	SEQ ID NOS: 14181 - 14182
VWCE	Von Willebrand factor C and EGF domains	SEQ ID NOS: 14183 - 14187
VWDE	Von Willebrand factor D and EGF domains	SEQ ID NOS: 14188 - 14193
VWF	Von Willebrand factor	SEQ ID NOS: 14194 - 14196
WDR25	WD repeat domain 25	SEQ ID NOS: 14197 - 14203
WDR81	WD repeat domain 81	SEQ ID NOS: 14204 - 14213

WDR90	WD repeat domain 90	SEQ ID NOS: 14214 - 14221
WFDC1	WAP four-disulfide core domain 1	SEQ ID NOS: 14222 - 14224
WFDC10A	WAP four-disulfide core domain 10A	SEQ ID NO: 14225
WFDC10B	WAP four-disulfide core domain 10B	SEQ ID NOS: 14226 - 14227
WFDC11	WAP four-disulfide core domain 11	SEQ ID NOS: 14228 - 14230
WFDC12	WAP four-disulfide core domain 12	SEQ ID NO: 14231
WFDC13	WAP four-disulfide core domain 13	SEQ ID NO: 14232
WFDC2	WAP four-disulfide core domain 2	SEQ ID NOS: 14233 - 14237
WFDC3	WAP four-disulfide core domain 3	SEQ ID NOS: 14238 - 14241
WFDC5	WAP four-disulfide core domain 5	SEQ ID NOS: 14242 - 14243
WFDC6	WAP four-disulfide core domain 6	SEQ ID NOS: 14244 - 14245
WFDC8	WAP four-disulfide core domain 8	SEQ ID NOS: 14246 - 14247
WFIKKN1	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	SEQ ID NO: 14248
WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	SEQ ID NOS: 14249 - 14250
WIF1	WNT inhibitory factor 1	SEQ ID NOS: 14255 - 14257
WISP1	WNT1 inducible signaling pathway protein 1	SEQ ID NOS: 14258 - 14262
WISP2	WNT1 inducible signaling pathway protein 2	SEQ ID NOS: 14263 - 14265
WISP3	WNT1 inducible signaling pathway protein 3	SEQ ID NOS: 14266 - 14273
WNK1	WNK lysine deficient protein kinase 1	SEQ ID NOS: 14274 - 14287
WNT1	Wingless-type MMTV integration site family, member 1	SEQ ID NOS: 14288 - 14289
WNT10B	Wingless-type MMTV integration site family, member 10B	SEQ ID NOS: 14290 - 14294
WNT11	Wingless-type MMTV integration site family, member 11	SEQ ID NOS: 14295 - 14297
WNT16	Wingless-type MMTV integration site family, member 16	SEQ ID NOS: 14298 - 14299
WNT2	Wingless-type MMTV integration site family member 2	SEQ ID NOS: 14300 - 14302

WNT3	Wingless-type MMTV integration site family, member 3	SEQ ID NO: 14303
WNT3A	Wingless-type MMTV integration site family, member 3A	SEQ ID NO: 14304
WNT5A	Wingless-type MMTV integration site family, member 5A	SEQ ID NOS: 14305 - 14308
WNT5B	Wingless-type MMTV integration site family, member 5B	SEQ ID NOS: 14309 - 14315
WNT6	Wingless-type MMTV integration site family, member 6	SEQ ID NO: 14316
WNT7A	Wingless-type MMTV integration site family, member 7A	SEQ ID NO: 14317
WNT7B	Wingless-type MMTV integration site family, member 7B	SEQ ID NOS: 14318 - 14322
WNT8A	Wingless-type MMTV integration site family, member 8A	SEQ ID NOS: 14323 - 14326
WNT8B	Wingless-type MMTV integration site family, member 8B	SEQ ID NO: 14327
WNT9A	Wingless-type MMTV integration site family, member 9A	SEQ ID NO: 14328
WNT9B	Wingless-type MMTV integration site family, member 9B	SEQ ID NOS: 14329 - 14331
WSB1	WD repeat and SOCS box containing 1	SEQ ID NOS: 14332 - 14341
WSCD1	WSC domain containing 1	SEQ ID NOS: 14342 - 14351
WSCD2	WSC domain containing 2	SEQ ID NOS: 14352 - 14355
XCL1	Chemokine (C motif) ligand 1	SEQ ID NO: 14356
XCL2	Chemokine (C motif) ligand 2	SEQ ID NO: 14357
XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	SEQ ID NOS: 14358 - 14359
XXbac-BPG116M5.17		SEQ ID NOS: 679 - 680
XXbac-BPG181M17.5		SEQ ID NO: 681
XXbac-BPG32J3.20		SEQ ID NO: 682
XXYLT1	Xyloside xylosyltransferase 1	SEQ ID NOS: 14360 - 14365
XYLT1	Xylosyltransferase I	SEQ ID NO: 14366
XYLT2	Xylosyltransferase II	SEQ ID NOS: 14367 - 14372
ZFYVE21	Zinc finger, FYVE domain containing 21	SEQ ID NOS: 14373 - 14377

ZG16	Zymogen granule protein 16	SEQ ID NO: 14378
ZG16B	Zymogen granule protein 16B	SEQ ID NOS: 14379 - 14382
ZIC4	Zic family member 4	SEQ ID NOS: 14383 - 14391
ZNF207	Zinc finger protein 207	SEQ ID NOS: 14392 - 14402
ZNF26	Zinc finger protein 26	SEQ ID NOS: 14403 - 14406
ZNF34	Zinc finger protein 34	SEQ ID NOS: 14407 - 14410
ZNF419	Zinc finger protein 419	SEQ ID NOS: 14411 - 14425
ZNF433	Zinc finger protein 433	SEQ ID NOS: 14426 - 14435
ZNF449	Zinc finger protein 449	SEQ ID NOS: 14436 - 14437
ZNF488	Zinc finger protein 488	SEQ ID NOS: 14438 - 14439
ZNF511	Zinc finger protein 511	SEQ ID NOS: 14440 - 14441
ZNF570	Zinc finger protein 570	SEQ ID NOS: 14442 - 14447
ZNF691	Zinc finger protein 691	SEQ ID NOS: 14448 - 14455
ZNF98	Zinc finger protein 98	SEQ ID NOS: 14456 - 14459
ZPBP	Zona pellucida binding protein	SEQ ID NOS: 14460 - 14463
ZPBP2	Zona pellucida binding protein 2	SEQ ID NOS: 14464 - 14467
ZSCAN29	Zinc finger and SCAN domain containing 29	SEQ ID NOS: 14468 - 14474

Cas-Clover

[0745] 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)

[0746] 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.

[0747] Amino acid sequence of Staphylococcus aureus Cas9 with an active catalytic site.

```
1    mkrnyilgld igitsvgygi idyetrdvid agvrlfkean vennegrrsk rgarrlkrrr
61   rhriqrvkkl lfdynlltdh selsginpye arvkglsqkl seeefsaall hlakrrgvhn
121  vneveedtgn elstkeqisr nskaleekyv aelqlerlkk dgevrgsinr fktsdyvkea
181  kqllkvqkay hqldqsfidt yidlletrrt yyegpgegsp fgwkdikewy emlmghctyf
241  peelrsvkya ynadlynaln dlnnlvitrd enekleyyek fqiienvfkq kkkptlkqia
301  keilvneedi kgyrvtstgk peftnlkvyh dikditarke iienaelldq iakiltiyqs
361  sediqeeltn lnseltqeei eqisnlkgyt gthnlslkai nlildelwht ndnqiaifnr
421  lklvpkkvdl sqqkeipttl vddfilspvv krsfiqsikv inaiikkygl pndiiielar
481  eknskdaqkm inemqkrnrq tnerieeiir ttgkenakyl iekiklhdmq egkclyslea
541  ipledllnnp fnyevdhiip rsvsfdnsfn nkvlvkqeen skkgnrtpfq ylsssdskis
601  yetfkkhiln lakgkgrisk tkkeylleer dinrfsvqkd finrnlvdtr yatrglmnll
661  rsyfrvnnld vkvksinggf tsflrrkwkf kkernkgykh haedaliian adfifkewkk
721  ldkakkvmen qmfeekqaes mpeieteqey keifitphqi khikdfkdyk yshrvdkkpn
781  relindtlys trkddkgntl ivnnlnglyd kdndklkkli nkspekllmy hhdpqtyqkl
841  klimeqygde knplykyyee tgnyltkysk kdngpvikki kyygnklnah lditddypns
901  rnkvvklslk pyrfdvyldn gvykfvtvkn ldvikkenyy evnskcyeea kklkkisnqa
961  efiasfynnd likingelyr vigvnndlln rievnmidit yreylenmnd krppriikti
1021 asktqsikky stdilgnlye vkskkhpqii kkg (SEQ ID NO: 18052)
```

Inactivated, small Cas9 (dSaCas9)

[0748] 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 comprise an effector comprising a type IIS endonuclease.

[0749] dSaCas9 Sequence: D10A and N580A mutations (bold, capitalized, and underlined) inactivate the catalytic site.

```
1    mkrnyilgl A igitsvgygi idyetrdvid agvrlfkean vennegrrsk rgarrlkrrr
61   rhriqrvkkl lfdynlltdh selsginpye arvkglsqkl seeefsaall hlakrrgvhn
121  vneveedtgn elstkeqisr nskaleekyv aelqlerlkk dgevrgsinr fktsdyvkea
181  kqllkvqkay hqldqsfidt yidlletrrt yyegpgegsp fgwkdikewy emlmghctyf
241  peelrsvkya ynadlynaln dlnnlvitrd enekleyyek fqiienvfkq kkkptlkqia
301  keilvneedi kgyrvtstgk peftnlkvyh dikditarke iienaelldq iakiltiyqs
361  sediqeeltn lnseltqeei eqisnlkgyt gthnlslkai nlildelwht ndnqiaifnr
421  lklvpkkvdl sqqkeipttl vddfilspvv krsfiqsikv inaiikkygl pndiiielar
481  eknskdaqkm inemqkrnrq tnerieeiir ttgkenakyl iekiklhdmq egkclyslea
541  ipledllnnp fnyevdhiip rsvsfdnsfn nkvlvkqee A skkgnrtpfq ylsssdskis
601  yetfkkhiln lakgkgrisk tkkeylleer dinrfsvqkd finrnlvdtr yatrglmnll
661  rsyfrvnnld vkvksinggf tsflrrkwkf kkernkgykh haedaliian adfifkewkk
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721  ldkakkvmen qmfeekqaes mpeieteqey keifitphqi khikdfkdyk yshrvdkkpn
781  relindtlys trkddkgntl ivnnlnglyd kdndklkkli nkspekllmy hhdpqtyqkl
841  klimeqygde knplykyyee tgnyltkysk kdngpvikki kyygnklnah lditddypns
901  rnkvvklslk pyrfdvyldn gvykfvtvkn ldvikkenyy evnskcyeea kklkkisnqa
961  efiasfynnd likingelyr vigvnndlln rievnmidit yreylenmnd krppriikti
1021 asktqsikky stdilgnlye vkskkhpqii kkg (SEQ ID NO: 18053)
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Inactivated Cas9 (dCas9)

[0750] 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, 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 IIS endonuclease.

[0751] In certain embodiments, the dCas9 of the disclosure comprises a dCas9 isolated or derived from Staphyloccocus 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 inactivate 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:

```
   1  XDKKYSIGLA IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE
  61  ATRLKRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSFFHR LEESFLVEED KKHERHPIFG
 121  NIVDEVAYHE KYPTIYHLRK KLVDSTDKAD LRLIYLALAH MIKFRGHFLI EGDLNPDNSD
 181  VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
 241  LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLDNLLA QIGDQYADLF LAAKNLSDAI
 301  LLSDILRVNT EITKAPLSAS MIKRYDEHHQ DLTLLKALVR QQLPEKYKEI FFDQSKNGYA
 361  GYIDGGASQE EFYKFIKPIL EKMDGTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH
 421  AILRRQEDFY PFLKDNREKI EKILTFRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE
 481  VVDKGASAQS FIERMTNFDK NLPNEKVLPK HSLLYEYFTV YNELTKVKYV TEGMRKPAFL
 541  SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLLKI
 601  IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKTYA HLFDDKVMKQ LKRRRYTGWG
 661  RLSRKLINGI RDKQSGKTIL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGDSL
 721  HEHIANLAGS PAIKKGILQT VKVVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER
 781  MKRIEEGIKE LGSQILKEHP VENTQLQNEK LYLYYLQNGR DMYVDQELDI NRLSDYDVDA
 841  IVPQSFLKDD SIDNKVLTRS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL
 901  TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILDSRMN TKYDENDKLI REVKVITLKS
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961 KLVSDFRKDF QFYKVREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGRDF
1081 ATVRKVLSMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDLIIKLPK
1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLKGSPE DNEQKQLFVE
1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA
1321 PAAFKYFDTT IDRKRYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD (SEQ ID NO: 18054).

