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(54) Titre : VESICULES EXTRACELLULAIRES AVEC DES OLIGONUCLEOTIDES ANTISENS STAT3
(54) Title: EXTRACELLULAR VESICLES WITH STAT3-ANTISENSE OLIGONUCLEOTIDES

(57) Abrégé/Abstract:

The present disclosure relates to modified extracellular vesicles, e.g., exosomes, comprising an antisense oligonucleotide (ASO), which is capable of reducing and/or inhibiting expression of STAT3 mRNA and/or STAT3 protein. ASOs that can be used with the modified extracellular vesicles are also disclosed. Also provided herein are methods for using the exosomes and ASOs to treat and/or prevent diseases, such as cancer.

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Abstract:

The present disclosure relates to modified extracellular vesicles, e.g., exosomes, comprising an antisense oligonucleotide (ASO), which is capable of reducing and/or inhibiting expression of STAT3 mRNA and/or STAT3 protein. ASOs that can be used with the modified extracellular vesicles are also disclosed. Also provided herein are methods for using the exosomes and ASOs to treat and/or prevent diseases, such as cancer.

EXTRACELLULAR VESICLES WITH STAT3-ANTISENSE OLIGONUCLEOTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority benefit of U.S. Provisional Application Nos. 62/886,901, filed August 14, 2019; 62/886,904, filed August 14, 2019; 62/900,376, filed September 13, 2019; and 62/900,371, filed September 13, 2019, each of which is herein incorporated by reference in its entirety.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY VIA EFS-WEB

[0002] The content of the electronically submitted sequence listing in ASCII text file (Name: 4000_060PC05_Seqlisting_ST25.txt; Size: 341,985 bytes; and Date of Creation: August 13, 2020), filed with the application, is incorporated herein by reference in its entirety.

FIELD OF DISCLOSURE

[0003] The present disclosure relates to extracellular vesicles (EVs), e.g., exosomes, comprising an antisense oligonucleotide (ASO), wherein the ASO comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within a STAT3 transcript. In certain aspects of the disclosure, the extracellular vesicle further comprises a scaffold protein.

BACKGROUND

[0004] Exosomes are small extracellular vesicles that are naturally produced by every eukaryotic cell. Exosomes comprise a membrane that encloses an internal space (*i.e.*, lumen). As drug delivery vehicles, EVs, e.g., exosomes, offer many advantages over traditional drug delivery methods as a new treatment modality in many therapeutic areas. In particular, exosomes have intrinsically low immunogenicity, even when administered to a different species.

[0005] Antisense oligonucleotides have emerged as a powerful means of regulating target gene expression *in vitro* or *in vivo*. However, there remains a need to improve the stability and delivery of ASOs *in vivo*.

SUMMARY OF THE DISCLOSURE

[0006] The present disclosure is related to compositions and methods for engineered-EVs (e.g., exosomes), particularly those that can be used to deliver therapeutic agents that can reduce the expression of a gene associated with a disease (e.g., N for cancer). One aspect of the disclosure is directed to an extracellular vesicle comprising an antisense oligonucleotide (ASO) which is an antagonist and comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within a *STAT3* transcript (SEQ ID NO: 1 or SEQ ID NO: 3). In some aspects, the extracellular vesicle comprises an ASO that is not TAAGCTGATAATTCAACTCA (SEQ ID NO: 5). In some aspects, the extracellular vesicle targets a macrophage. In some aspects, the ASO comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within nucleotides 1 to 56982 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 57003 to 75171 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 1 to 1287 of a *STAT3* transcript corresponding to SEQ ID NO: 3, or nucleotides 1306 to 2787 of a *STAT3* transcript corresponding to SEQ ID NO: 3. In some aspects, the contiguous nucleotide sequence is at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% complementary to the nucleic acid sequence within the *STAT3* transcript. In some aspects, the ASO is capable of reducing STAT3 protein expression in a human cell (e.g., HEK293 cell), wherein the human cell expresses the STAT3 protein.

[0007] In some aspects, the STAT3 protein expression is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to STAT3 protein expression in a human cell that is not exposed to the ASO. In some aspects, the ASO is capable of reducing a level of *STAT3* mRNA in a human cell (e.g., HEK293 cell), wherein the human cell expresses the *STAT3* mRNA. In some aspects, the level of *STAT3* mRNA is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to the level of the *STAT3* mRNA in a human cell that is not exposed to the ASO.

[0008] In some aspects, the ASO is a gapmer, a mixmer, or a totalmer. In some aspects, the ASO comprises one or more nucleoside analogs. In some aspects, the one or more nucleoside

analogs comprise a 2'-O-alkyl-RNA; 2'-O-methyl RNA (2'-OMe); 2'-alkoxy-RNA; 2'-O-methoxyethyl-RNA (2'-MOE); 2'-amino-DNA; 2'-fluoro-RNA; 2'-fluoro-DNA; arabino nucleic acid (ANA); 2'-fluoro-ANA; or bicyclic nucleoside analog. In some aspects, the nucleoside analog is a sugar modified nucleoside. In some aspects, the sugar modified nucleoside is an affinity enhancing 2' sugar modified nucleoside. In some aspects, the nucleoside analogs comprises a nucleoside comprising a bicyclic sugar. In some aspects, the nucleoside analogs comprises an LNA. In some aspects, one or more of the nucleotide analogs is selected from the group consisting of constrained ethyl nucleoside (cEt), 2',4'-constrained 2'-O-methoxyethyl (cMOE), α -L-LNA, β -D-LNA, 2'-O,4'-C-ethylene-bridged nucleic acids (ENA), amino-LNA, oxy-LNA, thio-LNA, and any combination thereof. In some aspects, the ASO comprises one or more 5'-methyl-cytosine nucleobases.

[0009] In some aspects, the contiguous nucleotide sequence is complementary to a nucleic acid sequence within (i) a 5' untranslated region (UTR); (ii) a coding region; or (iii) a 3' UTR of the *STAT3* transcript. In some aspects, the contiguous nucleotide sequence in the ASO is complementary to a nucleic acid sequence comprising (i) nucleotides 151 – 745 of SEQ ID NO: 3; (ii) nucleotides 642-1331 of SEQ ID NO: 3; (iii) nucleotides 1031 - 1704 of SEQ ID NO: 3; (iv) nucleotides 1521 – 2335 of SEQ ID NO: 3; (v) 2062 – 2776 of SEQ ID NO: 3; (vi) nucleotides 251 – 645 of SEQ ID NO: 3; (vii) nucleotides 742-1231 of SEQ ID NO: 3; (viii) nucleotides 1131 - 1604 of SEQ ID NO: 3; (ix) nucleotides 1621 – 2235 of SEQ ID NO: 3; (x) 2162 – 2676 of SEQ ID NO: 3; (xi) nucleotides 301 - 595 of SEQ ID NO: 3; (xii) nucleotides 792 - 1181 of SEQ ID NO: 3; (xiii) nucleotides 1181 - 1554 of SEQ ID NO: 3; (xiv) nucleotides 1671 - 2185 of SEQ ID NO: 3; (xv) 2212 - 2626 of SEQ ID NO: 3; (xvi) nucleotides 341 - 555 of SEQ ID NO: 3; (xvii) nucleotides 832 - 1141 of SEQ ID NO: 3; (xviii) nucleotides 1221 - 1514 of SEQ ID NO: 3; (xix) nucleotides 1711 - 2145 of SEQ ID NO: 3; or (xx) 2252 - 2586 of SEQ ID NO: 3. In some aspects, the contiguous nucleotide sequence is complementary to a nucleic acid sequence within (i) nucleotides 351 - 545 of SEQ ID NO: 3; (ii) nucleotides 842 - 1131 of SEQ ID NO: 3; (iii) nucleotides 1231 - 1504 of SEQ ID NO: 3; (iv) nucleotides 1721 - 2135 of SEQ ID NO: 3; or (v) 2262 - 2576 of SEQ ID NO: 3. In some aspects, the contiguous nucleotide sequence comprises a nucleotide sequence complementary to a sequence selected from the sequences in FIG. 1. In some aspects, the continuous nucleotide sequence is fully complementary to a nucleotide sequence within the *STAT3* transcript. In some aspects, the ASO comprises a nucleotide sequence selected from SEQ ID NOs: 100-199, with one or two mismatches. In some aspects, the ASO has a design selected from the group consisting of the designs in FIG. 1, wherein the upper case letter is a sugar

modified nucleoside and the lower case letter is DNA. In some aspects, the ASO is from 14 to 20 nucleotides in length. In some aspects, the contiguous nucleotide sequence comprises one or more modified internucleoside linkages. In some aspects, the one or more modified internucleoside linkages is a phosphorothioate linkage. In some aspects, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of internucleoside linkages are modified. In some aspects, each of the internucleoside linkages in the ASO is a phosphorothioate linkage.

[0010] In some aspects, the compositions and methods of the present disclosure comprise an anchoring moiety. In some aspects, the STAT3 antagonist is linked to the anchoring moiety. In some aspects, the compositions and methods of the present disclosure comprise an exogenous targeting moiety. In some aspects, the exogenous targeting moiety comprises a peptide, an antibody or an antigen-binding fragment thereof, a chemical compound, or any combination thereof. In some aspects, the exogenous targeting moiety comprises a peptide. In some aspects, the exogenous targeting moiety comprises a microprotein, a designed ankyrin repeat protein (darpin), an anticalin, an adnectin, an aptamer, a peptide mimetic molecule, a natural ligand for a receptor, a camelid nanobody, or any combination thereof. In some aspects, the exogenous targeting moiety comprises a full-length antibody, a single domain antibody, a heavy chain only antibody (VHH), a single chain antibody, a shark heavy chain only antibody (VNAR), an scFv, a Fv, a Fab, a Fab', a F(ab')₂, or any combination thereof. In some aspects, the antibody is a single chain antibody. In some aspects, the exogenous targeting moiety targets the exosome to the liver, heart, lungs, brain, kidneys, central nervous system, peripheral nervous system, muscle, bone, or any combination thereof. In some aspects, the exogenous targeting moiety targets the exosome to a tumor cell, dendritic cell, T cell, B cell, macrophage, neuron, hepatocyte, hematopoietic stem cell, or any combination thereof. In some aspects, the exogenous targeting moiety binds to CD33 or a fragment thereof. In some aspects, the EV comprises a scaffold moiety linking the exogenous targeting moiety to the EV. In some aspects, the anchoring moiety and/or the scaffold moiety is a Scaffold X. In some aspects, the anchoring moiety and/or the scaffold moiety is a Scaffold Y. In some aspects, the Scaffold X is a scaffold protein that is capable of anchoring the STAT3 antagonist on the luminal surface of the EV and/or on the exterior surface of the EV. In some aspects, the Scaffold X is selected from the group consisting of prostaglandin F₂ receptor negative regulator (the PTGFRN protein); basigin (the BSG protein); immunoglobulin superfamily member 2 (the IGSF2 protein); immunoglobulin superfamily member 3 (the IGSF3 protein); immunoglobulin superfamily member 8 (the IGSF8 protein); integrin beta-1 (the ITGB1 protein); integrin alpha-4 (the ITGA4 protein); 4F2 cell-surface antigen heavy chain (the SLC3A2 protein); a class of ATP

transporter proteins (the ATP1A1, ATP1A2, ATP1A3, ATP1A4, ATP1B3, ATP2B1, ATP2B2, ATP2B3, ATP2B4 proteins); a functional fragment thereof; and any combination thereof. In some aspects, the anchoring moiety and/or the scaffold moiety is PTGFRN protein or a functional fragment thereof. In some aspects, the anchoring moiety and/or the scaffold moiety comprises an amino acid sequence as set forth in SEQ ID NO: 302. In some aspects, the anchoring moiety and/or the scaffold moiety comprises an amino acid sequence at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or about 100% identical to SEQ ID NO: 301. In some aspects, the Scaffold Y is a scaffold protein that is capable of anchoring the STAT3 antagonist on the luminal surface of the EV and/or on the exterior surface of the EV.

[0011] In some aspects, the Scaffold Y is selected from the group consisting of myristoylated alanine rich Protein Kinase C substrate (the MARCKS protein), myristoylated alanine rich Protein Kinase C substrate like 1 (the MARCKSL1 protein), brain acid soluble protein 1 (the BASP1 protein), a functional fragment thereof, and any combination thereof. In some aspects, the Scaffold Y is a BASP1 protein or a functional fragment thereof. In some aspects, the Scaffold Y comprises an N terminus domain (ND) and an effector domain (ED), wherein the ND and/or the ED are associated with the luminal surface of the EV. In some aspects, the ND is associated with the luminal surface of the exosome via myristoylation. In some aspects, the ED is associated with the luminal surface of the exosome by an ionic interaction. In some aspects, the ED comprises (i) a basic amino acid or (ii) two or more basic amino acids in sequence, wherein the basic amino acid is selected from the group consisting of Lys, Arg, His, and any combination thereof. In some aspects, the basic amino acid is (Lys)_n, wherein n is an integer between 1 and 10. In some aspects, the ED comprises Lys (K), KK, KKK, KKKK (SEQ ID NO: 405), KKKKK (SEQ ID NO: 406), Arg (R), RR, RRR, RRRR (SEQ ID NO: 407); RRRRR (SEQ ID NO: 408), KR, RK, KKR, KRK, RKK, KRR, RRK, (K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 409), (K/R)(K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 410), or any combination thereof. In some aspects, the ND comprises the amino acid sequence as set forth in G:X2:X3:X4:X5:X6, wherein G represents Gly; wherein ":" represents a peptide bond, wherein each of the X2 to the X6 is independently an amino acid, and wherein the X6 comprises a basic amino acid. In some aspects, (i) the X2 is selected from the group consisting of Pro, Gly, Ala, and Ser; (ii) the X4 is selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln and Met; (iii) the X5 is selected from the group consisting of Pro, Gly, Ala, and Ser; (iv) the X6 is selected from the group consisting of Lys, Arg, and His; or (v) any combination of (i)-(iv). In some aspects, the ND

comprises the amino acid sequence of G:X2:X3:X4:X5:X6, wherein (i) G represents Gly; (ii) "." represents a peptide bond; (iii) the X2 is an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; (iv) the X3 is an amino acid; (v) the X4 is an amino acid selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln and Met; (vi) the X5 is an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; and (vii) the X6 is an amino acid selected from the group consisting of Lys, Arg, and His. In some aspects, the X3 is selected from the group consisting of Asn, Gln, Ser, Thr, Asp, Glu, Lys, His, and Arg. In some aspects, the ND and the ED are joined by a linker.

[0012] In some aspects, the linker comprises one or more amino acids. In some aspects, the ND comprises an amino acid sequence selected from the group consisting of (i) GGKLSKK (SEQ ID NO: 411), (ii) GAKLSKK (SEQ ID NO: 412), (iii) GGKQSKK (SEQ ID NO: 413), (iv) GGKLAKK (SEQ ID NO: 414), (v) GGKLSK (SEQ ID NO: 415), or (vi) any combination thereof. In some aspects, the ND comprises an amino acid sequence selected from the group consisting of (i) GGKLSKKK (SEQ ID NO: 438), (ii) GGKLSKKS (SEQ ID NO: 439), (iii) GAKLSKKK (SEQ ID NO: 440), (iv) GAKLSKKS (SEQ ID NO: 441), (v) GGKQSKKK (SEQ ID NO: 442), (vi) GGKQSKKS (SEQ ID NO: 443), (vii) GGKLAKKK (SEQ ID NO: 444), (viii) GGKLAKKS (SEQ ID NO: 445), and (ix) any combination thereof. In some aspects, the ND comprises the amino acid sequence GGKLSKK (SEQ ID NO: 411). In some aspects, the Scaffold Y is at least about 8, at least about 9, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, at least about 100, at least about 105, at least about 110, at least about 120, at least about 130, at least about 140, at least about 150, at least about 160, at least about 170, at least about 180, at least about 190, or at least about 200 amino acids in length. In some aspects, the Scaffold Y comprises (i) GGKLSKKKKGYNVN (SEQ ID NO: 446), (ii) GAKLSKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKGYSGG (SEQ ID NO: 450), (vi) GGKLSKKKKGSGGS (SEQ ID NO: 451), (vii) GGKLSKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 454), (x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456). In some aspects, the Scaffold Y consists of (i) GGKLSKKKKGYNVN (SEQ ID NO: 446), (ii)

GAKLSKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKGYSGG (SEQ ID NO: 450), (vi) GGKLSKKKKGSGGS (SEQ ID NO: 451), (vii) GGKLSKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 454), (x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456). In some aspects, the Scaffold Y does not comprise Met at the N terminus.

[0013] In some aspects, the Scaffold Y comprises a myristoylated amino acid residue at the N terminus of the scaffold protein. In some aspects, the amino acid residue at the N terminus of the Scaffold Y is Gly. In some aspects, the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety on the exterior of the EV. In some aspects, the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety on the luminal surface of the EV. In some aspects, the anchoring moiety comprises sterol, GM1, a lipid, a vitamin, a small molecule, a peptide, or a combination thereof. In some aspects, the anchoring moiety comprises cholesterol. In some aspects, the anchoring moiety comprises a phospholipid, a lysophospholipid, a fatty acid, a vitamin (e.g., vitamin D and/or vitamin E), or any combination thereof. In some aspects, the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety by a linker. In some aspects, the STAT3 ASO is linked to the EV by a linker. In some aspects, the linker is a polypeptide. In some aspects, the linker is a non-polypeptide moiety. In some aspects, the linker comprises ethylene glycol. In some aspects, the linker comprises HEG, TEG, PEG, or any combination thereof. In some aspects, the linker comprises acrylic phosphoramidite (e.g., ACRYDITE™), adenylation, azide (NHS Ester), digoxigenin (NHS Ester), cholesterol-TEG, I-LINKER™, an amino modifier (e.g., amino modifier C6, amino modifier C12, amino modifier C6 dT, or Uni-Link™ amino modifier), alkyne, 5' Hexynyl, 5-Octadiynyl dU, biotinylation (e.g., biotin, biotin (Azide), biotin dT, biotin-TEG, dual biotin, PC biotin, or desthiobiotin), thiol modification (thiol modifier C3 S-S, dithiol or thiol modifier C6 S-S), or any combination thereof. In some aspects, the linker is a cleavable linker. In some aspects, the linker comprises valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate. In some aspects, the linker comprises (i) a maleimide moiety and (ii) valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate. In some aspects, the EV is an exosome.

[0014] The compositions and methods of the present disclosure are directed in some aspects to an antisense oligonucleotide (ASO) comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within nucleotides 1 to 56982 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 57003 to 75171 of a

STAT3 transcript corresponding to SEQ ID NO: 1, nucleotides 1 to 1287 of a *STAT3* transcript corresponding to SEQ ID NO: 3, or nucleotides 1306 to 2787 of a *STAT3* transcript corresponding to SEQ ID NO: 3. In some aspects, the contiguous nucleotide sequence thereof is at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% complementary to the nucleic acid sequence within the *STAT3* transcript. In some aspects, the ASO is capable of reducing STAT3 protein expression in a human cell (e.g., HEK293 cell), wherein the human cell expresses the STAT3 protein. In some aspects, the STAT3 protein expression is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to STAT3 protein expression in a human cell that is not exposed to the ASO. In some aspects, the ASO is capable of reducing a level of STAT3 mRNA in a human cell (e.g., HEK293 cell), wherein the human cell expresses the *STAT3* mRNA. In some aspects, the level of *STAT3* mRNA is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to the level of the *STAT3* mRNA in a human cell that is not exposed to the ASO. In some aspects, the ASO is a gapmer, a mixmer, or a totalmer. In some aspects, the ASO comprises one or more nucleoside analogs. In some aspects, the nucleoside analogs comprises a 2'-O-alkyl-RNA; 2'-O-methyl RNA (2'-OMe); 2'-alkoxy-RNA; 2'-O-methoxyethyl-RNA (2'-MOE); 2'-amino-DNA; 2'-fluoro-RNA; 2'-fluoro-DNA; arabino nucleic acid (ANA); 2'-fluoro-ANA; or bicyclic nucleoside analog (LNA). In some aspects, one or more of the nucleoside analogs is a sugar modified nucleoside. In some aspects, the sugar modified nucleoside is an affinity enhancing 2' sugar modified nucleoside.

[0015] In some aspects, one or more of the nucleoside analogs comprises a nucleoside comprising a bicyclic sugar. In some aspects, one or more of the nucleoside analogs comprises an LNA. In some aspects, the LNA is selected from the group consisting of constrained ethyl nucleoside (cEt), 2',4'-constrained 2'-O-methoxyethyl (cMOE), α -L-LNA, β -D-LNA, 2'-O,4'-C-ethylene-bridged nucleic acids (ENA), amino-LNA, oxy-LNA, thio-LNA, and any combination thereof. In some aspects, the ASO comprises one or more 5'-methyl-cytosine nucleobases. In some aspects, the ASO comprises any one of SEQ ID NO: 100 to SEQ ID NO: 199. In some aspects, the ASO has a design selected from the group consisting of the designs in FIG. 1, wherein the upper case letter is a sugar modified nucleoside and the lower case letter is DNA. In some aspects, the

ASO is from 14 to 20 nucleotides in length. In some aspects, the contiguous nucleotide sequence comprises one or more modified internucleoside linkages. In some aspects, the one or more modified internucleoside linkages is a phosphorothioate linkage. In some aspects, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of internucleoside linkages are modified. In some aspects, each of the internucleoside linkages in the ASO is a phosphorothioate linkage. In some aspects, the ASO is covalently attached to at least one non-nucleotide or non-polynucleotide moiety. In some aspects, the non-nucleotide or non-polynucleotide moiety comprises a protein, a fatty acid chain, a sugar residue, a glycoprotein, a polymer, or any combinations thereof. In some aspects, an extracellular vesicle comprises the ASO or conjugate. The composition and methods of the present disclosure are also directed to a pharmaceutical composition comprising the extracellular vesicle comprising the ASO or the conjugate, and a pharmaceutically acceptable diluent, carrier, salt, or adjuvant. In some aspects, the pharmaceutically acceptable salt comprises a sodium salt, a potassium salt, an ammonium salt, or any combination thereof. In some aspects, the composition further comprises at least one additional therapeutic agent. In some aspects, the additional therapeutic agent is a STAT3 antagonist. In some aspects, the STAT3 antagonist is a chemical compound, an siRNA, an shRNA, an antisense oligonucleotide, a protein, or any combination thereof. In some aspects, the STAT3 antagonist is an anti- STAT3 antibody or fragment thereof. The compositions and methods of the present disclosure are also related to kits. In some aspects, the present compositions and methods are directed to a kit comprising the extracellular vesicle, the ASO, or the conjugate, or a pharmaceutical composition, and instructions for use. The compositions and methods of the present disclosure are also related to diagnostic kits. In some aspects, the present compositions and methods are directed to a diagnostic kit comprising the extracellular vesicle, the ASO, or the conjugate, or a pharmaceutical composition, and instructions for use.

[0016] The compositions and methods of the present disclosure are also directed to a method of inhibiting or reducing STAT3 protein expression in a cell, comprising administering the extracellular vesicle, the ASO, the conjugate, or a pharmaceutical composition to the cell expressing STAT3 protein, wherein the STAT3 protein expression in the cell is inhibited or reduced after the administration. In some aspects, the ASO inhibits or reduces expression of *STAT3* mRNA in the cell after the administration. In some aspects, a level of *STAT3* mRNA is reduced by at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% after the administration compared to the level of *STAT3* mRNA in a cell not exposed to the ASO. In some aspects, the

expression of STAT3 protein is reduced by at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% after the administration compared to the expression of STAT3 protein in a cell not exposed to the ASO. The compositions and methods of the present disclosure are also directed to a method of treating a cancer in a subject in need thereof, comprising administering an effective amount of the extracellular vesicle, the ASO, the conjugate, or a pharmaceutical composition to the subject.

[0017] The compositions and methods of the present disclosure are also directed to the use of the extracellular vesicle, the ASO, the conjugate, or a pharmaceutical composition in the manufacture of a medicament for the treatment of a cancer in a subject in need thereof. In some aspects, the compositions and methods of the present disclosure are directed to the extracellular vesicle, the ASO, the conjugate, or a pharmaceutical composition for use in the treatment of a cancer in a subject in need thereof. In some aspects, the extracellular vesicle, the ASO, the conjugate, or the pharmaceutical composition is administered intracardially, orally, parenterally, intrathecally, intra-cerebroventricularly, pulmorarily, topically, or intraventricularly. In some aspects, the cancer is selected from the group consisting of fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell cancer, squamous cell cancer of the head and neck cancer, colorectal cancer, lymphoma, leukemia, liver cancer, glioblastoma, melanoma, myeloma basal cell cancer, adenocarcinoma, sweat gland cancer, sebaceous gland cancer, papillary cancer, papillary adenocarcinomas, cystadenocarcinoma, medullary cancer, bronchogenic cancer, renal cell cancer, hepatoma, bile duct cancer, choriocarcinoma, seminoma, embryonal cancer, Wilms' tumor, cervical cancer, testicular cancer, lung cancer, small cell lung cancer, bladder cancer, epithelial cancer, glioma, glioblastoma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma, and any combination thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] FIG. 1 shows a table listing various STAT3 ASO sequences described herein and the location of the complimentary sequence for each in the mRNA sequence (*i.e.*, SEQ ID NO: 3). The ASOs are from 5' to 3'. The symbols in the chemical structures are as follows: Nb means

LNA; dN means DNA; 5MdC means 5-Methyl-dC; Nm means MOE, and s means phosphorothioate.

[0019] FIG. 2A-2N shows the knockdown efficiency of different STAT3 ASOs (circles). As a comparison, the effect of the STAT3 ASOs on GAPDH expression is also shown (square). FIG. 2A shows *STAT3* mRNA expression in cells treated with X51550 ASO. FIG. 2B shows *STAT3* mRNA expression in cells treated with X51577 ASO. FIG. 2C shows *STAT3* mRNA expression in cells treated with X51579 ASO. FIG. 2D shows mRNA expression in cells treated with X51578 ASO. FIG. 2E shows *STAT3* mRNA expression in cells treated with X51609 ASO. FIG. 2F shows *STAT3* mRNA expression in cells treated with X51553 ASO. FIG. 2G shows *STAT3* mRNA expression in cells treated with X51548. FIG. 2H shows *STAT3* mRNA expression in cells treated with X51562 ASO. FIG. 2I shows *STAT3* mRNA expression in cells treated with X52603 ASO. FIG. 2J shows *STAT3* mRNA expression in cells treated with X51603 ASO. FIG. 2K shows *STAT3* mRNA expression in cells treated with X51538 ASO. FIG. 2L shows *STAT3* mRNA expression in cells treated with X51608. FIG. 2M shows *STAT3* mRNA expression in cells treated with X51593 ASO. FIG. 2N shows *STAT3* mRNA expression in cells treated with X51588 ASO.

[0020] FIG. 3 shows a graph depicting the overall knockdown of both *STAT3* and *GAPDH* mRNAs in cells treated with different STAT3-specific ASOs. Knockdown is shown as the % of *STAT3* and *GAPDH* mRNA expression left in the treated cells. For each ASO tested ("Starting Nucleotide", which corresponds to the ASOs listed in FIG. 1 – see "Start" under the mRNA Position column), the left bar represents *STAT3* mRNA remaining, and the right bar represents *GAPDH* mRNA remaining.

[0021] FIGs. 4A-4C show a tumor volume response curve post-innoculation with STAT3 Exo-ASO (FIG. 4A) and STAT3 Free ASO MOE variants (FIG. 4B), as compared to control (PBS) (FIG. 4C). FIG. 4A shows STAT3 ASO delivered by an exosome (*i.e.*, linked to the exterior surface of the EVs), FIG. 4B shows STAT3 ASO delivered free (*i.e.*, not loaded in an exosome) in solution, and FIG. 4C shows a PBS buffer control. Each line represents a different ASO tested.

[0022] FIG. 5 shows a STAT3 gene expression profile response using negative control groups PBS, HEK-Exo, and Scramble Exo-ASO, positive control group C18-9 100mg/kg, and test groups STAT3 Exo-ASO, STAT3 Free ASO, and STAT3 Free ASO 2X. STAT3-Exo ASO shows STAT3 delivered by an exosome, while STAT3 Free ASO shows STAT3 delivered free in solution at a dose of 4 μ g, and STAT3 Free ASO 2X shows STAT3 delivered free in solution at a dose of 8 μ g. STAT3-Exo ASO (4 μ g) knock down STAT3 expression in the whole tumor lysate by 40%. STAT3 Free ASO (8 μ g) knocked down STAT3 expression in the whole tumor lysate by 25%.

[0023] FIGs. 6A-6C shows percentages of infiltrating MDSCs/CD45s (CD11b^{High} F40/80^{High}/CD45) cells after exposure to control group PBS, Scramble Exo-ASO, STAT3 Exo-ASO MOE, and STAT3 Free ASO MOE. FIG. 6A shows percentage of infiltrating CD45+ cells after dosing with each test group. FIG. 6B shows percentage of infiltrating macrophages/CD45 cells after dosing with each test group. FIG. 6C shows percentage of infiltrating MDSCs/CD45+ cells after dosing with each test group.

[0024] FIGs. 7A-7B shows percentages of infiltrating MDSCs/Total MDSCs (Ly6G^{High} CD11b^{High}/IA/IE^{Low}) after exposure to control group PBS, Scramble Exo-ASO, STAT3 Exo-ASO MOE, and STAT3 Free ASO MOE. FIG. 7A shows percentage of infiltrating gMDSCs/Total MDSCs after dosing with each test group. FIG. 7B shows percentage of infiltrating mMDSCs/Total MDSCs after dosing with each test group.

[0025] FIG. 8 shows a normalized STAT3 mRNA count after treatment with control group PBS, Scramble Exo-ASO, STAT3 Exo-ASO, and STAT3 Free ASO. STAT3-Exo ASO represents STAT3 delivered by an exosome (*i.e.*, linked to the exterior surface of the EV), while STAT3 Free ASO shows STAT3 delivered free in solution (*i.e.*, not linked to an EV).

[0026] FIGs. 9A-9D are schematic drawings of various CD47-Scaffold X fusion constructs. FIG. 9A shows constructs comprising the extracellular domain of wild-type CD47 (with a C15S substitution) fused to either a flag-tagged (1083 and 1084) or non-flag-tagged (1085 and 1086) full length Scaffold X (1083 and 1086) or a truncated Scaffold X (1084 and 1085). FIG. 9B shows constructs comprising the extracellular domain of Velcro-CD47 fused to either a flag-tagged (1087 and 1088) or non-flag-tagged (1089 and 1090) full length Scaffold X (1087 and 1090) or a truncated Scaffold X (1088 and 1089). FIG. 9C shows constructs wherein the first transmembrane domain of wild-type CD47 (with a C15S substitution; 1127 and 1128) or Velcro-CD47 (1129 and 1130) is replaced with a fragment of Scaffold X, comprising the transmembrane domain and the first extracellular motif of Scaffold X. FIG. 9D shows various constructs comprising a minimal "self" peptide (GNYTCEVTELREGETIIEELK; SEQ ID NO: 600) fused to either a flag-tagged (1158 and 1159) or non-flag-tagged (1160 and 1161) full length Scaffold X (1158 and 1161) or a truncated Scaffold X (1159 and 1160).

[0027] FIG. 10 shows the expression of of exemplary mouse CD47-Scaffold X fusion constructs that can be expressed on the surface of modified exosomes, along with an ASO targeting a STAT3 transcript. The constructs comprises the extracellular domain of wild-type murine CD47 (with a C15S substitution) fused to either a flag-tagged (1923 and 1925) or non-flag-tagged (1924 and 1922) full length Scaffold X (1923 and 1922) or a truncated Scaffold X (1925 and 1924).

[0028] FIG. 11A shows a schematic diagram of exemplary extracellular vesicle (e.g., exosome) targeting Trks using neurotrophin-Scaffold X fusion construct that can be delivered along with any other moieties, e.g., a biologically active moiety. Neurotrophins bind to Trk receptors as a homo dimer and allow the EV to target a sensory neuron.

[0029] FIG. 11B shows a schematic diagram of exemplary extracellular vesicle (e.g., exosome) having (i) neuro-tropism as well as (ii) an anti-phagocytic signal, e.g., CD47 and/or CD24, on the exterior surface of the EV that can be delivered along with (iii) an ASO targeting a *STAT3* transcript.

[0030] FIGs. 12A-12D show Exo-STAT3 dose-dependent knockdown of *STAT3* mRNA from two donors (e.g., black bars and white bars) (FIG. 12A) and Exo-STAT3 dose-dependent increase in M1 cytokine production (FIGs. 12B-12D) in primary human macrophages from three donors (e.g., white circles, black circles, shaded circles). FIG. 12B shows the results for TNF- α production. FIG. 12C shows the results for IL-23 production. FIG. 12D shows the results for IL-12 p40 production.