[0752] In certain embodiments, the amino acid sequence of the dCas9 comprises the sequence of:

1 MDKKYSIGL**A** IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE
61 ATRLKRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSFFHR LEESFLVEED KKHERHPIFG
121 NIVDEVAYHE KYPTIYHLRK KLVDSTDKAD LRLIYLALAH MIKFRGHFLI EGDLNPDNSD
181 VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
241 LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLDNLLA QIGDQYADLF LAAKNLSDAI
301 LLSDILRVNT EITKAPLSAS MIKRYDEHHQ DLTLLKALVR QQLPEKYKEI FFDQSKNGYA
361 GYIDGGASQE EFYKFIKPIL EKMDGTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH
421 AILRRQEDFY PFLKDNREKI EKILTFRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE
481 VVDKGASAQS FIERMTNFDK NLPNEKVLPK HSLLYEYFTV YNELTKVKYV TEGMRKPAFL
541 SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLLKI
601 IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKTYA HLFDDKVMKQ LKRRRYTGWG
661 RLSRKLINGI RDKQSGKTIL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGDSL
721 HEHIANLAGS PAIKKGILQT VKVVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER
781 MKRIEEGIKE LGSQILKEHP VENTQLQNEK LYLYYLQNGR DMYVDQELDI NRLSDYDV**A**
841 IVPQSFLKDD SIDNKVLTRS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL
901 TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILDSRMN TKYDENDKLI REVKVITLKS
961 KLVSDFRKDF QFYKVREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGRDF
1081 ATVRKVLSMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDLIIKLPK
1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLKGSPE DNEQKQLFVE
1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA
1321 PAAFKYFDTT IDRKRYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD (SEQ ID NO: 18055).

Clo051 Endonuclease

[0753] An exemplary Clo051 nuclease domain may comprise, consist essentially of or consist of, the amino acid sequence of:

EGIKSNISLLKDELRGQISHISHEYLSLIDLAFDSKQNRLFEMKVLELLVNEYGFKGRH LGGSRKPDGIVYSTTLEDNFGIIVDTKAYSEGYSLPISQADEMERYVRENSNRDEEVN PNKWWENFSEEVKKYYFVFISGSFKGKFEEQLRRLSMTTGVNGSAVNVVNLLLGAE KIRSGEMTIEELERAMFNNSEFILKY (SEQ ID NO: 18056).

Cas-Clover Fusion Protein

[0754] 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 (*Streptoccocus pyogenes*) in italics):

MAPKKKRKVEGIKSNISLLKDELRGQISHISHEYLSLIDLAFDSKQNRLFEMKVLELLVNEYGFKGRHLGGSRKP DGIVYSTTLEDNFGIIVDTKAYSEGYSLPISQADEMERYVRENSNRDEEVNPNKWWENFSEEVKKYYFVFISGSF KGKFEEQLRRLSMTTGVNGSAVNVVNLLLGAEKIRSGEMTIEELERAMFNNSEFILKY***GGGGS***DKKYSIGLAIGT NSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSN EMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEIT KAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE LLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFA WMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPA FLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGF ANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEM ARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDV DAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDK AGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAY LNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLI ETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT VAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRM LASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLD KVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLS QLGGDGSPKKKRKVSS (SEQ ID NO: 18057).

[0755] 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 *Streptoccocus pyogenes*):

```
   1 atggcaccaa agaagaaaag aaaagtggag ggcatcaagt caaacatcag cctgctgaaa
  61 gacgaactgc ggggacagat tagtcacatc agtcacgagt acctgtcact gattgatctg
 121 gccttcgaca gcaagcagaa tagactgttt gagatgaaag tgctggaact gctggtcaac
 181 gagtatggct tcaagggcag acatctgggc gggtctagga aacctgacgg catcgtgtac
 241 agtaccacac tggaagacaa cttcggaatc attgtcgata ccaaggctta ttccgagggc
 301 tactctctgc caattagtca ggcagatgag atggaaaggt acgtgcgcga aaactcaaat
 361 agggacgagg aagtcaaccc caataagtgg tgggagaatt tcagcgagga agtgaagaaa
 421 tactacttcg tctttatctc aggcagcttc aaagggaagt ttgaggaaca gctgcggaga
 481 ctgtccatga ctaccggggt gaacggatct gctgtcaacg tggtcaatct gctgctgggc
 541 gcagaaaaga tcaggtccgg ggagatgaca attgaggaac tggaacgcgc catgttcaac
 601 aattctgagt ttatcctgaa gtatggaggc gggggaagcg ataagaaata ctccatcgga
 661 ctggccattg gcaccaattc cgtgggctgg gctgtcatca cagacgagta caaggtgcca
 721 agcaagaagt tcaaggtcct ggggaacacc gatcgccaca gtatcaagaa aaatctgatt
 781 ggagccctgc tgttcgactc aggcgagact gctgaagcaa cccgactgaa gcggactgct
 841 aggcgccgat atacccggag aaaaaatcgg atctgctacc tgcaggaaat tttcagcaac
 901 gagatggcca aggtggacga tagtttcttt caccgcctgg aggaatcatt cctggtggag
 961 gaagataaga aacacgagcg gcatcccatc tttggcaaca ttgtggacga agtcgcttat
1021 cacgagaagt accctactat ctatcatctg aggaagaaac tggtggactc caccgataag
1081 gcagacctgc gcctgatcta tctggccctg gctcacatga tcaagttccg ggggcatttt
1141 ctgatcgagg gagatctgaa ccctgacaat tctgatgtgg acaagctgtt catccagctg
1201 gtccagacat acaatcagct gtttgaggaa aacccaatta atgcctcagg cgtggacgca
1261 aaggccatcc tgagcgccag actgtccaaa tctaggcgcc tggaaaacct gatcgctcag
1321 ctgccaggag agaagaaaaa cggcctgttt gggaatctga ttgcactgtc cctgggcctg
1381 acacccaact tcaagtctaa ttttgatctg gccgaggacg ctaagctgca gctgtccaaa
1441 gacacttatg acgatgacct ggataacctg ctggctcaga tcggcgatca gtacgcagac
1501 ctgttcctgg ccgctaagaa tctgagtgac gccatcctgc tgtcagatat tctgcgcgtg
1561 aacacagaga ttactaaggc cccactgagt gcttcaatga tcaaaagata tgacgagcac
1621 catcaggatc tgaccctgct gaaggctctg gtgaggcagc agctgcccga gaaatacaag
1681 gaaatcttct ttgatcagag caagaatgga tacgccggct atattgacgg cggggcttcc
1741 caggaggagt tctacaagtt catcaagccc attctggaaa agatggacgg caccgaggaa
1801 ctgctggtga agctgaatcg ggaggacctg ctgagaaaac agaggacatt tgataacgga
1861 agcatccctc accagattca tctgggcgaa ctgcacgcca tcctgcgacg gcaggaggac
1921 ttctacccat ttctgaagga taaccgcgag aaaatcgaaa agatcctgac cttcagaatc
1981 ccctactatg tggggcctct ggcacgggga aatagtagat ttgcctggat gacaagaaag
2041 tcagaggaaa ctatcacccc ctggaacttc gaggaagtgg tcgataaagg cgctagcgca
2101 cagtccttca ttgaaaggat gacaaatttt gacaagaacc tgccaaatga gaaggtgctg
2161 cccaaacaca gcctgctgta cgaatatttc acagtgtata acgagctgac taaagtgaag
2221 tacgtcaccg aagggatgcg caagcccgca ttcctgtccg gagagcagaa gaaagccatc
2281 gtggacctgc tgtttaagac aaatcggaaa gtgactgtca aacagctgaa ggaagactat
2341 ttcaagaaaa ttgagtgttt cgattcagtg gaaatcagcg gcgtcgagga caggtttaac
2401 gcctccctgg ggacctacca cgatctgctg aagatcatca aggataagga cttcctggac
2461 aacgaggaaa atgaggacat cctggaggac attgtgctga cactgactct gtttgaggat
2521 cgcgaaatga tcgaggaacg actgaagact tatgcccatc tgttcgatga caaagtgatg
2581 aagcagctga aaagaaggcg ctacaccgga tggggacgcc tgagccgaaa actgatcaat
2641 gggattagag acaagcagag cggaaaaact atcctggact ttctgaagtc cgatggcttc
2701 gccaacagga acttcatgca gctgattcac gatgactctc tgaccttcaa ggaggacatc
2761 cagaaagcac aggtgtctgg ccaggggac agtctgcacg agcatatcgc aaacctggcc
2821 ggcagccccg ccatcaagaa agggattctg cagaccgtga aggtggtgga cgaactggtc
2881 aaggtcatgg gacgacacaa acctgagaac atcgtgattg agatggcccg cgaaaatcag
2941 acaactcaga agggccagaa aaacagtcga gaacggatga agagaatcga ggaaggcatc
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```
3001 aaggagctgg ggtcacagat cctgaaggag catcctgtgg aaaacactca gctgcagaat
3061 gagaaactgt atctgtacta tctgcagaat ggacgggata tgtacgtgga ccaggagctg
3121 gatattaaca gactgagtga ttatgacgtg gatgccatcg tccctcagag cttcctgaag
3181 gatgactcca ttgacaacaa ggtgctgacc aggtccgaca agaaccgcgg caaatcagat
3241 aatgtgccaa gcgaggaagt ggtcaagaaa atgaagaact actggaggca gctgctgaat
3301 gccaagctga tcacacagcg gaaatttgat aacctgacta aggcagaaag aggaggcctg
3361 tctgagctgg acaaggccgg cttcatcaag cggcagctgg tggagacaag acagatcact
3421 aagcacgtcg ctcagattct ggatagcaga atgaacacaa agtacgatga aaacgacaag
3481 ctgatcaggg aggtgaaagt cattactctg aaatccaagc tggtgtctga ctttagaaag
3541 gatttccagt tttataaagt cagggagatc aacaactacc accatgctca tgacgcatac
3601 ctgaacgcag tggtcgggac cgccctgatt aagaaatacc ccaagctgga gtccgagttc
3661 gtgtacggag actataaagt gtacgatgtc cggaagatga tcgccaaatc tgagcaggaa
3721 attggcaagg ccaccgctaa gtatttcttt tacagtaaca tcatgaattt ctttaagacc
3781 gaaatcacac tggcaaatgg ggagatcaga aaaaggcctc tgattgagac caacggggag
3841 acaggagaaa tcgtgtggga caagggaagg gattttgcta ccgtgcgcaa agtcctgtcc
3901 atgccccaag tgaatattgt caagaaaact gaagtgcaga ccgggggatt ctctaaggag
3961 agtattctgc ctaagcgaaa ctctgataaa ctgatcgccc ggaagaaaga ctgggacccc
4021 aagaagtatg gcgggttcga ctctccaaca gtggcttaca gtgtcctggt ggtcgcaaag
4081 gtggaaaagg ggaagtccaa gaaactgaag tctgtcaaag agctgctggg aatcactatt
4141 atggaacgca gctccttcga gaagaatcct atcgattttc tggaagccaa gggctataaa
4201 gaggtgaaga aagacctgat cattaagctg ccaaaatact cactgtttga gctggaaaac
4261 ggacgaaagc gaatgctggc aagcgccgga gaactgcaga agggcaatga gctggccctg
4321 ccctccaaat acgtgaactt cctgtatctg gctagccact acgagaaact gaaggggtcc
4381 cctgaggata acgaacagaa gcagctgttt gtggagcagc acaaacatta tctggacgag
4441 atcattgaac agatttcaga gttcagcaag agagtgatcc tggctgacgc aaatctggat
4501 aaagtcctga gcgcatacaa caagcaccga gacaaaccaa tccgggagca ggccgaaaat
4561 atcattcatc tgttcaccct gacaaacctg ggcgcccctg cagccttcaa gtattttgac
4621 accacaatcg atcggaagag atacacttct accaaagagg tgctggatgc taccctgatc
4681 caccagagta ttaccggcct gtatgagaca cgcatcgacc tgtcacagct gggaggcgat
4741 gggagcccca agaaaaagcg gaaggtgtct agttaa (SEQ ID NO: 18058).
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[0756] 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.

[0757] 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 (*Streptoccocus pyogenes*) in italics):

```
   1 MPKKKRKVEG IKSNISLLKD ELRGQISHIS HEYLSLIDLA FDSKQNRLFE MKVLELLVNE
  61 YGFKGRHLGG SRKPDGIVYS TTLEDNFGII VDTKAYSEGY SLPISQADEM ERYVRENSNR
 121 DEEVNPNKWW ENFSEEVKKY YFVFISGSFK GKFEEQLRRL SMTTGVNGSA VNVVNLLLGA
 181 EKIRSGEMTI EELERAMFNN SEFILKYGGG GSDKKYSIGL AIGTNSVGWA VITDEYKVPS
 241 KKFKVLGNTD RHSIKKNLIG ALLFDSGETA EATRLKRTAR RRYTRRKNRI CYLQEIFSNE
 301 MAKVDDSFFH RLEESFLVEE DKKHERHPIF GNIVDEVAYH EKYPTIYHLR KKLVDSTDKA
 361 DLRLIYLALA HMIKFRGHFL IEGDLNPDNS DVDKLFIQLV QTYNQLFEEN PINASGVDAK
 421 AILSARLSKS RRLENLIAQL PGEKKNGLFG NLIALSLGLT PNFKSNFDLA EDAKLQLSKD
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 481 TYDDDLDNLL AQIGDQYADL FLAAKNLSDA ILLSDILRVN TEITKAPLSA SMIKRYDEHH
 541 QDLTLLKALV RQQLPEKYKE IFFDQSKNGY AGYIDGGASQ EEFYKFIKPI LEKMDGTEEL
 601 LVKLNREDLL RKQRTFDNGS IPHQIHLGEL HAILRRQEDF YPFLKDNREK IEKILTFRIP
 661 YYVGPLARGN SRFAWMTRKS EETITPWNFE EVVDKGASAQ SFIERMTNFD KNLPNEKVLP
 721 KHSLLYEYFT VYNELTKVKY VTEGMRKPAF LSGEQKKAIV DLLFKTNRKV TVKQLKEDYF
 781 KKIECFDSVE ISGVEDRFNA SLGTYHDLLK IIKDKDFLDN EENEDILEDI VLTLTLFEDR
 841 EMIEERLKTY AHLFDDKVMK QLKRRRYTGW GRLSRKLING IRDKQSGKTI LDFLKSDGFA
 901 NRNFMQLIHD DSLTFKEDIQ KAQVSGQGDS LHEHIANLAG SPAIKKGILQ TVKVVDELVK
 961 VMGRHKPENI VIEMARENQT TQKGQKNSRE RMKRIEEGIK ELGSQILKEH PVENTQLQNE
1021 KLYLYYLQNG RDMYVDQELD INRLSDYDVD AIVPQSFLKD DSIDNKVLTR SDKNRGKSDN
1081 VPSEEVVKKM KNYWRQLLNA KLITQRKFDN LTKAERGGLS ELDKAGFIKR QLVETRQITK
1141 HVAQILDSRM NTKYDENDKL IREVKVITLK SKLVSDFRKD FQFYKVREIN NYHHAHDAYL
1201 NAVVGTALIK KYPKLESEFV YGDYKVYDVR KMIAKSEQEI GKATAKYFFY SNIMNFFKTE
1261 ITLANGEIRK RPLIETNGET GEIVWDKGRD FATVRKVLSM PQVNIVKKTE VQTGGFSKES
1321 ILPKRNSDKL IARKKDWDPK KYGGFDSPTV AYSVLVVAKV EKGKSKKLKS VKELLGITIM
1381 ERSSFEKNPI DFLEAKGYKE VKKDLIIKLP KYSLFELENG RKRMLASAGE LQKGNELALP
1441 SKYVNFLYLA SHYEKLKGSP EDNEQKQLFV EQHKHYLDEI IEQISEFSKR VILADANLDK
1501 VLSAYNKHRD KPIREQAENI IHLFTLTNLG APAAFKYFDT TIDRKRYTST KEVLDATLIH
1561 QSITGLYETR IDLSQLGGDG SPKKKRKV
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(SEQ ID NO: 18059).