[0031] FIGs. 13A-13C show the knockdown efficiency of Exo-STAT3 disclosed in the present disclosure. The knockdown efficiency is shown by providing (i) relative *STAT3* mRNA expression (FIG. 13A), (ii) relative *mcl1* (a *STAT3* downstream target gene) mRNA expression (FIG. 13B), and (iii) relative *STAT3* protein expression (FIG. 13C) in Hep3B liver cells treated with various concentrations of the Exo-STAT3. The concentrations used are provided along the x-axis. In FIGs. 13A and 13B, untreated cells and cells treated with EVs comprising a scramble control ASO were used as controls. In FIG. 13C, EV comprising only Scaffold X (i.e., not fused to a *STAT3* ASO) was used as a control.

[0032] FIG. 14 shows Exo-STAT3 knockdown of *STAT3* mRNA in tumor lysates from intratumoral treatment of Hep3B subcutaneous xenograft models. The animals were treated with one of the following: (i) native EV (circle); (ii) *STAT3*-specific ASO only (i.e., not linked to an EV) (square); (iii) native EVs comprising only the *STAT3*-specific ASO (i.e., not fused to Scaffold X) (diamond); and (iv) EVs comprising *STAT3*-specific ASOs fused to Scaffold X (PTGFRN) and linked to the exterior surface of the EV ("triangle").

[0033] FIG. 15 shows the binding kinetics of AF568-labeled exosomes to CD33, as measured using Octet. "Soluble hP67.6" represents binding of the soluble anti-CD33 antibody to recombinant human CD33 extracellular domain. "PrX" and "PrX-AF568" represent binding of PTGFRN overexpressing exosomes, and PTGFRN overexpressing exosomes labeled with NHS-Alexa Fluor 568, to recombinant human CD33 extracellular domain, respectively. "ALFA" and

"ALFA-AF568" represent binding of ALFA nanobody expressing exosomes, with or without NHS-Alexa Fluor 568 labeling, to recombinant human CD33 extracellular domain. "Native" and "Native-AF568" represent binding of native exosomes, with or without NHS-Alexa Fluor 568 labeling, to recombinant human CD33 extracellular domain. "ALFA-hP67.6" and "ALFA-hP67.6-AF568" represent binding of ALFA nanobody expressing exosomes coupled to soluble ALFA-tagged hP67.6 aCD33 antibody, with and without NHS-Alexa Fluor 568 labeling, to recombinant human CD33 extracellular domain.

[0034] FIGs. 16A-16F shows increased uptake of CD33-targeted exosomes (*i.e.*, comprising an anti-CD33 targeting moiety) in AML cells. FIG. 16A shows exosome uptake in MV4-11 cells. FIG. 16B shows exosomes uptake in KG1 cells. FIG. 16C shows exosomes uptake in RAW264.7 cells. FIG. 16D shows exosome uptake in MV4-11, KG1, and RAW264.7 cells at MOI 1×10^6 . FIG. 16E shows exosome uptake in MV4-11, KG1, and RAW264.7 cells at MOI 1.25×10^5 . FIG. 16F shows exosome uptake in MV4-11, KG1, and RAW264.7 cells at MOI 1.56×10^4 .

DETAILED DESCRIPTION OF THE DISCLOSURE

[0035] The present disclosure is directed to an extracellular vesicle (EV), *e.g.*, an exosome, comprising a STAT3 antagonist. In some aspect, the STAT3 antagonist comprises an antisense oligonucleotide (ASO). In some aspects, the ASO comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within a *STAT3* transcript. In some aspects, the EV, *e.g.*, the exosome, further comprises a scaffold protein.

I. Definitions

[0036] In order that the present description can be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0037] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a nucleotide sequence," is understood to represent one or more nucleotide sequences. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0038] Furthermore, "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C"

is intended to encompass each of the following aspects: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0039] It is understood that wherever aspects are described herein with the language "comprising," otherwise analogous aspects described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0040] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

[0041] Units, prefixes, and symbols are denoted in their *Système International de Unites* (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, nucleotide sequences are written left to right in 5' to 3' orientation. Amino acid sequences are written left to right in amino to carboxy orientation. The headings provided herein are not limitations of the various aspects of the disclosure, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification in its entirety.

[0042] The term "about" is used herein to mean approximately, roughly, around, or in the regions of. When the term "about" is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term "about" can modify a numerical value above and below the stated value by a variance of, *e.g.*, 10 percent, up or down (higher or lower). For example, if it is stated that "the ASO reduces expression of STAT3 protein in a cell following administration of the ASO by at least about 60%," it is implied that the STAT3 levels are reduced by a range of 50% to 70%.

[0043] The term "antisense oligonucleotide" (ASO) refers to an oligomer or polymer of nucleosides, such as naturally-occurring nucleosides or modified forms thereof, that are covalently linked to each other through internucleotide linkages. The ASO useful for the disclosure includes at least one non-naturally occurring nucleoside. An ASO is at least partially complementary to a target nucleic acid, such that the ASO hybridizes to the target nucleic acid sequence.

[0044] The term "nucleic acids" or "nucleotides" is intended to encompass plural nucleic acids. In some aspects, the term "nucleic acids" or "nucleotides" refers to a target sequence, *e.g.*,

pre-mRNAs, mRNAs, or DNAs *in vivo* or *in vitro*. When the term refers to the nucleic acids or nucleotides in a target sequence, the nucleic acids or nucleotides can be naturally occurring sequences within a cell. In other aspects, "nucleic acids" or "nucleotides" refer to a sequence in the ASOs of the disclosure. When the term refers to a sequence in the ASOs, the nucleic acids or nucleotides can be non-naturally occurring, *i.e.*, chemically synthesized, enzymatically produced, recombinantly produced, or any combination thereof. In some aspects, the nucleic acids or nucleotides in the ASOs are produced synthetically or recombinantly, but are not a naturally occurring sequence or a fragment thereof. In some aspects, the nucleic acids or nucleotides in the ASOs are not naturally occurring because they contain at least one nucleoside analog that is not naturally occurring in nature.

[0045] The term "nucleotide" as used herein, refers to a glycoside comprising a sugar moiety, a base moiety and a covalently linked group (linkage group), such as a phosphate or phosphorothioate internucleotide linkage group, and covers both naturally occurring nucleotides, such as DNA or RNA, and non-naturally occurring nucleotides comprising modified sugar and/or base moieties, which are also referred to as "nucleotide analogs" herein. Herein, a single nucleotide can be referred to as a monomer or unit. In certain aspects, the term "nucleotide analogs" refers to nucleotides having modified sugar moieties. Non-limiting examples of the nucleotides having modified sugar moieties (*e.g.*, LNA) are disclosed elsewhere herein. In other aspects, the term "nucleotide analogs" refers to nucleotides having modified nucleobase moieties. The nucleotides having modified nucleobase moieties include, but are not limited to, 5-methyl-cytosine, isocytosine, pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-aminopurine, inosine, diaminopurine, and 2-chloro-6-aminopurine. In some aspects, the terms "nucleotide", "unit" and "monomer" are used interchangeably. It will be recognized that when referring to a sequence of nucleotides or monomers, what is referred to is the sequence of bases, such as A, T, G, C or U, and analogs thereof.

[0046] The term "nucleoside" as used herein is used to refer to a glycoside comprising a sugar moiety and a base moiety, and can therefore be used when referring to the nucleotide units, which are covalently linked by the internucleotide linkages between the nucleotides of the ASO. In the field of biotechnology, the term "nucleotide" is often used to refer to a nucleic acid monomer or unit. In the context of an ASO, the term "nucleotide" can refer to the base alone, *i.e.*, a nucleobase sequence comprising cytosine (DNA and RNA), guanine (DNA and RNA), adenine (DNA and RNA), thymine (DNA) and uracil (RNA), in which the presence of the sugar backbone and internucleotide linkages are implicit. Likewise, particularly in the case of oligonucleotides where

one or more of the internucleotide linkage groups are modified, the term "nucleotide" can refer to a "nucleoside." For example the term "nucleotide" can be used, even when specifying the presence or nature of the linkages between the nucleosides.

[0047] The term "nucleotide length" as used herein means the total number of the nucleotides (monomers) in a given sequence. For example, if a sequence has 20 nucleotides, the nucleotide length of the sequence is 20. The term "nucleotide length" is therefore used herein interchangeably with "nucleotide number."

[0048] As one of ordinary skill in the art would recognize, the 5' terminal nucleotide of an oligonucleotide does not comprise a 5' internucleotide linkage group, although it can comprise a 5' terminal group.

[0049] The compounds described herein can contain several asymmetric centers and can be present in the form of optically pure enantiomers, mixtures of enantiomers such as, for example, racemates, mixtures of diastereoisomers, diastereoisomeric racemates or mixtures of diastereoisomeric racemates. In some aspects, the asymmetric center can be an asymmetric carbon atom. The term "asymmetric carbon atom" means a carbon atom with four different substituents. According to the Cahn-Ingold-Prelog Convention an asymmetric carbon atom can be of the "R" or "S" configuration.

[0050] As used herein, the term "bicyclic sugar" refers to a modified sugar moiety comprising a 4 to 7 membered ring comprising a bridge connecting two atoms of the 4 to 7 membered ring to form a second ring, resulting in a bicyclic structure. In some aspects, the bridge connects the C2' and C4' of the ribose sugar ring of a nucleoside (*i.e.*, 2'-4' bridge), as observed in LNA nucleosides.

[0051] As used herein, a "coding region" or "coding sequence" is a portion of polynucleotide which consists of codons translatable into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is typically not translated into an amino acid, it can be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, untranslated regions ("UTRs"), and the like, are not part of a coding region. The boundaries of a coding region are typically determined by a start codon at the 5' terminus, encoding the amino terminus of the resultant polypeptide, and a translation stop codon at the 3' terminus, encoding the carboxyl terminus of the resulting polypeptide.

[0052] The term "non-coding region" as used herein means a nucleotide sequence that is not a coding region. Examples of non-coding regions include, but are not limited to, promoters, ribosome binding sites, transcriptional terminators, introns, untranslated regions ("UTRs"), non-

coding exons and the like. Some of the exons can be wholly or part of the 5' untranslated region (5' UTR) or the 3' untranslated region (3' UTR) of each transcript. The untranslated regions are important for efficient translation of the transcript and for controlling the rate of translation and half-life of the transcript.

[0053] The term "region" when used in the context of a nucleotide sequence refers to a section of that sequence. For example, the phrase "region within a nucleotide sequence" or "region within the complement of a nucleotide sequence" refers to a sequence shorter than the nucleotide sequence, but longer than at least 10 nucleotides located within the particular nucleotide sequence or the complement of the nucleotides sequence, respectively. The term "sub-sequence" or "subsequence" can also refer to a region of a nucleotide sequence.

[0054] The term "downstream," when referring to a nucleotide sequence, means that a nucleic acid or a nucleotide sequence is located 3' to a reference nucleotide sequence. In certain aspects, downstream nucleotide sequences relate to sequences that follow the starting point of transcription. For example, the translation initiation codon of a gene is located downstream of the start site of transcription.

[0055] The term "upstream" refers to a nucleotide sequence that is located 5' to a reference nucleotide sequence.

[0056] As used herein, the term "regulatory region" refers to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding region, and which influence the transcription, RNA processing, stability, or translation of the associated coding region. Regulatory regions can include promoters, translation leader sequences, introns, polyadenylation recognition sequences, RNA processing sites, effector binding sites, UTRs, and stem-loop structures. If a coding region is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

[0057] The term "transcript" as used herein can refer to a primary transcript that is synthesized by transcription of DNA and becomes a messenger RNA (mRNA) after processing, *i.e.*, a precursor messenger RNA (pre-mRNA), and the processed mRNA itself. The term "transcript" can be interchangeably used with "pre-mRNA" and "mRNA." After DNA strands are transcribed to primary transcripts, the newly synthesized primary transcripts are modified in several ways to be converted to their mature, functional forms to produce different proteins and RNAs, such as mRNA, tRNA, rRNA, lncRNA, miRNA and others. Thus, the term "transcript" can include exons, introns, 5' UTRs, and 3' UTRs.

[0058] The term "expression" as used herein refers to a process by which a polynucleotide produces a gene product, for example, a RNA or a polypeptide. It includes, without limitation, transcription of the polynucleotide into messenger RNA (mRNA) and the translation of an mRNA into a polypeptide. Expression produces a "gene product." As used herein, a gene product can be either a nucleic acid, *e.g.*, a messenger RNA produced by transcription of a gene, or a polypeptide which is translated from a transcript. Gene products described herein further include nucleic acids with post transcriptional modifications, *e.g.*, polyadenylation or splicing, or polypeptides with post translational modifications, *e.g.*, methylation, glycosylation, the addition of lipids, association with other protein subunits, or proteolytic cleavage.

[0059] The terms "identical" or percent "identity" in the context of two or more nucleic acids refer to two or more sequences that are the same or have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned (introducing gaps, if necessary) for maximum correspondence, not considering any conservative amino acid substitutions as part of the sequence identity. The percent identity can be measured using sequence comparison software or algorithms or by visual inspection. Various algorithms and software are known in the art that can be used to obtain alignments of amino acid or nucleotide sequences.

[0060] One such non-limiting example of a sequence alignment algorithm is the algorithm described in Karlin *et al.*, 1990, *Proc. Natl. Acad. Sci.*, 87:2264-2268, as modified in Karlin *et al.*, 1993, *Proc. Natl. Acad. Sci.*, 90:5873-5877, and incorporated into the NBLAST and XBLAST programs (Altschul *et al.*, 1991, *Nucleic Acids Res.*, 25:3389-3402). In certain aspects, Gapped BLAST can be used as described in Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402. BLAST-2, WU-BLAST-2 (Altschul *et al.*, 1996, *Methods in Enzymology*, 266:460-480), ALIGN, ALIGN-2 (Genentech, South San Francisco, California) or Megalign (DNASTAR) are additional publicly available software programs that can be used to align sequences. In certain aspects, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (*e.g.*, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 90 and a length weight of 1, 2, 3, 4, 5, or 6). In certain alternative aspects, the GAP program in the GCG software package, which incorporates the algorithm of Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) can be used to determine the percent identity between two amino acid sequences (*e.g.*, using either a BLOSUM 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5). Alternatively, in certain aspects, the percent identity between nucleotide or amino acid sequences is determined using the algorithm of Myers and Miller (CABIOS, 4:11-17 (1989)). For example, the percent identity can be determined

using the ALIGN program (version 2.0) and using a PAM120 with residue table, a gap length penalty of 12 and a gap penalty of 4. One skilled in the art can determine appropriate parameters for maximal alignment by particular alignment software. In certain aspects, the default parameters of the alignment software are used.

[0061] In certain aspects, the percentage identity "X" of a first nucleotide sequence to a second nucleotide sequence is calculated as $100 \times (Y/Z)$, where Y is the number of amino acid residues scored as identical matches in the alignment of the first and second sequences (as aligned by visual inspection or a particular sequence alignment program) and Z is the total number of residues in the second sequence. If the length of a first sequence is longer than the second sequence, the percent identity of the first sequence to the second sequence will be higher than the percent identity of the second sequence to the first sequence.

[0062] Different regions within a single polynucleotide target sequence that align with a polynucleotide reference sequence can each have their own percent sequence identity. It is noted that the percent sequence identity value is rounded to the nearest tenth. For example, 80.11, 80.12, 80.13, and 80.14 are rounded down to 80.1, while 80.15, 80.16, 80.17, 80.18, and 80.19 are rounded up to 80.2. It also is noted that the length value will always be an integer.

[0063] As used herein, the terms "homologous" and "homology" are interchangeable with the terms "identity" and "identical."

[0064] The term "naturally occurring variant thereof" refers to variants of the STAT3 polypeptide sequence or *STAT3* nucleic acid sequence (*e.g.*, transcript) which exist naturally within the defined taxonomic group, such as mammalian, such as mouse, monkey, and human. Typically, when referring to "naturally occurring variants" of a polynucleotide the term also can encompass any allelic variant of the *STAT3*-encoding genomic DNA which is found at Chromosomal position 17q21.2 (*i.e.*, nucleotides 5,001 to 80,171 of GenBank Accession No. NG_007370.1) by chromosomal translocation or duplication, and the RNA, such as mRNA derived therefrom. "Naturally occurring variants" can also include variants derived from alternative splicing of the *STAT3* mRNA. When referenced to a specific polypeptide sequence, *e.g.*, the term also includes naturally occurring forms of the protein, which can therefore be processed, *e.g.*, by co- or post-translational modifications, such as signal peptide cleavage, proteolytic cleavage, glycosylation, *etc.* When referenced to a specific polypeptide sequence, *e.g.*, the term also includes naturally occurring forms of the protein, which can therefore be processed, *e.g.*, by co- or post-translational modifications, such as signal peptide cleavage, proteolytic cleavage, glycosylation, *etc.*

[0065] In determining the degree of "complementarity" between the ASOs of the disclosure (or regions thereof) and the target region of the nucleic acid which encodes mammalian STAT3 (e.g., the *STAT3* gene), such as those disclosed herein, the degree of "complementarity" (also, "homology" or "identity") is expressed as the percentage identity (or percentage homology) between the sequence of the ASO (or region thereof) and the sequence of the target region (or the reverse complement of the target region) that best aligns therewith. The percentage is calculated by counting the number of aligned bases that are identical between the two sequences, dividing by the total number of contiguous monomers in the ASO, and multiplying by 100. In such a comparison, if gaps exist, it is preferable that such gaps are merely mismatches rather than areas where the number of monomers within the gap differs between the ASO of the disclosure and the target region.

[0066] The term "complement" as used herein indicates a sequence that is complementary to a reference sequence. It is well known that complementarity is the base principle of DNA replication and transcription as it is a property shared between two DNA or RNA sequences, such that when they are aligned antiparallel to each other, the nucleotide bases at each position in the sequences will be complementary, much like looking in the mirror and seeing the reverse of things. Therefore, for example, the complement of a sequence of 5'ATGC'3' can be written as 3'TACG'5' or 5'GCAT'3'. The terms "reverse complement", "reverse complementary", and "reverse complementarity" as used herein are interchangeable with the terms "complement", "complementary", and "complementarity." In some aspects, the term "complementary" refers to 100% match or complementarity (i.e., fully complementary) to a contiguous nucleic acid sequence within a *STAT3* transcript. In some aspects, the term "complementary" refers to at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% match or complementarity to a contiguous nucleic acid sequence within a *STAT3* transcript.

[0067] The terms "corresponding to" and "corresponds to," when referencing two separate nucleic acid or nucleotide sequences can be used to clarify regions of the sequences that correspond or are similar to each other based on homology and/or functionality, although the nucleotides of the specific sequences can be numbered differently. For example, different isoforms of a gene transcript can have similar or conserved portions of nucleotide sequences whose numbering can differ in the respective isoforms based on alternative splicing and/or other modifications. In addition, it is recognized that different numbering systems can be employed when characterizing

a nucleic acid or nucleotide sequence (*e.g.*, a gene transcript and whether to begin numbering the sequence from the translation start codon or to include the 5'UTR). Further, it is recognized that the nucleic acid or nucleotide sequence of different variants of a gene or gene transcript can vary. As used herein, however, the regions of the variants that share nucleic acid or nucleotide sequence homology and/or functionality are deemed to "correspond" to one another. For example, a nucleotide sequence of a *STAT3* transcript corresponding to nucleotides X to Y of SEQ ID NO: 1 ("reference sequence") refers to an *STAT3* transcript sequence (*e.g.*, *STAT3* pre-mRNA or mRNA) that has an identical sequence or a similar sequence to nucleotides X to Y of SEQ ID NO: 1, wherein X is the start site and Y is the end site (as shown in FIG. 1). A person of ordinary skill in the art can identify the corresponding X and Y residues in the *STAT3* transcript sequence (SEQ ID NO: 3) by aligning the *STAT3* transcript sequence with SEQ ID NO: 1

[0068] The terms "corresponding nucleotide analog" and "corresponding nucleotide" are intended to indicate that the nucleobase in the nucleotide analog and the naturally occurring nucleotide have the same pairing, or hybridizing, ability. For example, when the 2-deoxyribose unit of the nucleotide is linked to an adenine, the "corresponding nucleotide analog" contains a pentose unit (different from 2-deoxyribose) linked to an adenine.

[0069] The annotation of ASO chemistry is as follows Beta-D-oxy LNA nucleotides are designated by OxyB where B designates a nucleotide base such as thymine (T), uridine (U), cytosine (C), 5-methylcytosine (MC), adenine (A) or guanine (G), and thus include OxyA, OxyT, OxyMC, OxyC and OxyG. DNA nucleotides are designated by DNAb, where the lower case b designates a nucleotide base such as thymine (T), uridine (U), cytosine (C), 5-methylcytosine (Mc), adenine (A) or guanine (G), and thus include DNAa, DNAt, DNA and DNAG. The letter M before C or c indicates 5-methylcytosine. The letter "s" indicates a phosphorothioate internucleotide linkage.

[0070] The term "ASO Number" or "ASO No." as used herein refers to a unique number given to a nucleotide sequence having the detailed chemical structure of the components, *e.g.*, nucleosides (*e.g.*, DNA), nucleoside analogs (*e.g.*, beta-D-oxy-LNA), nucleobase (*e.g.*, A, T, G, C, U, or MC), and backbone structure (*e.g.*, phosphorothioate or phosphorodiester). For example, ASO-STAT3-2559 can refer to STAT3-2559 (SEQ ID NO: 100).

[0071] "Potency" is normally expressed as an IC₅₀ or EC₅₀ value, in μ M, nM or pM unless otherwise stated. Potency can also be expressed in terms of percent inhibition. IC₅₀ is the median inhibitory concentration of a therapeutic molecule. EC₅₀ is the median effective concentration of a therapeutic molecule relative to a vehicle or control (*e.g.*, saline). In functional assays, IC₅₀ is the

concentration of a therapeutic molecule that reduces a biological response, *e.g.*, transcription of mRNA or protein expression, by 50% of the biological response that is achieved by the therapeutic molecule. In functional assays, EC₅₀ is the concentration of a therapeutic molecule that produces 50% of the biological response, *e.g.*, transcription of mRNA or protein expression. IC₅₀ or EC₅₀ can be calculated by any number of means known in the art.

[0072] As used herein, the term "inhibiting," *e.g.*, the expression of *STAT3* gene transcript and/or STAT3 protein refers to the ASO reducing the expression of the *STAT3* gene transcript and/or STAT3 protein in a cell or a tissue. In some aspects, the term "inhibiting" refers to complete inhibition (100% inhibition or non-detectable level) of *STAT3* gene transcript or STAT3 protein. In other aspects, the term "inhibiting" refers to at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or at least 99% inhibition of *STAT3* gene transcript and/or STAT3 protein expression in a cell or a tissue.

[0073] As used herein, the term "extracellular vesicle" or "EV" refers to a cell-derived vesicle comprising a membrane that encloses an internal space. Extracellular vesicles comprise all membrane-bound vesicles (*e.g.*, exosomes, nanovesicles) that have a smaller diameter than the cell from which they are derived. In some aspects, extracellular vesicles range in diameter from 20 nm to 1000 nm, and can comprise various macromolecular payload either within the internal space (*i.e.*, lumen), displayed on the external surface of the extracellular vesicle, and/or spanning the membrane. In some aspects, the payload can comprise nucleic acids, proteins, carbohydrates, lipids, small molecules, and/or combinations thereof. In certain aspects, an extracellular vehicle comprises a scaffold moiety. By way of example and without limitation, extracellular vesicles include apoptotic bodies, fragments of cells, vesicles derived from cells by direct or indirect manipulation (*e.g.*, by serial extrusion or treatment with alkaline solutions), vesiculated organelles, and vesicles produced by living cells (*e.g.*, by direct plasma membrane budding or fusion of the late endosome with the plasma membrane). Extracellular vesicles can be derived from a living or dead organism, explanted tissues or organs, prokaryotic or eukaryotic cells, and/or cultured cells. In some aspects, the extracellular vesicles are produced by cells that express one or more transgene products.

[0074] As used herein, the term "exosome" refers to an extracellular vesicle with a diameter between 20-300 nm (*e.g.*, between 40-200 nm). Exosomes comprise a membrane that encloses an internal space (*i.e.*, lumen), and, in some aspects, can be generated from a cell (*e.g.*, producer cell) by direct plasma membrane budding or by fusion of the late endosome with the plasma membrane.

In certain aspects, an exosome comprises a scaffold moiety. As described *infra*, exosome can be derived from a producer cell, and isolated from the producer cell based on its size, density, biochemical parameters, or a combination thereof. In some aspects, the EVs, *e.g.*, exosomes, of the present disclosure are produced by cells that express one or more transgene products.

[0075] As used herein, the term "nanovesicle" refers to an extracellular vesicle with a diameter between 20-250 nm (*e.g.*, between 30-150 nm) and is generated from a cell (*e.g.*, producer cell) by direct or indirect manipulation such that the nanovesicle would not be produced by the cell without the manipulation. Appropriate manipulations of the cell to produce the nanovesicles include but are not limited to serial extrusion, treatment with alkaline solutions, sonication, or combinations thereof. In some aspects, production of nanovesicles can result in the destruction of the producer cell. In some aspects, population of nanovesicles described herein are substantially free of vesicles that are derived from cells by way of direct budding from the plasma membrane or fusion of the late endosome with the plasma membrane. In certain aspects, a nanovesicle comprises a scaffold moiety. Nanovesicles, once derived from a producer cell, can be isolated from the producer cell based on its size, density, biochemical parameters, or a combination thereof.

[0076] As used herein the term "surface-engineered EVs, *e.g.*, exosomes" (*e.g.*, Scaffold X-engineered EVs, *e.g.*, exosomes) refers to an EV, *e.g.*, exosome, with the membrane or the surface of the EV, *e.g.*, exosome, modified in its composition so that the surface of the engineered EV, *e.g.*, exosome, is different from that of the EV, *e.g.*, exosome, prior to the modification or of the naturally occurring EV, *e.g.*, exosome. The engineering can be on the surface of the EV, *e.g.*, exosome, or in the membrane of the EV, *e.g.*, exosome, so that the surface of the EV, *e.g.*, exosome, is changed. For example, the membrane is modified in its composition of a protein, a lipid, a small molecule, a carbohydrate, *etc.* The composition can be changed by a chemical, a physical, or a biological method or by being produced from a cell previously or concurrently modified by a chemical, a physical, or a biological method. Specifically, the composition can be changed by a genetic engineering or by being produced from a cell previously modified by genetic engineering. In some aspects, a surface-engineered EV, *e.g.*, exosome, comprises an exogenous protein (*i.e.*, a protein that the EV, *e.g.*, exosome, does not naturally express) or a fragment or variant thereof that can be exposed to the surface of the EV, *e.g.*, exosome, or can be an anchoring point (attachment) for a moiety exposed on the surface of the EV, *e.g.*, exosome. In other aspects, a surface-engineered EV, *e.g.*, exosome, comprises a higher expression (*e.g.*, higher number) of a natural exosome protein (*e.g.*, Scaffold X) or a fragment or variant thereof that can be exposed to the surface of the

EV, *e.g.*, exosome, or can be an anchoring point (attachment) for a moiety exposed on the surface of the EV, *e.g.*, exosome.

[0077] As used herein the term "lumen-engineered exosome" (*e.g.*, Scaffold Y-engineered exosome) refers to an EV, *e.g.*, exosome, with the membrane or the lumen of the EV, *e.g.*, exosome, modified in its composition so that the lumen of the engineered EV, *e.g.*, exosome, is different from that of the EV, *e.g.*, exosome, prior to the modification or of the naturally occurring EV, *e.g.*, exosome. The engineering can be directly in the lumen or in the membrane of the EV, *e.g.*, exosome so that the lumen of the EV, *e.g.*, exosome is changed. For example, the membrane is modified in its composition of a protein, a lipid, a small molecule, a carbohydrate, *etc.* so that the lumen of the EV, *e.g.*, exosome is modified. The composition can be changed by a chemical, a physical, or a biological method or by being produced from a cell previously modified by a chemical, a physical, or a biological method. Specifically, the composition can be changed by a genetic engineering or by being produced from a cell previously modified by genetic engineering. In some aspects, a lumen-engineered exosome comprises an exogenous protein (*i.e.*, a protein that the EV, *e.g.*, exosome does not naturally express) or a fragment or variant thereof that can be exposed in the lumen of the EV, *e.g.*, exosome or can be an anchoring point (attachment) for a moiety exposed on the inner layer of the EV, *e.g.*, exosome. In other aspects, a lumen-engineered EV, *e.g.*, exosome, comprises a higher expression of a natural exosome protein (*e.g.*, Scaffold X or Scaffold Y) or a fragment or variant thereof that can be exposed to the lumen of the exosome or can be an anchoring point (attachment) for a moiety exposed in the lumen of the exosome.

[0078] The term "modified," when used in the context of EVs, *e.g.*, exosomes described herein, refers to an alteration or engineering of an EV, *e.g.*, exosome and/or its producer cell, such that the modified EV, *e.g.*, exosome is different from a naturally-occurring EV, *e.g.*, exosome. In some aspects, a modified EV, *e.g.*, exosome described herein comprises a membrane that differs in composition of a protein, a lipid, a small molecular, a carbohydrate, *etc.* compared to the membrane of a naturally-occurring EV, *e.g.*, exosome (*e.g.*, membrane comprises higher density or number of natural exosome proteins and/or membrane comprises proteins that are not naturally found in exosomes (*e.g.*, an ASO). In certain aspects, such modifications to the membrane changes the exterior surface of the EV, *e.g.*, exosome (*e.g.*, surface-engineered EVs, *e.g.*, exosomes described herein). In certain aspects, such modifications to the membrane changes the lumen of the EV, *e.g.*, exosome (*e.g.*, lumen-engineered EVs, *e.g.*, exosomes described herein).

[0079] As used herein, the term "scaffold moiety" refers to a molecule that can be used to anchor a payload or any other compound of interest (*e.g.*, an ASO) to the EV, *e.g.*, exosome either

on the luminal surface or on the exterior surface of the EV, *e.g.*, exosome. In certain aspects, a scaffold moiety comprises a synthetic molecule. In some aspects, a scaffold moiety comprises a non-polypeptide moiety. In other aspects, a scaffold moiety comprises a lipid, carbohydrate, or protein that naturally exists in the EV, *e.g.*, exosome. In some aspects, a scaffold moiety comprises a lipid, carbohydrate, or protein that does not naturally exist in the EV, *e.g.*, exosome. In certain aspects, a scaffold moiety is Scaffold X. In some aspects, a scaffold moiety is Scaffold Y. In further aspects, a scaffold moiety comprises both Scaffold X and Scaffold Y. Non-limiting examples of other scaffold moieties that can be used with the present disclosure include: aminopeptidase N (CD13); Neprilysin, AKA membrane metalloendopeptidase (MME); ectonucleotide pyrophosphatase/phosphodiesterase family member 1 (ENPP1); Neuropilin-1 (NRP1); CD9, CD63, CD81, PDGFR, GPI anchor proteins, lactadherin (MFGE8), LAMP2, and LAMP2B.

[0080] As used herein, the term "Scaffold X" refers to exosome proteins that have recently been identified on the surface of exosomes. *See, e.g.*, U.S. Pat. No. 10,195,290, which is incorporated herein by reference in its entirety. Non-limiting examples of Scaffold X proteins include: prostaglandin F2 receptor negative regulator ("the PTGFRN protein"); basigin ("the BSG protein"); immunoglobulin superfamily member 2 ("the IGSF2 protein"); immunoglobulin superfamily member 3 ("the IGSF3 protein"); immunoglobulin superfamily member 8 ("the IGSF8 protein"); integrin beta-1 ("the ITGB1 protein"); integrin alpha-4 ("the ITGA4 protein"); 4F2 cell-surface antigen heavy chain ("the SLC3A2 protein"); a class of ATP transporter proteins ("the ATP1A1 protein," "the ATP1A2 protein," "the ATP1A3 protein," "the ATP1A4 protein," "the ATP1B3 protein," "the ATP2B1 protein," "the ATP2B2 protein," "the ATP2B3 protein," "the ATP2B protein"); and a functional fragment thereof. In some aspects, a Scaffold X protein can be a whole protein or a fragment thereof (*e.g.*, functional fragment, *e.g.*, the smallest fragment that is capable of anchoring another moiety on the exterior surface or on the luminal surface of the EV, *e.g.*, exosome). In some aspects, a Scaffold X can anchor a moiety (*e.g.*, an ASO) to the external surface or the luminal surface of the exosome.

[0081] As used herein, the term "Scaffold Y" refers to exosome proteins that were newly identified within the lumen of exosomes. *See, e.g.*, International Publ. No. WO/2019/099942, which is incorporated herein by reference in its entirety. Non-limiting examples of Scaffold Y proteins include: myristoylated alanine rich Protein Kinase C substrate ("the MARCKS protein"); myristoylated alanine rich Protein Kinase C substrate like 1 ("the MARCKSL1 protein"); and brain acid soluble protein 1 ("the BASP1 protein"). In some aspects, a Scaffold Y protein can be a whole protein or a fragment thereof (*e.g.*, functional fragment, *e.g.*, the smallest fragment that is capable

of anchoring a moiety to the luminal surface of the exosome). In some aspects, a Scaffold Y can anchor a moiety (*e.g.*, an ASO) to the luminal surface of the EV, *e.g.*, exosome. In some aspects, a Scaffold Y can anchor a moiety (*e.g.*, an ASO) to the exterior surface of the EV, *e.g.*, exosome.