[0758] 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 *Streptoccocus pyogenes*):

```
   1 atgcctaaga agaagcggaa ggtggaaggc atcaaaagca acatctccct cctgaaagac
  61 gaactccggg ggcagattag ccacattagt cacgaatacc tctccctcat cgacctggct
 121 ttcgatagca agcagaacag gctctttgag atgaaagtgc tggaactgct cgtcaatgag
 181 tacgggttca agggtcgaca cctcggcgga tctaggaaac cagacggcat cgtgtatagt
 241 accacactgg aagacaactt tgggatcatt gtggatacca aggcatactc tgagggttat
 301 agtctgccca tttcacaggc cgacgagatg gaacggtacg tgcgcgagaa ctcaaataga
 361 gatgaggaag tcaaccctaa caagtggtgg gagaacttct ctgaggaagt gaagaaatac
 421 tacttcgtct ttatcagcgg gtccttcaag ggtaaatttg aggaacagct caggagactg
 481 agcatgacta ccggcgtgaa tggcagcgcc gtcaacgtgg tcaatctgct cctgggcgct
 541 gaaaagattc ggagcggaga gatgaccatc gaagagctgg agagggcaat gtttaataat
 601 agcgagttta tcctgaaata cggtggcggt ggatccgata aaaagtattc tattggttta
 661 gccatcggca ctaattccgt tggatgggct gtcataaccg atgaatacaa agtaccttca
 721 aagaaattta aggtgttggg gaacacagac cgtcattcga ttaaaaagaa tcttatcggt
 781 gccctcctat tcgatagtgg cgaaacggca gaggcgactc gcctgaaacg aaccgctcgg
 841 agaaggtata cacgtcgcaa gaaccgaata tgttacttac aagaaatttt tagcaatgag
 901 atggccaaag ttgacgattc tttctttcac cgtttggaag agtccttcct tgtcgaagag
 961 gacaagaaac atgaacggca ccccatcttt ggaaacatag tagatgaggt ggcatatcat
1021 gaaaagtacc caacgattta tcacctcaga aaaaagctag ttgactcaac tgataaagcg
1081 gacctgaggt taatctactt ggctcttgcc catatgataa agttccgtgg gcactttctc
1141 attgagggtg atctaaatcc ggacaactcg gatgtcgaca aactgttcat ccagttagta
1201 caaacctata atcagttgtt tgaagagaac cctataaatg caagtggcgt ggatgcgaag
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1261 gctattctta gcgcccgcct ctctaaatcc cgacggctag aaaacctgat cgcacaatta
1321 cccggagaga agaaaaatgg gttgttcggt aaccttatag cgctctcact aggcctgaca
1381 ccaaatttta agtcgaactt cgacttagct gaagatgcca aattgcagct tagtaaggac
1441 acgtacgatg acgatctcga caatctactg gcacaaattg gagatcagta tgcggactta
1501 tttttggctg ccaaaaacct tagcgatgca atcctcctat ctgacatact gagagttaat
1561 actgagatta ccaaggcgcc gttatccgct tcaatgatca aaaggtacga tgaacatcac
1621 caagacttga cacttctcaa ggccctagtc cgtcagcaac tgcctgagaa atataaggaa
1681 atattctttg atcagtcgaa aaacgggtac gcaggttata ttgacggcgg agcgagtcaa
1741 gaggaattct acaagtttat caaacccata ttagagaaga tggatgggac ggaagagttg
1801 cttgtaaaac tcaatcgcga agatctactg cgaaagcagc ggactttcga caacggtagc
1861 attccacatc aaatccactt aggcgaattg catgctatac ttagaaggca ggaggatttt
1921 tatccgttcc tcaaagacaa tcgtgaaaag attgagaaaa tcctaacctt tcgcatacct
1981 tactatgtgg gacccctggc ccgagggaac tctcggttcg catggatgac aagaaagtcc
2041 gaagaaacga ttactccatg gaattttgag gaagttgtcg ataaaggtgc gtcagctcaa
2101 tcgttcatcg agaggatgac caactttgac aagaatttac cgaacgaaaa agtattgcct
2161 aagcacagtt tactttacga gtatttcaca gtgtacaatg aactcacgaa agttaagtat
2221 gtcactgagg gcatgcgtaa acccgccttt ctaagcggag aacagaagaa agcaatagta
2281 gatctgttat tcaagaccaa ccgcaaagtg acagttaagc aattgaaaga ggactacttt
2341 aagaaaattg aatgcttcga ttctgtcgag atctccgggg tagaagatcg atttaatgcg
2401 tcacttggta cgtatcatga cctcctaaag ataattaaag ataaggactt cctggataac
2461 gaagagaatg aagatatctt agaagatata gtgttgactc ttaccctctt tgaagatcgg
2521 gaaatgattg aggaaagact aaaaacatac gctcacctgt tcgacgataa ggttatgaaa
2581 cagttaaaga ggcgtcgcta tacgggctgg ggacgattgt cgcggaaact tatcaacggg
2641 ataagagaca agcaaagtgg taaaactatt ctcgattttc taaagagcga cggcttcgcc
2701 aataggaact ttatgcagct gatccatgat gactctttaa ccttcaaaga ggatatacaa
2761 aaggcacagg tttccggaca aggggactca ttgcacgaac atattgcgaa tcttgctggt
2821 tcgccagcca tcaaaaaggg catactccag acagtcaaag tagtggatga gctagttaag
2881 gtcatgggac gtcacaaacc ggaaaacatt gtaatcgaga tggcacgcga aaatcaaacg
2941 actcagaagg ggcaaaaaaa cagtcgagag cggatgaaga gaatagaaga gggtattaaa
3001 gaactgggca gccagatctt aaaggagcat cctgtggaaa atacccaatt gcagaacgag
3061 aaactttacc tctattacct acaaaatgga agggacatgt atgttgatca ggaactggac
3121 ataaaccgtt tatctgatta cgacgtcgat gccattgtac cccaatcctt tttgaaggac
3181 gattcaatcg acaataaagt gcttacacgc tcggataaga accgagggaa aagtgacaat
3241 gttccaagcg aggaagtcgt aaagaaaatg aagaactatt ggcggcagct cctaaatgcg
3301 aaactgataa cgcaaagaaa gttcgataac ttaactaaag ctgagagggg tggcttgtct
3361 gaacttgaca aggccggatt tattaaacgt cagctcgtgg aaacccgcca aatcacaaag
3421 catgttgcac agatactaga ttcccgaatg aatacgaaat acgacgagaa cgataagctg
3481 attcgggaag tcaaagtaat cactttaaag tcaaaattgg tgtcggactt cagaaaggat
3541 tttcaattct ataaagttag ggagataaat aactaccacc atgcgcacga cgcttatctt
3601 aatgccgtcg tagggaccgc actcattaag aaatacccga agctagaaag tgagtttgtg
3661 tatggtgatt acaaagttta tgacgtccgt aagatgatcg cgaaaagcga acaggagata
3721 ggcaaggcta cagccaaata cttcttttat tctaacatta tgaatttctt taagacggaa
3781 atcactctgg caaacggaga gatacgcaaa cgacctttaa ttgaaaccaa tggggagaca
3841 ggtgaaatcg tatgggataa gggccgggac ttcgcgacgg tgagaaaagt tttgtccatg
3901 ccccaagtca acatagtaaa gaaaactgag gtgcagaccg gagggttttc aaaggaatcg
3961 attcttccaa aaaggaatag tgataagctc atcgctcgta aaaaggactg ggacccgaaa
4021 aagtacggtg gcttcgatag ccctacagtt gcctattctg tcctagtagt ggcaaaagtt
4081 gagaagggaa aatccaagaa actgaagtca gtcaaagaat tattggggat aacgattatg
4141 gagcgctcgt cttttgaaaa gaaccccatc gacttccttg aggcgaaagg ttacaaggaa
4201 gtaaaaaagg atctcataat taaactacca aagtatagtc tgtttgagtt agaaaatggc
4261 cgaaaacgga tgttggctag cgccggagag cttcaaaagg ggaacgaact cgcactaccg
4321 tctaaatacg tgaatttcct gtatttagcg tcccattacg agaagttgaa aggttcacct
4381 gaagataacg aacagaagca acttttgtt gagcagcaca aacattatct cgacgaaatc
4441 atagagcaaa tttcggaatt cagtaagaga gtcatcctag ctgatgccaa tctggacaaa
4501 gtattaagcg catacaacaa gcacagggat aaacccatac gtgagcaggc ggaaaatatt
4561 atccatttgt ttactcttac caacctcggc gctccagccg cattcaagta ttttgacaca

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4621 acgatagatc gcaaacgata cacttctacc aaggaggtgc tagacgcgac actgattcac
4681 caatccatca cgggattata tgaaactcgg atagatttgt cacagcttgg gggtgacgga
4741 tcccccaaga agaagaggaa agtctga
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(SEQ ID NO: 18060).

[0759] 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: Construction and *in vitro* Characterization of PSMA5 and PSMA8 CARTyrins

[0760] PSMA5 and PSMA8 CARTyrins were constructed as shown in Figures 1, 2, 3A-3C and 4A-4C. Figure 5 depicts the structure of the anti-PSMA CARTyrins.

[0761] Surface expression of CARTyrins of the disclosure was evaluated by flow cytometry 24 hours following mRNA electroporation of a sequence encoding a PSMA5 or PSMA8 CARTyrin into human pan T cells (Figure 6A). By flow cytometry, surface PSMA protein expression was detected on LNCaP tumor cell lines and K562 cell lines transfected with PSMA (Figure 6B). Functionality of CARTyrin-expressing T cells was measured by degranulation against tumor lines. Degranulation of RNA-electroporated PSMA CARTyrin T cells against PSMA+ tumor cell lines was observed (Figure 6C). PSMA surface protein expression was detected by flow cytometry following transfection of K562 cells lines using increasing amounts of PSMA mRNA (Figure 6D). Degranulation of RNA-electroporated PSMA CARTyrin T cells against K562 expressing various amounts of PSMA protein was observed (Figure 6E). Together, these data shows that PSMA5 and PSMA8 CARTyrins can be expressed on the surface of T cells and facilitate cytotoxic function against PSMA+ cell targets.

[0762] To support *in vivo* evaluation of PSMA CARTyrins, P-PSMA5-101 and P-PSMA8-101 were constructed using using the piggyBac DNA modification system. PSMA CARTyrin was detected on the surface of primary human T cells from a representative donor that were transposed with either P-PSMA5-101 or P-PSMA8-101 plasmids (Figure 7A). Flow cytometry analysis using surface expression markers showed that T cells expressing PSMA CARTyrin had markers of T stem cell memory phenotype but not activation and/or functiona

T cell exhaustion phenotype (Figure 7B-7C). ELISA analysis showed that T cells expressing PSMA CARTyrins caused IFNγ secretion in cells expressing PSMA (LNCaP and K562.PSMA cells), demonstrating effector function of the T cells (Figure 7D). T cells expressing PSMA CARTyrins showed strong cytotoxic function by a standard killing assay and a cell proliferation assay (Figure 7E-7F). Together, these data show that surface expression of P-PSMA5-101 and P-PSMA8-101 PSMA CARTyrins on T cells demonstrated cytotoxic function and proliferative capacity in vitro against PSMA+ cell targets. Following this strong performance *in vitro*, the ability of the PSMA CARTyrins to function *in vivo* was evaluated.

Example 2: *In vivo* Characterization of PSMA5 and PSMA8 CARTyrins using a murine xenograft model

[0763] Figure 8A depicts the treatment schedule for an in vivo study in mice using the P-PSMA8-101 CARTyrin. Anti-tumor activity was evaluated by survival (Figure 8B), P-PSMA8-101 CD8+ T cell expansion and detection in the blood (Figure 8C), tumor volume assessment by caliper measurement (Figure 8D), and bioluminescence of LNCaP tumor (Figure 8E-F). P-PSMA8-101 at 'stress' and standard doses demonstrated significantly enhanced anti-tumor efficacy and survival in comparison to 'No T cells' control mice against established SC LNCaP.luc solid tumors in NSG mice. Specifically, there was no survival in control animals, 50% survival in animal treated with an 'ultra-low' dose of P-PSMA8-101, and 100% survival in animals treated with either the 'stress' or standard dose of P-PSMA8-101. P-PSMA8-101 at the standard dose eliminated established LNCaP tumor in 100% of animals for the duration of the study (42 days post-treatment), while 2/3 of the 'stress' dosed animals remained tumor-free. In the peripheral blood, P-PSMA8-101 expanded and gave rise to differentiated effector PSMA8 CARTyrin+ T-cells that were concomitant with a decrease in tumor burden below detectable caliper and bioluminescent imaging limits. P-PSMA8-101 then contracted, yet persisted in the peripheral blood. Together this data demonstrates that animals expressing the PSMA8 CARTyrin demonstrate a reduce tumor burden compared to controls.

[0764] Figure 9A depicts the treatment schedule for an in vivo study in mice using the P-PSMA5-101 and P-PSMA8-101 CARTyrins at a "stress" dose of (4x10^6) using a murine xenograft model. Anti-tumor activity was evaluated by survival (Figure 9B), CD8+ T cell

expansion and detection in the blood (Figure 9C), tumor volume assessment by caliper measurement (Figure 9D), and bioluminescence of LNCaP tumor (Figure 9E-F). P-PSMA5-101 and P-PSMA8-101 at a 'stress' dose demonstrated significantly enhanced anti-tumor efficacy and survival in comparison to the T cells (no CAR) control mice against established SC LNCaP.luc solid tumors in NSG mice. Specifically, there was no survival in T cells (no CAR) control animals, 25% survival in the P-BCMA-101 treated group, 75% survival in the P-PSMA5-101 treated group, and 100% survival in animals treated with a 'stress' dose of P-PSMA8-101. In the peripheral blood, P-PSMA5-101 and P-PSMA8-101 expanded and gave rise to differentiated effector CARTyrin+ T-cells that were concomitant with a decrease in tumor burden below detectable caliper and bioluminescent imaging limits. These cells then contracted, yet persisted in the peripheral blood.

Example 3: Expression and Function of piggyBac integrated iC9 safety switch into human pan T-cells

[0765] Human pan T-cells were nucleofected using an Amaxa 4D nucleofector with one of four piggyBac transposons. Modified T cells receiving the "mock" condition were nucleofected with an empty piggyBac transposon. Modified T cells received either a piggyBac transposon containing a therapeutic agent alone (a sequence encoding a CARTyrin) or a piggyBac transposon containing an integrated iC9 sequence and a therapeutic agent (a sequence encoding a CARTyrin).

[0766] Figure 8 provides a schematic diagram of the iC9 safety switch, which contains a ligand binding region, a linker, and a truncated caspase 9 polypeptide. Specifically, the iC9 polypeptide contains a ligand binding region comprising a FK506 binding protein 12 (FKBP12) polypeptide including 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 GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026). In certain embodiments, the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG

GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027). In certain embodiments, the induction agent specific for the ligand binding region may comprise a FK506 binding protein 12 (FKBP12) polypeptide having a substitution of valine (V) for phenylalanine (F) at position 36 (F36V) comprises AP20187 and/or AP1903, both synthetic drugs.

[0767] In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the linker region is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028) or a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029). In certain embodiments, the nucleic acid sequence encoding the linker does not comprise a restriction site.

[0768] In certain embodiments of the truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an arginine (R) at position 87 of the sequence. Alternatively, or in addition, in certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid sequence that does not comprise an alanine (A) at position 282 the sequence. In certain embodiments of the inducible proapoptotic polypeptides, inducible caspase polypeptides or truncated caspase 9 polypeptides of the disclosure, the truncated caspase 9 polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030) or a nucleic acid sequence comprising GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT

TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA
AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT
GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG
AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT
CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG
AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA
AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG
TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG
CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG
CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT
CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT
TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA
ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT
GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

[0769] In certain embodiments of the inducible proapoptotic polypeptides, wherein the polypeptide comprises a truncated caspase 9 polypeptide, the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising
GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI
RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS
GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR
RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG
AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE
SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE
TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18032) or the nucleic acid sequence comprising
ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg
ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag
gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg
ccacccagggatcattcccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg
ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt
aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta

gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

[0770] To test the iC9 safety switch, each of the four modified T cells were incubated for 24 hours with 0, 0.1 nM, 1 nM, 10 nM, 100 nM or 1000 nM AP1903 (an induction agent for AP1903). Viability was assessed by flow cytometry using 7-aminoactinomycin D (7-AAD), a fluorescent intercalator, as a marker for cells undergoing apoptosis.

[0771] Cell viability was assessed at day 12 (see Figure 9). The data demonstrate a shift of cell populations from the lower right to the upper left quadrants with increasing concentration of the induction agent in cells containing the iC9 construct; however, this effect is not observed in cells lacking the iC9 construct (those receiving only the CARTyrin), in which cells are evenly distributed among these two areas regardless of the concentration of the induction agent. Moreover, cell viability was assessed at day 19 (see Figure 10). The data reveal the same trend as shown in Figure 9 (day 12 post-nucleofection); however, the population shift to the upper left quadrant is more pronounced at this later time point (day 19 post-nucleofection).

[0772] A quantification of the aggregated results was performed and is provided in Figure 11, showing the significant impact of the iC9 safety switch on the percent cell viability as a function of the concentration of the induction agent (AP1903) of the iC9 switch for each modified cell type at either day 12 (Figure 9 and left graph) or day 19 (Figure 10 and right graph). The presence of the iC9 safety switch induces apoptosis in a significant majority of cells by day 12 and the effect is even more dramatic by day 19.

[0773] The results of this study show that the iC9 safety switch is extremely effective at eliminating active cells upon contact with an induction agent (e.g. AP1903) because AP1903 induces apoptosis at even the lowest concentrations of the study (0.1 nM). Furthermore, the iC9 safety switch may be functionally expressed as part of a tricistronic vector.

Example 4: Knock down efficiency of checkpoint signaling proteins on armored T-cells

[0774] To create armored T-cells which have enhanced therapeutic potential, genetic modifications may be made in order to render the T-cells less sensitive to immunologic and/or metabolic checkpoints. 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, TGFβR2, 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 (Figure 13). 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 5: Strategies for the expression of null or switch intracellular signaling proteins on armored T-cells

[0775] 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 TGFβRII of T-cells, which bind to the PD-L1 ligand and TGFβ cytokine, respectively. Figure 14 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 TGFβRII (bottom panel)). To design Null receptors, the intracellular domain (ICD) of PD1 or TGFβRII 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 wildtype receptor. This results in dilution of the overall level of checkpoint signaling effectively delivered to the T-cell, thus, reducing or blocking checkpoint inhibition. Figure 15 also shows switch receptor design strategies for the inhibitory receptors PD-1 (top panel) and TGFβRII (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 1. Inhibitory molecules include but are not limited to CTLA4, PD1, Lag3 and the examples listed in Tables 1 and 9. 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.

Example 6: Enhancing surface expression of PD1 and TGFβRII null or switch intracellular signaling proteins on armored T-cells

[0776] 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. Figure 15A shows schematic diagrams of several null receptor constructs for PD-1 (top) and TGFβRII (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 CD8a receptor (red arrows). Each of the six truncated null constructs shown in Figure 15A 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 (Figure 15B). By flow cytometry, replacement of the WT SP with the alternative CD8a (02.8aSP-PD-1 and 02.8aSP-TGFβRII) 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-TGFβRII Null receptor exhibited an MFI of 13,809, which is 102-fold higher than endogenous T cell TGFβRII expression and 1.8-fold higher than the WT TGFβRII Null receptor. These results show that replacement of

wildtype SP with the alternative CD8a SP for both PD1 and TGFβRII 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 endogenous ligand(s).

Example 7: Design of NF-KB inducible vectors for expression in modified T-cells

[0777] Two T cell activation NF-KB inducible vectors were developed (Figures 16A and 16B); 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 8: NF-KB inducible vectors for GFP expression in modified T-cells

[0778] T cells were nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR mutein 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). 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 NFκB activity (see Figure 17). 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 NFκB activity is lower. GFP expression is still observed at Day 19, which may due to the long half-life of GFP protein (~30hr), or, basal level of NFκB activity through, for example, a TCR, a CAR, a cytokine receptor, or a growth factor receptor signal.

Example 9: NF-KB inducible vectors for anti-BCMA CAR-mediated GFP expression in modified T-cells

[0779] T cells were either unmodified (Mock T cells) or nucleofected with a piggyBac vector expressing an anti-BCMA CAR and a DHFR mutein 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), BMCA+ (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 (Figure 18). Little difference in GFP expression was observed between the pNFKB-GFP forward- and reverse-transposed cells that were cocultured with BCMA+ tumor cells.

Example 10: Control of anti-BCMA CAR-mediated expression in modified T-cells

[0780] 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 EF1a promoter (Figure 19). 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.

INCORPORATION BY REFERENCE

[0781] 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

[0782] 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.

CLAIMS

What is claimed is:

1. A chimeric antigen receptor (CAR) comprising:

(a) an ectodomain comprising an antigen recognition region, wherein the antigen recognition region comprises at least one prostate-specific membrane antigen (PSMA)-specific Centyrin;

(b) a transmembrane domain, and

(c) an endodomain comprising at least one costimulatory domain.

2. The CAR of claim 1, wherein the ectodomain of (a) further comprises a signal peptide.

3. The CAR of claim 1 or 2, wherein the ectodomain of (a) further comprises a hinge between the antigen recognition region and the transmembrane domain.

4. The CAR of claim 2 or 3, wherein the signal peptide comprises a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR signal peptide.

5. The CAR of claim 2 or 3, wherein the signal peptide comprises a sequence encoding a human CD8α signal peptide.

6. The CAR of claim 5, wherein the signal peptide comprises an amino acid sequence comprising MALPVTALLLPLALLLHAARP (SEQ ID NO: 18004).

7. The CAR of claim 5 or 6, wherein the signal peptide is encoded by a nucleic acid sequence comprising atggcactgccagtcaccgccctgctgctgcctctggctctgctgctgcacgcagctagacca (SEQ ID NO: 18005).

8. The CAR of any one of the preceding claims, wherein the transmembrane domain comprises a sequence encoding a human CD2, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD8α, CD19, CD28, 4-1BB or GM-CSFR transmembrane domain.

9. The CAR of any one of the preceding claims, wherein the transmembrane domain comprises a sequence encoding a human CD8α transmembrane domain.

10. The CAR of claim 9, wherein the transmembrane domain comprises an amino acid sequence comprising IYIWAPLAGTCGVLLLSLVITLYC (SEQ ID NO: 18006).

11. The CAR of claim 9 or 10, wherein the transmembrane domain is encoded by a nucleic acid sequence comprising atctacatttgggcaccactggccgggacctgtggagtgctgctgctgagcctggtcatcacactgtactgc (SEQ ID NO: 18007).

12. The CAR of any one of the preceding claims, wherein the endodomain comprises a human CD3ζ endodomain.

13. The CAR of any one of the preceding claims, wherein the at least one costimulatory domain comprises a human 4-1BB, CD28, CD40, ICOS, MyD88, OX-40 intracellular segment, or any combination thereof.

14. The CAR of any one of the preceding claims, wherein the at least one costimulatory domain comprises a human CD28 and/or a 4-1BB costimulatory domain.

15. The CAR of claim 13 or 14, wherein the CD3ζ costimulatory domain comprises an amino acid sequence comprising RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 18008).

16. The CAR of claim 15, wherein the CD28 costimulatory domain is encoded by a nucleic acid sequence comprising cgcgtgaagtttagtcgatcagcagatgccccagcttacaaacagggacagaaccagctgtataacgagctgaatctgggccgccga gaggaatatgacgtgctggataagcggagaggacgcgaccccgaaatgggaggcaagcccaggcgcaaaaaccctcaggaagg cctgtataacgagctgcagaaggacaaaatggcagaagcctattctgagatcggcatgaaggggagcgacggagaggcaaagg gcacgatgggctgtaccagggactgagcaccgccacaaaggacacctatgatgctctgcatatgcaggcactgcctccaagg (SEQ ID NO: 18010).

17. The CAR of claim 13 or 14, wherein the 4-1BB costimulatory domain comprises an amino acid sequence comprising KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL (SEQ ID NO: 18011).

18. The CAR of claim 17, wherein the 4-1BB costimulatory domain is encoded by a nucleic acid sequence comprising aagagaggcaggaagaaactgctgtatattttcaaacagcccttcatgcgccccgtgcagactacccaggaggaagacgggtgctcc tgtcgattccctgaggaagaggaaggcgggtgtgagctg (SEQ ID NO: 18013).

19. The CAR of any one of claims 14-18, wherein the 4-1BB costimulatory domain is located between the transmembrane domain and the CD28 costimulatory domain.

20. The CAR of any one of claims 2-19, wherein the hinge comprises a sequence derived from a human CD8α, IgG4, and/or CD4 sequence.

21. The CAR of any one of claims 2-19, wherein the hinge comprises a sequence derived from a human CD8α sequence.

22. The CAR of claim 20 or 21, wherein the hinge comprises an amino acid sequence comprising TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD (SEQ ID NO: 18014).

23. The CAR of claim 22, wherein the hinge is encoded by a nucleic acid sequence comprising ACCACAACCCCTGCCCCCAGACCTCCCACACCCGCCCCTACCATCGCGAGTCAGC CCCTGAGTCTGAGACCTGAGGCCTGCAGGCCAGCTGCAGGAGGAGCTGTGCACA CCAGGGGCCTGGACTTCGCCTGCGAC (SEQ ID NO: 18016).

24. The CAR of any one of the preceding claims, wherein the at least one PSMA-specific Centyrin comprises at least one fibronectin type III (FN3) domain.

25. The CAR of any one of the preceding claims, wherein the at least one PSMA-specific Centyrin is capable of specifically binding a sequence of prostate-specific membrane antigen (PSMA).

26. The CAR of claim 25, wherein the at least one PSMA-specific Centyrin comprises or consists of the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18000).

27. The CAR of claim 26, wherein the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 70% identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWDIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18000).

28. The CAR of claim 25 or 26, wherein the at least one PSMA-specific Centyrin comprises or consists of the nucleic acid sequence of ATGCTGCCTGCACCAAAGAACCTGGTGGTGTCTCGGGTGACCGAGGACTCTGCC AGACTGAGCTGGGACATCGATGAGCAGAGGGATTGGTTCGAGAGCTTTCTGATC CAGTATCAGGAGTCCGAGAAAGTGGGCGAGGCCATCGTGCTGACAGTGCCTGGC AGCGAGCGGTCCTATGACCTGACCGGCCTGAAGCCAGGCACAGAGTACACCGTG TCCATCTACGGCGTGTATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTCAC CACA (SEQ ID NO: 18001).

29. The CAR of claim 25, wherein the at least one PSMA-specific Centyrin comprises or consists of the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18002).

30. The CAR of claim 29, wherein the at least one PSMA-specific Centyrin comprises an amino acid sequence having at least 70% identity to the amino acid sequence of MLPAPKNLVVSRVTEDSARLSWAIDEQRDWFESFLIQYQESEKVGEAIVLTVPGSERS YDLTGLKPGTEYTVSIYGVYHVYRSNPLSAIFTT (SEQ ID NO: 18002).

31. The CAR of claim 25 or 29, wherein the at least one PSMA-specific Centyrin comprises or consists of the nucleic acid sequence of ATGCTGCCTGCACCAAAGAACCTGGTGGTGTCTCGGGTGACCGAGGACTCTGCC AGACTGAGCTGGGCCATCGACGAGCAGAGGGATTGGTTCGAGAGCTTTCTGATC CAGTATCAGGAGTCCGAGAAAGTGGGCGAGGCCATCGTGCTGACAGTGCCTGGC AGCGAGCGGTCCTATGATCTGACCGGCCTGAAGCCAGGCACAGAGTACACCGTG TCCATCTACGGCGTGTATCACGTGTACAGGTCCAATCCTCTGTCTGCCATCTTCAC CACA (SEQ ID NO: 18003).