[0082] As used herein, the term "fragment" of a protein (*e.g.*, therapeutic protein, Scaffold X, or Scaffold Y) refers to an amino acid sequence of a protein that is shorter than the naturally-occurring sequence, N- and/or C-terminally deleted or any part of the protein deleted in comparison to the naturally occurring protein. As used herein, the term "functional fragment" refers to a protein fragment that retains protein function. Accordingly, in some aspects, a functional fragment of a Scaffold X protein retains the ability to anchor a moiety on the luminal surface or on the exterior surface of the EV, *e.g.*, exosome. Similarly, in certain aspects, a functional fragment of a Scaffold Y protein retains the ability to anchor a moiety on the luminal surface or exterior surface of the EV, *e.g.*, exosome. Whether a fragment is a functional fragment can be assessed by any art known methods to determine the protein content of EVs, *e.g.*, exosomes including Western Blots, FACS analysis and fusions of the fragments with autofluorescent proteins like, *e.g.*, GFP. In certain aspects, a functional fragment of a Scaffold X protein retains at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 100% of the ability, *e.g.*, an ability to anchor a moiety, of the naturally occurring Scaffold X protein. In some aspects, a functional fragment of a Scaffold Y protein retains at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 100% of the ability, *e.g.*, an ability to anchor another molecule, of the naturally occurring Scaffold Y protein.

[0083] As used herein, the term "variant" of a molecule (*e.g.*, functional molecule, antigen, Scaffold X and/or Scaffold Y) refers to a molecule that shares certain structural and functional identities with another molecule upon comparison by a method known in the art. For example, a variant of a protein can include a substitution, insertion, deletion, frameshift or rearrangement in another protein.

[0084] In some aspects, a variant of a Scaffold X comprises a variant having at least about 70% identity to the full-length, mature PTGFRN, BSG, IGSF2, IGSF3, IGSF8, ITGB1, ITGA4, SLC3A2, or ATP transporter proteins or a fragment (*e.g.*, functional fragment) of the PTGFRN, BSG, IGSF2, IGSF3, IGSF8, ITGB1, ITGA4, SLC3A2, or ATP transporter proteins. In some aspects, variants or variants of fragments of PTGFRN share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with PTGFRN according to SEQ ID NO: 301 or with a functional fragment thereof. In some aspects variants or variants of fragments

of BSG share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with BSG according to SEQ ID NO: 303 or with a functional fragment thereof. In some aspects variants or variants of fragments of IGSF2 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with IGSF2 according to SEQ ID NO: 308 or with a functional fragment thereof. In some aspects variants or variants of fragments of IGSF3 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with IGSF3 according to SEQ ID NO: 309 or with a functional fragment thereof. In some aspects variants or variants of fragments of IGSF8 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with IGSF8 according to SEQ ID NO: 304 or with a functional fragment thereof. In some aspects variants or variants of fragments of ITGB1 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ITGB1 according to SEQ ID NO: 305 or with a functional fragment thereof. In some aspects variants or variants of fragments of ITGA4 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ITGA4 according to SEQ ID NO: 306 or with a functional fragment thereof. In some aspects variants or variants of fragments of SLC3A2 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with SLC3A2 according to SEQ ID NO: 307 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP1A1 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP1A1 according to SEQ ID NO: 310 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP1A2 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP1A2 according to SEQ ID NO: 311 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP1A3 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at

least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP1A3 according to SEQ ID NO: 312 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP1A4 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP1A4 according to SEQ ID NO: 313 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP1B3 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP1B3 according to SEQ ID NO: 314 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP2B1 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP2B1 according to SEQ ID NO: 315 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP2B2 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP2B2 according to SEQ ID NO: 316 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP2B3 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP2B3 according to SEQ ID NO: 317 or with a functional fragment thereof. In some aspects variants or variants of fragments of ATP2B4 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with ATP2B4 according to SEQ ID NO: 318 or with a functional fragment thereof. In some aspects, the variant or variant of a fragment of Scaffold X protein disclosed herein retains the ability to be specifically targeted to EVs, *e.g.*, exosomes. In some aspects, the Scaffold X includes one or more mutations, for example, conservative amino acid substitutions.

[0085] In some aspects, a variant of a Scaffold Y comprises a variant having at least 70% identity to MARCKS, MARCKSL1, BASP1, or a fragment of MARCKS, MARCKSL1, or BASP1. In some aspects variants or variants of fragments of MARCKS share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with MARCKS according to SEQ ID NO: 401 or with a functional fragment thereof. In some aspects variants or

variants of fragments of MARCKSL1 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with MARCKSL1 according to SEQ ID NO: 402 or with a functional fragment thereof. In some aspects variants or variants of fragments of BASP1 share at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity with BASP1 according to SEQ ID NO: 403 or with a functional fragment thereof. In some aspects, the variant or variant of a fragment of Scaffold Y protein retains the ability to be specifically targeted to the luminal surface of EVs, *e.g.*, exosomes. In some aspects, the Scaffold Y includes one or more mutations, *e.g.*, conservative amino acid substitutions.

[0086] A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, if an amino acid in a polypeptide is replaced with another amino acid from the same side chain family, the substitution is considered to be conservative. In another aspect, a string of amino acids can be conservatively replaced with a structurally similar string that differs in order and/or composition of side chain family members.

[0087] The term "percent sequence identity" or "percent identity" between two polynucleotide or polypeptide sequences refers to the number of identical matched positions shared by the sequences over a comparison window, taking into account additions or deletions (*i.e.*, gaps) that must be introduced for optimal alignment of the two sequences. A matched position is any position where an identical nucleotide or amino acid is presented in both the target and reference sequence. Gaps presented in the target sequence are not counted since gaps are not nucleotides or amino acids. Likewise, gaps presented in the reference sequence are not counted since target sequence nucleotides or amino acids are counted, not nucleotides or amino acids from the reference sequence.

[0088] The percentage of sequence identity is calculated by determining the number of positions at which the identical amino-acid residue or nucleic acid base occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total

number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. The comparison of sequences and determination of percent sequence identity between two sequences may be accomplished using readily available software both for online use and for download. Suitable software programs are available from various sources, and for alignment of both protein and nucleotide sequences. One suitable program to determine percent sequence identity is *bl2seq*, part of the BLAST suite of programs available from the U.S. government's National Center for Biotechnology Information BLAST web site (blast.ncbi.nlm.nih.gov). *Bl2seq* performs a comparison between two sequences using either the BLASTN or BLASTP algorithm. BLASTN is used to compare nucleic acid sequences, while BLASTP is used to compare amino acid sequences. Other suitable programs are, *e.g.*, *Needle*, *Stretcher*, *Water*, or *Matcher*, part of the EMBOSS suite of bioinformatics programs and also available from the European Bioinformatics Institute (EBI) at worldwideweb.ebi.ac.uk/Tools/psa.

[0089] Different regions within a single polynucleotide or polypeptide target sequence that aligns with a polynucleotide or polypeptide reference sequence can each have their own percent sequence identity. It is noted that the percent sequence identity value is rounded to the nearest tenth. For example, 80.11, 80.12, 80.13, and 80.14 are rounded down to 80.1, while 80.15, 80.16, 80.17, 80.18, and 80.19 are rounded up to 80.2. It also is noted that the length value will always be an integer.

[0090] One skilled in the art will appreciate that the generation of a sequence alignment for the calculation of a percent sequence identity is not limited to binary sequence-sequence comparisons exclusively driven by primary sequence data. Sequence alignments can be derived from multiple sequence alignments. One suitable program to generate multiple sequence alignments is *ClustalW2*, available from worldwideweb.clustal.org. Another suitable program is *MUSCLE*, available from worldwideweb.drive5.com/muscle/. *ClustalW2* and *MUSCLE* are alternatively available, *e.g.*, from the EBI.

[0091] It will also be appreciated that sequence alignments can be generated by integrating sequence data with data from heterogeneous sources such as structural data (*e.g.*, crystallographic protein structures), functional data (*e.g.*, location of mutations), or phylogenetic data. A suitable program that integrates heterogeneous data to generate a multiple sequence alignment is *T-Coffee*, available at worldwideweb.tcoffee.org, and alternatively available, *e.g.*, from the EBI. It will also be appreciated that the final alignment used to calculate percent sequence identity may be curated either automatically or manually.

[0092] The polynucleotide variants can contain alterations in the coding regions, non-coding regions, or both. In one aspect, the polynucleotide variants contain alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. In another aspect, nucleotide variants are produced by silent substitutions due to the degeneracy of the genetic code. In other aspects, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination. Polynucleotide variants can be produced for a variety of reasons, *e.g.*, to optimize codon expression for a particular host (change codons in the human mRNA to others, *e.g.*, a bacterial host such as *E. coli*).

[0093] Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present disclosure. Alternatively, non-naturally occurring variants can be produced by mutagenesis techniques or by direct synthesis.

[0094] Using known methods of protein engineering and recombinant DNA technology, variants can be generated to improve or alter the characteristics of the polypeptides. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. Ron *et al.*, *J. Biol. Chem.* 268: 2984-2988 (1993), incorporated herein by reference in its entirety, reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli *et al.*, *J. Biotechnology* 7:199-216 (1988), incorporated herein by reference in its entirety.)

[0095] Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (*J. Biol. Chem* 268:22105-22111 (1993), incorporated herein by reference in its entirety) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

[0096] As stated above, polypeptide variants include, *e.g.*, modified polypeptides. Modifications include, *e.g.*, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation (Mei *et al.*, *Blood* 116:270-79 (2010), which is incorporated herein by reference in its entirety), proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. In some aspects, Scaffold X and/or Scaffold Y is modified at any convenient location.

[0097] As used herein the term "linked to" or "conjugated to" are used interchangeably and refer to a covalent or non-covalent bond formed between a first moiety and a second moiety, *e.g.*, Scaffold X and an ASO, respectively, *e.g.*, a scaffold moiety expressed in or on the extracellular vesicle and an ASO, *e.g.*, Scaffold X (*e.g.*, a PTGFRN protein), respectively, in the luminal surface of or on the external surface of the extracellular vesicle.

[0098] The term "encapsulated", or grammatically different forms of the term (*e.g.*, encapsulation, or encapsulating) refers to a status or process of having a first moiety (*e.g.*, an ASO) inside a second moiety (*e.g.*, an EV, *e.g.*, exosome) without chemically or physically linking the two moieties. In some aspects, the term "encapsulated" can be used interchangeably with "in the lumen of." Non-limiting examples of encapsulating a first moiety (*e.g.*, an ASO) into a second moiety (*e.g.*, EVs, *e.g.*, exosomes) are disclosed elsewhere herein.

[0099] As used herein, the term "producer cell" refers to a cell used for generating an EV, *e.g.*, exosome. A producer cell can be a cell cultured *in vitro*, or a cell *in vivo*. A producer cell includes, but not limited to, a cell known to be effective in generating EVs, *e.g.*, exosomes, *e.g.*, HEK293 cells, Chinese hamster ovary (CHO) cells, mesenchymal stem cells (MSCs), BJ human foreskin fibroblast cells, fHDF fibroblast cells, AGE.HN[®] neuronal precursor cells, CAP[®] amniocyte cells, adipose mesenchymal stem cells, RPTEC/TERT1 cells. In certain aspects, a producer cell is not an antigen-presenting cell. In some aspects, a producer cell is not a dendritic cell, a B cell, a mast cell, a macrophage, a neutrophil, Kupffer-Browicz cell, cell derived from any of these cells, or any combination thereof. In some aspects, the EVs, *e.g.*, exosomes useful in the present disclosure do not carry an antigen on MHC class I or class II molecule exposed on the

surface of the EV, *e.g.*, exosome, but instead can carry an antigen in the lumen of the EV, *e.g.*, exosome or on the surface of the EV, *e.g.*, exosome by attachment to Scaffold X and/or Scaffold Y.

[0100] As used herein, the terms "isolate," "isolated," and "isolating" or "purify," "purified," and "purifying" as well as "extracted" and "extracting" are used interchangeably and refer to the state of a preparation (*e.g.*, a plurality of known or unknown amount and/or concentration) of desired EVs, that have undergone one or more processes of purification, *e.g.*, a selection or an enrichment of the desired EV preparation. In some aspects, isolating or purifying as used herein is the process of removing, partially removing (*e.g.*, a fraction) of the EVs from a sample containing producer cells. In some aspects, an isolated EV composition has no detectable undesired activity or, alternatively, the level or amount of the undesired activity is at or below an acceptable level or amount. In other aspects, an isolated EV composition has an amount and/or concentration of desired EVs at or above an acceptable amount and/or concentration. In other aspects, the isolated EV composition is enriched as compared to the starting material (*e.g.*, producer cell preparations) from which the composition is obtained. This enrichment can be by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, 99.999%, 99.9999%, or greater than 99.9999% as compared to the starting material. In some aspects, isolated EV preparations are substantially free of residual biological products. In some aspects, the isolated EV preparations are 100% free, 99% free, 98% free, 97% free, 96% free, 95% free, 94% free, 93% free, 92% free, 91% free, or 90% free of any contaminating biological matter. Residual biological products can include abiotic materials (including chemicals) or unwanted nucleic acids, proteins, lipids, or metabolites. Substantially free of residual biological products can also mean that the EV composition contains no detectable producer cells and that only EVs are detectable.

[0101] As used herein, the term "payload" refers to an agent that acts on a target (*e.g.*, a target cell) that is contacted with the EV. A non-limiting examples of payload that can be included on the EV, *e.g.*, exosome, is an ASO. Payloads that can be introduced into an EV, *e.g.*, exosome, and/or a producer cell include agents such as, nucleotides (*e.g.*, nucleotides comprising a detectable moiety or a toxin or that disrupt transcription), nucleic acids (*e.g.*, DNA or mRNA molecules that encode a polypeptide such as an enzyme, or RNA molecules that have regulatory function such as miRNA, dsDNA, lncRNA, and siRNA), amino acids (*e.g.*, amino acids comprising a detectable moiety or a toxin or that disrupt translation), polypeptides (*e.g.*, enzymes), lipids, carbohydrates, and small molecules (*e.g.*, small molecule drugs and toxins). In certain aspects, a payload

comprises an ASO. As used herein, the term "antibody" encompasses an immunoglobulin whether natural or partly or wholly synthetically produced, and fragments thereof. The term also covers any protein having a binding domain that is homologous to an immunoglobulin binding domain. "Antibody" further includes a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. As used herein, the term "antigen" refers to any agent that when introduced into a subject elicits an immune response (cellular or humoral) to itself. Use of the term antibody is meant to include whole antibodies, polyclonal, monoclonal and recombinant antibodies, fragments thereof, and further includes single-chain antibodies, humanized antibodies, murine antibodies, chimeric, mouse-human, mouse-primate, primate-human monoclonal antibodies, anti-idiotypic antibodies, antibody fragments, such as, *e.g.*, scFv, (scFv)₂, Fab, Fab', and F(ab')₂, F(ab1)₂, Fv, dAb, and Fd fragments, diabodies, and antibody-related polypeptides. Antibody includes bispecific antibodies and multispecific antibodies so long as they exhibit the desired biological activity or function.

[0102] The terms "individual," "subject," "host," and "patient," are used interchangeably herein and refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired, particularly humans. The compositions and methods described herein are applicable to both human therapy and veterinary applications. In some aspects, the subject is a mammal, and in other aspects the subject is a human. As used herein, a "mammalian subject" includes all mammals, including without limitation, humans, domestic animals (*e.g.*, dogs, cats and the like), farm animals (*e.g.*, cows, sheep, pigs, horses and the like) and laboratory animals (*e.g.*, monkey, rats, mice, rabbits, guinea pigs and the like).

[0103] The term "pharmaceutical composition" refers to a preparation which is in such form as to permit the biological activity of the active ingredient to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the composition would be administered. Such composition can be sterile.

[0104] As used herein, the term "substantially free" means that the sample comprising EVs, *e.g.*, exosomes, comprise less than 10% of macromolecules by mass/volume (m/v) percentage concentration. Some fractions may contain less than 0.001%, less than 0.01%, less than 0.05%, less than 0.1%, less than 0.2%, less than 0.3%, less than 0.4%, less than 0.5%, less than 0.6%, less than 0.7%, less than 0.8%, less than 0.9%, less than 1%, less than 2%, less than 3%, less than 4%, less than 5%, less than 6%, less than 7%, less than 8%, less than 9%, or less than 10% (m/v) of macromolecules.

[0105] As used herein, the term "macromolecule" means nucleic acids, contaminant proteins, lipids, carbohydrates, metabolites, or a combination thereof.

[0106] As used herein, the term "conventional exosome protein" means a protein previously known to be enriched in exosomes, including but is not limited to CD9, CD63, CD81, PDGFR, GPI anchor proteins, lactadherin (MFGE8), LAMP2, and LAMP2B, a fragment thereof, or a peptide that binds thereto.

[0107] "Administering," as used herein, means to give a composition comprising an EV, *e.g.*, exosome, disclosed herein to a subject via a pharmaceutically acceptable route. Routes of administration can be intravenous, *e.g.*, intravenous injection and intravenous infusion. Additional routes of administration include, *e.g.*, subcutaneous, intramuscular, oral, nasal, and pulmonary administration. EVs, *e.g.*, exosomes can be administered as part of a pharmaceutical composition comprising at least one excipient.

[0108] An "effective amount" of, *e.g.*, an ASO or an extracellular vesicle as disclosed herein, is an amount sufficient to carry out a specifically stated purpose. An "effective amount" can be determined empirically and in a routine manner, in relation to the stated purpose.

[0109] "Treat," "treatment," or "treating," as used herein refers to, *e.g.*, the reduction in severity of a disease or condition; the reduction in the duration of a disease course; the amelioration or elimination of one or more symptoms associated with a disease or condition; the provision of beneficial effects to a subject with a disease or condition, without necessarily curing the disease or condition. The term also includes prophylaxis or prevention of a disease or condition or its symptoms thereof. In one aspect, the "treating" or "treatment" includes inducing hematopoiesis in a subject in need thereof. In some aspects, the disease or condition is associated with a hematopoiesis or a deficiency thereof. In certain aspects, the disease or condition is a cancer. In some aspects, the treating enhances hematopoiesis in a subject having a cancer, wherein the enhanced hematopoiesis comprises increased proliferation and/or differentiation of one or more immune cell in the subject.

[0110] "Prevent" or "preventing," as used herein, refers to decreasing or reducing the occurrence or severity of a particular outcome. In some aspects, preventing an outcome is achieved through prophylactic treatment. In some aspects, an EV, *e.g.*, an exosome, comprising an ASO, described herein, is administered to a subject prophylactically. In some aspects, the subject is at risk of developing cancer. In some aspects, the subject is at risk of developing a hematopoietic disorder.

II. Antisense Oligonucleotides (ASOs)

[0111] The present disclosure employs antisense oligonucleotides (ASOs) for use in modulating the function of nucleic acid molecules encoding mammalian STAT3, such as the *STAT3* nucleic acid, *e.g.*, *STAT3* transcript, including *STAT3* pre-mRNA, and *STAT3* mRNA, or naturally occurring variants of such nucleic acid molecules encoding mammalian STAT3. The term "ASO" in the context of the present disclosure, refers to a molecule formed by covalent linkage of two or more nucleotides (*i.e.*, an oligonucleotide). The ASOs useful for the present invention are not naturally occurring and cannot be found in nature. In some aspects, the ASOs are chemically modified.

[0112] The ASO comprises a contiguous nucleotide sequence of from about 10 to about 50, *e.g.*, about 10 to about 30, such as 10–20, 14–20, 16–20, or 15–25, nucleotides in length. The terms "antisense ASO," "antisense oligonucleotide," and "oligomer" as used herein are interchangeable with the term "ASO." The ASOs useful for the present invention are not naturally occurring and cannot be found in nature. In some aspects, the ASOs are chemically modified.

[0113] A reference to a SEQ ID number includes a particular nucleobase sequence, but does not include any design or full chemical structure. Furthermore, any design shown associated with an ASO disclosed herein is not intended to be limiting, unless otherwise indicated. For example, when a claim (or this specification) refers to SEQ ID NO: 100, it includes the nucleotide sequence of SEQ ID NO: 100 only. The design of any ASO disclosed herein can be written as SEQ ID NO: 100, wherein each of the first nucleotide, the second nucleotide, the third nucleotide, the sixth nucleotide, the tenth nucleotide, the thirteenth nucleotide, the fourteenth nucleotide, and the fifteenth nucleotide from the 5' end is a modified nucleotide, *e.g.*, LNA or 5MdC, and each of the other nucleotides is a non-modified nucleotide (*e.g.*, DNA).

[0114] In various aspects, the ASO of the disclosure does not comprise RNA (units). In some aspects, the ASO comprises one or more DNA units. In one aspect, the ASO according to the disclosure is a linear molecule or is synthesized as a linear molecule. In some aspects, the ASO is a single stranded molecule, and does not comprise short regions of, for example, at least 3, 4 or 5 contiguous nucleotides, which are complementary to equivalent regions within the same ASO (*i.e.* duplexes) - in this regard, the ASO is not (essentially) double stranded. In some aspects, the ASO is essentially not double stranded. In some aspects, the ASO is not a siRNA. In various aspects, the ASO of the disclosure can consist entirely of the contiguous nucleotide region. Thus, in some aspects the ASO is not substantially self-complementary.

[0115] In other aspects, the present disclosure includes fragments of ASOs. For example, the disclosure includes at least one nucleotide, at least two contiguous nucleotides, at least three contiguous nucleotides, at least four contiguous nucleotides, at least five contiguous nucleotides, at least six contiguous nucleotides, at least seven contiguous nucleotides, at least eight contiguous nucleotides, or at least nine contiguous nucleotides of the ASOs disclosed herein. Fragments of any of the sequences disclosed herein are contemplated as part of the disclosure.

[0116] In some aspects, the ASOs for the present disclosure include a phosphorodiamidate Morpholino oligomer (PMO) or a peptide-conjugated phosphorodiamidate morpholino oligomer (PPMO).

II.A. The Target (STAT3)

[0117] Suitably the ASOs of the disclosure are capable of down-regulating (*e.g.*, reducing or removing) expression of the *STAT3* mRNA or protein. In this regard, the ASO of the disclosure can affect indirect inhibition of STAT3 protein through the reduction in *STAT3* mRNA levels, typically in a mammalian cell, such as a human cell, such as a tumor cell. In particular, the present disclosure is directed to ASOs that target one or more regions of the *STAT3* pre-mRNA (*e.g.*, intron regions, exon regions, and/or exon-intron junction regions). Unless indicated otherwise, the term "STAT3," as used herein, can refer to STAT3 from one or more species (*e.g.*, humans, non-human primates, dogs, cats, guinea pigs, rabbits, rats, mice, horses, cattle, and bears).

[0118] Signal Transducer and Activator of Transcription 3 (STAT3) is a signal transducer and activator of transcription that transmits signals from cell surface receptors to the nucleus. STAT3 is frequently hyperactivated in many human cancers. High levels of activated STAT3 are often found to correlate with poor prognosis in human breast cancer patients in terms of metastatic progression (Ranger et al. 2009). Therefore, STAT3 represents a promising target for the prevention and treatment of both ER-positive and ER-negative breast cancer and also other cancers such as pancreatic, head/neck, prostate and lung cancers. However, current strategies of inhibiting STAT3 activity by means of blocking peptides, blockade of translocation, disrupting dimerization, or modulating phosphatase activity have not sufficiently inhibited STAT3 activity in cancer cells. Under normal conditions, STAT3 activation is transient and tightly regulated. Upon cellular stimulation by ligands such as growth factors or cytokines, STAT3 becomes phosphorylated on a critical tyrosine residue (Tyr705) and consequently induces STAT3 dimerization through two reciprocal phosphotyrosine (pTyr)-Src-homology 2 (SH2) interactions. The STAT3 dimers then translocate to the nucleus and bind to specific DNA-response elements in the promoters of target

genes thereby activating transcription. The association of aberrant STAT3 activation with many types of human malignancies and solid tumors has made STAT3 an attractive molecular target for the development of novel cancer therapeutics.

[0119] STAT3 is often found to be constitutively activated in tumor cells and contribute to tumor progression through the modulation of target genes, such as antiapoptotic genes Bcl-xL, Bcl-2, Mcl-1 and survivin along with genes driving cell cycle progression, c-Myc and cyclin-D1. Aberrant activation of STAT3 is frequent in almost all blood malignancies and solid tumors, including lymphoma and leukemia, breast, prostate, lung head and neck, brain and colon cancer, which have made STAT3 an attractive target for the development of anticancer agents. The specificity of STAT activation is due to specific cytokines, i.e. each STAT is responsive to a small number of specific cytokines. Other non-cytokine signaling molecules, such as growth factors, have also been found to activate STATs. Binding of these factors to a cell surface receptor associated with protein tyrosine kinase also results in phosphorylation of STAT. STAT3 in particular has been found to be responsive to interleukin-6 (IL-6) as well as epidermal growth factor (EGF) (Darnell, Jr., J. E., et al., Science, 1994, 264, 1415-1421). Evidence exists suggesting that STAT3 may be regulated by the MAPK pathway. ERK2 induces serine phosphorylation and also associates with STAT3 (Jain, N., et al., Oncogene, 1998, 17, 3157-3167). STAT3 is expressed in most cell types and is also involved in the induction of expression of genes involved in response to tissue injury and inflammation. Aberrant expression of or constitutive expression of STAT3 is associated with a number of disease processes. STAT3 has been found to be constitutively active in myeloma tumor cells, both in culture and in bone marrow mononuclear cells from patients with multiple myeloma. These cells are resistant to Fas-mediated apoptosis and express high levels of Bcl-xL. The STAT3 SH2 domain is required for promoting dimerization. One of the limitations of targeting protein dimerization is the practicality of targeting the dimer interface, which is challenging owing to the planarity of the large surface area.

[0120] Signal transducer and activator of transcription 3 (STAT3) is known in the art by various names. Such names include: DNA-binding protein APRF, and acute-phase response factor. The mRNA encoding human STAT3 can be found at Genbank Accession Number NM_003150.3, and is represented by the sequence (SEQ ID NO: 3):

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GGTTTCCGGAGCTGCGGCGGCGCAGACTGGGAGGGGGAGCCGGGGTTCCGACGTGCGAG
CCGAGGGAACAAGCCCCAACCGGATCCTGGACAGGCACCCCGGCTTGGCGCTGTCTCTCC
CCCTCGGCTCGGAGAGGCCCTTCGGCCTGAGGGAGCCTCGCCGCCCGTCCCCGGCACACG
CGCAGCCCCGGCCTCTCGGCCTCTGCCGGAGAAACAGGATGGCCCCAATGGAATCAGCTAC
AGCAGCTTGACACACGGTACCTGGAGCAGCTCCATCAGCTCTACAGTGACAGCTTCCCAA
TGGAGCTGCGGCAGTTTCTGGCCCCTTGGATTGAGAGTCAAGATTGGGCATATGCGGCCA
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GCAAAGAATCACATGCCACTTTGGTGTTCATAATCTCCTGGGAGAGATTGACCAGCAGT
ATAGCCGCTTCCTGCAAGAGTCAATGTTCTCTATCAGCACAATCTACGAAGAATCAAGC
AGTTTTCTTCAGAGCAGGTATCTTGAGAAGCCAATGGAGATTGCCCGGATTGTGGCCCCGT
GCCTGTGGGAAGAATCACGCCTTCTACAGACTGCAGCCACTGCGGCCAGCAAGGGGGCC
AGGCCAACACCCACAGCAGCCGTGGTGACGGAGAAGCAGCAGATGCTGGAGCAGCACC
TTCAGGATGTCCGGAAGAGAGTGCAGGATCTAGAACAGAAAATGAAAGTGGTAGAGAATC
TCCAGGATGACTTTGATTTCAACTATAAAACCTCAAGAGTCAAGGAGACATGCAAGATC
TGAATGGAACAACACAGTCAGTGACCAGGCAGAAGATGCAGCAGCTGGAACAGATGCTCA
CTGCGCTGGACCAGATGCGGAGAAGCATCGTGAGTGAGCTGGCGGGCTTTTGTACCGA
TGGAGTACGTGCAGAAAACCTCTCACGGACGAGGAGCTGGCTGACTGGAAGAGGCGGCAAC
AGATTGCCTGCATTGGAGGCCCCGCCAACATCTGCCTAGATCGGCTAGAAAACCTGGATAA
CGTCATTAGCAGAATCTCAACTTCAGACCCGTCAACAAATTAAGAAACTGGAGGAGTTGC
AGCAAAAAGTTTTCTACAAAGGGGACCCCATTTGTACAGCACCGGCCGATGCTGGAGGAGA
GAATCGTGGAGCTGTTTAGAAAACCTTAATGAAAAGTGCCCTTTGTGGTGGAGCGGCAGCCCT
GCATGCCCATGCATCCTGACCGGCCCCCTCGTCATCAAGACCGGCGTCCAGTTCACTACTA
AAGTCAGTTGCTGGTCAAATTCCTGAGTTGAATTATCAGCTTAAATTAAGTGTGCA
TTGACAAAGACTCTGGGGACGTTGCAGCTCTCAGAGGATCCCGGAAATTTAACATTCTGG
GCACAAACACAAAAGTGATGAACATGGAAGAATCCAACAACGGCAGCCTCTCTGCAGAAT
TCAAACACTTGACCCTGAGGGAGCAGAGATGTGGGAATGGGGGCGGAGCCAATTGTGATG
CTTCCCTGATTGTGACTGAGGAGCTGCACCTGATCACCTTTGAGACCGAGGTGTATCACC
AAGGCCTCAAGATTGACCTAGAGACCCACTCCTTGCCAGTTGTGGTGTATCTCCAACATCT
GTCAGATGCCAAATGCCTGGGCGTCCATCCTGTGGTACAACATGCTGACCAACAATCCCA
AGAATGTAACTTTTTTACCAAGCCCCCAATTGGAACCTGGGATCAAGTGGCCGAGGTCC
TGAGCTGGCAGTTCTCCTCCACCACCAAGCAGGACTGAGCATCGAGCAGCTGACTACAC
TGGCAGAGAAAACCTTTGGGACCTGGTGTGAATTATTCAGGGTGTGAGTACATGGGCTA
AATTTTGCAAAGAAAACATGGCTGGCAAGGGCTTCTCCTTCTGGGTCTGGCTGGACAATA
TCATTGACCTTGTGAAAAGTACATCCTGGCCCTTTGGAACGAAGGTACATCATGGGCT
TTATCAGTAAGGAGCGGGAGCGGGCCATCTTGAGCACTAAGCCTCCAGGCACCTTCTGCT
TAAGATTTCAGTGAAAGCAGCAAAGAAGGAGGCGTCACTTTCACTTTGGGTGGAGAAGGACA
TCAGCGGTAAAGACCAGATCCAGTCCGTGGAACCATACACAAAGCAGCAGCTGAACAACA
TGAGCTGGCTGAAATCATCATGGGCTATAAGATCATGGATGCTACCAATATCCTGGTGT
CTCCACTGGTCTATCTCTATCCTGACATTCCCAAGGAGGAGGCATTTCGAAAAGTATTGTC
GGCCAGAGAGCCAGGAGCATCCTGAAGCTGACCCAGGCGCTGCCCCATACCTGAAGACCA
AGTTTATCTGTGTGACACCAACGACCTGCAGCAATACCATTGACCTGCCGATGTCCCCC
GCACCTTAGATTCAATTGATGCAGTTTGGAAATAATGGTGAAGGTGCTGAACCTCAGCAG
GAGGGCAGTTTGAGTCCCTCACCTTTGACATGGAGTTGACCTCGGAGTGCGCTACCTCCC
CCATGTGAGGAGCTGAGAACGGAAGCTGCAGAAAGATACGACTGAGGCGCCTACCTGCAT
TCTGCCACCCCTCACACAGCCAAACCCAGATCATCTGAAACTACTAATTTGTGGTTCC
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GAGAAATGAGTGAATGTGGGTGATCTGCTTTTATCTAAATGCAAATAAGGATGTGTTCTC
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CCACAGGCCACCTATAGCTACATACTCCTGGCATTGCACTTTTTAACCTTGCTGACATCC
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TTAAAGGGCAAAAAACACTGTATCAGCATAGCCTTTCTGTATTTAAGAAACTTAAGCAGC
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GTCAGGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAGTACA
AAAAATTAGCTGGGTGTGGTGGTGGGCGCCTGTAGTCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATCGCTTGAACCTGAGAGGCGGAGGTTGCAGTGAGCCAAAATTGCACCACTGCA
CACTGCACTCCATCCTGGGCGACAGTCTGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAA
AGAAACTTCAGTTAACAGCCTCCTTGGTGCTTTAAGCATTGAGCTTCTTCAGGCTGGTA
ATTTATATAATCCCTGAAACGGGCTTCAGGTCAAACCCCTAAGACATCTGAAGCTGCAAC
CTGGCCTTTGGTGTGAAATAGGAAGGTTTAAGGAGAATCTAAGCATTTTAGACTTTTTT
TTATAAATAGACTTATTTTTCTTTGTAATGTATTGGCCTTTTAGTGAGTAAGGCTGGGCA
GAGGGTGTCTTACAACCTTGACTCCCTTTCTCCCTGGACTTGATCTGCTGTTTCAGAGGCT
AGGTTGTTTTCTGTGGGTGCCTTATCAGGGCTGGGATACTTCTGATTCTGGCTTCTTCTCT
GCCCCACCCCTCCCGACCCAGTCCCCCTGATCCTGCTAGAGGCATGTCTCCTTGCGTGTCT
TAAAGGTCCCTCATCCTGTTTGTGTTTAGGAATCCTGGTCTCAGGACCTCATGGAAGAAGA

GGGGGAGAGAGTTACAGGTTGGACATGATGCACACTATGGGGCCCCAGCGACGTGTCTGG
 TTGAGCTCAGGGAATATGGTTCTTAGCCAGTTTCTTGGTGATATCCAGTGGCACTTGTA
 TGGCGTCTTCATTAGTTTATGCAGGGCAAAGGCTTACTGATAAACTTGAGTCTGCCCTC
 GTATGAGGGTGTATACCTGGCCTCCCTCTGAGGCTGGTGA CTCTCCCTGCTGGGGCCCC
 ACAGGTGAGGCAGAACAGCTAGAGGGCCTCCCCGCCTGCCCGCCTTGGCTGGCTAGCTCG
 CCTCTCCTGTGCGTATGGGAACACCTAGCACGTGCTGGATGGGCTGCCTCTGACTCAGAG
 GCATGGCCGGATTTGGCAACTCAAACACCTTGCCTCAGCTGATCAGAGTTTCTGTGGA
 ATTCTGTTTGTAAATCAAATTAGCTGGTCTCTGAATTAAGGGGGAGACGACCTTCTCTA
 AGATGAACAGGGTTTCGCCCCAGTCTCTCTGGAGACAGTTGATGTGTCTATGCAGAGC
 TCTTACTTCTCCAGCAACACTCTTCAGTACATAATAAGCTTAACTGATAAACAGAATATT
 TAGAAAGGTGAGACTTGGGCTTACCATTGGGTTTAAATCATAGGGACCTAGGGCGAGGGT
 TCAGGGCTTCTCTGGAGCAGATATTGTCAAGTTCATGGCCTTAGGTAGCATGTATCTGGT
 CTTAACTCTGATTGTAGCAAAAGTTCTGAGAGGAGCTGAGCCCTGTTGTGGCCCATTA
 GAACAGGGTCTCAGGCCCTGCCCGCTTCTGTCCACTGCCCCCTCCCCATCCCCAGCCC
 AGCCGAGGGAATCCCGTGGGTTGCTTACCTACCTATAAGGTGGTTTATAAGCTGCTGTCC
 TGGCCACTGCATTCAAATCCAATGTGTACTTTCATAGTGTAAAAATTTATATTATTGTGA
 GGTTTTTTGTCTTTTTTTTTTTTTTTTTTTTTTTTGGTATATTGCTGTATCTACTTTAACTT
 CCAGAAATAAACGTTATATAGGAACCGTAAAAA

[0121] The STAT3 protein sequence can be found at UniProt ID: P40763, and is represented by the sequence (SEQ ID NO: 2):

MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMIARIVARCLWEESRLLQTAA
 TAAQQGGQANHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDDFNYKTLK
 SQGDMQDLNGNNSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEEL
 ADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYPKQDPIVQ
 HRPMLERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNY
 QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
 GGRANCASLIVTEELHLITFETEVYHQLKIDLETHSLPVVVISNICQMPNAWASILWY
 NMLTNNPKNVNFFTTPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTLAELKLLGPGVNYS
 GCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST
 KPPGTFLRRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQLNNMSFAEIMGYKIM
 DATNILVSPPLVLYPDIPKBEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPPTCSN
 TIDLPMSPRTLDSLMQFGNNGEGAEPSSAGGQFESLTFDMELTSECATSPM

[0122] Natural variants of the human *STAT3* gene product are known. For example, natural variants of human STAT3 protein can contain one or more amino acid substitutions selected from: R382L, R382Q, OR R382W, and any combinations thereof. Additional variants of human STAT3 protein resulting from alternative splicing are also known in the art, such as: R382W, F384L, F384S, T389I, N395Y, R423Q, N425Y, H437Y, Del-463, S611N, F621V, T622I, V637L, V637M, Del-644, Y657C, P330S, K392R, N646K, K658N, Del-701, or T716M. Therefore, the ASOs of the present disclosure can be designed to reduce or inhibit expression of the natural variants of the STAT3 protein.