32. The CAR of claim 25, wherein the at least one fibronectin type III (FN3) domain is derived from a human protein.

33. The CAR of claim 32, wherein the human protein is Tenascin-C.

34. The CAR of any one of claims 25 or 32-34, wherein the consensus sequence comprises LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDL TGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18018).

35. The CAR of any one of claims 25 or 32-34, wherein the consensus sequence comprises MLPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYD LTGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18019).

36. The CAR of any one of claims 25 or 32-34, wherein the consensus sequence comprises a sequence having at least 70% identity to the amino acid sequence of LPAPKNLVVSEVTEDSLRLSWTAPDAAFDSFLIQYQESEKVGEAINLTVPGSERSYDL TGLKPGTEYTVSIYGVKGGHRSNPLSAEFTT (SEQ ID NO: 18018).

37. The CAR of any one of claims 25 or 32-34, wherein 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 (SEQ ID NO: 18020) at positions 13-16 of the consensus sequence;

(b) a B-C loop comprising or consisting of the amino acid residues TAPDAAF (SEQ ID NO: 18021) 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: 18022) 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: 18023) 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: 18024) 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: 18025) at positions 75-81 of the consensus sequence; or

(g) any combination of (a)-(f).

38. The CAR of any one of claims 25 or 32-37, comprising a consensus sequence of at least 5 fibronectin type III (FN3) domains.

39. The CAR of any one of claims 25 or 332-38, comprising a consensus sequence of at least 10 fibronectin type III (FN3) domains.

40. The CAR of any one of claims 25 or 32-39, comprising a consensus sequence of at least 15 fibronectin type III (FN3) domains.

41. The CAR of any one of claims 1-40, wherein the at least one Centryin 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.

42. The CAR of claim 41, wherein the K_D is determined by surface plasmon resonance.

43. A composition comprising the CAR of any one of the preceding claims and at least one pharmaceutically acceptable carrier.

44. A transposon comprising the CAR of any one of claims 1-42.

45. The transposon of claim 44, wherein the transposon further comprises a selection gene.

46. The transposon of claim 45, wherein the selection gene encodes a gene product essential for cell viability and survival.

47. The transposon of claim 45, wherein the selection gene encodes a gene product essential for cell viability and survival when challenged by selective cell culture conditions.

48. The transposon of claim 47, wherein the selective cell culture conditions comprise a compound harmful to cell viability or survival and wherein the gene product confers resistance to the compound.

49. The transposon of claim 44, wherein the selection gene comprises *neo,* TYMS (Thymidylate Synthetase), MGMT (O(6)-methylguanine-DNA methyltransferase), multidrug

resistance gene (MDR1), DHFR, ALDH1 (Aldehyde dehydrogenase 1 family, member A1), FRANCF, RAD51C (RAD51 Paralog C), GCS (glucosylceramide synthase), NKX2.2 (NK2 Homeobox 2) or any combination thereof.

50. The transposon of any one of claims 44-49, wherein the 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.

51. The transposon of claim 50, wherein the non-human sequence is a restriction site.

52. The transposon of claim 50 or 51, wherein the ligand binding region inducible caspase polypeptide comprises a FK506 binding protein 12 (FKBP12) polypeptide.

53. The transposon of claim 52, wherein the amino acid sequence of the FK506 binding protein 12 (FKBP12) polypeptide comprises a modification at position 36 of the sequence.

54. The transposon of claim 53, wherein the modification is a substitution of valine (V) for phenylalanine (F) at position 36 (F36V).

55. The transposon of any one of claims 52-54, wherein the FKBP12 polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026).

56. The transposon of claim 55, wherein the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising

GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG
GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG
GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA
GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC
AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC
ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027).

57. The transposon of any one of claims 50-56, wherein the linker region of the inducible proapoptotic polypeptide is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028).

58. The transposon of claim 57, wherein the linker region of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029).

59. The transposon of any one of claims 50-58, wherein 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.

60. The transposon of any one of claims 50-59, wherein 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.

61. The transposon of any one of claims 50-60, wherein the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by an amino acid comprising
GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR
RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG
AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE
SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE

TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030).

62. The transposon of claim 61, wherein the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

63. The transposon of any one of claims 50-62, wherein of the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE

TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18032).

64. The transposon of claim 63, wherein of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg ccacccagggatcattccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

65. The transposon of any one of claims 50-64, wherein the transposon comprises at least one self-cleaving peptide.

66. The transposon of any one of claims 50-65, wherein the transposon comprises at least one self-cleaving peptide and wherein a self-cleaving peptide is located between the CAR and the selection gene.

67. The transposon of any one of claims 50-66, wherein the transposon comprises at least one self-cleaving peptide and wherein a self-cleaving peptide is located between the CAR and the inducible proapoptotic polypeptide.

68. The transposon of any one of claims 50-67, wherein the transposon comprises at least two self-cleaving peptides and wherein a first self-cleaving peptide is located upstream of the inducible proapoptotic polypeptide and a second self-cleaving peptide is located downstream of the inducible proapoptotic polypeptide.

69. The transposon of any one of claims 50-68, wherein the transposon comprises at least one self-cleaving peptide and wherein a first self-cleaving peptide is located upstream of the CAR and a second self-cleaving peptide is located downstream of the CAR.

70. The transposon of any one of claims 65-69, wherein the at least one self-cleaving peptide comprises T2A peptide, 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.

71. The transposon of claim 70, wherein the T2A peptide comprises an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034).

72. The transposon of claim 70, wherein the GSG-T2A peptide comprises an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18035).

73. The transposon of claim 70, wherein the E2A peptide comprises an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18036).

74. The transposon of claim 70, wherein the GSG-E2A peptide comprises an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18037).

75. The transposon of claim 70, wherein the F2A peptide comprises an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18038).

76. The transposon of claim 70, wherein the GSG-F2A peptide comprises an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18039).

77. The transposon of claim 70, wherein the P2A peptide comprises an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18040).

78. The transposon of claim 70, wherein the GSG-P2A peptide comprises an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18041).

79. The transposon of any one of claims 44-78, further comprising a sequence encoding a chimeric stimulatory receptor (CSR).

80. The transposon of claim 79, wherein the CSR comprises:
(a) an ectodomain comprising an activation component;
(b) a transmembrane domain; and
(c) an endodomain comprising at least one signal transduction domain;
wherein the combination of (a), (b) and (c) is non-naturally occurring.

81. The transposon of claim 80, wherein the activation component of (a) is isolated or derived from a first protein.

82. The transposon of claim 81, wherein the at least one signal transduction domain of (c) is isolated or derived from a second protein.

83. The transposon of claim 81 or 82, wherein the first protein and the second protein are not identical.

84. The transposon of any one of claims 80-83, wherein the Activation component comprises one or more of a component of a human transmembrane receptor, a human cell-surface receptor, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor.

85. The transposon of claim 84, wherein the activation component comprises a portion of one or more of a component of a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor to which an agonist of the Activation component binds.

86. The transposon of any one of claims 80-85, wherein the Activation component comprises a CD2 protein or a portion thereof to which an agonist binds.

87. The transposon of any one of claims 80-86, wherein the signal transduction domain comprises one or more of a component of a human signal transduction domain, T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor.

88. The transposon of claim 87, wherein the signal transduction domain comprises a CD3 protein.

89. The transposon of claim 88, wherein the CD3 protein comprises a CD3ζ protein.

90. The transposon of any one of claims 80-89, wherein the endodomain further comprises a cytoplasmic domain.

91. The transposon of claim 90, wherein the cytoplasmic domain is isolated or derived from a third protein.

92. The transposon of claim 91, wherein the first protein and the third protein are identical.

93. The transposon of any one of claims 80-92, wherein the ectodomain further comprises a signal peptide.

94. The transposon of claim 93, wherein the signal peptide is derived from a fourth protein.

95. The transposon of claim 94, wherein the first protein and the fourth protein are identical.

96. The transposon of any one of claims 80-95, wherein the transmembrane domain is isolated or derived from a fifth protein.

97. The transposon of claim 96, wherein the first protein and the fifth protein are identical.

98. The transposon of any one of claims 80-97, wherein the Activation component does not bind a naturally-occurring molecule.

99. The transposon of any one of claims 80-97, wherein the CSR does not transduce a signal upon binding of the activation component to a naturally-occurring molecule.

100. The transposon of claim 80, wherein the ectodomain comprises a modification.

101. The transposon of claim 100, wherein the modification comprises a mutation or a truncation of a sequence encoding the activation component when compared to a wild type sequence of the first protein.

102. The transposon of any one of claims 80-101, wherein the Activation component binds to a non-naturally occurring molecule.

103. The transposon of any one of claims 80-102, wherein the CSR selectively transduces a signal upon binding of the Activation component to a non-naturally occurring molecule.

104. The transposon of any one of claims 45-103, wherein the transposon is a piggyBac or a piggyBac-like transposon.

105. The transposon of any one of claims 45-103,wherein the transposon is a TcBuster transposon.

106. The transposon of any one of claims 45-103, wherein the transposon is a Sleeping Beauty transposon.

107. The transposon of any one of claims 45-103, wherein the transposon is a Helraiser transposon.

108. The transposon of any one of claims 45-103, wherein the transposon is a Tol2 transposon.

109. A composition comprising the transposon of any one of claims 45-108.

110. The composition of claim 109, further comprising a plasmid comprising a sequence encoding a transposase enzyme.

111. The composition of claim 110, wherein the sequence encoding a transposase enzyme is an mRNA sequence.

112. The composition of any one of claims 109-111, wherein the transposon is a piggyBac or a piggyBac-like transposon and wherein the transposase is a piggyBac or a piggyBac-like transposase.

113. The composition of claim 112, wherein the piggyBac transposase comprises an amino acid sequence comprising SEQ ID NO: 14487.

114. The composition of claim 112 or 113, wherein 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: 14487.

115. The composition of claim 114, wherein the amino acid substitution at position 30 of SEQ ID NO: 14487 is a substitution of a valine (V) for an isoleucine (I) (I30V).

116. The composition of claim 114, wherein the amino acid substitution at position 165 of SEQ ID NO: 14487 is a substitution of a serine (S) for a glycine (G) (G165S).

117. The composition of claim 114, wherein the amino acid substitution at position 282 of SEQ ID NO: 14487 is a substitution of a valine (V) for a methionine (M) (M282V).

118. The composition of claim 114, wherein the amino acid substitution at position 538 of SEQ ID NO: 14487 is a substitution of a lysine (K) for an asparagine (N) (N538K).

119. The composition of any one of claims 110-118, wherein the transposase is a Super piggyBac (sPBo) transposase.

120. The composition of claim 119, wherein the Super piggyBac (sPBo) transposase comprises an amino acid sequence comprising SEQ ID NO: 14484.

121. The composition of any one of claims 109-111, wherein the transposon is a TcBuster transposon and wherein the transposase enzyme is a TcBuster transposase enzyme.

122. The composition of claim 121, wherein the TcBuster transposase enzyme is a hyperactive TcBuster transposase enzyme.

123. The composition of claim 121 or 122, wherein the TcBuster transposase enzyme comprises a sequence having at least 75% identity to:

MMLNWLKSGK LESQSQEQSS CYLENSNCLP PTLDSTDIIG EENKAGTTSR KKRKYDEDYL
NFGFTWTGDK DEPNGLCVIC EQVVNNSSLN PAKLKRHLDT KHPTLKGKSE YFKRKCNELN
QKKHTFERYV RDDNKNLLKA SYLVSLRIAK QGEAYTIAEK LIKPCTKDLT TCVFGEKFAS
KVDLVPLSDT TISRRIEDMS YFCEAVLVNR LENAKCGFTL QMDESTDVAG LAILLVFVRY
IHESSFEEDM LFCKALPTQT TGEEIFNLLN AYFEKHSIPW NLCYHICTDG AKAMVGVIKG
VIARIKKLVP DIKASHCCLH RHALAVKRIP NALHEVLNDA VKMINFIKSR PLNARVFALL
CDDLGSLHKN LLLHTEVRWL SRGKVLTRFW ELRDEIRIFF NEREFAGKLN DTSWLQNLAY
IADIFSYLNE VNLSLQGPNS TIFKVNSRIN SIKSKLKLWE ECITKNNTEC FANLNDFLET
SNTALDPNLK SNILEHLNGL KNTFLEYFPP TCNNISWVEN PFNECGNVDT LPIKEREQLI
DIRTDTTLKS SFVPDGIGPF WIKLMDEFPE ISKRAVKELM PFVTTYLCEK SFSVYVATKT
KYRNRLDAED DMRLQLTTIH PDIDNLCNNK QAQKSH (SEQ ID NO: 17900).

124. The composition of any one of claims 109-111, wherein the transposon is a Sleeping Beauty transposon and wherein the transposase enzyme is a Sleeping Beauty transposase enzyme.

125. The composition of claim 124, wherein the Sleeping Beauty transposase enzyme comprises the sequence of SEQ ID NO: 14485.

126. The composition of claim 124, wherein the Sleeping Beauty transposase enzyme is a hyperactive Sleeping Beauty transposase (SB100X).

127. The composition of claim 126, wherein the hyperactive Sleeping Beauty transposase (SB100X) comprises the sequence of SEQ ID NO: 14486.

128. The composition of any one of claims 109-111, wherein the transposon is a Helraiser transposon and wherein the transposase enzyme is a Helraiser transposase enzyme.

129. The composition of claim 128, wherein the Helraiser transposase enzyme comprises the sequence of SEQ ID NO: 14501.

130. The composition of any one of claims 109-111, wherein the transposon is a Tol2 transposon and wherein the transposase enzyme is a Tol2 transposase enzyme.

131. The composition of claim 130, wherein the Tol2 transposase enzyme comprises the sequence of SEQ ID NO: 14502.

132. A vector comprising the CAR of any one of claims 1-42.

133. The vector of claim 132, wherein the vector is a viral vector.

134. The vector of claim 133, wherein the viral vector comprises a sequence isolated or derived from a retrovirus, a lentivirus, an adenovirus, an adeno-associated virus or any combination thereof.

135. The vector of claim 133 or 134, wherein the viral vector comprises a sequence isolated or derived from an adeno-associated virus.

136. The vector of any one of claims 133-135, wherein the viral vector is a recombinant vector.

137. The vector of claim 132, wherein the vector is a nanoparticle vector.

138. The vector of claim 137, wherein the nanoparticle vector comprises a nucleic acid, an amino acid, a polymers, a micelle, lipid, an organic molecule, an inorganic molecule or any combination thereof.

139. The vector of any one of claims 132-138, wherein the vector further comprises a selection gene.

140. The vector of claim 139, wherein the selection gene encodes a gene product essential for cell viability and survival.

141. The vector of claim 140, wherein the selection gene encodes a gene product essential for cell viability and survival when challenged by selective cell culture conditions.

142. The vector of claim 138, wherein the selective cell culture conditions comprise a compound harmful to cell viability or survival and wherein the gene product confers resistance to the compound.

143. The vector of any one of claims 139-142, wherein the selection gene comprises *neo,* 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.

144. The vector of any one of claims 132-143, wherein the vector 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.

145. The vector of claim 144, wherein the non-human sequence is a restriction site.

146. The vector of claim 144 or 145, wherein the ligand binding region inducible caspase polypeptide comprises a FK506 binding protein 12 (FKBP12) polypeptide.

147. The vector of claim 146, wherein the amino acid sequence of the FK506 binding protein 12 (FKBP12) polypeptide comprises a modification at position 36 of the sequence.

148. The vector of claim 147, wherein the modification is a substitution of valine (V) for phenylalanine (F) at position 36 (F36V).

149. The vector of any one of claims 147 or 148, wherein the FKBP12 polypeptide is encoded by an amino acid sequence comprising

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE (SEQ ID NO: 18026).

150. The vector of claim 149, wherein the FKBP12 polypeptide is encoded by a nucleic acid sequence comprising GGGGTCCAGGTCGAGACTATTTCACCAGGGGATGGGCGAACATTTCCAAAAAGG GGCCAGACTTGCGTCGTGCATTACACCGGGATGCTGGAGGACGGGAAGAAAGTG GACAGCTCCAGGGATCGCAACAAGCCCTTCAAGTTCATGCTGGGAAAGCAGGAA GTGATCCGAGGATGGGAGGAAGGCGTGGCACAGATGTCAGTCGGCCAGCGGGCC AAACTGACCATTAGCCCTGACTACGCTTATGGAGCAACAGGCCACCCAGGGATC ATTCCCCCTCATGCCACCCTGGTCTTCGAT GTGGAACTGCTGAAGCTGGAG (SEQ ID NO: 18027).

151. The vector of any one of claims 144-150, wherein the linker region of the inducible proapoptotic polypeptide is encoded by an amino acid comprising GGGGS (SEQ ID NO: 18028).

152. The vector of claim 151, wherein the linker region of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising GGAGGAGGAGGATCC (SEQ ID NO: 18029).

153. The vector of any one of claims 144-152, wherein 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.

154. The vector of any one of claims 144-153, wherein 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.

155. The vector of any one of claims 144-154, wherein the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by an amino acid comprising GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID NO: 18030).

156. The vector of claim 155, wherein the truncated caspase 9 polypeptide of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising GGATTTGGGGACGTGGGGGCCCTGGAGTCTCTGCGAGGAAATGCCGATCTGGCT TACATCCTGAGCATGGAACCCTGCGGCCACTGTCTGATCATTAACAATGTGAACT TCTGCAGAGAAAGCGGACTGCGAACACGGACTGGCTCCAATATTGACTGTGAGA AGCTGCGGAGAAGGTTCTCTAGTCTGCACTTTATGGTCGAAGTGAAAGGGGATCT GACCGCCAAGAAAATGGTGCTGGCCCTGCTGGAGCTGGCTCAGCAGGACCATGG AGCTCTGGATTGCTGCGTGGTCGTGATCCTGTCCCACGGGTGCCAGGCTTCTCAT CTGCAGTTCCCCGGAGCAGTGTACGGAACAGACGGCTGTCCTGTCAGCGTGGAG AAGATCGTCAACATCTTCAACGGCACTTCTTGCCCTAGTCTGGGGGGAAAGCCAA AACTGTTCTTTATCCAGGCCTGTGGCGGGGAACAGAAAGATCACGGCTTCGAGG TGGCCAGCACCAGCCCTGAGGACGAATCACCAGGGAGCAACCCTGAACCAGATG CAACTCCATTCCAGGAGGGACTGAGGACCTTTGACCAGCTGGATGCTATCTCAAG CCTGCCCACTCCTAGTGACATTTTCGTGTCTTACAGTACCTTCCCAGGCTTTGTCT CATGGCGCGATCCCAAGTCAGGGAGCTGGTACGTGGAGACACTGGACGACATCT TTGAACAGTGGGCCCATTCAGAGGACCTGCAGAGCCTGCTGCTGCGAGTGGCAA ACGCTGTCTCTGTGAAGGGCATCTACAAACAGATGCCCGGGTGCTTCAATTTTCT GAGAAAGAAACTGTTCTTTAAGACTTCC (SEQ ID NO: 18031).

157. The vector of any one of claims 144-156, wherein of the inducible proapoptotic polypeptide is encoded by an amino acid sequence comprising

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVI
RGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGGGS
GFGDVGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRR
RFSSLHFMVEVKGDLTAKKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPG
AVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDE
SPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVE
TLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS (SEQ ID
NO: 18032).

158. The vector of claim 157, wherein of the inducible proapoptotic polypeptide is encoded by a nucleic acid sequence comprising
ggggtccaggtcgagactatttcaccaggggatgggcgaacatttccaaaaaggggccagacttgcgtcgtgcattacaccgggatg
ctggaggacgggaagaaagtggacagctccagggatcgcaacaagcccttcaagttcatgctgggaaagcaggaagtgatccgag
gatgggaggaaggcgtggcacagatgtcagtcggccagcgggccaaactgaccattagccctgactacgcttatggagcaacagg
ccacccagggatcattcccccctcatgccaccctggtcttcgatgtggaactgctgaagctggagggaggaggaggatccggatttgg
ggacgtgggggccctggagtctctgcgaggaaatgccgatctggcttacatcctgagcatggaaccctgcggccactgtctgatcatt
aacaatgtgaacttctgcagagaaagcggactgcgaacacggactggctccaatattgactgtgagaagctgcggagaaggttctcta
gtctgcactttatggtcgaagtgaaaggggatctgaccgccaagaaaatggtgctggccctgctggagctggctcagcaggaccatg
gagctctggattgctgcgtggtcgtgatcctgtcccacgggtgccaggcttctcatctgcagttccccggagcagtgtacggaacaga
cggctgtcctgtcagcgtggagaagatcgtcaacatcttcaacggcacttcttgccctagtctgggggggaaagccaaaactgttctttat
ccaggcctgtggcggggaacagaaagatcacggcttcgaggtggccagcaccagccctgaggacgaatcaccagggagcaaccc
tgaaccagatgcaactccattccaggagggactgaggacctttgaccagctggatgctatctcaagcctgcccactcctagtgacatttt
cgtgtcttacagtaccttcccaggctttgtctcatggcgcgatcccaagtcagggagctggtacgtggagacactggacgacatctttga
acagtgggcccattcagaggacctgcagagcctgctgctgcgagtggcaaacgctgtctctgtgaagggcatctacaaacagatgcc
cgggtgcttcaattttctgagaaagaaactgttctttaagacttcc(SEQ ID NO: 18033).

159. The vector of any one of claims 132-158, wherein the vector comprises at least one self-cleaving peptide.

160. The vector of any one of claims 132-158, wherein the vector comprises at least one self-cleaving peptide and wherein a self-cleaving peptide is located between the CAR and a selection gene.

161. The vector of any one of claims 132-158, wherein the transposon comprises at least one self-cleaving peptide and wherein a self-cleaving peptide is located between the CAR and the inducible proapoptotic polypeptide.

162. The vector of any one of claims 132-158, wherein the transposon comprises at least two self-cleaving peptides and wherein a first self-cleaving peptide is located upstream of the inducible proapoptotic polypeptide and a second self-cleaving peptide is located downstream of the inducible proapoptotic polypeptide.

163. The vector of any one of claims 132-162, wherein the vector comprises at least one self-cleaving peptide and wherein a first self-cleaving peptide is located upstream of the CAR and a second self-cleaving peptide is located downstream of the CAR.

164. The vector of any one of claims 159-163, wherein the at least one self-cleaving peptide comprises aT2A peptide, 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.

165. The vector of claim 164, wherein the T2A peptide comprises an amino acid sequence comprising EGRGSLLTCGDVEENPGP (SEQ ID NO: 18034).

166. The vector of claim 164, wherein the GSG-T2A peptide comprises an amino acid sequence comprising GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 18035).

167. The vector of claim 164, wherein the E2A peptide comprises an amino acid sequence comprising QCTNYALLKLAGDVESNPGP (SEQ ID NO: 18036).

168. The vector of claim 164, wherein the GSG-E2A peptide comprises an amino acid sequence comprising GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 18037).

169. The vector of claim 164, wherein the F2A peptide comprises an amino acid sequence comprising VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18038).

170. The vector of claim 164, wherein the GSG-F2A peptide comprises an amino acid sequence comprising GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 18039).

171. The vector of claim 164, wherein the P2A peptide comprises an amino acid sequence comprising ATNFSLLKQAGDVEENPGP (SEQ ID NO: 18040).

172. The vector of claim 164, wherein the GSG-P2A peptide comprises an amino acid sequence comprising GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 18041).

173. A composition comprising the vector of any one of claims 132-172.

174. A cell comprising the CAR of any one of claims 1-42.

175. A cell of claim 174, further comprising a chimeric stimulatory receptor (CSR) comprising:

(a) an ectodomain comprising a activation component;

(b) a transmembrane domain; and

(c) an endodomain comprising at least one signal transduction domain;

wherein the combination of (a), (b) and (c) is non-naturally occurring.

176. The cell of claim 175, wherein the Activation component of (a) is isolated or derived from a first protein.

177. The cell of claim 176, wherein the at least one signal transduction domain of (c) is isolated or derived from a second protein.

178. The cell of claim 176 or 177, wherein the first protein and the second protein are not identical.

179. The cell of any one of claims 175-178, wherein the Activation component comprises one or more of a component of a human transmembrane receptor, a human cell-surface receptor, a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor.

180. The cell of claim 179, wherein the Activation component comprises a portion of one or more of a component of a T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor to which an agonist of the Activation component binds.

181. The cell of any one of claims 175-180, wherein the Activation component comprises a CD2 protein or a portion thereof to which an agonist binds.

182. The cell of any one of claims 175-181, wherein the signal transduction domain comprises one or more of a component of a human signal transduction domain, T-cell Receptor (TCR), a component of a TCR complex, a component of a TCR co-receptor, a component of a TCR co-stimulatory protein, a component of a TCR inhibitory protein, a cytokine receptor, and a chemokine receptor.

183. The cell of claim 182, wherein the signal transduction domain comprises a CD3 protein.

184. The cell of claim 183, wherein the CD3 protein comprises a CD3ζ protein.

185. The cell of any one of claims 175-184, wherein the endodomain further comprises a cytoplasmic domain.

186. The cell of claim 185, wherein the cytoplasmic domain is isolated or derived from a third protein.

187. The cell of claim 186, wherein the first protein and the third protein are identical.

188. The cell of any one of claims 175-187, wherein the ectodomain further comprises a signal peptide.

189. The cell of claim 188, wherein the signal peptide is derived from a fourth protein.