[0123] SEQ ID NO: 1 is identical to a *STAT3* pre-mRNA sequence except that nucleotide "t" in SEQ ID NO: 1 is shown as "u" in pre-mRNA. In certain aspects, the "target nucleic acid"

comprises an intron of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, and RNA nucleic acids derived therefrom, *e.g.*, pre-mRNA. In other aspects, the target nucleic acid comprises an exon region of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, and RNA nucleic acids derived therefrom, *e.g.*, pre-mRNA. In yet other aspects, the target nucleic acid comprises an exon-intron junction of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, and RNA nucleic acids derived therefrom, *e.g.*, pre-mRNA. In some aspects, for example when used in research or diagnostics the "target nucleic acid" can be a cDNA or a synthetic oligonucleotide derived from the above DNA or RNA nucleic acid targets. The human STAT3 protein sequence encoded by the *STAT3* pre-mRNA is shown as SEQ ID NO: 2. In other aspects, the target nucleic acid comprises an untranslated region of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, *e.g.*, 5' UTR, 3' UTR, or both.

[0124] In yet other aspects, the target nucleic acid comprises an exon-intron junction of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, and RNA nucleic acids derived therefrom, *e.g.*, pre-mRNA. In some aspects, for example when used in research or diagnostics the "target nucleic acid" can be a cDNA or a synthetic oligonucleotide derived from the above DNA or RNA nucleic acid targets. The human STAT3 protein sequence encoded by the *STAT3* pre-mRNA is shown as SEQ ID NO: 3. In other aspects, the target nucleic acid comprises an untranslated region of a STAT3 protein-encoding nucleic acids or naturally occurring variants thereof, *e.g.*, 5' UTR, 3' UTR, or both.

[0125] In some aspects, an ASO of the disclosure hybridizes to a region within the introns of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In certain aspects, an ASO of the disclosure hybridizes to a region within the exons of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In other aspects, an ASO of the disclosure hybridizes to a region within the exon-intron junction of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In some aspects, an ASO of the disclosure hybridizes to a region within a *STAT3* transcript (*e.g.*, an intron, exon, or exon-intron junction), *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3, wherein the ASO has a design according to formula: 5' A-B-C 3' as described elsewhere herein.

[0126] In some aspects, the ASO targets a mRNA encoding a particular isoform of STAT3 protein (*e.g.*, Isoform 1). In some aspects, the ASO targets all isoforms of STAT3 protein. In other aspects, the ASO targets two isoforms (*e.g.*, Isoform 1 (UniProt ID: P40763-1) and Isoform 2 (SEQ ID NO: 7) (UniProt ID: P40763-2), Isoform 2 and Isoform 3 (SEQ ID NO: 8) (UniProt ID: P40763-3) of STAT3 protein.

[0127] In some aspects, an ASO of the disclosure hybridizes to a region within the introns of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In certain aspects, an ASO of the disclosure hybridizes to a region within the exons of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In other aspects, an ASO of the disclosure hybridizes to a region within the exon-intron junction of a *STAT3* transcript, *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3. In some aspects, an ASO of the disclosure hybridizes to a region within a *STAT3* transcript (*e.g.*, an intron, exon, or exon-intron junction), *e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3, wherein the ASO has a design according to formula: 5' A-B-C 3' as described elsewhere herein.

[0128] In some aspects, the ASO comprises a contiguous nucleotide sequence that hybridizes to a nucleic acid sequence, or a region within the sequence, of a *STAT3* transcript ("target region"), wherein the nucleic acid sequence corresponds to (i) nucleotides 251 – 645 of SEQ ID NO: 3; (ii) nucleotides 742-1231 of SEQ ID NO: 3; (iii) nucleotides 1131 - 1604 of SEQ ID NO: 3; (iv) nucleotides 1621 – 2235 of SEQ ID NO: 3; (v) 2162 – 2676 of SEQ ID NO: 3 and wherein, optionally, the ASO has one of the designs described herein (*e.g.*, Section II.G) or a chemical structure shown elsewhere herein.

[0129] In some aspects, the ASO comprises a contiguous nucleotide sequence that hybridizes to a nucleic acid sequence, or a region within the sequence, of a *STAT3* transcript ("target region"), wherein the nucleic acid sequence corresponds to (i) nucleotides 301 - 595 of SEQ ID NO: 3; (ii) nucleotides 792 - 1181 of SEQ ID NO: 3; (iii) nucleotides 1181 - 1554 of SEQ ID NO: 3; (iv) nucleotides 1671 - 2185 of SEQ ID NO: 3; (v) 2212 - 2626 of SEQ ID NO: 3 and wherein, optionally, the ASO has one of the designs described herein (*e.g.*, Section II.G) or a chemical structure shown elsewhere herein.

[0130] In some aspects, the ASO comprises a contiguous nucleotide sequence that hybridizes to a nucleic acid sequence, or a region within the sequence, of a *STAT3* transcript ("target region"), wherein the nucleic acid sequence corresponds to (i) nucleotides 341 - 555 of SEQ ID NO: 3; (ii) nucleotides 832 - 1141 of SEQ ID NO: 3; (iii) nucleotides 1221 - 1514 of SEQ ID NO: 3; (iv) nucleotides 1711 - 2145 of SEQ ID NO: 3; or (v) 2252 - 2586 of SEQ ID NO: 3 and wherein, optionally, the ASO has one of the designs described herein (*e.g.*, Section II.G) or a chemical structure shown elsewhere herein.

[0131] In some aspects, the ASO comprises a contiguous nucleotide sequence that hybridizes to a nucleic acid sequence, or a region within the sequence, of a *STAT3* transcript ("target region"), wherein the nucleic acid sequence corresponds to (i) nucleotides 351 - 545 of

SEQ ID NO: 3; (ii) nucleotides 842 - 1131 of SEQ ID NO: 3; (iii) nucleotides 1231 - 1504 of SEQ ID NO: 3; (iv) nucleotides 1721 - 2135 of SEQ ID NO: 3; or (v) 2262 - 2576 of SEQ ID NO: 3.

[0132] In some aspects, the target region corresponds to nucleotides 2559-2576 of SEQ ID NO: 3 (e.g., ASO-STAT3-2559; SEQ ID NO: 100). In some aspects, the target region corresponds to nucleotides 2556-2576 of SEQ ID NO: 3 (e.g., ASO-STAT3-2556; SEQ ID NO: 101). In some aspects, the target region corresponds to nucleotides 2557-2577 of SEQ ID NO: 3 (e.g., ASO-STAT3-2557; SEQ ID NO: 102). In some aspects, the target region corresponds to nucleotides 1046-1061 of SEQ ID NO: 3 (e.g., ASO-STAT3-1046; SEQ ID NO: 103). In some aspects, the target region corresponds to nucleotides 351-371 of SEQ ID NO: 3 (e.g., ASO-STAT3-351; SEQ ID NO: 104). In some aspects, the target region corresponds to nucleotides 450-470 of SEQ ID NO: 3 (e.g., ASO-STAT3-450; SEQ ID NO: 105). In some aspects, the target region corresponds to nucleotides 2558-2575 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 106). In some aspects, the target region corresponds to nucleotides 2558-2578 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 107). In some aspects, the target region corresponds to nucleotides 865-885 of SEQ ID NO: 3 (e.g., ASO-STAT3-865; SEQ ID NO: 108). In some aspects, the target region corresponds to nucleotides 894-910 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 109). In some aspects, the target region corresponds to nucleotides 1778-1798 of SEQ ID NO: 3 (e.g., ASO-STAT3-1778; SEQ ID NO: 110). In some aspects, the target region corresponds to nucleotides 2558-2574 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 111). In some aspects, the target region corresponds to nucleotides 1482-1498 of SEQ ID NO: 3 (e.g., ASO-STAT3-1482; SEQ ID NO: 112). In some aspects, the target region corresponds to nucleotides 892-912 of SEQ ID NO: 3 (e.g., ASO-STAT3-892; SEQ ID NO: 113). In some aspects, the target region corresponds to nucleotides 2262-2282 of SEQ ID NO: 3 (e.g., ASO-STAT3-2262; SEQ ID NO: 114). In some aspects, the target region corresponds to nucleotides 2267-2282 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 115). In some aspects, the target region corresponds to nucleotides 411-431 of SEQ ID NO: 3 (e.g., ASO-STAT3-411; SEQ ID NO: 116). In some aspects, the target region corresponds to nucleotides 2267-2284 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 117). In some aspects, the target region corresponds to nucleotides 896-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-896; SEQ ID NO: 118). In some aspects, the target region corresponds to nucleotides 2555-2575 of SEQ ID NO: 3 (e.g., ASO-STAT3-2555; SEQ ID NO: 119). In some aspects, the target region corresponds to nucleotides 525-545 of SEQ ID NO: 3 (e.g., ASO-STAT3-525; SEQ ID NO: 120). In some aspects, the target region corresponds to nucleotides 1766-1786 of SEQ ID NO: 3 (e.g., ASO-STAT3-1766; SEQ ID NO: 121). In some aspects, the

target region corresponds to nucleotides 1114-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1114; SEQ ID NO: 122). In some aspects, the target region corresponds to nucleotides 2557-2574 of SEQ ID NO: 3 (e.g., ASO-STAT3-2557; SEQ ID NO: 123). In some aspects, the target region corresponds to nucleotides 995-1015 of SEQ ID NO: 3 (e.g., ASO-STAT3-995; SEQ ID NO: 124). In some aspects, the target region corresponds to nucleotides 2263-2283 of SEQ ID NO: 3 (e.g., ASO-STAT3-2263; SEQ ID NO: 125). In some aspects, the target region corresponds to nucleotides 511-531 of SEQ ID NO: 3 (e.g., ASO-STAT3-511; SEQ ID NO: 126). In some aspects, the target region corresponds to nucleotides 511-527 of SEQ ID NO: 3 (e.g., ASO-STAT3-511; SEQ ID NO: 127). In some aspects, the target region corresponds to nucleotides 1043-1063 of SEQ ID NO: 3 (e.g., ASO-STAT3-1043; SEQ ID NO: 128). In some aspects, the target region corresponds to nucleotides 1780-1800 of SEQ ID NO: 3 (e.g., ASO-STAT3-1780; SEQ ID NO: 129). In some aspects, the target region corresponds to nucleotides 458-478 of SEQ ID NO: 3 (e.g., ASO-STAT3-458; SEQ ID NO: 130). In some aspects, the target region corresponds to nucleotides 894-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 131). In some aspects, the target region corresponds to nucleotides 1779-1799 of SEQ ID NO: 3 (e.g., ASO-STAT3-1779; SEQ ID NO: 132). In some aspects, the target region corresponds to nucleotides 2274-2294 of SEQ ID NO: 3 (e.g., ASO-STAT3-2274; SEQ ID NO: 133). In some aspects, the target region corresponds to nucleotides 1039-1059 of SEQ ID NO: 3 (e.g., ASO-STAT3-1039; SEQ ID NO: 134). In some aspects, the target region corresponds to nucleotides 1238-1258 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 135). In some aspects, the target region corresponds to nucleotides 1239-1259 of SEQ ID NO: 3 (e.g., ASO-STAT3-1239; SEQ ID NO: 136). In some aspects, the target region corresponds to nucleotides 516-536 of SEQ ID NO: 3 (e.g., ASO-STAT3-516; SEQ ID NO: 137). In some aspects, the target region corresponds to nucleotides 1238-1254 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 138). In some aspects, the target region corresponds to nucleotides 1034-1054 of SEQ ID NO: 3 (e.g., ASO-STAT3-1034; SEQ ID NO: 139). In some aspects, the target region corresponds to nucleotides 1239-1254 of SEQ ID NO: 3 (e.g., ASO-STAT3-1239; SEQ ID NO: 140). In some aspects, the target region corresponds to nucleotides 1113-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1113; SEQ ID NO: 141). In some aspects, the target region corresponds to nucleotides 1484-1504 of SEQ ID NO: 3 (e.g., ASO-STAT3-1484; SEQ ID NO: 142). In some aspects, the target region corresponds to nucleotides 2556-2571 of SEQ ID NO: 3 (e.g., ASO-STAT3-2556; SEQ ID NO: 143). In some aspects, the target region corresponds to nucleotides 461-481 of SEQ ID NO: 3 (e.g., ASO-STAT3-461; SEQ ID NO: 144). In some aspects, the target region corresponds to nucleotides 2273-2293 of SEQ ID NO: 3 (e.g.,

ASO-STAT3-2273; SEQ ID NO: 145). In some aspects, the target region corresponds to nucleotides 1783-1803 of SEQ ID NO: 3 (e.g., ASO-STAT3-1783; SEQ ID NO: 146). In some aspects, the target region corresponds to nucleotides 891-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-891; SEQ ID NO: 147). In some aspects, the target region corresponds to nucleotides 510-530 of SEQ ID NO: 3 (e.g., ASO-STAT3-510; SEQ ID NO: 148). In some aspects, the target region corresponds to nucleotides 2115-2135 of SEQ ID NO: 3 (e.g., ASO-STAT3-2115; SEQ ID NO: 149). In some aspects, the target region corresponds to nucleotides 1482-1502 of SEQ ID NO: 3 (e.g., ASO-STAT3-1482; SEQ ID NO: 150). In some aspects, the target region corresponds to nucleotides 986-1006 of SEQ ID NO: 3 (e.g., ASO-STAT3-986; SEQ ID NO: 151). In some aspects, the target region corresponds to nucleotides 893-913 of SEQ ID NO: 3 (e.g., ASO-STAT3-893; SEQ ID NO: 152). In some aspects, the target region corresponds to nucleotides 1237-1252 of SEQ ID NO: 3 (e.g., ASO-STAT3-1237; SEQ ID NO: 153). In some aspects, the target region corresponds to nucleotides 1111-1131 of SEQ ID NO: 3 (e.g., ASO-STAT3-1111; SEQ ID NO: 154). In some aspects, the target region corresponds to nucleotides 1236-1252 of SEQ ID NO: 3 (e.g., ASO-STAT3-1236; SEQ ID NO: 155). In some aspects, the target region corresponds to nucleotides 2557-2572 of SEQ ID NO: 3 (e.g., ASO-STAT3-2557; SEQ ID NO: 156). In some aspects, the target region corresponds to nucleotides 2264-2284 of SEQ ID NO: 3 (e.g., ASO-STAT3-2264; SEQ ID NO: 157). In some aspects, the target region corresponds to nucleotides 1234-1249 of SEQ ID NO: 3 (e.g., ASO-STAT3-1234; SEQ ID NO: 158). In some aspects, the target region corresponds to nucleotides 1241-1258 of SEQ ID NO: 3 (e.g., ASO-STAT3-1241; SEQ ID NO: 159). In some aspects, the target region corresponds to nucleotides 524-544 of SEQ ID NO: 3 (e.g., ASO-STAT3-524; SEQ ID NO: 160). In some aspects, the target region corresponds to nucleotides 890-910 of SEQ ID NO: 3 (e.g., ASO-STAT3-890; SEQ ID NO: 161). In some aspects, the target region corresponds to nucleotides 1114-1131 of SEQ ID NO: 3 (e.g., ASO-STAT3-1114; SEQ ID NO: 162). In some aspects, the target region corresponds to nucleotides 1108-1128 of SEQ ID NO: 3 (e.g., ASO-STAT3-1108; SEQ ID NO: 163). In some aspects, the target region corresponds to nucleotides 409-429 of SEQ ID NO: 3 (e.g., ASO-STAT3-409; SEQ ID NO: 164). In some aspects, the target region corresponds to nucleotides 1356-1376 of SEQ ID NO: 3 (e.g., ASO-STAT3-1356; SEQ ID NO: 165). In some aspects, the target region corresponds to nucleotides 1231-1246 of SEQ ID NO: 3 (e.g., ASO-STAT3-1231; SEQ ID NO: 166). In some aspects, the target region corresponds to nucleotides 2267-2287 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 167). In some aspects, the target region corresponds to nucleotides 1238-1253 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 168). In some

aspects, the target region corresponds to nucleotides 1237-1253 of SEQ ID NO: 3 (e.g., ASO-STAT3-1237; SEQ ID NO: 169). In some aspects, the target region corresponds to nucleotides 522-542 of SEQ ID NO: 3 (e.g., ASO-STAT3-522; SEQ ID NO: 170). In some aspects, the target region corresponds to nucleotides 2266-2286 of SEQ ID NO: 3 (e.g., ASO-STAT3-2266; SEQ ID NO: 171). In some aspects, the target region corresponds to nucleotides 1998-2018 of SEQ ID NO: 3 (e.g., ASO-STAT3-1998; SEQ ID NO: 172). In some aspects, the target region corresponds to nucleotides 881-901 of SEQ ID NO: 3 (e.g., ASO-STAT3-881; SEQ ID NO: 173). In some aspects, the target region corresponds to nucleotides 513-533 of SEQ ID NO: 3 (e.g., ASO-STAT3-513; SEQ ID NO: 174). In some aspects, the target region corresponds to nucleotides 1107-1127 of SEQ ID NO: 3 (e.g., ASO-STAT3-1107; SEQ ID NO: 175). In some aspects, the target region corresponds to nucleotides 1235-1250 of SEQ ID NO: 3 (e.g., ASO-STAT3-1235; SEQ ID NO: 176). In some aspects, the target region corresponds to nucleotides 882-902 of SEQ ID NO: 3 (e.g., ASO-STAT3-882; SEQ ID NO: 177). In some aspects, the target region corresponds to nucleotides 1112-1132 of SEQ ID NO: 3 (e.g., ASO-STAT3-1112; SEQ ID NO: 178). In some aspects, the target region corresponds to nucleotides 521-541 of SEQ ID NO: 3 (e.g., ASO-STAT3-521; SEQ ID NO: 179). In some aspects, the target region corresponds to nucleotides 1110-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1110; SEQ ID NO: 180). In some aspects, the target region corresponds to nucleotides 1475-1495 of SEQ ID NO: 3 (e.g., ASO-STAT3-1475; SEQ ID NO: 181). In some aspects, the target region corresponds to nucleotides 894-914 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 182). In some aspects, the target region corresponds to nucleotides 519-539 of SEQ ID NO: 3 (e.g., ASO-STAT3-519; SEQ ID NO: 183). In some aspects, the target region corresponds to nucleotides 2553-2573 of SEQ ID NO: 3 (e.g., ASO-STAT3-2553; SEQ ID NO: 184). In some aspects, the target region corresponds to nucleotides 2552-2572 of SEQ ID NO: 3 (e.g., ASO-STAT3-2552; SEQ ID NO: 185). In some aspects, the target region corresponds to nucleotides 883-903 of SEQ ID NO: 3 (e.g., ASO-STAT3-883; SEQ ID NO: 186). In some aspects, the target region corresponds to nucleotides 842-862 of SEQ ID NO: 3 (e.g., ASO-STAT3-842; SEQ ID NO: 187). In some aspects, the target region corresponds to nucleotides 851-871 of SEQ ID NO: 3 (e.g., ASO-STAT3-851; SEQ ID NO: 188). In some aspects, the target region corresponds to nucleotides 2265-2285 of SEQ ID NO: 3 (e.g., ASO-STAT3-2265; SEQ ID NO: 189). In some aspects, the target region corresponds to nucleotides 520-540 of SEQ ID NO: 3 (e.g., ASO-STAT3-520; SEQ ID NO: 190). In some aspects, the target region corresponds to nucleotides 985-1005 of SEQ ID NO: 3 (e.g., ASO-STAT3-985; SEQ ID NO: 191). In some aspects, the target region corresponds to nucleotides 524-541 of SEQ ID NO: 3 (e.g., ASO-STAT3-524; SEQ ID NO:

192). In some aspects, the target region corresponds to nucleotides 1106-1126 of SEQ ID NO: 3 (e.g., ASO-STAT3-1106; SEQ ID NO: 193). In some aspects, the target region corresponds to nucleotides 517-537 of SEQ ID NO: 3 (e.g., ASO-STAT3-517; SEQ ID NO: 194). In some aspects, the target region corresponds to nucleotides 1721-1741 of SEQ ID NO: 3 (e.g., ASO-STAT3-1721; SEQ ID NO: 195). In some aspects, the target region corresponds to nucleotides 1113-1133 of SEQ ID NO: 3 (e.g., ASO-STAT3-1113; SEQ ID NO: 196). In some aspects, the target region corresponds to nucleotides 992-1008 of SEQ ID NO: 3 (e.g., ASO-STAT3-992; SEQ ID NO: 197). In some aspects, the target region corresponds to nucleotides 993-1008 of SEQ ID NO: 3 (e.g., ASO-STAT3-993; SEQ ID NO: 198). In some aspects, the target region corresponds to nucleotides 1104-1124 of SEQ ID NO: 3 (e.g., ASO-STAT3-1104; SEQ ID NO: 199).

[0133] In some aspects, the target region corresponds to nucleotides 2559-2576 of SEQ ID NO: 3 (e.g., ASO-STAT3-2559; SEQ ID NO: 100) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2556-2576 of SEQ ID NO: 3 (e.g., ASO-STAT3-2556; SEQ ID NO: 101) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2557-2577 of SEQ ID NO: 3 (e.g., ASO-STAT3-2557; SEQ ID NO: 102) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1046-1061 of SEQ ID NO: 3 (e.g., ASO-STAT3-1046; SEQ ID NO: 103) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 351-371 of SEQ ID NO: 3 (e.g., ASO-STAT3-351; SEQ ID NO: 104) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 450-470 of SEQ ID NO: 3 (e.g., ASO-STAT3-450; SEQ ID NO: 105) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2558-2575 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 106) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2558-2578 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 107) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 865-885 of SEQ ID NO: 3 (e.g., ASO-STAT3-865; SEQ ID NO: 108) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 894-910 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 109).

$\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1778-1798 of SEQ ID NO: 3 (e.g., ASO-STAT3-1778; SEQ ID NO: 110) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2558-2574 of SEQ ID NO: 3 (e.g., ASO-STAT3-2558; SEQ ID NO: 111) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1482-1498 of SEQ ID NO: 3 (e.g., ASO-STAT3-1482; SEQ ID NO: 112) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 892-912 of SEQ ID NO: 3 (e.g., ASO-STAT3-892; SEQ ID NO: 113) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2262-2282 of SEQ ID NO: 3 (e.g., ASO-STAT3-2262; SEQ ID NO: 114) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2267-2282 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 115) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 411-431 of SEQ ID NO: 3 (e.g., ASO-STAT3-411; SEQ ID NO: 116) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2267-2284 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 117) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 896-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-896; SEQ ID NO: 118) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2555-2575 of SEQ ID NO: 3 (e.g., ASO-STAT3-2555; SEQ ID NO: 119) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 525-545 of SEQ ID NO: 3 (e.g., ASO-STAT3-525; SEQ ID NO: 120) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1766-1786 of SEQ ID NO: 3 (e.g., ASO-STAT3-1766; SEQ ID NO: 121) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1114-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1114; SEQ ID NO: 122) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2557-2574 of SEQ ID NO: 3

(e.g., ASO-STAT3-2557; SEQ ID NO: 123) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 995-1015 of SEQ ID NO: 3 (e.g., ASO-STAT3-995; SEQ ID NO: 124) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2263-2283 of SEQ ID NO: 3 (e.g., ASO-STAT3-2263; SEQ ID NO: 125) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 511-531 of SEQ ID NO: 3 (e.g., ASO-STAT3-511; SEQ ID NO: 126) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 511-527 of SEQ ID NO: 3 (e.g., ASO-STAT3-511; SEQ ID NO: 127) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1043-1063 of SEQ ID NO: 3 (e.g., ASO-STAT3-1043; SEQ ID NO: 128) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1780-1800 of SEQ ID NO: 3 (e.g., ASO-STAT3-1780; SEQ ID NO: 129) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 458-478 of SEQ ID NO: 3 (e.g., ASO-STAT3-458; SEQ ID NO: 130) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 894-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 131) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1779-1799 of SEQ ID NO: 3 (e.g., ASO-STAT3-1779; SEQ ID NO: 132) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2274-2294 of SEQ ID NO: 3 (e.g., ASO-STAT3-2274; SEQ ID NO: 133) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1039-1059 of SEQ ID NO: 3 (e.g., ASO-STAT3-1039; SEQ ID NO: 134) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1238-1258 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 135) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1239-1259 of SEQ ID NO: 3 (e.g., ASO-STAT3-1239; SEQ ID NO: 136) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 516-536 of SEQ ID NO: 3

(e.g., ASO-STAT3-516; SEQ ID NO: 137) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1238-1254 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 138) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1034-1054 of SEQ ID NO: 3 (e.g., ASO-STAT3-1034; SEQ ID NO: 139) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1239-1254 of SEQ ID NO: 3 (e.g., ASO-STAT3-1239; SEQ ID NO: 140) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1113-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1113; SEQ ID NO: 141) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1484-1504 of SEQ ID NO: 3 (e.g., ASO-STAT3-1484; SEQ ID NO: 142) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2556-2571 of SEQ ID NO: 3 (e.g., ASO-STAT3-2556; SEQ ID NO: 143) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 461-481 of SEQ ID NO: 3 (e.g., ASO-STAT3-461; SEQ ID NO: 144) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2273-2293 of SEQ ID NO: 3 (e.g., ASO-STAT3-2273; SEQ ID NO: 145) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1783-1803 of SEQ ID NO: 3 (e.g., ASO-STAT3-1783; SEQ ID NO: 146) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 891-911 of SEQ ID NO: 3 (e.g., ASO-STAT3-891; SEQ ID NO: 147) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 510-530 of SEQ ID NO: 3 (e.g., ASO-STAT3-510; SEQ ID NO: 148) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2115-2135 of SEQ ID NO: 3 (e.g., ASO-STAT3-2115; SEQ ID NO: 149) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1482-1502 of SEQ ID NO: 3 (e.g., ASO-STAT3-1482; SEQ ID NO: 150) $\pm 10, \pm 20, \pm 30, \pm 40, \pm 50, \pm 60, \pm 70, \pm 80$, or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds

to nucleotides 986-1006 of SEQ ID NO: 3 (e.g., ASO-STAT3-986; SEQ ID NO: 151) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 893-913 of SEQ ID NO: 3 (e.g., ASO-STAT3-893; SEQ ID NO: 152) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1237-1252 of SEQ ID NO: 3 (e.g., ASO-STAT3-1237; SEQ ID NO: 153) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1111-1131 of SEQ ID NO: 3 (e.g., ASO-STAT3-1111; SEQ ID NO: 154) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1236-1252 of SEQ ID NO: 3 (e.g., ASO-STAT3-1236; SEQ ID NO: 155) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2557-2572 of SEQ ID NO: 3 (e.g., ASO-STAT3-2557; SEQ ID NO: 156) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2264-2284 of SEQ ID NO: 3 (e.g., ASO-STAT3-2264; SEQ ID NO: 157) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1234-1249 of SEQ ID NO: 3 (e.g., ASO-STAT3-1234; SEQ ID NO: 158) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1241-1258 of SEQ ID NO: 3 (e.g., ASO-STAT3-1241; SEQ ID NO: 159) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 524-544 of SEQ ID NO: 3 (e.g., ASO-STAT3-524; SEQ ID NO: 160) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 890-910 of SEQ ID NO: 3 (e.g., ASO-STAT3-890; SEQ ID NO: 161) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1114-1131 of SEQ ID NO: 3 (e.g., ASO-STAT3-1114; SEQ ID NO: 162) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1108-1128 of SEQ ID NO: 3 (e.g., ASO-STAT3-1108; SEQ ID NO: 163) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 409-429 of SEQ ID NO: 3 (e.g., ASO-STAT3-409; SEQ ID NO: 164) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects,

the target region corresponds to nucleotides 1356-1376 of SEQ ID NO: 3 (e.g., ASO-STAT3-1356; SEQ ID NO: 165) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1231-1246 of SEQ ID NO: 3 (e.g., ASO-STAT3-1231; SEQ ID NO: 166) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2267-2287 of SEQ ID NO: 3 (e.g., ASO-STAT3-2267; SEQ ID NO: 167) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1238-1253 of SEQ ID NO: 3 (e.g., ASO-STAT3-1238; SEQ ID NO: 168) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1237-1253 of SEQ ID NO: 3 (e.g., ASO-STAT3-1237; SEQ ID NO: 169) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 522-542 of SEQ ID NO: 3 (e.g., ASO-STAT3-522; SEQ ID NO: 170) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2266-2286 of SEQ ID NO: 3 (e.g., ASO-STAT3-2266; SEQ ID NO: 171) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1998-2018 of SEQ ID NO: 3 (e.g., ASO-STAT3-1998; SEQ ID NO: 172) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 881-901 of SEQ ID NO: 3 (e.g., ASO-STAT3-881; SEQ ID NO: 173) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 513-533 of SEQ ID NO: 3 (e.g., ASO-STAT3-513; SEQ ID NO: 174) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1107-1127 of SEQ ID NO: 3 (e.g., ASO-STAT3-1107; SEQ ID NO: 175) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1235-1250 of SEQ ID NO: 3 (e.g., ASO-STAT3-1235; SEQ ID NO: 176) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 882-902 of SEQ ID NO: 3 (e.g., ASO-STAT3-882; SEQ ID NO: 177) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1112-1132 of SEQ ID NO: 3 (e.g., ASO-STAT3-1112; SEQ ID NO: 178) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end

and/or the 5' end. In some aspects, the target region corresponds to nucleotides 521-541 of SEQ ID NO: 3 (e.g., ASO-STAT3-521; SEQ ID NO: 179) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1110-1130 of SEQ ID NO: 3 (e.g., ASO-STAT3-1110; SEQ ID NO: 180) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1475-1495 of SEQ ID NO: 3 (e.g., ASO-STAT3-1475; SEQ ID NO: 181) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 894-914 of SEQ ID NO: 3 (e.g., ASO-STAT3-894; SEQ ID NO: 182) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 519-539 of SEQ ID NO: 3 (e.g., ASO-STAT3-519; SEQ ID NO: 183) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2553-2573 of SEQ ID NO: 3 (e.g., ASO-STAT3-2553; SEQ ID NO: 184) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2552-2572 of SEQ ID NO: 3 (e.g., ASO-STAT3-2552; SEQ ID NO: 185) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 883-903 of SEQ ID NO: 3 (e.g., ASO-STAT3-883; SEQ ID NO: 186) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 842-862 of SEQ ID NO: 3 (e.g., ASO-STAT3-842; SEQ ID NO: 187) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 851-871 of SEQ ID NO: 3 (e.g., ASO-STAT3-851; SEQ ID NO: 188) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 2265-2285 of SEQ ID NO: 3 (e.g., ASO-STAT3-2265; SEQ ID NO: 189) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 520-540 of SEQ ID NO: 3 (e.g., ASO-STAT3-520; SEQ ID NO: 190) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 985-1005 of SEQ ID NO: 3 (e.g., ASO-STAT3-985; SEQ ID NO: 191) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 524-541 of SEQ ID NO: 3 (e.g., ASO-STAT3-524; SEQ ID NO: 192) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end

and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1106-1126 of SEQ ID NO: 3 (e.g., ASO-STAT3-1106; SEQ ID NO: 193) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 517-537 of SEQ ID NO: 3 (e.g., ASO-STAT3-517; SEQ ID NO: 194) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1721-1741 of SEQ ID NO: 3 (e.g., ASO-STAT3-1721; SEQ ID NO: 195) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1113-1133 of SEQ ID NO: 3 (e.g., ASO-STAT3-1113; SEQ ID NO: 196) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 992-1008 of SEQ ID NO: 3 (e.g., ASO-STAT3-992; SEQ ID NO: 197) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 993-1008 of SEQ ID NO: 3 (e.g., ASO-STAT3-993; SEQ ID NO: 198) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end. In some aspects, the target region corresponds to nucleotides 1104-1124 of SEQ ID NO: 3 (e.g., ASO-STAT3-1104; SEQ ID NO: 199) ± 10 , ± 20 , ± 30 , ± 40 , ± 50 , ± 60 , ± 70 , ± 80 , or ± 90 nucleotides at the 3' end and/or the 5' end.

[0134] In some aspects, the ASO of the present disclosure hybridizes to multiple target regions within the *STAT3* transcript (e.g., genomic sequence, SEQ ID NO: 1). In some aspects, the ASO hybridizes to two different target regions within the *STAT3* transcript. In some aspects, the ASO hybridizes to three different target regions within the *STAT3* transcript. The sequences of exemplary ASOs that hybridizes to multiple target regions, and the start/end sites of the different target regions are provided in FIG. 1. In some aspects, the ASOs that hybridizes to multiple regions within the *STAT3* transcript (e.g., genomic sequence, SEQ ID NO: 1) are more potent (e.g., having lower EC₅₀) at reducing *STAT3* expression compared to ASOs that hybridizes to a single region within the *STAT3* transcript (e.g., genomic sequence, SEQ ID NO: 1).

[0135] In some aspects, the ASO of the disclosure is capable of hybridizing to the target nucleic acid (e.g., *STAT3* transcript) under physiological condition, i.e., *in vivo* condition. In some aspects, the ASO of the disclosure is capable of hybridizing to the target nucleic acid (e.g., *STAT3* transcript) *in vitro*. In some aspects, the ASO of the disclosure is capable of hybridizing to the target nucleic acid (e.g., *STAT3* transcript) *in vitro* under stringent conditions. Stringency conditions for hybridization *in vitro* are dependent on, *inter alia*, productive cell uptake, RNA accessibility, temperature, free energy of association, salt concentration, and time (see, e.g.,

Stanley T Crooke, *Antisense Drug Technology: Principles, Strategies and Applications*, 2nd Edition, CRC Press (2007)). Generally, conditions of high to moderate stringency are used for *in vitro* hybridization to enable hybridization between substantially similar nucleic acids, but not between dissimilar nucleic acids. An example of stringent hybridization conditions includes hybridization in 5X saline-sodium citrate (SSC) buffer (0.75 M sodium chloride/0.075 M sodium citrate) for 1 hour at 40°C, followed by washing the sample 10 times in 1X SSC at 40°C and 5 times in 1X SSC buffer at room temperature. *In vivo* hybridization conditions consist of intracellular conditions (*e.g.*, physiological pH and intracellular ionic conditions) that govern the hybridization of antisense oligonucleotides with target sequences. *In vivo* conditions can be mimicked *in vitro* by relatively low stringency conditions. For example, hybridization can be carried out *in vitro* in 2X SSC (0.3 M sodium chloride/0.03 M sodium citrate), 0.1% SDS at 37°C. A wash solution containing 4X SSC, 0.1% SDS can be used at 37°C, with a final wash in 1X SSC at 45°C.

[0136] In some aspects, the ASO of the present disclosure is capable of targeting a *STAT3* transcript from one or more species (*e.g.*, humans, non-human primates, dogs, cats, guinea pigs, rabbits, rats, mice, horses, cattle, and bears). In certain aspects, the ASO disclosed herein is capable of targeting both human and rodent (*e.g.*, mice or rats) *STAT3* transcript. Accordingly, in some aspects, the ASO is capable of down-regulating (*e.g.*, reducing or removing) expression of the *STAT3* mRNA or protein both in humans and in rodents (*e.g.*, mice or rats).

II.B. ASO Sequences (STAT3)

[0137] The ASOs of the disclosure comprise a contiguous nucleotide sequence which corresponds to the complement of a region of *STAT3* transcript, *e.g.*, a nucleotide sequence corresponding to SEQ ID NO: 1 or SEQ ID NO: 3.

[0138] In certain aspects, the disclosure provides an ASO from 10 – 30, such as 10 – 15 nucleotides, 10 – 20 nucleotides, 20 nucleotides in length, or 10 – 25 nucleotides in length, wherein the contiguous nucleotide sequence has at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% sequence identity to a region within the complement of a *STAT3* transcript, such as SEQ ID NO: 1 or SEQ ID NO: 3, or naturally occurring variant thereof. Thus, for example, the ASO hybridizes to a single stranded nucleic acid molecule having the sequence of SEQ ID NO: 1 or a portion thereof. In some aspects, the ASO hybridizes to a single stranded nucleic acid molecule having the sequence of SEQ ID NO: 3 or a portion thereof.

[0139] The ASO can comprise a contiguous nucleotide sequence which is fully complementary (perfectly complementary) to the equivalent region of a nucleic acid which encodes a mammalian STAT3 protein (*e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3). The ASO can comprise a contiguous nucleotide sequence which is fully complementary (perfectly complementary) to a nucleic acid sequence, or a region within the sequence, corresponding to nucleotides X-Y of SEQ ID NO: 3, wherein X and Y are the start site and the end site, respectively, as shown in FIG. 1.

[0140] The ASO can comprise a contiguous nucleotide sequence which is fully complementary (perfectly complementary) to the equivalent region of a mRNA which encodes a mammalian STAT3 protein (*e.g.*, SEQ ID NO: 2). The ASO can comprise a contiguous nucleotide sequence which is fully complementary (perfectly complementary) to a mRNA sequence, or a region within the sequence, corresponding to nucleotides X-Y of SEQ ID NO: 1 or 3, wherein X and Y are the start site and the end site, respectively.

[0141] In some aspects, the nucleotide sequence of the ASOs of the disclosure or the contiguous nucleotide sequence has at least about 80% sequence identity to a sequence selected from SEQ ID NOs: 100-199 to STAT3 (*i.e.*, the sequences in FIG. 1), such as at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96% sequence identity, at least about 97% sequence identity, at least about 98% sequence identity, at least about 99% sequence identity, such as about 100% sequence identity (homologous). In some aspects, the ASO has a design described elsewhere herein or a chemical structure shown elsewhere herein.

[0142] In some aspects the ASO (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NOs: 100-199 to STAT3 or a region of at least 10 contiguous nucleotides thereof, wherein the ASO (or contiguous nucleotide portion thereof) can optionally comprise one, two, three, or four mismatches when compared to the corresponding *STAT3* transcript (*e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3).

[0143] In some aspects, the ASO comprises a sequence selected from the group consisting of SEQ ID NO: 100 (*e.g.*, ASO-STAT3-2559), SEQ ID NO: 101 (*e.g.*, ASO-STAT3-2556), SEQ ID NO: 102 (*e.g.*, ASO-STAT3-2557), SEQ ID NO: 103 (*e.g.*, ASO-STAT3-1046), SEQ ID NO: 104 (*e.g.*, ASO-STAT3-351), SEQ ID NO: 105 (*e.g.*, ASO-STAT3-450), SEQ ID NO: 106 (*e.g.*, ASO-STAT3-2558), SEQ ID NO: 107 (*e.g.*, ASO-STAT3-2558), SEQ ID NO: 108 (*e.g.*, ASO-STAT3-865), SEQ ID NO: 109 (*e.g.*, ASO-STAT3-894), SEQ ID NO: 110 (*e.g.*, ASO-STAT3-1778), SEQ ID NO: 111 (*e.g.*, ASO-STAT3-2558), SEQ ID NO: 112 (*e.g.*, ASO-STAT3-1482),

SEQ ID NO: 113 (e.g., ASO-STAT3-892), SEQ ID NO: 114 (e.g., ASO-STAT3-2262), SEQ ID NO: 115 (e.g., ASO-STAT3-2267), SEQ ID NO: 116 (e.g., ASO-STAT3-411), SEQ ID NO: 117 (e.g., ASO-STAT3-2267), SEQ ID NO: 118 (e.g., ASO-STAT3-896), SEQ ID NO: 119 (e.g., ASO-STAT3-2555), SEQ ID NO: 120 (e.g., ASO-STAT3-525), SEQ ID NO: 121 (e.g., ASO-STAT3-1766), SEQ ID NO: 122 (e.g., ASO-STAT3-1114), SEQ ID NO: 123 (e.g., ASO-STAT3-2557), SEQ ID NO: 124 (e.g., ASO-STAT3-995), SEQ ID NO: 125 (e.g., ASO-STAT3-2263), SEQ ID NO: 126 (e.g., ASO-STAT3-511), SEQ ID NO: 127 (e.g., ASO-STAT3-511), SEQ ID NO: 128 (e.g., ASO-STAT3-1043), SEQ ID NO: 129 (e.g., ASO-STAT3-1780), SEQ ID NO: 130 (e.g., ASO-STAT3-458), SEQ ID NO: 131 (e.g., ASO-STAT3-894), SEQ ID NO: 132 (e.g., ASO-STAT3-1779), SEQ ID NO: 133 (e.g., ASO-STAT3-2274), SEQ ID NO: 134 (e.g., ASO-STAT3-1039), SEQ ID NO: 135 (e.g., ASO-STAT3-1238), SEQ ID NO: 136 (e.g., ASO-STAT3-1239), SEQ ID NO: 137 (e.g., ASO-STAT3-516), SEQ ID NO: 138 (e.g., ASO-STAT3-1238), SEQ ID NO: 139 (e.g., ASO-STAT3-1034), SEQ ID NO: 140 (e.g., ASO-STAT3-1239), SEQ ID NO: 141 (e.g., ASO-STAT3-1113), SEQ ID NO: 142 (e.g., ASO-STAT3-1484), SEQ ID NO: 143 (e.g., ASO-STAT3-2556), SEQ ID NO: 144 (e.g., ASO-STAT3-461), SEQ ID NO: 145 (e.g., ASO-STAT3-2273), SEQ ID NO: 146 (e.g., ASO-STAT3-1783), SEQ ID NO: 147 (e.g., ASO-STAT3-891), SEQ ID NO: 148 (e.g., ASO-STAT3-510), SEQ ID NO: 149 (e.g., ASO-STAT3-2115), SEQ ID NO: 150 (e.g., ASO-STAT3-1482), SEQ ID NO: 151 (e.g., ASO-STAT3-986), SEQ ID NO: 152 (e.g., ASO-STAT3-893), SEQ ID NO: 153 (e.g., ASO-STAT3-1237), SEQ ID NO: 154 (e.g., ASO-STAT3-1111), SEQ ID NO: 155 (e.g., ASO-STAT3-1236), SEQ ID NO: 156 (e.g., ASO-STAT3-2557), SEQ ID NO: 157 (e.g., ASO-STAT3-2264), SEQ ID NO: 158 (e.g., ASO-STAT3-1234), SEQ ID NO: 159 (e.g., ASO-STAT3-1241), SEQ ID NO: 160 (e.g., ASO-STAT3-524), SEQ ID NO: 161 (e.g., ASO-STAT3-890), SEQ ID NO: 162 (e.g., ASO-STAT3-1114), SEQ ID NO: 163 (e.g., ASO-STAT3-1108), SEQ ID NO: 164 (e.g., ASO-STAT3-409), SEQ ID NO: 165 (e.g., ASO-STAT3-1356), SEQ ID NO: 166 (e.g., ASO-STAT3-1231), SEQ ID NO: 167 (e.g., ASO-STAT3-2267), SEQ ID NO: 168 (e.g., ASO-STAT3-1238), SEQ ID NO: 169 (e.g., ASO-STAT3-1237), SEQ ID NO: 170 (e.g., ASO-STAT3-522), SEQ ID NO: 171 (e.g., ASO-STAT3-2266), SEQ ID NO: 172 (e.g., ASO-STAT3-1998), SEQ ID NO: 173 (e.g., ASO-STAT3-881), SEQ ID NO: 174 (e.g., ASO-STAT3-513), SEQ ID NO: 175 (e.g., ASO-STAT3-1107), SEQ ID NO: 176 (e.g., ASO-STAT3-1235), SEQ ID NO: 177 (e.g., ASO-STAT3-882), SEQ ID NO: 178 (e.g., ASO-STAT3-1112), SEQ ID NO: 179 (e.g., ASO-STAT3-521), SEQ ID NO: 180 (e.g., ASO-STAT3-1110), SEQ ID NO: 181 (e.g., ASO-STAT3-1475), SEQ ID NO: 182 (e.g., ASO-STAT3-894), SEQ ID NO: 183 (e.g., ASO-STAT3-519), SEQ ID NO: 184 (e.g., ASO-STAT3-

2553), SEQ ID NO: 185 (e.g., ASO-STAT3-2552), SEQ ID NO: 186 (e.g., ASO-STAT3-883), SEQ ID NO: 187 (e.g., ASO-STAT3-842), SEQ ID NO: 188 (e.g., ASO-STAT3-851), SEQ ID NO: 189 (e.g., ASO-STAT3-2265), SEQ ID NO: 190 (e.g., ASO-STAT3-520), SEQ ID NO: 191 (e.g., ASO-STAT3-985), SEQ ID NO: 192 (e.g., ASO-STAT3-524), SEQ ID NO: 193 (e.g., ASO-STAT3-1106), SEQ ID NO: 194 (e.g., ASO-STAT3-517), SEQ ID NO: 195 (e.g., ASO-STAT3-1721), SEQ ID NO: 196 (e.g., ASO-STAT3-1113), SEQ ID NO: 197 (e.g., ASO-STAT3-992), SEQ ID NO: 198 (e.g., ASO-STAT3-993), or SEQ ID NO: 199 (e.g., ASO-STAT3-1104).

[0144] In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 100 (e.g., ASO-STAT3-2559). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 101 (e.g., ASO-STAT3-2556). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 102 (e.g., ASO-STAT3-2557). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 103 (e.g., ASO-STAT3-1046). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 104 (e.g., ASO-STAT3-351). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 105 (e.g., ASO-STAT3-450). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 106 (e.g., ASO-STAT3-2558). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 107 (e.g., ASO-STAT3-2558). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 108 (e.g., ASO-STAT3-865). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 109 (e.g., ASO-STAT3-894). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 110 (e.g., ASO-STAT3-1778). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 111 (e.g., ASO-STAT3-2558). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 112 (e.g., ASO-STAT3-1482). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 113 (e.g., ASO-STAT3-892). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 114 (e.g., ASO-STAT3-2262). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 115 (e.g., ASO-STAT3-2267). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 116 (e.g., ASO-STAT3-411). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 117 (e.g., ASO-STAT3-2267). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 118 (e.g., ASO-STAT3-896). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 119 (e.g., ASO-STAT3-2555). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 120 (e.g., ASO-STAT3-525). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 121 (e.g., ASO-STAT3-1766). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 122 (e.g., ASO-STAT3-

1114). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 123 (e.g., ASO-STAT3-2557). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 124 (e.g., ASO-STAT3-995). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 125 (e.g., ASO-STAT3-2263). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 126 (e.g., ASO-STAT3-511). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 127 (e.g., ASO-STAT3-511). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 128 (e.g., ASO-STAT3-1043). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 129 (e.g., ASO-STAT3-1780). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 130 (e.g., ASO-STAT3-458). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 131 (e.g., ASO-STAT3-894). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 132 (e.g., ASO-STAT3-1779). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 133 (e.g., ASO-STAT3-2274). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 134 (e.g., ASO-STAT3-1039). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 135 (e.g., ASO-STAT3-1238). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 136 (e.g., ASO-STAT3-1239). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 137 (e.g., ASO-STAT3-516). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 138 (e.g., ASO-STAT3-1238). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 139 (e.g., ASO-STAT3-1034). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 140 (e.g., ASO-STAT3-1239). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 141 (e.g., ASO-STAT3-1113). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 142 (e.g., ASO-STAT3-1484). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 143 (e.g., ASO-STAT3-2556). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 144 (e.g., ASO-STAT3-461). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 145 (e.g., ASO-STAT3-2273). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 146 (e.g., ASO-STAT3-1783). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 147 (e.g., ASO-STAT3-891). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 148 (e.g., ASO-STAT3-510). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 149 (e.g., ASO-STAT3-2115). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 150 (e.g., ASO-STAT3-1482). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 151 (e.g., ASO-STAT3-986). In some aspects, the ASO

comprises the sequence as set forth in SEQ ID NO: 152 (e.g., ASO-STAT3-893). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 153 (e.g., ASO-STAT3-1237). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 154 (e.g., ASO-STAT3-1111). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 155 (e.g., ASO-STAT3-1236). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 156 (e.g., ASO-STAT3-2557). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 157 (e.g., ASO-STAT3-2264). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 158 (e.g., ASO-STAT3-1234). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 159 (e.g., ASO-STAT3-1241). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 160 (e.g., ASO-STAT3-524). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 161 (e.g., ASO-STAT3-890). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 162 (e.g., ASO-STAT3-1114). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 163 (e.g., ASO-STAT3-1108). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 164 (e.g., ASO-STAT3-409). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 165 (e.g., ASO-STAT3-1356). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 166 (e.g., ASO-STAT3-1231). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 167 (e.g., ASO-STAT3-2267). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 168 (e.g., ASO-STAT3-1238). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 169 (e.g., ASO-STAT3-1237). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 170 (e.g., ASO-STAT3-522). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 171 (e.g., ASO-STAT3-2266). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 172 (e.g., ASO-STAT3-1998). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 173 (e.g., ASO-STAT3-881). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 174 (e.g., ASO-STAT3-513). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 175 (e.g., ASO-STAT3-1107). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 176 (e.g., ASO-STAT3-1235). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 177 (e.g., ASO-STAT3-882). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 178 (e.g., ASO-STAT3-1112). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 179 (e.g., ASO-STAT3-521). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 180 (e.g., ASO-STAT3-1110). In some aspects, the ASO comprises the sequence as set forth in

SEQ ID NO: 181 (e.g., ASO-STAT3-1475). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 182 (e.g., ASO-STAT3-894). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 183 (e.g., ASO-STAT3-519). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 184 (e.g., ASO-STAT3-2553). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 185 (e.g., ASO-STAT3-2552). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 186 (e.g., ASO-STAT3-883). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 187 (e.g., ASO-STAT3-842). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 188 (e.g., ASO-STAT3-851). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 189 (e.g., ASO-STAT3-2265). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 190 (e.g., ASO-STAT3-520). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 191 (e.g., ASO-STAT3-985). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 192 (e.g., ASO-STAT3-524). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 193 (e.g., ASO-STAT3-1106). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 194 (e.g., ASO-STAT3-517). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 195 (e.g., ASO-STAT3-1721). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 196 (e.g., ASO-STAT3-1113). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 197 (e.g., ASO-STAT3-992). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 198 (e.g., ASO-STAT3-993). In some aspects, the ASO comprises the sequence as set forth in SEQ ID NO: 199 (e.g., ASO-STAT3-1104).

[0145] In some aspects, the ASOs of the disclosure bind to the target nucleic acid sequence (e.g., *STAT3* transcript) and are capable of inhibiting or reducing expression of the *STAT3* transcript by at least 10% or 20% compared to the normal (i.e., control) expression level in the cell, e.g., at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% compared to the normal expression level (e.g., expression level in cells that have not been exposed to the ASO).

[0146] In some aspects, the ASOs of the disclosure are capable of reducing expression of *STAT3* mRNA *in vitro* by at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100%

in cells when the cells are in contact with 25 μ M of the ASO compared to cells that are not in contact with the ASO (*e.g.*, contact with saline).

[0147] In some aspects, the ASO can tolerate 1, 2, 3, or 4 (or more) mismatches, when hybridizing to the target sequence and still sufficiently bind to the target to show the desired effect, *i.e.*, down-regulation of the target mRNA and/or protein. Mismatches can, for example, be compensated by increased length of the ASO nucleotide sequence and/or an increased number of nucleotide analogs, which are disclosed elsewhere herein.

[0148] In some aspects, the ASO of the disclosure comprises no more than three mismatches when hybridizing to the target sequence. In other aspects, the contiguous nucleotide sequence comprises no more than two mismatches when hybridizing to the target sequence. In other aspects, the contiguous nucleotide sequence comprises no more than one mismatch when hybridizing to the target sequence.

II.C. ASO Length

[0149] The ASOs can comprise a contiguous nucleotide sequence of a total of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 contiguous nucleotides in length. It should be understood that when a range is given for an ASO, or contiguous nucleotide sequence length, the range includes the lower and upper lengths provided in the range, for example from (or between) 10–30, includes both 10 and 30.

[0150] In some aspects, the ASOs comprise a contiguous nucleotide sequence of a total of about 14–20, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleotides in length. In certain aspects, the ASOs comprise a contiguous nucleotide sequence of a total of about 20 contiguous nucleotides in length. In certain aspects, ASOs of the present disclosure are 14 nucleotides in length. In certain aspects, the ASO is 14 nucleotides in length. In certain aspects, the ASO is 13 nucleotides in length. In certain aspects, the ASO is 12 nucleotides in length. In certain aspects, the ASO is 11 nucleotides in length. In certain aspects, the ASO is 10 nucleotides in length. In certain aspects, ASOs of the present disclosure are 15 nucleotides in length. In certain aspects, ASOs of the present disclosure are 16 nucleotides in length. In certain aspects, ASOs of the present disclosure are 17 nucleotides in length. In certain aspects, ASOs of the present disclosure are 18 nucleotides in length. In certain aspects, ASOs of the present disclosure are 19 nucleotides in length.

[0151] In some aspects, the ASO comprises a contiguous nucleotide sequence of from about 10 to about 50 nucleotides in length, *e.g.*, about 10 to about 45, about 10 to about 40, about 10 or about 35, or about 10 to about 30. In certain aspects, the ASO is 21 nucleotides in length. In

certain aspects, the ASO is 22 nucleotides in length. In certain aspects, the ASO is 23 nucleotides in length. In certain aspects, the ASO is 24 nucleotides in length. In certain aspects, the ASO is 25 nucleotides in length. In certain aspects, the ASO is 26 nucleotides in length. In certain aspects, the ASO is 27 nucleotides in length. In certain aspects, the ASO is 28 nucleotides in length. In certain aspects, the ASO is 29 nucleotides in length. In certain aspects, the ASO is 30 nucleotides in length. In certain aspects, the ASO is 31 nucleotides in length. In certain aspects, the ASO is 32 nucleotides in length. In certain aspects, the ASO is 33 nucleotides in length. In certain aspects, the ASO is 34 nucleotides in length. In certain aspects, the ASO is 35 nucleotides in length. In certain aspects, the ASO is 36 nucleotides in length. In certain aspects, the ASO is 37 nucleotides in length. In certain aspects, the ASO is 38 nucleotides in length. In certain aspects, the ASO is 39 nucleotides in length. In certain aspects, the ASO is 40 nucleotides in length. In certain aspects, the ASO is 41 nucleotides in length. In certain aspects, the ASO is 42 nucleotides in length. In certain aspects, the ASO is 43 nucleotides in length. In certain aspects, the ASO is 44 nucleotides in length. In certain aspects, the ASO is 45 nucleotides in length. In certain aspects, the ASO is 46 nucleotides in length. In certain aspects, the ASO is 47 nucleotides in length. In certain aspects, the ASO is 48 nucleotides in length. In certain aspects, the ASO is 49 nucleotides in length. In certain aspects, the ASO is 50 nucleotides in length.

II.D. Nucleosides and Nucleoside analogs

[0152] In one aspect of the disclosure, the ASOs comprise one or more non-naturally occurring nucleoside analogs. "Nucleoside analogs" as used herein are variants of natural nucleosides, such as DNA or RNA nucleosides, by virtue of modifications in the sugar and/or base moieties. Analogs could in principle be merely "silent" or "equivalent" to the natural nucleosides in the context of the oligonucleotide, *i.e.* have no functional effect on the way the oligonucleotide works to inhibit target gene expression. Such "equivalent" analogs can nevertheless be useful if, for example, they are easier or cheaper to manufacture, or are more stable to storage or manufacturing conditions, or represent a tag or label. In some aspects, however, the analogs will have a functional effect on the way in which the ASO works to inhibit expression; for example by producing increased binding affinity to the target and/or increased resistance to intracellular nucleases and/or increased ease of transport into the cell. Specific examples of nucleoside analogs are described by *e.g.* Freier & Altmann; *Nucl. Acid Res.*, 1997, 25, 4429-4443 and Uhlmann; *Curr. Opinion in Drug Development*, 2000, 3(2), 293-213, and in Scheme 1. The ASOs of the present disclosure can contain more than one, more than two, more than three, more than four, more than

five, more than six, more than seven, more than eight, more than nine, more than 10, more than 11, more than 12, more than 13, more than 14, more than 15, more than 16, more than 18, more than 19, or more than 20 nucleoside analogs. In some aspects, the nucleoside analogs in the ASOs are the same. In other aspects, the nucleoside analogs in the ASOs are different. The nucleotide analogs in the ASOs can be any one of or combination of the following nucleoside analogs.

[0153] In some aspects, the nucleoside analog comprises a 2'-O-alkyl-RNA; 2'-O-methyl RNA (2'-OMe); 2'-alkoxy-RNA; 2'-O-methoxyethyl-RNA (2'-MOE); 2'-amino-DNA; 2'-fluoro-RNA; 2'-fluoro-DNA; arabino nucleic acid (ANA); 2'-fluoro-ANA; bicyclic nucleoside analog; or any combination thereof. In some aspects, the nucleoside analog comprises a sugar modified nucleoside. In some aspects, the nucleoside analog comprises a nucleoside comprising a bicyclic sugar. In some aspects, the nucleoside analog comprises an LNA.

[0154] In some aspects, the nucleoside analog is selected from the group consisting of constrained ethyl nucleoside (cEt), 2',4'-constrained 2'-O-methoxyethyl (cMOE), α -L-LNA, β -D-LNA, 2'-O,4'-C-ethylene-bridged nucleic acids (ENA), amino-LNA, oxy-LNA, thio-LNA, and any combination thereof. In some aspects, the ASO comprises one or more 5'-methyl-cytosine nucleobases.

II.D.1. Nucleobase

[0155] The term nucleobase includes the purine (*e.g.*, adenine and guanine) and pyrimidine (*e.g.*, uracil, thymine and cytosine) moiety present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. In the context of the present disclosure, the term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization. In some aspects, the nucleobase moiety is modified by modifying or replacing the nucleobase. In this context, "nucleobase" refers to both naturally occurring nucleobases such as adenine, guanine, cytosine, thymidine, uracil, xanthine and hypoxanthine, as well as non-naturally occurring variants. Such variants are for example described in Hirao *et al.*, (2012) *Accounts of Chemical Research* vol 45 page 2055 and Bergstrom (2009) *Current Protocols in Nucleic Acid Chemistry* Suppl. 37 1.4.1.

[0156] In some aspects, the nucleobase moiety is modified by changing the purine or pyrimidine into a modified purine or pyrimidine, such as substituted purine or substituted pyrimidine, such as a nucleobase selected from isocytosine, pseudoisocytosine, 5-methyl-cytosine, 5-thiazolo-cytosine, 5-propynyl-cytosine, 5-propynyl-uracil, 5-bromouracil, 5-thiazolo-uracil, 2-

thio-uracil, 2'thio-thymine, inosine, diaminopurine, 6-aminopurine, 2-aminopurine, 2,6-diaminopurine, and 2-chloro-6-aminopurine.

[0157] The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, *e.g.*, A, T, G, C, or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the nucleobase moieties are selected from A, T, G, C, and 5-methyl-cytosine. Optionally, for LNA gapmers, 5-methyl-cytosine LNA nucleosides may be used.

II.D.2. Sugar Modification

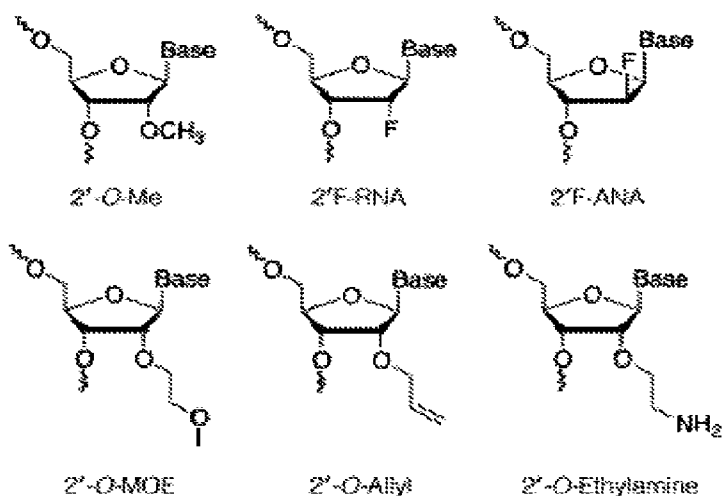
[0158] The ASO of the disclosure can comprise one or more nucleosides which have a modified sugar moiety, *i.e.* a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA. Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance.

[0159] Such modifications include those where the ribose ring structure is modified, *e.g.* by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradical bridge between the C2' and C4' carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2' and C3' carbons (*e.g.*, UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleic acids (WO2011/017521) or tricyclic nucleic acids (WO2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example in the case of peptide nucleic acids (PNA), or morpholino nucleic acids.

[0160] Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2'-OH group naturally found in RNA nucleosides. Substituents may, for example be introduced at the 2', 3', 4', or 5' positions. Nucleosides with modified sugar moieties also include 2' modified nucleosides, such as 2' substituted nucleosides. Indeed, much focus has been spent on developing 2' substituted nucleosides, and numerous 2' substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides, such as enhanced nucleoside resistance and enhanced affinity.

H.D.2.a 2' modified nucleosides

[0161] A 2' sugar modified nucleoside is a nucleoside which has a substituent other than H or -OH at the 2' position (2' substituted nucleoside) or comprises a 2' linked biradical, and includes 2' substituted nucleosides and LNA (2' – 4' biradical bridged) nucleosides. For example, the 2' modified sugar may provide enhanced binding affinity (*e.g.*, affinity enhancing 2' sugar modified nucleoside) and/or increased nuclease resistance to the oligonucleotide. Examples of 2' substituted modified nucleosides are 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, 2'-Fluoro-DNA, arabino nucleic acids (ANA), and 2'-Fluoro-ANA nucleoside. For further examples, please *see, e.g.*, Freier & Altmann; *Nucl. Acid Res.*, 1997, 25, 4429-4443; Uhlmann, *Curr. Opinion in Drug Development*, 2000, 3(2), 293-213; and Delcavey and Damha, *Chemistry and Biology* 2012, 19, 937. Below are illustrations of some 2' substituted modified nucleosides.