190. The cell of claim 189, wherein the first protein and the fourth protein are identical.

191. The cell of any one of claims 175-190, wherein the transmembrane domain is isolated or derived from a fifth protein.

192. The cell of claim 191, wherein the first protein and the fifth protein are identical.

193. The cell of any one of claim 175-192, wherein the Activation component does not bind a naturally-occurring molecule.

194. The cell of any one of claim 175-192, wherein the CSR does not transduce a signal upon binding of the activation component to a naturally-occurring molecule.

195. The cell of claim 194, wherein the ectodomain comprises a modification.

196. The cell of claim 195, wherein the modification comprises a mutation or a truncation of a sequence encoding the activation component when compared to a wild type sequence of the first protein.

197. The cell of any one of claims 175-196, wherein the Activation component binds to a non-naturally occurring molecule.

198. The cell of any one of claim 175-197, wherein the CSR selectively transduces a signal upon binding of the Activation component to a non-naturally occurring molecule.

199. A cell comprising the transposon or transposase of any one of claims 44-95.

200. A cell comprising the vector of any one of claims 132-172.

201. The cell of any one of claims 198-200, wherein the cell expresses the CAR on the cell surface.

202. The cell of any one of claims 198-200, wherein the cell is an immune cell.

203. The cell of claim 202, wherein the immune cell is a T-cell, a Natural Killer (NK) cell, a Natural Killer (NK)-like cell, a Cytokine Induced Killer (CIK) cell), a hematopoeitic progenitor cell, a peripheral blood (PB) derived T cell or an umbilical cord blood (UCB) derived T-cell.

204. The cell of claim 203, wherein the immune cell is a T-cell.

205. The cell of any one of claims 175-204, further comprising:a sequence encoding an inducible proapoptotic polypeptide

206. The cell of claim 204 or 205, wherein T-cell is an early memory cell, a stem-like T-cell, a T_{SCM}-like cell, a T_{SCM} or a T_{CM}.

207. The cell of claim 26, wherein T-cell is a T_{SCM}.

208. The cell of any one of claims 174-207, wherein the cell is an artificial antigen presenting cell.

209. The cell of any one of claims 174-207, wherein the cell is a tumor cell.

210. The cell of any one of claims 174-209, wherein the cell is autologous.

211. A composition comprising the cell of any one of claims 174-210.

212. A method for expressing a chimeric antigen receptor (CAR) on the surface of a cell, comprising:

(a) obtaining a cell population;

(b) contacting the cell population to a composition comprising a CAR according to any one of claims 1-42 or a sequence encoding the CAR, under conditions sufficient to transfer the CAR across a cell membrane of at least one cell in the cell population, thereby generating a modified cell population;

(c) culturing the modified cell population under conditions suitable for integration of the CAR;

(d) expanding and/or selecting at least one cell from the modified cell population that express the CAR on the cell surface.

213. The method of claim 212, wherein the cell population comprises leukocytes.

214. The method of claim 212 or 213, wherein the cell population comprises CD4+ and CD8+ leukocytes in an optimized ratio.

215. The method of claim 214, wherein the optimized ratio of CD4+ to CD8+ leukocytes does not naturally occur *in vivo*.

216. The method of claim 212, wherein a transposon or vector comprises the CAR or the sequence encoding the CAR.

217. The method of claim 216, wherein a transposon of any one of claims 42-77 comprises the CAR or the sequence encoding the CAR.

218. The method of claim 216 or 217, wherein the transposon comprises a piggyBac transposon.

219. The method of claim 216 or 217, wherein the transposon comprises a TcBuster transposon.

220. The method of any one of claims 215-219, further comprising a composition comprising a plasmid comprising a sequence encoding a transposase enzyme.

221. The method of claim 220, wherein the sequence encoding a transposase enzyme is an mRNA sequence.

222. The method of any one of claims 220 or 221, wherein the transposase is a piggyBac transposase.

223. The method of claim 222, wherein the piggyBac transposase comprises an amino acid sequence comprising SEQ ID NO: 14487.

224. The method of claim 222 or 223, wherein 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: 14487.

225. The method of claim 224, wherein the amino acid substitution at position 30 of SEQ ID NO: 14487 is a substitution of a valine (V) for an isoleucine (I) (I30V).

226. The method of claim 224, wherein the amino acid substitution at position 165 of SEQ ID NO: 14487 is a substitution of a serine (S) for a glycine (G) (G165S).

227. The method of claim 224, wherein the amino acid substitution at position 282 of SEQ ID NO: 14487 is a substitution of a valine (V) for a methionine (M) (M282V).

228. The method of claim 224, wherein the amino acid substitution at position 538 of SEQ ID NO: 14487 is a substitution of a lysine (K) for an asparagine (N) (N538K).

229. The method of any one of claims 220 or 221, wherein the transposase is a Super piggyBac (sPBo) transposase.

230. The method of claim 229, wherein the Super piggyBac (sPBo) transposase comprises an amino acid sequence comprising SEQ ID NO: 14484.

231. The method of claim 200, wherein a vector comprises the CAR or the sequence encoding the CAR.

232. The method of any one of claims 212-231 , wherein the conditions sufficient to transfer the sequence encoding the CAR across a cell membrane of at least one cell in the cell population comprise nucleofection.

233. The method of any one of claims 212-231, wherein the conditions sufficient to transfer the sequence encoding the CAR across a cell membrane of at least one cell in the cell population of (b) comprise at least one of an application of one or more pulses of electricity at a specified voltage, a buffer, and one or more supplemental factor(s).

234. The method of claim 233, wherein the buffer comprises PBS, HBSS, OptiMEM, BTXpress, Amaxa Nucleofector, Human T cell nucleofection buffer or any combination thereof.

235. The method of claim 233 or 234, wherein the one or more supplemental factor(s) comprise

(a) a recombinant human cytokine, a chemokine, an interleukin or any combination thereof;

(b) a salt, a mineral, a metabolite or any combination thereof;

(c) a cell medium;

(d) an inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof; and

(e) a reagent that modifies or stabilizes one or more nucleic acids.

236. The method of claim 235, wherein the recombinant human cytokine, the chemokine, the interleukin or any combination thereof comprise 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 or any combination thereof.

237. The method of claim 235, wherein the salt, the mineral, the metabolite or any combination thereof comprise 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, Pop313, Crown-5, or any combination thereof.

238. The method of claim 235, wherein the cell medium comprises 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.

239. The method of claim 235, wherein the inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof comprise 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, glycogen synthase kinase-3β (GSK-3 β), TWS119, Bafilomycin, Chloroquine, Quinacrine, AC-YVAD-CMK, Z-VAD-FMK, Z-IETD-FMK or any combination thereof.

240. The method of claim 235, wherein the reagent that modifies or stabilizes one or more nucleic acids comprises a pH modifier, a DNA-binding protein, a lipid, a phospholipid, CaPO4, a net neutral charge DNA binding peptide with or without a NLS sequence, a TREX1 enzyme or any combination thereof.

241. The method of any one of claims 212-231, wherein the conditions suitable for integration of the CAR or the sequence encoding the CAR comprise at least one of a buffer and one or more supplemental factor(s).

242. The method of claim 241, wherein the buffer comprises PBS, HBSS, OptiMEM, BTXpress, Amaxa Nucleofector, Human T cell nucleofection buffer or any combination thereof.

243. The method of claim 241 or 242, wherein the one or more supplemental factor(s) comprise

(a) a recombinant human cytokine, a chemokine, an interleukin or any combination thereof;

(b) a salt, a mineral, a metabolite or any combination thereof;

(c) a cell medium;

(d) an inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof; and

(e) a reagent that modifies or stabilizes one or more nucleic acids.

244. The method of claim 243, wherein the recombinant human cytokine, the chemokine, the interleukin or any combination thereof comprise 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 or any combination thereof.

245. The method of claim 243, wherein the salt, the mineral, the metabolite or any combination thereof comprise 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, CINa, Glucose, Ca(NO3)2, Tris/HCl, K2HPO4, KH2PO4, Polyethylenimine, Poly-ethylene-glycol, Poloxamer 188, Poloxamer 181, Poloxamer 407, Poly-vinylpyrrolidone, Pop313, Crown-5, or any combination thereof.

246. The method of claim 243, wherein the cell medium comprises 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.

247. The method of claim 243, wherein the inhibitor of cellular DNA sensing, metabolism, differentiation, signal transduction, one or more apoptotic pathway(s) or combinations thereof comprise 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,

glycogen synthase kinase-3β (GSK-3β), TWS119, Bafilomycin, Chloroquine, Quinacrine, AC-YVAD-CMK, Z-VAD-FMK, Z-IETD-FMK or any combination thereof.

248. The method of claim 243, wherein the reagent that modifies or stabilizes one or more nucleic acids comprises a pH modifier, a DNA-binding protein, a lipid, a phospholipid, CaPO4, a net neutral charge DNA binding peptide with or without a NLS sequence, a TREX1 enzyme or any combination thereof.

249. The method of any one of claims 212-248, wherein the expansion and selection of (d) occur sequentially.

250. The method of claim 249, wherein the expansion occurs prior to selection.

251. The method of claim 249, wherein the expansion occurs following selection.

252. The method of claim 249, wherein a further selection occurs following expansion.

253. The method of any one of claims 212-252, wherein the expansion and selection of (d) occur simultaneously.

254. The method of any one of claims 212-253, wherein the expansion comprises contacting at least one cell of the modified cell population with an antigen to stimulate the at least one cell through the CAR.

255. The method of claim 254, wherein the antigen is presented on the surface of a substrate.

256. The method of claim 255, wherein the substrate is a bead or a plurality of beads.

257. The method of claim 256, wherein the bead or plurality of beads is/are separated from the modified cell population following expansion.

258. The method of claim 257, wherein the antigen is presented on the surface of a cell.

259. The method of claim 258, wherein the antigen is presented on the surface of an artificial antigen presenting cell.

260. The method of any one of claims 212-259, wherein the transposon or vector comprises a selection gene and wherein the selection step comprises contacting at least one cell of the modified cell population with a compound to which the selection gene confers resistance, thereby identifying a cell expressing the selection gene as surviving the selection and identifying a cell failing to express the selection gene as failing to survive the selection step.

261. The method of any one of claims 212-260, wherein the expansion and selection steps proceed for a period of 10 to 14 days, inclusive of the endpoints.

262. A composition comprising the expanded and selected cell population of any one of claims 212-261.

263. A method of treating cancer in a subject in need thereof, comprising administering to the subject the composition of any one of claims 43, 109-123, 173, 211, or 262, wherein the CAR specifically binds to an antigen on a tumor cell.

264. The method of claim 263, wherein the tumor cell is a malignant tumor cell.

265. The method of claim 263 or 264, comprising administering to the subject the composition of claim 211 or 262, wherein the cell or cell population is autologous.

266. The method of claim 263 or 264, comprising administering to the subject the composition of claim 211 or 262, wherein the cell or cell population is allogeneic.

267. A method of modifying a cell therapy in a subject in need thereof, comprising administering to the subject a composition comprising a cell comprising a transposon of any

one of claims 44-80, wherein apoptosis may be selectively induced in the cell by contacting the cell with an induction agent.

268. A method of modifying a cell therapy in a subject in need thereof, comprising administering to the subject a composition comprising a cell comprising a vector of any one of claims 96-136, wherein apoptosis may be selectively induced in the cell by contacting the cell with an induction agent.

269. The method of claim 267 or 268, wherein the cell is autologous.

270. The method of claim any one of claims 267-269, wherein the cell therapy is an adoptive cell therapy.

271. The method of claim any one of claims 267-269, wherein the modifying is a termination of the cell therapy.

272. The method of claim any one of claims 267-271, wherein the modifying is a depletion of a portion of the cells provided in the cell therapy.

273. The method of claim any one of claims 267-272, further comprising the step of administering an inhibitor of the induction agent to inhibit modification of the cell therapy, thereby restoring the function and/or efficacy of the cell therapy.