***H.D.2.b Locked Nucleic Acid Nucleosides (LNA).***

[0162] LNA nucleosides are modified nucleosides which comprise a linker group (referred to as a biradical or a bridge) between C2' and C4' of the ribose sugar ring of a nucleoside (*i.e.*, 2'-4' bridge), which restricts or locks the conformation of the ribose ring. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature. The locking of the conformation of the ribose is associated with an enhanced affinity of hybridization (duplex stabilization) when the LNA is incorporated into an oligonucleotide for a complementary RNA or DNA molecule. This can be routinely determined by measuring the melting temperature of the oligonucleotide/complement duplex.

hydrogen. In certain aspects of $-X-$, one of R^a and R^b is methyl and the other one is hydrogen. In other aspects of $-X-$, R^a and R^b are both methyl at the same time.

[0167] In some aspects, $-Y-$, R^a is hydrogen or alkyl, in particular hydrogen or methyl. In certain aspects of $-Y-$, R^b is hydrogen or alkyl, in particular hydrogen or methyl. In other aspects of $-Y-$, one or both of R^a and R^b are hydrogen. In some aspects of $-Y-$, only one of R^a and R^b is hydrogen. In other aspects of $-Y-$, one of R^a and R^b is methyl and the other one is hydrogen. In some aspects of $-Y-$, R^a and R^b are both methyl at the same time.

[0168] In some aspects, R^1 , R^2 , R^3 , R^5 and R^{5*} are independently selected from hydrogen and alkyl, in particular hydrogen and methyl.

[0169] In some aspects, R^1 , R^2 , R^3 , R^5 and R^{5*} are all hydrogen at the same time.

[0170] In some aspects, R^1 , R^2 , R^3 , are all hydrogen at the same time, one of R^5 and R^{5*} is hydrogen and the other one is as defined above, in particular alkyl, more particularly methyl.

[0171] In some aspects, R^1 , R^2 , R^3 , are all hydrogen at the same time, one of R^5 and R^{5*} is hydrogen and the other one is azide.

[0172] In some aspects, $-X-Y-$ is $-O-CH_2-$, W is oxygen and R^1 , R^2 , R^3 , R^5 and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are disclosed in WO 99/014226, WO 00/66604, WO 98/039352 and WO 2004/046160, which are all hereby incorporated by reference, and include what are commonly known in the art as beta-D-oxy LNA and alpha-L-oxy LNA nucleosides.

[0173] In some aspects, $-X-Y-$ is $-S-CH_2-$, W is oxygen and R^1 , R^2 , R^3 , R^5 and R^{5*} are all hydrogen at the same time. Such thio LNA nucleosides are disclosed in WO 99/014226 and WO 2004/046160 which are hereby incorporated by reference.

[0174] In some aspects, $-X-Y-$ is $-NH-CH_2-$, W is oxygen and R^1 , R^2 , R^3 , R^5 and R^{5*} are all hydrogen at the same time. Such amino LNA nucleosides are disclosed in WO 99/014226 and WO 2004/046160, which are hereby incorporated by reference.

[0175] In some aspects, $-X-Y-$ is $-O-CH_2CH_2-$ or $-OCH_2CH_2CH_2-$, W is oxygen, and R^1 , R^2 , R^3 , R^5 and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are disclosed in WO 00/047599 and Morita *et al.*, *Bioorganic & Med.Chem. Lett.* 12, 73-76, which are hereby incorporated by reference, and include what are commonly known in the art as 2'-O-4'C-ethylene bridged nucleic acids (ENA).

[0176] In some aspects, $-X-Y-$ is $-O-CH_2-$, W is oxygen, R^1 , R^2 , R^3 are all hydrogen at the same time, one of R^5 and R^{5*} is hydrogen and the other one is not hydrogen, such as alkyl, for example methyl. Such 5' substituted LNA nucleosides are disclosed in WO 2007/134181, which is hereby incorporated by reference.

[0177] In some aspects, -X-Y- is -O-CR^aR^b-, wherein one or both of R^a and R^b are not hydrogen, in particular alkyl such as methyl, W is oxygen, R¹, R², R³ are all hydrogen at the same time, one of R⁵ and R^{5*} is hydrogen and the other one is not hydrogen, in particular alkyl, for example methyl. Such bis modified LNA nucleosides are disclosed in WO 2010/077578, which is hereby incorporated by reference.

[0178] In some aspects, -X-Y- is -O-CH(CH₂-O-CH₃)- ("2' O-methoxyethyl bicyclic nucleic acid", Seth *et al.*, *J. Org. Chem.* 2010, Vol 75(5) pp. 1569-81).

[0179] In some aspects, -X-Y- is -O-CHR^a-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6'-substituted LNA nucleosides are disclosed in WO 2010/036698 and WO 2007/090071, which are both hereby incorporated by reference. In such 6'-substituted LNA nucleosides, R^a is in particular C1-C6 alkyl, such as methyl.

[0180] In some aspects, -X-Y- is -O-CH(CH₂-O-CH₃)-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such LNA nucleosides are also known in the art as cyclic MOEs (cMOE) and are disclosed in WO 2007/090071.

[0181] In some aspects, -X-Y- is -O-CH(CH₃)-.

[0182] In some aspects, -X-Y- is -O-CH₂-O-CH₂- (Seth *et al.*, *J. Org. Chem.* 2010 op. cit.)

[0183] In some aspects, -X-Y- is -O-CH(CH₃)-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6'-methyl LNA nucleosides are also known in the art as cET nucleosides, and may be either (S)-cET or (R)-cET diastereoisomers, as disclosed in WO 2007/090071 (beta-D) and WO 2010/036698 (alpha-L) which are both hereby incorporated by reference.

[0184] In some aspects, -X-Y- is -O-CR^aR^b-, wherein neither R^a nor R^b is hydrogen, W is oxygen, and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In certain aspects, R^a and R^b are both alkyl at the same time, in particular both methyl at the same time. Such 6'-di-substituted LNA nucleosides are disclosed in WO 2009/006478 which is hereby incorporated by reference.

[0185] In some aspects, -X-Y- is -S-CHR^a-, W is oxygen, and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such 6'-substituted thio LNA nucleosides are disclosed in WO 2011/156202, which is hereby incorporated by reference. In certain aspects of such 6'-substituted thio LNA, R^a is alkyl, in particular methyl.

[0186] In some aspects, -X-Y- is -C(=CH₂)C(R^aR^b)-, such as, W is oxygen, and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. Such vinyl carbo LNA nucleosides are disclosed in WO 2008/154401 and WO 2009/067647, which are both hereby incorporated by reference.

[0187] In some aspects, -X-Y- is -N(OR^a)-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In some aspects, R^a is alkyl such as methyl. Such LNA nucleosides are also known as N substituted LNAs and are disclosed in WO 2008/150729, which is hereby incorporated by reference.

[0188] In some aspects, -X-Y- is -O-NCH₃- (Seth *et al.*, *J. Org. Chem* 2010 op. cit.).

[0189] In some aspects, -X-Y- is ON(R^a)-N(R^a)-O-, -NR^a-CR^aR^b-CR^aR^b-, or -NR^a-CR^aR^b-, W is oxygen, and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In certain aspects, R^a is alkyl, such as methyl. (Seth *et al.*, *J. Org. Chem* 2010 op. cit.).

[0190] In some aspects, R⁵ and R^{5*} are both hydrogen at the same time. In other aspects, one of R⁵ and R^{5*} is hydrogen and the other one is alkyl, such as methyl. In such aspects, R¹, R² and R³ can be in particular hydrogen and -X-Y- can be in particular -O-CH₂- or -O-CHC(R^a)₃-, such as -O-CH(CH₃)-.

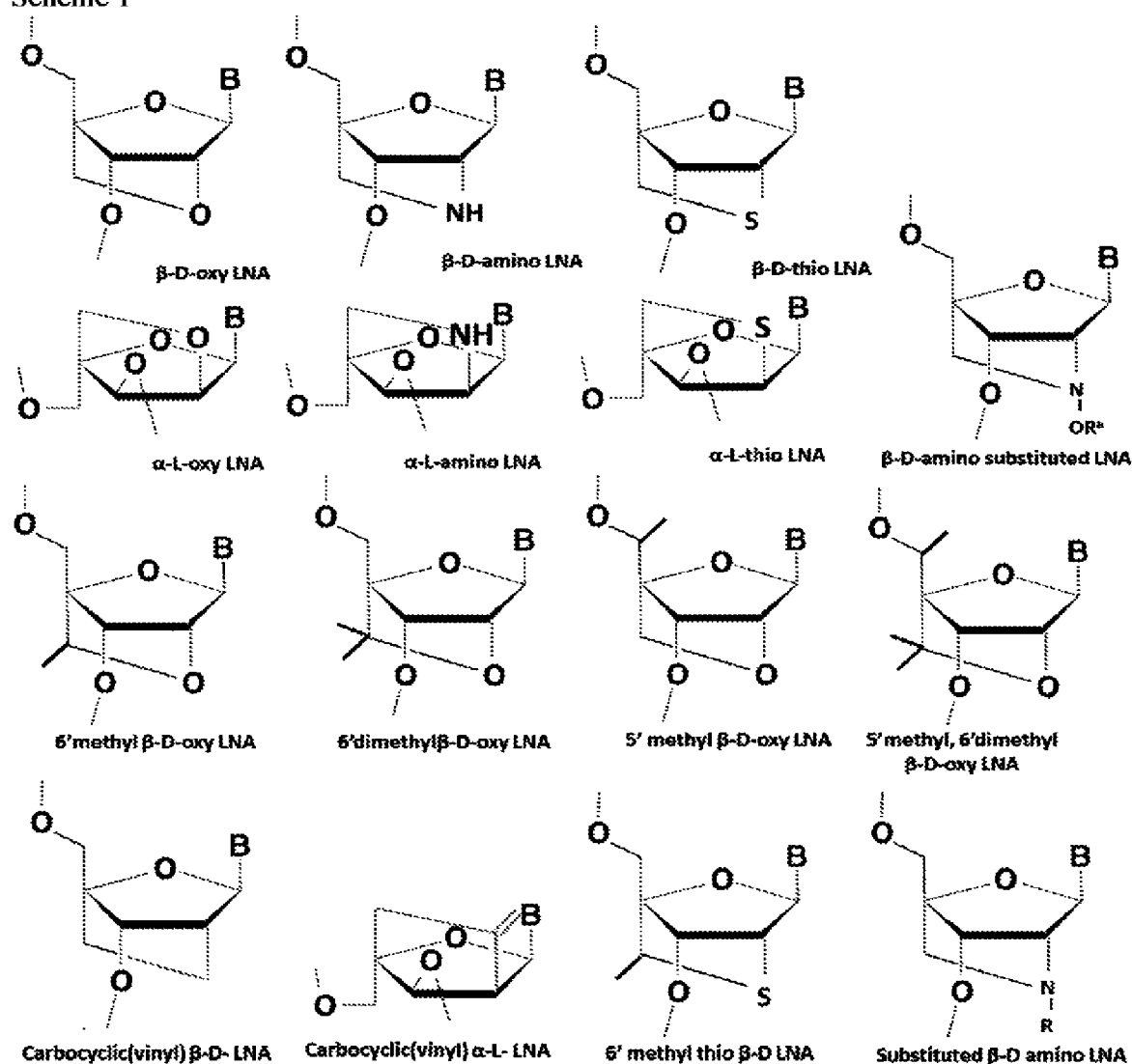
[0191] In some aspects, -X-Y- is -CR^aR^b-O-CR^aR^b-, such as -CH₂-O-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In such aspects, R^a can be in particular alkyl such as methyl. Such LNA nucleosides are also known as conformationally restricted nucleotides (CRNs) and are disclosed in WO 2013/036868, which is hereby incorporated by reference.

[0192] In some aspects, -X-Y- is -O-CR^aR^b-O-CR^aR^b-, such as -O-CH₂-O-CH₂-, W is oxygen and R¹, R², R³, R⁵ and R^{5*} are all hydrogen at the same time. In certain aspects, R^a can be in particular alkyl such as methyl. Such LNA nucleosides are also known as COC nucleotides and are disclosed in Mitsuoka *et al.*, *Nucleic Acids Research* 2009, 37(4), 1225-1238, which is hereby incorporated by reference.

[0193] It will be recognized than, unless specified, the LNA nucleosides may be in the beta-D or alpha-L stereoisofom.

[0194] Certain examples of LNA nucleosides are presented in Scheme 1.

Scheme 1



[0195] As illustrated elsewhere, in some aspects of the disclosure the LNA nucleosides in the oligonucleotides are beta-D-oxy-LNA nucleosides.

II.E. Nuclease mediated degradation

[0196] Nuclease mediated degradation refers to an oligonucleotide capable of mediating degradation of a complementary nucleotide sequence when forming a duplex with such a sequence.

[0197] In some aspects, the oligonucleotide may function via nuclease mediated degradation of the target nucleic acid, where the oligonucleotides of the disclosure are capable of recruiting a nuclease, particularly an endonuclease, preferably an endoribonuclease (RNase), such as RNase H. Examples of oligonucleotide designs which operate via nuclease mediated

mechanisms are oligonucleotides which typically comprise a region of at least 5 or 6 DNA nucleosides and are flanked on one side or both sides by affinity enhancing nucleosides, for example gapmers.

II.F. RNase H Activity and Recruitment

[0198] The RNase H activity of an antisense oligonucleotide refers to its ability to recruit RNase H when in a duplex with a complementary RNA molecule and induce degradation of the complementary RNA molecule. WO01/23613 provides *in vitro* methods for determining RNaseH activity, which may be used to determine the ability to recruit RNaseH. Typically, an oligonucleotide is deemed capable of recruiting RNase H if, when provided with a complementary target nucleic acid sequence, it has an initial rate, as measured in pmol/l/min, of at least 5%, such as at least 10% or more than 20% of the of the initial rate determined when using a oligonucleotide having the same base sequence as the modified oligonucleotide being tested, but containing only DNA monomers, with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613.

[0199] In some aspects, an oligonucleotide is deemed essentially incapable of recruiting RNaseH if, when provided with the complementary target nucleic acid, the RNaseH initial rate, as measured in pmol/l/min, is less than 20%, such as less than 10%, such as less than 5% of the initial rate determined when using a oligonucleotide having the same base sequence as the oligonucleotide being tested, but containing only DNA monomers, with no 2' substitutions, with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613.

II.G. ASO Design

[0200] The ASO of the disclosure can comprise a nucleotide sequence which comprises both nucleosides and nucleoside analogs, and can be in the form of a gapmer. In some aspects, the ASOs are gapmers. In some aspects, the ASOs are mixmers. In some aspects, the ASOs are totalmers. Examples of configurations of a gapmer that can be used with the ASO of the disclosure are described in U.S. Patent Appl. Publ. No. 2012/0322851, which is incorporated herein by reference in its entirety.

[0201] The term "gapmer" as used herein refers to an antisense oligonucleotide which comprises a region of RNase H recruiting oligonucleotides (gap) which is flanked 5' and 3' by one or more affinity enhancing modified nucleosides (flanks). The term "LNA gapmer" is a gapmer

oligonucleotide wherein at least one of the affinity enhancing modified nucleosides is an LNA nucleoside. The term "mixed wing gapmer" refers to an LNA gapmer wherein the flank regions comprise at least one LNA nucleoside and at least one DNA nucleoside or non-LNA modified nucleoside, such as at least one 2' substituted modified nucleoside, such as, for example, 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, 2'-Fluro-DNA, arabino nucleic acid (ANA), and 2'-Fluoro-ANA nucleoside(s).

[0202] In some aspects, in addition to enhancing affinity of the ASO for the target region, some nucleoside analogs also mediate RNase (*e.g.*, RNaseH) binding and cleavage. Since α -L-LNA monomers recruit RNaseH activity to a certain extent, in some aspects, gap regions (*e.g.*, region B as referred to herein) of ASOs containing α -L-LNA monomers consist of fewer monomers recognizable and cleavable by the RNaseH, and more flexibility in the mixmer construction is introduced.

II.H. Gapmer Design

[0203] In some aspects, the ASO of the disclosure is a gapmer and comprises a contiguous stretch of nucleotides (*e.g.*, one or more DNA) which is capable of recruiting an RNase, such as RNaseH, referred to herein in as region B (B), wherein region B is flanked at both 5' and 3' by regions of nucleoside analogs 5' and 3' to the contiguous stretch of nucleotides of region B—these regions are referred to as regions A (A) and C (C), respectively. In some aspects, the nucleoside analogs are sugar modified nucleosides (*e.g.*, high affinity sugar modified nucleosides). In certain aspects, the sugar modified nucleosides of regions A and C enhance the affinity of the ASO for the target nucleic acid (*i.e.*, affinity enhancing 2' sugar modified nucleosides). In some aspects, the sugar modified nucleosides are 2' sugar modified nucleosides, such as high affinity 2' sugar modifications, such as LNA and/or 2'-MOE.

[0204] In a gapmer, the 5' and 3' most nucleosides of region B are DNA nucleosides, and are positioned adjacent to nucleoside analogs (*e.g.*, high affinity sugar modified nucleosides) of regions A and C, respectively. In some aspects, regions A and C can be further defined by having nucleoside analogs at the end most distant from region B (*i.e.*, at the 5' end of region A and at the 3' end of region C).

[0205] In some aspects, the ASOs of the present disclosure comprise a nucleotide sequence of formula (5' to 3') A-B-C, wherein: (A) (5' region or a first wing sequence) comprises at least one nucleoside analog (*e.g.*, 3-5 LNA units); (B) comprises at least four consecutive nucleosides (*e.g.*, 4-24 DNA units), which are capable of recruiting RNase (when formed in a duplex with a

complementary RNA molecule, such as the pre-mRNA or mRNA target); and (C) (3' region or a second wing sequence) comprises at least one nucleoside analog (*e.g.*, 3-5 LNA units).

[0206] In some aspects, region A comprises 3-5 nucleoside analogs, such as LNA, region B consists of 6-24 (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, or 14) DNA units, and region C consists of 3 or 4 nucleoside analogs, such as LNA. Such designs include (A-B-C) 3-14-3, 3-11-3, 3-12-3, 3-13-3, 4-9-4, 4-10-4, 4-11-4, 4-12-4, and 5-10-5. In some aspects, the ASO has a design of LLLD_nLLL, LLLLD_nLLLL, or LLLLLD_nLLLLL, wherein the L is a nucleoside analog, the D is DNA, and n can be any integer between 4 and 24. In some aspects, n can be any integer between 6 and 14. In some aspects, n can be any integer between 8 and 12. In some aspects, n can be any integer between 6 and 14. In some aspects, n can be any integer between 8 and 12. In some aspects, the ASO has a design of LLLMMD_nMMLLL, LLLMD_nMLLL, LLLLMMMD_nMMLLLL, LLLLMD_nMLLLL, LLLLLLMMMD_nMMLLLLL, or LLLLLLMD_nMLLLLL, wherein the D is DNA, n can be any integer between 3 and 15, the L is LNA, and the M is 2'MOE.

[0207] Further gapmer designs are disclosed in WO2004/046160, WO 2007/146511, and WO2008/113832, each of which is hereby incorporated by reference in its entirety.

II.I. Internucleotide Linkages

[0208] The monomers of the ASOs described herein are coupled together via linkage groups. Suitably, each monomer is linked to the 3' adjacent monomer via a linkage group.

[0209] The person having ordinary skill in the art would understand that, in the context of the present disclosure, the 5' monomer at the end of an ASO does not comprise a 5' linkage group, although it may or may not comprise a 5' terminal group.

[0210] In some aspects, the contiguous nucleotide sequence comprises one or more modified internucleoside linkages. The terms "linkage group" or "internucleoside linkage" are intended to mean a group capable of covalently coupling together two nucleosides. Non-limiting examples include phosphate groups and phosphorothioate groups.

[0211] The nucleosides of the ASO of the disclosure or contiguous nucleosides sequence thereof are coupled together via linkage groups. Suitably, each nucleoside is linked to the 3' adjacent nucleoside via a linkage group.

[0212] In some aspects, the internucleoside linkage is modified from its normal phosphodiester to one that is more resistant to nuclease attack, such as phosphorothioate, which is cleavable by RNaseH, also allows that route of antisense inhibition in reducing the expression of the target gene. In some aspects, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%,

at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of internucleoside linkages are modified.

III. Extracellular Vesicles, *e.g.*, Exosomes

[0213] Disclosed herein are EVs, *e.g.*, exosomes, comprising a STAT3 antagonist. In some aspects, the STAT3 antagonist is an antisense oligonucleotide (ASO). The ASO can be any ASO described herein or a functional fragment thereof. In certain aspects, the ASO reduces the level of a *STAT3* mRNA or a STAT3 protein in a target cell.

[0214] In some aspects, the EV, *e.g.*, the exosome, targets an immune cell. In some aspects the immune cell is selected from a macrophage, a dendritic cell, a B cell, a T cell, and any combination thereof. In certain aspects, an EV of the present disclosure targets a tumor cell. In certain aspects, the EV, *e.g.*, the exosome, targets a macrophage. In certain aspects, the EV, *e.g.*, the exosome, targets a dendritic cell. In certain aspects, the EV, *e.g.*, the exosome, targets a B cell. In certain aspects, the EV, *e.g.*, the exosome, targets a T cell.

[0215] In some aspects, the EV, *e.g.*, the exosome, treats a cancer in a subject in need thereof. In some aspects, the cancer is selected from fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell cancer, squamous cell cancer of the head and neck cancer, colorectal cancer, lymphoma, leukemia, liver cancer, glioblastoma, melanoma, myeloma basal cell cancer, adenocarcinoma, sweat gland cancer, sebaceous gland cancer, papillary cancer, papillary adenocarcinomas, cystadenocarcinoma, medullary cancer, bronchogenic cancer, renal cell cancer, hepatoma, bile duct cancer, choriocarcinoma, seminoma, embryonal cancer, Wilms' tumor, cervical cancer, testicular cancer, lung cancer, small cell lung cancer, bladder cancer, epithelial cancer, glioma, glioblastoma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma, acute myeloid leukemia, gastric cancer, hepatocellular carcinoma, and any combination thereof.

[0216] As described *supra*, EVs, *e.g.*, exosomes, described herein are extracellular vesicles with a diameter between about 20-300 nm. In certain aspects, an EV, *e.g.*, exosome, of the present disclosure has a diameter between about 20-290 nm, 20-280 nm, 20-270 nm, 20-260 nm, 20-250 nm, 20-240 nm, 20-230 nm, 20-220 nm, 20-210 nm, 20-200 nm, 20-190 nm, 20-180 nm, 20-170

nm, 20-160 nm, 20-150 nm, 20-140 nm, 20-130 nm, 20-120 nm, 20-110 nm, 20-100 nm, 20-90 nm, 20-80 nm, 20-70 nm, 20-60 nm, 20-50 nm, 20-40 nm, 20-30 nm, 30-300 nm, 30-290 nm, 30-280 nm, 30-270 nm, 30-260 nm, 30-250 nm, 30-240 nm, 30-230 nm, 30-220 nm, 30-210 nm, 30-200 nm, 30-190 nm, 30-180 nm, 30-170 nm, 30-160 nm, 30-150 nm, 30-140 nm, 30-130 nm, 30-120 nm, 30-110 nm, 30-100 nm, 30-90 nm, 30-80 nm, 30-70 nm, 30-60 nm, 30-50 nm, 30-40 nm, 40-300 nm, 40-290 nm, 40-280 nm, 40-270 nm, 40-260 nm, 40-250 nm, 40-240 nm, 40-230 nm, 40-220 nm, 40-210 nm, 40-200 nm, 40-190 nm, 40-180 nm, 40-170 nm, 40-160 nm, 40-150 nm, 40-140 nm, 40-130 nm, 40-120 nm, 40-110 nm, 40-100 nm, 40-90 nm, 40-80 nm, 40-70 nm, 40-60 nm, 40-50 nm, 50-300 nm, 50-290 nm, 50-280 nm, 50-270 nm, 50-260 nm, 50-250 nm, 50-240 nm, 50-230 nm, 50-220 nm, 50-210 nm, 50-200 nm, 50-190 nm, 50-180 nm, 50-170 nm, 50-160 nm, 50-150 nm, 50-140 nm, 50-130 nm, 50-120 nm, 50-110 nm, 50-100 nm, 50-90 nm, 50-80 nm, 50-70 nm, 50-60 nm, 60-300 nm, 60-290 nm, 60-280 nm, 60-270 nm, 60-260 nm, 60-250 nm, 60-240 nm, 60-230 nm, 60-220 nm, 60-210 nm, 60-200 nm, 60-190 nm, 60-180 nm, 60-170 nm, 60-160 nm, 60-150 nm, 60-140 nm, 60-130 nm, 60-120 nm, 60-110 nm, 60-100 nm, 60-90 nm, 60-80 nm, 60-70 nm, 70-300 nm, 70-290 nm, 70-280 nm, 70-270 nm, 70-260 nm, 70-250 nm, 70-240 nm, 70-230 nm, 70-220 nm, 70-210 nm, 70-200 nm, 70-190 nm, 70-180 nm, 70-170 nm, 70-160 nm, 70-150 nm, 70-140 nm, 70-130 nm, 70-120 nm, 70-110 nm, 70-100 nm, 70-90 nm, 70-80 nm, 80-300 nm, 80-290 nm, 80-280 nm, 80-270 nm, 80-260 nm, 80-250 nm, 80-240 nm, 80-230 nm, 80-220 nm, 80-210 nm, 80-200 nm, 80-190 nm, 80-180 nm, 80-170 nm, 80-160 nm, 80-150 nm, 80-140 nm, 80-130 nm, 80-120 nm, 80-110 nm, 80-100 nm, 80-90 nm, 90-300 nm, 90-290 nm, 90-280 nm, 90-270 nm, 90-260 nm, 90-250 nm, 90-240 nm, 90-230 nm, 90-220 nm, 90-210 nm, 90-200 nm, 90-190 nm, 90-180 nm, 90-170 nm, 90-160 nm, 90-150 nm, 90-140 nm, 90-130 nm, 90-120 nm, 90-110 nm, 90-100 nm, 100-300 nm, 110-290 nm, 120-280 nm, 130-270 nm, 140-260 nm, 150-250 nm, 160-240 nm, 170-230 nm, 180-220 nm, or 190-210 nm. The size of the EV, *e.g.*, exosome, described herein can be measured according to methods described, *infra*.

[0217] In some aspects, an EV, *e.g.*, exosome, of the present disclosure comprises a bi-lipid membrane ("EV, *e.g.*, exosome, membrane"), comprising an interior (luminal) surface and an exterior surface. In certain aspects, the interior (luminal) surface faces the inner core (*i.e.*, lumen) of the EV, *e.g.*, exosome. In certain aspects, the exterior surface can be in contact with the endosome, the multivesicular bodies, or the membrane/cytoplasm of a producer cell or a target cell

[0218] In some aspects, the EV, *e.g.*, exosome, membrane comprises lipids and fatty acids. In some aspects, the EV, *e.g.*, exosome, membrane comprises phospholipids, glycolipids, fatty acids, sphingolipids, phosphoglycerides, sterols, cholesterol, and phosphatidylserines.

[0219] In some aspects, the EV, *e.g.*, exosome, membrane comprises an inner leaflet and an outer leaflet. The composition of the inner and outer leaflet can be determined by transbilayer distribution assays known in the art, *see, e.g.*, Kuypers *et al.*, *Biochim Biophys Acta* 1985 819:170. In some aspects, the composition of the outer leaflet is between approximately 70-90% choline phospholipids, between approximately 0-15% acidic phospholipids, and between approximately 5-30% phosphatidylethanolamine. In some aspects, the composition of the inner leaflet is between approximately 15-40% choline phospholipids, between approximately 10-50% acidic phospholipids, and between approximately 30-60% phosphatidylethanolamine.

[0220] In some aspects, the EV, *e.g.*, exosome, membrane comprises one or more polysaccharide, such as glycan.

[0221] In some aspects, the EV, *e.g.*, exosome, of the present disclosure comprises an ASO, wherein the ASO is linked to the EV via a scaffold moiety, either on the exterior surface of the EV or on the luminal surface of the EV.

[0222] In some aspects, the EV, *e.g.*, exosome, comprising an ASO comprises an anchoring moiety, which optionally comprising a linker, between the ASO and the exosome membrane. In some aspects, the ASO is exogenous. In some aspects, the ASO is not a part of exosome produced by a producer cell.

[0223] In some aspects, the EV, *e.g.*, the exosome, comprises at least one ASO. In some aspects, the EV, *e.g.*, the exosome, comprises at least two ASOs, *e.g.*, a first ASO comprising a first nucleotide sequence and a second ASO comprising a second nucleotide sequence. In some aspects, the EV, *e.g.*, the exosome, comprises at least three ASOs, at least four ASOs, at least five ASOs, at least six ASOs, or more than six ASOs. In some aspects, each of the first ASO, the second ASO, the third ASO, the fourth ASO, the fifth ASO, the sixth ASO, and/or the Nth ASO is different.

[0224] In some aspects, the EV, *e.g.* the exosome, comprises a first ASO and a second ASO, wherein the first ASO comprises a first nucleotide sequence that is complimentary to a first target sequence in a first transcript, and wherein the second ASO comprises a second nucleotide sequence that is complimentary to a second target sequence in the first transcript. In some aspects, the first target sequence does not overlap with the second target sequence. In some aspects, the first target sequence comprises at least one nucleotide that is within the 5'UTR of the transcript, and the second target sequence does not comprise a nucleotide that is within the 5'UTR. In some aspects, the first target sequence comprises at least one nucleotide that is within the 3'UTR of the transcript, and the second target sequence does not comprise a nucleotide that is within the 3'UTR.

In some aspects, the first target sequence comprises at least one nucleotide that is within the 5'UTR of the transcript, and the second target sequence comprises at least one nucleotide that is within the 3'UTR.

[0225] In some aspects, the first ASO targets a sequence within an exon-intron junction, and the second ASO targets a sequence within an exon-intron junction. In some aspects, the first ASO targets a sequence within an exon-intron junction, and the second ASO targets a sequence within an exon. In some aspects, the first ASO targets a sequence within an exon-intron junction, and the second ASO targets a sequence within an intron. In some aspects, the first ASO targets a sequence within an exon, and the second ASO targets a sequence within an exon. In some aspects, the first ASO targets a sequence within an intron, and the second ASO targets a sequence within an exon. In some aspects, the first ASO targets a sequence within an intron, and the second ASO targets a sequence within an intron.

[0226] In some aspects, the EV, *e.g.* the exosome, comprises a first ASO and a second ASO, wherein the first ASO comprises a first nucleotide sequence that is complimentary to a first target sequence in a first transcript, and wherein the second ASO comprises a second nucleotide sequence that is complimentary to a second target sequence in a second transcript, wherein the first transcript is not the product of the same gene as the second transcript.

[0227] In some aspects, the ASOs for the present disclosure include a phosphorodiamidate Morpholino oligomer (PMO) or a peptide-conjugated phosphorodiamidate morpholino oligomer (PPMO).

[0228] Non-limiting examples of the linkers are disclosed elsewhere herein.

III.A. Anchoring moieties (AM)

[0229] One or more anchoring moieties (AMs) can be used to anchor an ASO to the EV of the present disclosure. In some aspects, the ASO is linked directly to the anchoring moiety or via a linker. In some aspects, the ASO can be attached to an anchoring moiety or linker combination via reaction between a "reactive group" (RG; *e.g.*, amine, thiol, hydroxy, carboxylic acid, or azide) with a "reactive moiety" (RM; *e.g.*, maleimide, succinate, NHS). Several potential synthetic routes are envisioned, for example:

[AM]-/Reactive moiety/	+	/Reactive group/-[ASO]
[AM]-[Linker] <i>n</i> -/Reactive moiety/	+	/Reactive group/-[ASO]
[AM]-/Reactive moiety/	+	/Reactive group/-[Linker] <i>n</i> -[ASO]
[AM]- [Linker] <i>n</i> -/Reactive moiety/	+	/Reactive group/-[Linker] <i>n</i> -[ASO]

[0230] The anchoring moiety can insert into the lipid bilayer of an EV, e.g., an exosome, allowing the loading of the exosome with an ASO. Currently, a predominant obstacle to the commercialization of exosomes as a delivery vehicle for polar ASOs, is highly inefficient loading. This obstacle can be overcome by modifying polar ASOs, prior to loading them into exosomes. Thus, as described herein, modification of ASOs facilitates their loading into exosomes.

[0231] The methods of loading exosomes with modified polar ASOs set forth herein significantly improve loading efficiency as compared to the loading efficiency previously reported for introducing unmodified ASOs into exosomes by, for example, electroporation or cationic lipid transfection.

[0232] In some aspects, the modifications increase the hydrophobicity of the an ASO by at least about 1, at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 fold relative to native (non-modified) ASO. In some aspects, the modifications increase the hydrophobicity of the ASO by at least about 1, at least about 2, at least about 3, at least about 4, at least about 5, at least about 6, at least about 7, at least about 8, at least about 9, or at least about 10 orders of magnitude relative to native (non-modified) ASO.

[0233] In some aspects, the modifications increase the hydrophobicity of the ASO by at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 100%, at least about 125%, at least about 150%, at least about 175%, at least about 200%, at least about 250%, at least about 300%, at least about 350%, at least about 400%, at least about 450%, at least about 500%, at least about 600%, at least about 700%, at least about 800%, at least about 900%, or at least about 1000% relative to native (non-modified) ASO, e.g., the corresponding unmodified ASO. Increases in hydrophobicity can be assessed using any suitable method. For example, hydrophobicity can be determined by measuring the percentage solubility in an organic solvent, such as octanol, as compared to solubility in an aqueous solvent, such as water.

[0234] In some aspect, an anchoring moiety can be chemically conjugated to an ASO to enhance its hydrophobic character. In exemplary aspects, the anchoring moiety is a sterol (e.g., cholesterol), GM1, a lipid, a vitamin, a small molecule, a peptide, or a combination thereof. In some aspects, the moiety is a lipid. In some aspects, the anchoring moiety is a sterol, e.g., cholesterol. Additional hydrophobic moieties include, for example, phospholipids, lysophospholipids, fatty acids, or vitamins (e.g., vitamin D or vitamin E).

[0235] In some aspects, the anchoring moiety is conjugated at the termini of the ASO either directly or via one or more linkers (i.e., "terminal modification"). In other aspects, the anchoring moiety is conjugated to other portions of the ASO.

[0236] In some aspects, the ASO can include a detectable label. Exemplary labels include fluorescent labels and/or radioactive labels. In some aspects, where ASOs are fluorescently labeled, the detectable label can be, for example, Cy3. Adding a detectable label to ASOs can be used as a way of labeling exosomes, and following their biodistribution. In other aspects, a detectable label can be attached to exosomes directly, for example, by way of labeling an exosomal lipid and/or an exosomal peptide.

[0237] The different components of an ASO (i.e., anchoring moieties, linkers and linker combinations, and ASOs) can be linked by amide, ester, ether, thioether, disulfide, phosphoramidate, phosphotriester, phosphorodithioate, methyl phosphonate, phosphodiester, or phosphorothioate linkages or, alternatively any or other linkage.

[0238] In some aspects, the different components of an ASO can be linker using bifunctional linkers (i.e., linkers containing two functional groups), such as N-succinimidyl-3-(2-pyridyldithio)propionate, N-4-maleimide butyric acid, S-(2-pyridyldithio)cysteamine, iodoacetoxysuccinimide, N-(4-maleimidebutyloxy) succinimide, N-[5-(3'-maleimide propylamide)-1-carboxypentyl]iminodiacetic acid, N-(5-aminopentyl)-iminodiacetic acid, and the like.

III.B.1. Anchoring moieties

[0239] Suitable anchoring moieties capable of anchoring an ASO to the surface of an EV, e.g., an exosome, comprise for example sterols (e.g., cholesterol), lipids, lysophospholipids, fatty acids, or fat-soluble vitamins, as described in detail below.

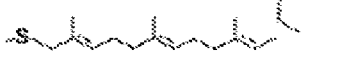
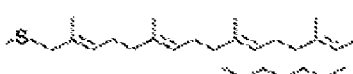
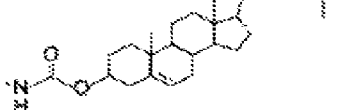
[0240] In some aspects, the anchoring moiety can be a lipid. A lipid anchoring moiety can be any lipid known in the art, e.g., palmitic acid or glycosylphosphatidylinositols. In some aspects, the lipid, is a fatty acid, phosphatide, phospholipid (e.g., phosphatidyl choline, phosphatidyl serine, or phosphatidyl ethanolamine), or analogue thereof (e.g. phosphatidylcholine, lecithin, phosphatidylethanolamine, cephalin, or phosphatidylserine or analogue or portion thereof, such as a partially hydrolyzed portion thereof). In some aspects, the anchoring moiety is a cholesterol.

[0241] Generally, anchoring moieties are chemically attached. However, an anchoring moiety can be attached to an ASO enzymatically. In some aspects, it is possible to attach an anchoring moiety to an ASO via modification of cell culture conditions. For example, by using a

culture medium where myristic acid is limiting, some other fatty acids including shorter-chain and unsaturated, can be attached to an N-terminal glycine. For example, in BK channels, myristate has been reported to be attached posttranslationally to internal serine/threonine or tyrosine residues via a hydroxyester linkage.

[0242] The anchoring moiety can be conjugated to an ASO directly or indirectly via a linker combination, at any chemically feasible location, e.g., at the 5' and/or 3' end of the ASO. In one aspect, the anchoring moiety is conjugated only to the 3' end of the ASO. In one aspect, the anchoring moiety is conjugated only to the 5' end of the ASO. In one aspect, the anchoring moiety is conjugated at a location which is not the 3' end or 5' end of the ASO.

[0243] Some types of membrane anchors that can be used to practice the methods of the present disclosure presented in the following table:

Modification	Modifying Group
S-Palmitoylation	
N-Palmitoylation	
N-Myristoylation	
O-Acylation	
Farnesylation	
Geranylgeranylation	
Cholesterol	

[0244] In some aspects, an anchoring moiety of the present disclosure can comprise two or more types of anchoring moieties disclosed herein. For example, in some aspects, an anchoring moiety can comprise two lipids, e.g., a phospholipids and a fatty acid, or two phospholipids, or two fatty acids, or a lipid and a vitamin, or cholesterol and a vitamin, etc. which taken together have 6-80 carbon atoms (i.e., an equivalent carbon number (ECN) of 6-80).

[0245] In some aspects, the combination of anchoring moieties, e.g., a combination of the lipids (e.g., fatty acids) has an ECN of 6-80, 8-80, 10-80, 12-80, 14-80, 16-80, 18-80, 20-80, 22-80, 24-80, 26-80, 28-80, 30-80, 4-76, 6-76, 8-76, 10-76, 12-76, 14-76, 16-76, 18-76, 20-76, 22-76,

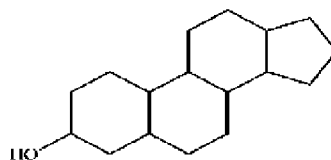
24-76, 26-76, 28-76, 30-76, 6-72, 8-72, 10-72, 12-72, 14-72, 16-72, 18-72, 20-72, 22-72, 24-72, 26-72, 28-72, 30-72, 6-68, 8-68, 10-68, 12-68, 14-68, 16-68, 18-68, 20-68, 22-68, 24-68, 26-68, 28-68, 30-68, 6-64, 8-64, 10-64, 12-64, 14-64, 16-64, 18-64, 20-64, 22-64, 24-64, 26-64, 28-64, 30-64, 6-60, 8-60, 10-60, 12-56, 14-56, 16-56, 18-56, 20-56, 22-56, 24-56, 26-56, 28-56, 30-56, 6-52, 8-52, 10-52, 12-52, 14-52, 16-52, 18-52, 20-52, 22-52, 24-52, 26-52, 28-52, 30-52, 6-48, 8-48, 10-48, 12-48, 14-48, 16-48, 18-48, 20-48, 22-48, 24-48, 26-48, 28-48, 30-48, 6-44, 8-44, 10-44, 12-44, 14-44, 16-44, 18-44, 20-44, 22-44, 24-44, 26-44, 28-44, 30-44, 6-40, 8-40, 10-40, 12-40, 14-40, 16-40, 18-40, 20-40, 22-40, 24-40, 26-40, 28-40, 30-40, 6-36, 8-36, 10-36, 12-36, 14-36, 16-36, 18-36, 20-36, 22-36, 24-36, 26-36, 28-36, 30-36, 6-32, 8-32, 10-32, 12-32, 14-32, 16-32, 18-32, 20-32, 22-32, 24-32, 26-32, 28-32, or 30-32.

III.B.1.a. Cholesterol and other sterols

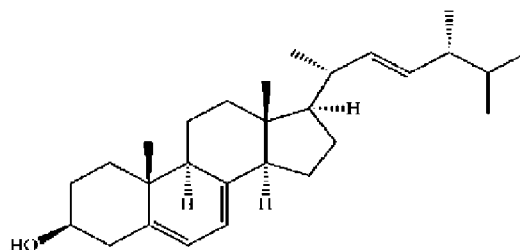
[0246] In some aspects, the anchoring moiety comprises a sterol, steroid, hopanoid, hydroxysteroid, secosteroid, or analog thereof with lipophilic properties. In some aspects, the anchoring moiety comprises a sterol, such as a phytosterol, mycosterol, or zoosterol. Exemplary zoosterols include cholesterol and 24S-hydroxycholesterol; exemplary phytosterols include ergosterol (mycosterol), campesterol, sitosterol, and stigmasterol. In some aspects, the sterol is selected from ergosterol, 7-dehydrocholesterol, cholesterol, 24S-hydroxycholesterol, lanosterol, cycloartenol, fucosterol, saringosterol, campesterol, β -sitosterol, sitostanol, coprostanol, avenasterol, or stigmasterol. Sterols may be found either as free sterols, acylated (sterol esters), alkylated (steryl alkyl ethers), sulfated (sterol sulfate), or linked to a glycoside moiety (steryl glycosides), which can be itself acylated (acylated sterol glycosides).

[0247] In some aspects, the anchoring moiety comprises a steroid. In some aspects, the steroid is selected from dihydrotestosterone, uvaol, hecigenin, diosgenin, progesterone, or cortisol.

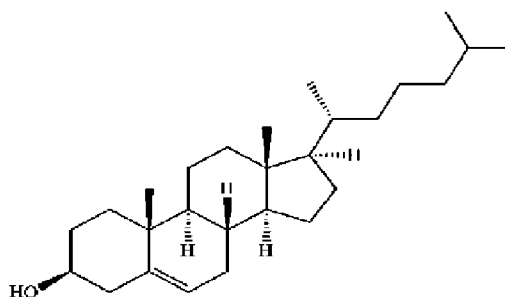
[0248] For example, sterols may be conjugated to the ASO directly or via a linker combination at the available —OH group of the sterol. Exemplary sterols have the general skeleton shown below:



[0249] As a further example, ergosterol has the structure below:



[0250] Cholesterol has the structure below:



[0251] Accordingly, in some embodiments, the free —OH group of a sterol or steroid is used to conjugate the ASO directly or via a linker combination, to the sterol (e.g., cholesterol) or steroid.

III.B.1.b. Fatty acids

[0252] In some aspects, the anchoring moiety is a fatty acid. In some aspects, the fatty acid is a short-chain, medium-chain, or long-chain fatty acid. In some aspects, the fatty acid is a saturated fatty acid. In some aspects, the fatty acid is an unsaturated fatty acid. In some aspects, the fatty acid is a monounsaturated fatty acid. In some aspects, the fatty acid is a polyunsaturated fatty acid, such as an ω -3 (omega-3) or ω -6 (omega-6) fatty acid.

[0253] In some aspects, the lipid, e.g., fatty acid, has a C₂-C₆₀ chain. In some embodiments, the lipid, e.g., fatty acid, has a C₂-C₂₈ chain. In some aspects, the fatty acid, has a C₂-C₄₀ chain. In some aspects, the fatty acid, has a C₂-C₁₂ or C₄-C₁₂ chain. In some aspects, the fatty acid, has a C₄-C₄₀ chain. In some aspects, the fatty acid, has a C₄-C₄₀, C₂-C₃₈, C₂-C₃₆, C₂-C₃₄, C₂-C₃₂, C₂-C₃₀, C₄-C₃₀, C₂-C₂₈, C₄-C₂₈, C₂-C₂₆, C₄-C₂₆, C₂-C₂₄, C₄-C₂₄, C₆-C₂₄, C₈-C₂₄, C₁₀-C₂₄, C₂-C₂₂, C₄-C₂₂, C₆-C₂₂, C₈-C₂₂, C₁₀-C₂₂, C₂-C₂₀, C₄-C₂₀, C₆-C₂₀, C₈-C₂₀, C₁₀-C₂₀, C₂-C₁₈, C₄-C₁₈, C₆-C₁₈, C₈-C₁₈, C₁₀-C₁₈, C₁₂-C₁₈, C₁₄-C₁₈, C₁₆-C₁₈, C₂-C₁₆, C₄-C₁₆, C₆-C₁₆, C₈-C₁₆, C₁₀-C₁₆, C₁₂-C₁₆, C₁₄-C₁₆, C₂-C₁₅, C₄-C₁₅, C₆-C₁₅, C₈-C₁₅, C₉-C₁₅, C₁₀-C₁₅, C₁₁-C₁₅, C₁₂-C₁₅, C₁₃-C₁₅, C₂-C₁₄, C₄-C₁₄, C₆-C₁₄, C₈-C₁₄, C₉-C₁₄, C₁₀-C₁₄, C₁₁-C₁₄, C₁₂-C₁₄, C₂-C₁₃, C₄-C₁₃, C₆-C₁₃, C₇-C₁₃, C₈-C₁₃, C₉-C₁₃, C₁₀-C₁₃, C₁₀-C₁₃, C₁₁-C₁₃, C₂-C₁₂, C₄-C₁₂, C₆-C₁₂, C₇-C₁₂, C₈-C₁₂, C₉-C₁₂, C₁₀-C₁₂, C₂-C₁₁, C₄-C₁₁, C₆-C₁₁, C₇-C₁₁, C₈-C₁₁, C₉-C₁₁, C₂-C₁₀, C₄-C₁₀, C₂-C₉, C₄-C₉, C₂-C₈, C₂-C₇, C₄-C₇, C₂-C₆, or C₄-C₆, chain. In some

aspects, the fatty acid, has a C₂, C₃, C₄, C₅, C₆, C₇, C₈, C₉, C₁₀, C₁₁, C₁₂, C₁₃, C₁₄, C₁₅, C₁₆, C₁₇, C₁₈, C₁₉, C₂₀, C₂₁, C₂₂, C₂₃, C₂₄, C₂₅, C₂₆, C₂₇, C₂₈, C₂₉, C₃₀, C₃₁, C₃₂, C₃₃, C₃₄, C₃₅, C₃₆, C₃₇, C₃₈, C₃₉, C₄₀, C₄₁, C₄₂, C₄₃, C₄₄, C₄₅, C₄₆, C₄₇, C₄₈, C₄₉, C₅₀, C₅₁, C₅₂, C₅₃, C₅₄, C₅₅, C₅₆, C₅₇, C₅₈, C₅₉, or C₆₀ chain.

[0254] In some aspects, the anchoring moiety comprises two fatty acids, each of which is independently selected from a fatty acid having a chain with any one of the foregoing ranges or numbers of carbon atoms. In some aspects, one of the fatty acids is independently a fatty acid with a C₆-C₂₁ chain and one is independently a fatty acid with a C₁₂-C₃₆ chain. In some embodiments, each fatty acid independently has a chain of 11, 12, 13, 14, 15, 16, or 17 carbon atoms.

[0255] Suitable fatty acids include saturated straight-chain fatty acids, saturated branched fatty acids, unsaturated fatty acids, hydroxy fatty acids, and polycarboxylic acids. In some aspects, such fatty acids have up to 32 carbon atoms.

[0256] Examples of useful saturated straight-chain fatty acids include those having an even number of carbon atoms, such as butyric acid, caproic acid, caprylic acid, capric acid, lauric acid, myristic acid, palmitic acid, stearic acid, arachic acid, behenic acid, lignoceric acid, hexacosanoic acid, octacosanoic acid, triacontanoic acid and n-dotriacontanoic acid, and those having an odd number of carbon atoms, such as propionic acid, n-valeric acid, enanthic acid, pelargonic acid, hendecanoic acid, tridecanoic acid, pentadecanoic acid, heptadecanoic acid, nonadecanoic acid, heneicosanoic acid, tricosanoic acid, pentacosanoic acid, and heptacosanoic acid.

[0257] Examples of suitable saturated branched fatty acids include isobutyric acid, isocaproic acid, isocaprylic acid, isocapric acid, isolauric acid, 11-methyldodecanoic acid, isomyristic acid, 13-methyl-tetradecanoic acid, isopalmitic acid, 15-methyl-hexadecanoic acid, isostearic acid, 17-methyloctadecanoic acid, isoarachic acid, 19-methyl-eicosanoic acid, α -ethyl-hexanoic acid, α -hexyldecanoic acid, α -heptylundecanoic acid, 2-decyltetradecanoic acid, 2-undecyltetradecanoic acid, 2-decylpentadecanoic acid, 2-undecylpentadecanoic acid, and Fine oxocol 1800 acid (product of Nissan Chemical Industries, Ltd.). Suitable saturated odd-carbon branched fatty acids include anteiso fatty acids terminating with an isobutyl group, such as 6-methyl-octanoic acid, 8-methyl-decanoic acid, 10-methyl-dodecanoic acid, 12-methyl-tetradecanoic acid, 14-methyl-hexadecanoic acid, 16-methyl-octadecanoic acid, 18-methyl-eicosanoic acid, 20-methyl-docosanoic acid, 22-methyl-tetracosanoic acid, 24-methyl-hexacosanoic acid, and 26-methyloctacosanoic acid.

[0258] Examples of suitable unsaturated fatty acids include 4-decenoic acid, caproleic acid, 4-dodecenoic acid, 5-dodecenoic acid, lauroleic acid, 4-tetradecenoic acid, 5-tetradecenoic acid,

9-tetradecenoic acid, palmitoleic acid, 6-octadecenoic acid, oleic acid, 9-octadecenoic acid, 11-octadecenoic acid, 9-eicosenoic acid, cis-11-eicosenoic acid, cetoleic acid, 13-docosenoic acid, 15-tetracosenoic acid, 17-hexacosenoic acid, 6,9,12,15-hexadecatetraenoic acid, linoleic acid, linolenic acid, α -eleostearic acid, β -eleostearic acid, punicic acid, 6,9,12,15-octadecatetraenoic acid, parinaric acid, 5,8,11,14-eicosatetraenoic acid, 5,8,11,14,17-eicosapentaenoic acid, 7,10,13,16,19-docosapentaenoic acid, 4,7,10,13,16,19-docosaheptaenoic acid, and the like.

[0259] Examples of suitable hydroxy fatty acids include α -hydroxy lauric acid, α -hydroxymyristic acid, α -hydroxypalmitic acid, α -hydroxystearic acid, ω -hydroxy lauric acid, α -hydroxyarachic acid, 9-hydroxy-12-octadecenoic acid, ricinoleic acid, α -hydroxybehenic acid, 9-hydroxy-trans-10,12-octadecadienic acid, kamolenic acid, ipurolic acid, 9,10-dihydroxystearic acid, 12-hydroxystearic acid and the like.

[0260] Examples of suitable polycarboxylic acids include oxalic acid, malonic acid, succinic acid, glutaric acid, adipic acid, pimelic acid, suberic acid, azelaic acid, sebacic acid, D,L-malic acid, and the like.

[0261] In some aspects, each fatty acid is independently selected from propionic acid, butyric acid, valeric acid, caproic acid, enanthic acid, caprylic acid, pelargonic acid, capric acid, undecylic acid, lauric acid, tridecylic acid, myristic acid, pentadecylic acid, palmitic acid, margaric acid, stearic acid, nonadecylic acid, arachidic acid, heneicosylic acid, behenic acid, tricosylic acid, lignoceric acid, pentacosylic acid, cerotic acid, heptacosylic acid, montanic acid, nonacosylic acid, melissic acid, henatriacontylic acid, lacceroic acid, psyllic acid, geddic acid, ceroplastic acid, hexatriacontylic acid, heptatriacontanoic acid, or octatriacontanoic acid.

[0262] In some aspects, each fatty acid is independently selected from α -linolenic acid, stearidonic acid, eicosapentaenoic acid, docosaheptaenoic acid, linoleic acid, gamma-linoleic acid, dihomogamma-linoleic acid, arachidonic acid, docosatetraenoic acid, palmitoleic acid, vaccenic acid, paullinic acid, oleic acid, elaidic acid, gondoic acid, eucic acid, nervonic acid, mead acid, adrenic acid, bosseopentaenoic acid, ozubondo acid, sardine acid, herring acid, docosaheptaenoic acid, or tetracosanolpentaenoic acid, or another monounsaturated or polyunsaturated fatty acid.

[0263] In some aspects, one or both of the fatty acids is an essential fatty acid. In view of the beneficial health effects of certain essential fatty acids, the therapeutic benefits of disclosed therapeutic-loaded exosomes may be increased by including such fatty acids in the therapeutic agent. In some aspects, the essential fatty acid is an n-6 or n-3 essential fatty acid selected from the group consisting of linolenic acid, gamma-linolenic acid, dihomogamma-linolenic acid,

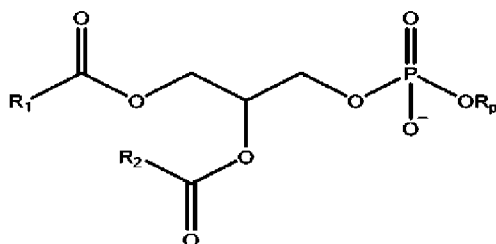
arachidonic acid, adrenic acid, docosapentaenoic n-6 acid, alpha-linolenic acid, stearidonic acid, the 20:4n-3 acid, eicosapentaenoic acid, docosapentaenoic n-3 acid, or docosahexaenoic acid.

[0264] In some aspects, each fatty acid is independently selected from all-cis-7,10,13-hexadecatrienoic acid, α -linolenic acid, stearidonic acid, eicosatrienoic acid, eicosatetraenoic acid, eicosapentaenoic acid (EPA), docosapentaenoic acid, docosahexaenoic acid (DHA), tetracosapentaenoic acid, tetracosahexaenoic acid, or lipoic acid. In other aspects, the fatty acid is selected from eicosapentaenoic acid, docosahexaenoic acid, or lipoic acid. Other examples of fatty acids include all-cis-7,10,13-hexadecatrienoic acid, α -linolenic acid (ALA or all-cis-9,12,15-octadecatrienoic acid), stearidonic acid (STD or all-cis-6,9,12,15-octadecatetraenoic acid), eicosatrienoic acid (ETE or all-cis-11,14,17-eicosatrienoic acid), eicosatetraenoic acid (ETA or all-cis-8,11,14,17-eicosatetraenoic acid), eicosapentaenoic acid (EPA), docosapentaenoic acid (DPA, clupanodonic acid or all-cis-7,10,13,16,19-docosapentaenoic acid), docosahexaenoic acid (DHA or all-cis-4,7,10,13,16,19-docosahexaenoic acid), tetracosapentaenoic acid (all-cis-9,12,15,18,21-docosahexaenoic acid), or tetracosahexaenoic acid (nisinic acid or all-cis-6,9,12,15,18,21-tetracosenoic acid). In some aspects, the fatty acid is a medium-chain fatty acid such as lipoic acid.

[0265] Fatty acid chains differ greatly in the length of their chains and may be categorized according to chain length, e.g. as short to very long. Short-chain fatty acids (SCFA) are fatty acids with chains of about five or less carbons (e.g. butyric acid). In some aspects, the fatty acid is a SCFA. Medium-chain fatty acids (MCFA) include fatty acids with chains of about 6-12 carbons, which can form medium-chain triglycerides. In some aspects, the fatty acid is a MCFA. Long-chain fatty acids (LCFA) include fatty acids with chains of 13-21 carbons. In some aspects, the fatty acid is a LCFA. In some aspects, the fatty acid is a LCFA. Very long chain fatty acids (VLCFA) include fatty acids with chains of 22 or more carbons, such as 22-60, 22-50, or 22-40 carbons. In some aspects, the fatty acid is a VLCFA.

III.B.1.c. Phospholipids

[0266] In some aspects, the anchoring moiety comprises a phospholipid. Phospholipids are a class of lipids that are a major component of all cell membranes. They can form lipid bilayers because of their amphiphilic characteristic. The structure of the phospholipid molecule generally consists of two hydrophobic fatty acid "tails" and a hydrophilic "head" consisting of a phosphate group. For example, a phospholipid can be a lipid according to the following formula:



in which R_p represents a phospholipid moiety and R_1 and R_2 represent fatty acid moieties with or without unsaturation that may be the same or different.

[0267] A phospholipid moiety may be selected, for example, from the non-limiting group consisting of phosphatidyl choline, phosphatidyl ethanolamine, phosphatidyl glycerol, phosphatidyl serine, phosphatidic acid, 2 lysophosphatidyl choline, and a sphingomyelin.

[0268] Particular phospholipids may facilitate fusion to a lipid bilayer, e.g., the lipid bilayer of an exosomal membrane. For example, a cationic phospholipid may interact with one or more negatively charged phospholipids of a membrane. Fusion of a phospholipid to a membrane may allow one or more elements of a lipid-containing composition to bind to the membrane or to pass through the membrane.

[0269] A fatty acid moiety may be selected, for example, from the non-limiting group consisting of lauric acid, myristic acid, myristoleic acid, palmitic acid, palmitoleic acid, stearic acid, oleic acid, linoleic acid, alpha-linolenic acid, erucic acid, phytanoic acid, arachidic acid, arachidonic acid, eicosapentaenoic acid, behenic acid, docosapentaenoic acid, and docosaheptaenoic acid.

[0270] The phospholipids using as anchoring moieties in the present disclosure can be natural or non-natural phospholipids. Non-natural phospholipid species including natural species with modifications and substitutions including branching, oxidation, cyclization, and alkynes are also contemplated. For example, a phospholipid may be functionalized with or cross-linked to one or more alkynes (e.g., an alkenyl group in which one or more double bonds is replaced with a triple bond). Under appropriate reaction conditions, an alkyne group may undergo a copper-catalyzed cycloaddition upon exposure to an azide.

[0271] Phospholipids include, but are not limited to, glycerophospholipids such as phosphatidylcholines, phosphatidylethanolamines, phosphatidylserines, phosphatidylinositols, phosphatidyl glycerols, and phosphatidic acids.

[0272] Examples of phospholipids that can be used in the anchoring moieties disclosed herein include

- **Phosphatidylethanolamines:** E.g., dilauroylphosphatidyl ethanolamine, dimyristoylphosphatidyl ethanolamine, dipalmitoylphosphatidyl ethanolamine, distearoylphosphatidyl ethanolamine, dioleoylphosphatidyl ethanolamine, 1-palmitoyl-2-oleylphosphatidyl ethanolamine, 1-oleyl-2-palmitoylphosphatidyl ethanolamine, and dierucoylphosphatidyl ethanolamine;
- **Phosphatidyl glycerols:** E.g., dilauroylphosphatidyl glycerol, dimyristoylphosphatidyl glycerol, dipalmitoylphosphatidyl glycerol, distearoylphosphatidyl glycerol, dioleoylphosphatidyl glycerol, 1-palmitoyl-2-oleyl-phosphatidyl glycerol, 1-oleyl-2-palmitoyl-phosphatidyl glycerol, and dierucoylphosphatidyl glycerol;
- **Phosphatidyl serines:** E.g., such as dilauroylphosphatidyl serine, dimyristoylphosphatidyl serine, dipalmitoylphosphatidyl serine, distearoylphosphatidyl serine, dioleoylphosphatidyl serine, 1-palmitoyl-2-oleyl-phosphatidyl serine, 1-oleyl-2-palmitoyl-phosphatidyl serine, and dierucoylphosphatidyl serine;
- **Phosphatidic acids:** E.g., dilauroylphosphatidic acid, dimyristoylphosphatidic acid, dipalmitoylphosphatidic acid, distearoylphosphatidic acid, dioleoylphosphatidic acid, 1-palmitoyl-2-oleylphosphatidic acid, 1-oleyl-2-palmitoyl-phosphatidic acid, and dierucoylphosphatidic acid; and,
- **Phosphatidyl inositols:** E.g., dilauroylphosphatidyl inositol, dimyristoylphosphatidyl inositol, dipalmitoylphosphatidyl inositol, distearoylphosphatidyl inositol, dioleoylphosphatidyl inositol, 1-palmitoyl-2-oleyl-phosphatidyl inositol, 1-oleyl-2-palmitoyl-phosphatidyl inositol, and dierucoylphosphatidyl inositol.

[0273] Phospholipids may be of a symmetric or an asymmetric type. As used herein, the term "symmetric phospholipid" includes glycerophospholipids having matching fatty acid moieties and sphingolipids in which the variable fatty acid moiety and the hydrocarbon chain of the sphingosine backbone include a comparable number of carbon atoms. As used herein, the term "asymmetric phospholipid" includes lysolipids, glycerophospholipids having different fatty acid moieties (e.g., fatty acid moieties with different numbers of carbon atoms and/or unsaturations (e.g., double bonds)), and sphingolipids in which the variable fatty acid moiety and the hydrocarbon chain of the sphingosine backbone include a dissimilar number of carbon atoms (e.g., the variable fatty acid moiety include at least two more carbon atoms than the hydrocarbon chain or at least two fewer carbon atoms than the hydrocarbon chain).

[0274] In some aspects, the anchoring moiety comprises at least one symmetric phospholipid. Symmetric phospholipids may be selected from the non-limiting group consisting of

1,2-dipropionyl-*sn*-glycero-3-phosphocholine (03:0 PC),
 1,2-dibutyryl-*sn*-glycero-3-phosphocholine (04:0 PC),
 1,2-dipentanoyl-*sn*-glycero-3-phosphocholine (05:0 PC),
 1,2-dihexanoyl-*sn*-glycero-3-phosphocholine (06:0 PC),
 1,2-diheptanoyl-*sn*-glycero-3-phosphocholine (07:0 PC),
 1,2-dioctanoyl-*sn*-glycero-3-phosphocholine (08:0 PC),
 1,2-dinonanoyl-*sn*-glycero-3-phosphocholine (09:0 PC),
 1,2-didecanoyl-*sn*-glycero-3-phosphocholine (10:0 PC),
 1,2-diundecanoyl-*sn*-glycero-3-phosphocholine (11:0 PC, DUPC),
 1,2-dilauroyl-*sn*-glycero-3-phosphocholine (12:0 PC),
 1,2-ditridecanoyl-*sn*-glycero-3-phosphocholine (13:0 PC),
 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine (14:0 PC, DMPC),
 1,2-dipentadecanoyl-*sn*-glycero-3-phosphocholine (15:0 PC),
 1,2-dipalmitoyl-*sn*-glycero-3-phosphocholine (16:0 PC, DPPC),
 1,2-diphytanoyl-*sn*-glycero-3-phosphocholine (4ME 16:0 PC),
 1,2-diheptadecanoyl-*sn*-glycero-3-phosphocholine (17:0 PC),
 1,2-distearoyl-*sn*-glycero-3-phosphocholine (18:0 PC, DSPC),
 1,2-dinonadecanoyl-*sn*-glycero-3-phosphocholine (19:0 PC),
 1,2-diarachidoyl-*sn*-glycero-3-phosphocholine (20:0 PC),
 1,2-dihenarachidoyl-*sn*-glycero-3-phosphocholine (21:0 PC),
 1,2-dibehenoyl-*sn*-glycero-3-phosphocholine (22:0 PC),
 1,2-ditricosanoyl-*sn*-glycero-3-phosphocholine (23:0 PC),
 1,2-dilignoceroyl-*sn*-glycero-3-phosphocholine (24:0 PC),
 1,2-dimyristoleoyl-*sn*-glycero-3-phosphocholine (14:1 (Δ^9 -Cis) PC),
 1,2-dimyristelaidoyl-*sn*-glycero-3-phosphocholine (14:1 (Δ^9 -Trans) PC),
 1,2-dipalmitoleoyl-*sn*-glycero-3-phosphocholine (16:1 (Δ^9 -Cis) PC),
 1,2-dipalmitelaidoyl-*sn*-glycero-3-phosphocholine (16:1 (Δ^9 -Trans) PC),
 1,2-dipetroselenoyl-*sn*-glycero-3-phosphocholine (18:1 (Δ^6 -Cis) PC),
 1,2-dioleoyl-*sn*-glycero-3-phosphocholine (18:1 (Δ^9 -Cis) PC, DOPC),
 1,2-dielaaidoyl-*sn*-glycero-3-phosphocholine (18:1 (Δ^9 -Trans) PC),

1,2-dilinoleoyl-*sn*-glycero-3-phosphocholine (18:2 (Cis) PC, DLPC),
 1,2-dilinolenoyl-*sn*-glycero-3-phosphocholine (18:3 (Cis) PC, DLnPC),
 1,2-dieicosenoyl-*sn*-glycero-3-phosphocholine (20:1 (Cis) PC),
 1,2-diarachidonoyl-*sn*-glycero-3-phosphocholine (20:4 (Cis) PC, DAPC),
 1,2-dierucoyl-*sn*-glycero-3-phosphocholine (22:1 (Cis) PC),
 1,2-didocosahexaenoyl-*sn*-glycero-3-phosphocholine (22:6 (Cis) PC, DHAPC),
 1,2-dinervonoyl-*sn*-glycero-3-phosphocholine (24:1 (Cis) PC),
 1,2-dihexanoyl-*sn*-glycero-3-phosphoethanolamine (06:0 PE),
 1,2-dioctanoyl-*sn*-glycero-3-phosphoethanolamine (08:0 PE),
 1,2-didecanoyl-*sn*-glycero-3-phosphoethanolamine (10:0 PE),
 1,2-dilauroyl-*sn*-glycero-3-phosphoethanolamine (12:0 PE),
 1,2-dimyristoyl-*sn*-glycero-3-phosphoethanolamine (14:0 PE),
 1,2-dipentadecanoyl-*sn*-glycero-3-phosphoethanolamine (15:0 PE),
 1,2-dipalmitoyl-*sn*-glycero-3-phosphoethanolamine (16:0 PE),
 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (4ME 16:0 PE),
 1,2-diheptadecanoyl-*sn*-glycero-3-phosphoethanolamine (17:0 PE),
 1,2-distearoyl-*sn*-glycero-3-phosphoethanolamine (18:0 PE, DSPE),
 1,2-dipalmitoleoyl-*sn*-glycero-3-phosphoethanolamine (16:1 PE),
 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (18:1 (Δ^9 -Cis) PE, DOPE),
 1,2-dielaidoyl-*sn*-glycero-3-phosphoethanolamine (18:1 (Δ^9 -Trans) PE),
 1,2-dilinoleoyl-*sn*-glycero-3-phosphoethanolamine (18:2 PE, DLPE),
 1,2-dilinolenoyl-*sn*-glycero-3-phosphoethanolamine (18:3 PE, DLnPE),
 1,2-diarachidonoyl-*sn*-glycero-3-phosphoethanolamine (20:4 PE, DAPE),
 1,2-didocosahexaenoyl-*sn*-glycero-3-phosphoethanolamine (22:6 PE, DHAPE),
 1,2-di-O-octadecenyl-*sn*-glycero-3-phosphocholine (18:0 Diether PC),
 1,2-dioleoyl-*sn*-glycero-3-phospho-*rac*-(1-glycerol) sodium salt (DOPG), and any combination thereof.

[0275] In some aspects, the anchoring moiety comprises at least one symmetric phospholipid selected from the non-limiting group consisting of DLPC, DMPC, DOPC, DPPC, DSPC, DUPC, 18:0 Diether PC, DLnPC, DAPC, DHAPC, DOPE, 4ME 16:0 PE, DSPE, DLPE, DLnPE, DAPE, DHAPE, DOPG, and any combination thereof.

[0276] In some aspects, the anchoring moiety comprises at least one asymmetric phospholipid. Asymmetric phospholipids may be selected from the non-limiting group consisting of

1-myristoyl-2-palmitoyl-*sn*-glycero-3-phosphocholine (14:0-16:0 PC, MPPC),
 1-myristoyl-2-stearoyl-*sn*-glycero-3-phosphocholine (14:0-18:0 PC, MSPC),
 1-palmitoyl-2-acetyl-*sn*-glycero-3-phosphocholine (16:0-02:0 PC),
 1-palmitoyl-2-myristoyl-*sn*-glycero-3-phosphocholine (16:0-14:0 PC, PMPC),
 1-palmitoyl-2-stearoyl-*sn*-glycero-3-phosphocholine (16:0-18:0 PC, PSPC),
 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (16:0-18:1 PC, POPC),
 1-palmitoyl-2-linoleoyl-*sn*-glycero-3-phosphocholine (16:0-18:2 PC, PLPC),
 1-palmitoyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine (16:0-20:4 PC),
 1-palmitoyl-2-docosahexaenoyl-*sn*-glycero-3-phosphocholine (14:0-22:6 PC),
 1-stearoyl-2-myristoyl-*sn*-glycero-3-phosphocholine (18:0-14:0 PC, SMPC),
 1-stearoyl-2-palmitoyl-*sn*-glycero-3-phosphocholine (18:0-16:0 PC, SPPC),
 1-stearoyl-2-oleoyl-*sn*-glycero-3-phosphocholine (18:0-18:1 PC, SOPC),
 1-stearoyl-2-linoleoyl-*sn*-glycero-3-phosphocholine (18:0-18:2 PC),
 1-stearoyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine (18:0-20:4 PC),
 1-stearoyl-2-docosahexaenoyl-*sn*-glycero-3-phosphocholine (18:0-22:6 PC),
 1-oleoyl-2-myristoyl-*sn*-glycero-3-phosphocholine (18:1-14:0 PC, OMPC),
 1-oleoyl-2-palmitoyl-*sn*-glycero-3-phosphocholine (18:1-16:0 PC, OPPC),
 1-oleoyl-2-stearoyl-*sn*-glycero-3-phosphocholine (18:1-18:0 PC, OSPC),
 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphoethanolamine (16:0-18:1 PE, POPE),
 1-palmitoyl-2-linoleoyl-*sn*-glycero-3-phosphoethanolamine (16:0-18:2 PE),
 1-palmitoyl-2-arachidonoyl-*sn*-glycero-3-phosphoethanolamine (16:0-20:4 PE),
 1-palmitoyl-2-docosahexaenoyl-*sn*-glycero-3-phosphoethanolamine (16:0-22:6 PE),
 1-stearoyl-2-oleoyl-*sn*-glycero-3-phosphoethanolamine (18:0-18:1 PE),
 1-stearoyl-2-linoleoyl-*sn*-glycero-3-phosphoethanolamine (18:0-18:2 PE),
 1-stearoyl-2-arachidonoyl-*sn*-glycero-3-phosphoethanolamine (18:0-20:4 PE),
 1-stearoyl-2-docosahexaenoyl-*sn*-glycero-3-phosphoethanolamine (18:0-22:6 PE),
 1-oleoyl-2-cholesterylhemisuccinoyl-*sn*-glycero-3-phosphocholine (OChemsPC), and
 any combination thereof.

[0277] To provide more remarkable nuclease resistance, cellular uptake efficiency, and a more remarkable RNA interference effect, phosphatidylethanolamines may be used as anchoring

moieties, for example, dimyristoylphosphatidyl ethanolamine, dipalmitoylphosphatidyl ethanolamine, 1-palmitoyl-2-oleyl-phosphatidyl ethanolamine, and dioleoylphosphatidyl ethanolamine.

[0278] The binding site of lipid (e.g., a phospholipid) and a linker combination or BAM, e.g., an ASO, may be suitably selected according to the types of lipid and linker or ASO. Any position other than hydrophobic groups of the lipid may be linked to the linker or ASO by a chemical bond. For example, when using a phosphatidylethanolamine, the linkage may be made by forming an amide bond, etc. between the amino group of phosphatidylethanolamine and the linker or ASO. When using a phosphatidylglycerol, the linkage may be made by forming an ester bond, an ether bond, etc. between the hydroxyl group of the glycerol residue and the linker or ASO. When using a phosphatidylserine, the linkage may be made by forming an amide bond or an ester bond, etc. between the amino group or carboxyl group of the serine residue and the linker or ASO. When using a phosphatidic acid, the linkage may be made by forming a phosphoester bond, etc. between the phosphate residue and the linker or ASO. When using a phosphatidylinositol, the linkage may be made by forming an ester bond, an ether bond, etc. between the hydroxyl group of the inositol residue and the linker or ASO.

III.A.1.d. Lysolipids (e.g., lysophospholipids)

[0279] In some aspects, the anchoring moiety comprises a lysolipid, e.g., a lysophospholipid. Lysolipids are derivatives of a lipid in which one or both fatty acyl chains have been removed, generally by hydrolysis. Lysophospholipids are derivatives of a phospholipid in which one or both fatty acyl chains have been removed by hydrolysis.

[0280] In some aspects, the anchoring moiety comprises any of the phospholipids disclosed above, in which one or both acyl chains have been removed via hydrolysis, and therefore the resulting lysophospholipid comprises one or no fatty acid acyl chain.

[0281] In some aspects, the anchoring moiety comprises a lysoglycerophospholipid, a lysoglycosphingolipid, a lysophosphatidylcholine, a lysophosphatidylethanolamine, a lysophosphatidylinositol, or a lysophosphatidylserine.

[0282] In some aspect, the anchoring moiety comprises a lysolipid selected from the non-limiting group consisting of

1-hexanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (06:0 Lyso PC),

1-heptanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (07:0 Lyso PC),

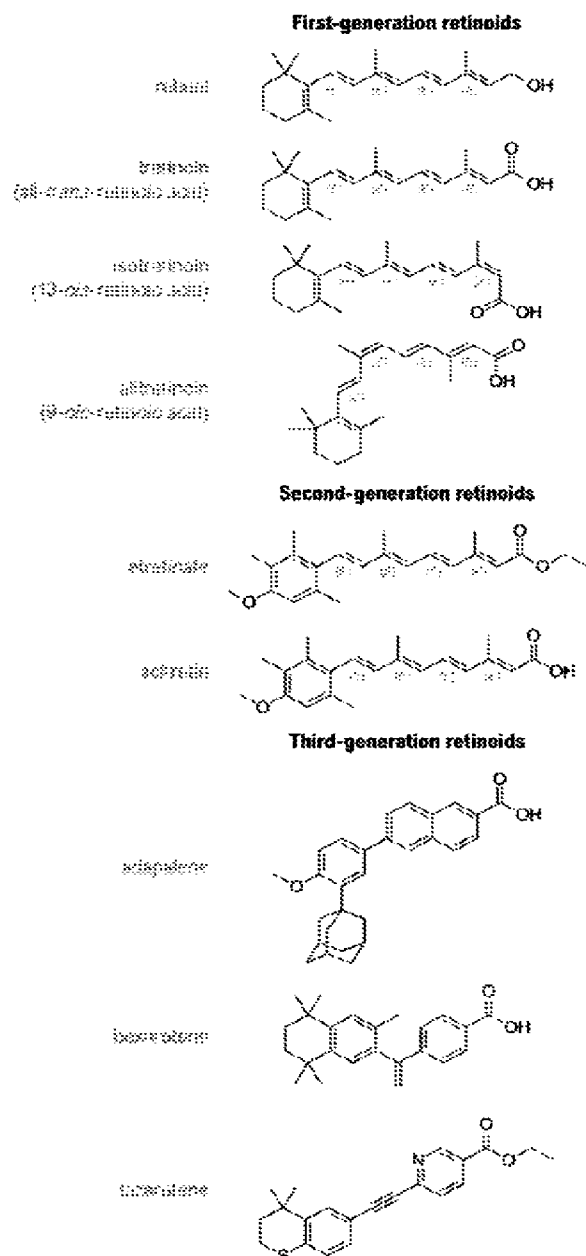
1-octanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (08:0 Lyso PC),
1-nonanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (09:0 Lyso PC),
1-decanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (10:0 Lyso PC),
1-undecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (11:0 Lyso PC),
1-lauroyl-2-hydroxy-*sn*-glycero-3-phosphocholine (12:0 Lyso PC),
1-tridecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (13:0 Lyso PC),
1-myristoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (14:0 Lyso PC),
1-pentadecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (15:0 Lyso PC),
1-palmitoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (16:0 Lyso PC),
1-heptadecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (17:0 Lyso PC),
1-stearoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (18:0 Lyso PC),
1-oleoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (18:1 Lyso PC),
1-nonadecanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (19:0 Lyso PC),
1-arachidoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (20:0 Lyso PC),
1-behenoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (22:0 Lyso PC),
1-lignoceroyl-2-hydroxy-*sn*-glycero-3-phosphocholine (24:0 Lyso PC),
1-hexacosanoyl-2-hydroxy-*sn*-glycero-3-phosphocholine (26:0 Lyso PC),
1-myristoyl-2-hydroxy-*sn*-glycero-3-phosphoethanolamine (14:0 Lyso PE),
1-palmitoyl-2-hydroxy-*sn*-glycero-3-phosphoethanolamine (16:0 Lyso PE),
1-stearoyl-2-hydroxy-*sn*-glycero-3-phosphoethanolamine (18:0 Lyso PE),
1-oleoyl-2-hydroxy-*sn*-glycero-3-phosphoethanolamine (18:1 Lyso PE),
1-hexadecyl-*sn*-glycero-3-phosphocholine (C16 Lyso PC), and
any combination thereof.

III.A.1.e. Vitamins

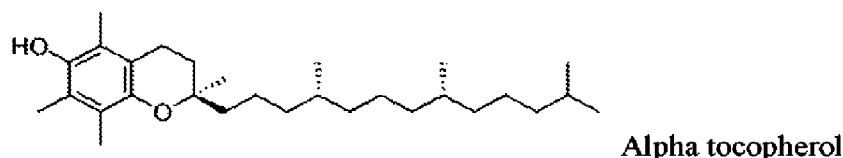
[0283] In some aspects, the anchoring moiety comprises a lipophilic vitamin, e.g., folic acid, vitamin A, vitamin E, or vitamin K.

[0284] In some aspects, the anchoring moiety comprises vitamin A. Vitamin A is a group of unsaturated nutritional organic compounds that includes retinol, retinal, retinoic acid, and several provitamin A carotenoids (most notably beta-carotene). In some aspects, the anchoring moiety comprises retinol. In some aspects, the anchoring moiety comprises a retinoid. Retinoids are a class of chemical compounds that are vitamers of vitamin A or are chemically related to it.

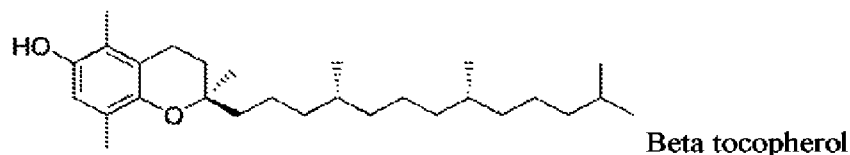
In some aspects, the anchoring moiety comprises a first generation retinoid (e.g., retinol, tretinoin, isotretinoin, or alitretinoin), a second-generation retinoid (e.g., etretinate or acitretin), a third-generation retinoid (e.g., adapalene, bexarotene, or tazarotene), or any combination thereof.



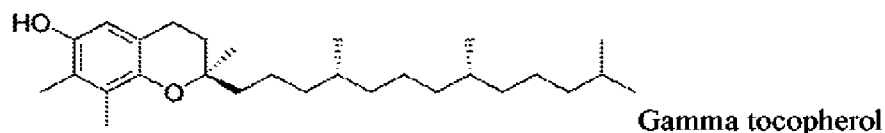
[0285] In some aspects, the anchoring moiety comprises vitamin E. Tocopherols are a class of methylated phenols many of which have vitamin E activity. Thus, in some aspects, the anchoring moiety comprises alpha-tocopherol, beta-tocopherol, gamma-tocopherol, delta-tocopherol, or a combination thereof.



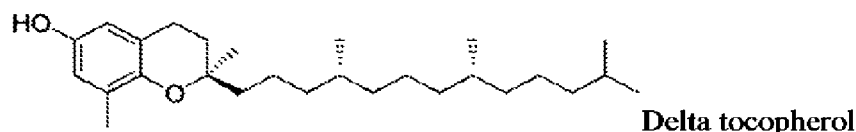
Alpha tocopherol



Beta tocopherol

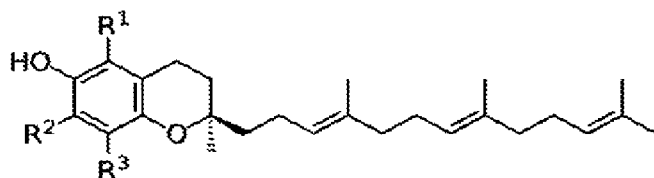


Gamma tocopherol



Delta tocopherol

[0286] Tocotrienols also have vitamin E activity. The critical chemical structural difference between tocotrienols and tocopherols is that tocotrienols have unsaturated isoprenoid side chain with three carbon-carbon double bonds versus saturated side chains for tocopherols. In some aspects, the anchoring moiety comprises alpha-tocotrienol, beta-tocotrienol, gamma-tocotrienol, delta-tocotrienol, or a combination thereof. Tocotrienols can be represented by the formula below



alpha(α)-Tocotrienol: R¹ = Me, R² = Me, R³ = Me;

beta(β)-Tocotrienol: R¹ = Me, R² = H, R³ = Me;

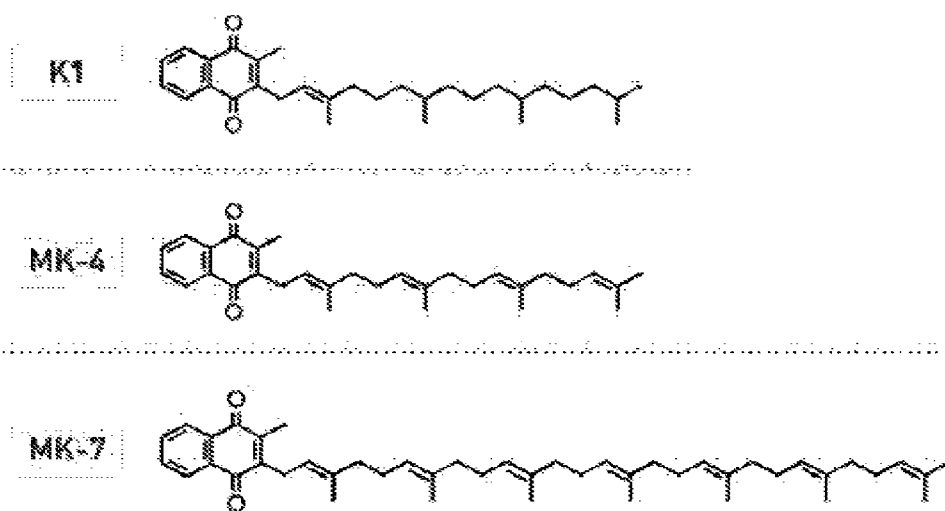
gamma(γ)-Tocotrienol: R¹ = H, R² = Me, R³ = Me;

delta(δ)-Tocotrienol: R¹ = H, R² = H, R³ = Me.

[0287] In some aspects, the anchoring moiety comprises vitamin K. Chemically, the vitamin K family comprises 2-methyl-1,4-naphthoquinone (3-) derivatives. Vitamin K includes two natural vitamins: vitamin K₁ and vitamin K₂. The structure of vitamin K₁ (also known as phytonadione, phylloquinone, or (E)-phytonadione) is marked by the presence of a phytyl group. The structures of vitamin K₂ (menaquinones) are marked by the polyisoprenyl side chain present in the molecule that can contain six to 13 isoprenyl units. Thus, vitamin K₂ consists of a number

of related chemical subtypes, with differing lengths of carbon side chains made of isoprenoid groups of atoms. MK-4 is the most common form of vitamin K₂. Long chain forms, such as MK-7, MK-8 and MK-9 are predominant in fermented foods. Longer chain forms of vitamin K₂ such as MK-10 to MK-13 are synthesized by bacteria, but they are not well absorbed and have little biological function. In addition to the natural forms of vitamin K, there is a number of synthetic forms of vitamin K such as vitamin K₃ (menadione; 2-methylnaphthalene-1,4-dione), vitamin K₄, and vitamin K₅.

[0288] Accordingly, in some aspects, the anchoring moiety comprises vitamin K₁, K₂ (e.g., MK-4, MK-5, MK-6, MK-7, MK-8, MK-9, MK-10, MK-11, MK-12, or MK-13), K₃, K₄, K₅, or any combination thereof.



III.A.2. Linker combinations

[0289] In some aspects, an ASO is linked to a hydrophobic membrane anchoring moiety disclosed herein via a linker combination, which can comprise any combination of cleavable and/or non-cleavable linkers. The main function of a linker combination is to provide the optimal spacing between the anchoring moiety or moieties and the BAM target. For example, in the case of an ASO, the linker combination should reduce steric hindrances and position the ASO so it can interact with a target nucleic acid, e.g., a mRNA or a miRNA.

[0290] Linkers may be susceptible to cleavage ("cleavable linker") thereby facilitating release of the biologically active molecule. Thus, in some aspects, a linker combination disclosed herein can comprise a cleavable linker. Such cleavable linkers may be susceptible, for example, to acid-induced cleavage, photo-induced cleavage, peptidase-induced cleavage, esterase-induced

cleavage, and disulfide bond cleavage, at conditions under which the biologically active molecule remains active. Alternatively, linkers may be substantially resistant to cleavage ("non-cleavable linker"). In some aspects, the cleavable linker comprises a spacer. In some aspects the spacer is PEG.

[0291] In some aspects, a linker combination comprises at least 2, at least 3, at least 4, at least 5, or at least 6 or more different linkers disclosed herein. In some aspects, linkers in a linker combination can be linked by an ester linkage (e.g., phosphodiester or phosphorothioate ester).

[0292] In some aspects, the linker is direct bond between an anchoring moiety and a BAM, e.g., an ASO.

III.B.2.a. Non-cleavable linkers

[0293] In some aspects, the linker combination comprises a "non-cleavable liker. " Non-cleavable linkers are any chemical moiety capable of linking two or more components of a modified biologically active molecule of the present disclosure (e.g., a biologically active molecule and an anchoring moiety; a biologically active molecule and a cleavable linker; an anchoring moiety and a cleavable linker) in a stable, covalent manner and does not fall off under the categories listed above for cleavable linkers. Thus, non-cleavable linkers are substantially resistant to acid-induced cleavage, photo-induced cleavage, peptidase-induced cleavage, esterase-induced cleavage and disulfide bond cleavage.

[0294] Furthermore, non-cleavable refers to the ability of the chemical bond in the linker or adjoining to the linker to withstand cleavage induced by an acid, photolabile-cleaving agent, a peptidase, an esterase, or a chemical or physiological compound that cleaves a disulfide bond, at conditions under which a cyclic dinucleotide and/or the antibody does not lose its activity. In some aspects, the biologically active molecule is attached to the linker via another linker, e.g., a self-immolative linker.

[0295] In some aspects, the linker combination comprises a non-cleavable linker comprising, e.g., tetraethylene glycol (TEG), hexaethylene glycol (HEG), polyethylene glycol (PEG), succinimide, or any combination thereof. In some aspects, the non-cleavable linker comprises a spacer unit to link the biologically active molecule to the non-cleavable linker.

[0296] In some aspects, one or more non-cleavable linkers comprise smaller units (e.g., HEG, TEG, glycerol, C2 to C12 alkyl, and the like) linked together. In one aspect, the linkage is an ester linkage (e.g., phosphodiester or phosphorothioate ester) or other linkage.

III.B.2.b. Ethylene Glycols (HEG, TEG, PEG)

[0297] In some aspects, the linker combination comprises a non-cleavable linker, wherein the non-cleavable linker comprises a polyethylene glycol (PEG) characterized by a formula $R^3-(O-CH_2-CH_2)_n-$ or $R^3-(O-CH_2-CH_2)_n-O-$ with R^3 being hydrogen, methyl or ethyl and n having a value from 2 to 200. In some aspects, the linker comprises a spacer, wherein the spacer is PEG.

[0298] In some aspects, the PEG linker is an oligo-ethylene glycol, e.g., diethylene glycol, triethylene glycol, tetra ethylene glycol (TEG), pentaethylene glycol, or a hexaethylene glycol (HEG) linker.

[0299] In some aspects, n has a value of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, or 200.

[0300] In some aspects, n is between 2 and 10, between 10 and 20, between 20 and 30, between 30 and 40, between 40 and 50, between 50 and 60, between 60 and 70, between 70 and 80, between 80 and 90, between 90 and 100, between 100 and 110, between 110 and 120, between 120 and 130, between 130 and 140, between 140 and 150, between 150 and 160, between 160 and 170, between 170 and 180, between 180 and 190, or between 190 and 200.

[0301] In some specific aspects, n has a value from 3 to 200, from 3 to 20, from 10 to 30, or from 9 to 45.

[0302] In some aspects, the PEG is a branched PEG. Branched PEGs have three to ten PEG chains emanating from a central core group.

[0303] In certain embodiments, the PEG moiety is a monodisperse polyethylene glycol. In the context of the present disclosure, a monodisperse polyethylene glycol (mdPEG) is a PEG that has a single, defined chain length and molecular weight. mdPEGs are typically generated by separation from the polymerization mixture by chromatography. In certain formulae, a monodisperse PEG moiety is assigned the abbreviation mdPEG.

[0304] In some aspects, the PEG is a Star PEG. Star PEGs have 10 to 100 PEG chains emanating from a central core group.

[0305] In some aspects, the PEG is a Comb PEGs. Comb PEGs have multiple PEG chains normally grafted onto a polymer backbone.

[0306] In certain aspects, the PEG has a molar mass between 100 g/mol and 3000 g/mol, particularly between 100 g/mol and 2500 g/mol, more particularly of approx. 100 g/mol to 2000 g/mol. In certain aspects, the PEG has a molar mass between 200 g/mol and 3000 g/mol, particularly between 300 g/mol and 2500 g/mol, more particularly of approx. 400 g/mol to 2000 g/mol.

[0307] In some aspects, the PEG is PEG₁₀₀, PEG₂₀₀, PEG₃₀₀, PEG₄₀₀, PEG₅₀₀, PEG₆₀₀, PEG₇₀₀, PEG₈₀₀, PEG₉₀₀, PEG₁₀₀₀, PEG₁₁₀₀, PEG₁₂₀₀, PEG₁₃₀₀, PEG₁₄₀₀, PEG₁₅₀₀, PEG₁₆₀₀, PEG₁₇₀₀, PEG₁₈₀₀, PEG₁₉₀₀, PEG₂₀₀₀, PEG₂₁₀₀, PEG₂₂₀₀, PEG₂₃₀₀, PEG₂₄₀₀, PEG₂₅₀₀, PEG₁₆₀₀, PEG₁₇₀₀, PEG₁₈₀₀, PEG₁₉₀₀, PEG₂₀₀₀, PEG₂₁₀₀, PEG₂₂₀₀, PEG₂₃₀₀, PEG₂₄₀₀, PEG₂₅₀₀, PEG₂₆₀₀, PEG₂₇₀₀, PEG₂₈₀₀, PEG₂₉₀₀, or PEG₃₀₀₀. In one particular aspect, the PEG is PEG₄₀₀. In another particular aspect, the PEG is PEG₂₀₀₀.

[0308] In some aspects, a linker combination of the present disclosure can comprise several PEG linkers, e.g., a cleavable linker flanked by PEG, HEG, or TEG linkers.

[0309] In some aspects, the linker combination comprises (HEG)_n and/or (TEG)_n, wherein n is an integer between 1 and 50, and each unit is connected, e.g., via a phosphate ester linker, a phosphorothioate ester linkage, or a combination thereof.

III.B.2.c. Glycerol and Polyglycerols (PG)

[0310] In some aspects, the linker combination comprises a non-cleavable linker comprising a glycerol unit or a polyglycerol (PG) described by the formula ((R₃—O—(CH₂—CHOH—CH₂O)_n—) with R₃ being hydrogen, methyl or ethyl, and n having a value from 3 to 200. In some aspects, n has a value from 3 to 20. In some aspects, n has a value from 10 to 30.

[0311] In some aspects, the PG linker is a diglycerol, triglycerol, tetraglycerol (TG), pentaglycerol, or a hexaglycerol (HG) linker.

[0312] In some aspects, n has a value of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115,

116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, or 200.

[0313] In some aspects, n is between 2 and 10, between 10 and 20, between 20 and 30, between 30 and 40, between 40 and 50, between 50 and 60, between 60 and 70, between 70 and 80, between 80 and 90, between 90 and 100, between 100 and 110, between 110 and 120, between 120 and 130, between 130 and 140, between 140 and 150, between 150 and 160, between 160 and 170, between 170 and 180, between 180 and 190, or between 190 and 200.

[0314] In some alternatives of these embodiments, n has a value from 9 to 45. In some aspects, the heterologous moiety is a branched polyglycerol described by the formula $(R^3-O-(CH_2-CHOR^5-CH_2-O)_n-)$ with R^5 being hydrogen or a linear glycerol chain described by the formula $(R^3-O-(CH_2-CHOH-CH_2-O)_n-)$ and R^3 being hydrogen, methyl or ethyl. In some aspects, the heterologous moiety is a hyperbranched polyglycerol described by the formula $(R^3-O-(CH_2-CHOR^5-CH_2-O)_n-)$ with R^5 being hydrogen or a glycerol chain described by the formula $(R^3-O-(CH_2-CHOR^6-CH_2-O)_n-)$, with R^6 being hydrogen or a glycerol chain described by the formula $(R^3-O-(CH_2-CHOR^7-CH_2-O)_n-)$, with R^7 being hydrogen or a linear glycerol chain described by the formula $(R^3-O-(CH_2-CHOH-CH_2-O)_n-)$ and R^3 being hydrogen, methyl or ethyl. Hyperbranched glycerol and methods for its synthesis are described in Oudshorn et al. (2006) *Biomaterials* 27:5471-5479; Wilms et al. (2010) *Acc. Chem. Res.* 43, 129-41, and references cited therein.

[0315] In certain aspects, the PG has a molar mass between 100 g/mol and 3000 g/mol, particularly between 100 g/mol and 2500 g/mol, more particularly of approx. 100 g/mol to 2000 g/mol. In certain aspects, the PG has a molar mass between 200 g/mol and 3000 g/mol, particularly between 300 g/mol and 2500 g/mol, more particularly of approx. 400 g/mol to 2000 g/mol.

[0316] In some aspects, the PG is PG₁₀₀, PG₂₀₀, PG₃₀₀, PG₄₀₀, PG₅₀₀, PG₆₀₀, PG₇₀₀, PG₈₀₀, PG₉₀₀, PG₁₀₀₀, PG₁₁₀₀, PG₁₂₀₀, PG₁₃₀₀, PG₁₄₀₀, PG₁₅₀₀, PG₁₆₀₀, PG₁₇₀₀, PG₁₈₀₀, PG₁₉₀₀, PG₂₀₀₀, PG₂₁₀₀, PG₂₂₀₀, PG₂₃₀₀, PG₂₄₀₀, PG₂₅₀₀, PG₂₆₀₀, PG₂₇₀₀, PG₂₈₀₀, PG₂₉₀₀, or PG₃₀₀₀. In one particular aspect, the PG is PG₄₀₀. In another particular aspect, the PG is PG₂₀₀₀.

[0317] In some aspects, the linker combination comprises (glycerol)_n, and/or (HG)_n and/or (TG)_n, wherein n is an integer between 1 and 50, and each unit is connected, e.g., via a phosphate ester linker, a phosphorothioate ester linkage, or a combination thereof.

III.B.2.d. Aliphatic (Alkyl) linkers

[0318] In some aspects, the linker combination comprises at least one aliphatic (alkyl) linker, e.g., propyl, butyl, hexyl, or C2-C12 alkyl, such as C2-C10 alkyl or C2-C6 alkyl.

[0319] In some aspects, the linker combination comprises an alkyl chain, e.g., an unsubstituted alkyl. In some aspects, the linker combination comprises an substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclalkyl, heterocyclalkenyl, heterocyclalkynyl, Aryl, heteroaryl, heterocycl, cycloalkyl, cycloalkenyl, alkylarylalkyl, alkylarylalkenyl, alkylarylalkynyl, alkenylarylalkyl, alkenyl Aryl alkenyl, alkenyl aryl alkynyl, alkynyl aryl alkyl, alkynyl aryl alkenyl, alkynyl aryl alkynyl, alkyl heteroaryl alkyl, alkyl heteroaryl alkyl, alkyl heteroaryl alkenyl, alkyl heteroaryl alkynyl, alkenyl heteroaryl alkyl, alkenyl heteroaryl alkenyl, alkenyl heteroaryl alkynyl, alkynyl Heteroarylalkyl, alkynylheteroarylalkenyl, alkynylheteroarylalkynyl, alkylheterocyclalkyl, alkylheterocyclalkenyl, alkylheterocyclalkynyl, alkenylheterocyclalkyl, alkenylheterocyclalkenyl, or alkenylheterocyclalkynyl.

[0320] Optionally these components are substituted. Substituents include alcohol, alkoxy (such as methoxy, ethoxy, and propoxy), straight or branched chain alkyl (such as C1-C12 alkyl), amine, aminoalkyl (such as amino C1-C12 alkyl), phosphoramidite, phosphate, phosphoramidate, phosphorodithioate, thiophosphate, hydrazide, hydrazine, halogen, (such as F, Cl, Br, or I), amide, alkylamide (such as amide C1-C12 alkyl), carboxylic acid, carboxylic ester, carboxylic anhydride, carboxylic acid halide, ether, sulfonyl halide, imidate ester, isocyanate, isothiocyanate, haloformate, carbodiimide adduct, aldehydes, ketone, sulfhydryl, haloacetyl, alkyl halide, alkyl sulfonate, C(=O)CH=CHC(=O) (maleimide), thioether, cyano, sugar (such as mannose, galactose, and glucose), α,β-unsaturated carbonyl, alkyl mercurial, or α,β-unsaturated sulfone.

[0321] The term "alkyl," by itself or as part of another substituent, means, unless otherwise stated, a straight or branched chain hydrocarbon radical having the number of carbon atoms designated (e.g., C₁-C₁₀ means one to ten carbon atoms). Typically, an alkyl group will have from 1 to 24 carbon atoms, for example having from 1 to 10 carbon atoms, from 1 to 8 carbon atoms or from 1 to 6 carbon atoms. A "lower alkyl" group is an alkyl group having from 1 to 4 carbon

atoms. The term "alkyl" includes di- and multivalent radicals. For example, the term "alkyl" includes "alkylene" wherever appropriate, *e.g.*, when the formula indicates that the alkyl group is divalent or when substituents are joined to form a ring. Examples of alkyl radicals include, but are not limited to, methyl, ethyl, *n*-propyl, *iso*-propyl, *n*-butyl, *tert*-butyl, *iso*-butyl, *sec*-butyl, as well as homologs and isomers of, for example, *n*-pentyl, *n*-hexyl, *n*-heptyl and *n*-octyl.

[0322] The term "alkylene" by itself or as part of another substituent means a divalent (diradical) alkyl group, wherein alkyl is defined herein. "Alkylene" is exemplified, but not limited, by $-\text{CH}_2\text{CH}_2\text{CH}_2\text{CH}_2-$. Typically, an "alkylene" group will have from 1 to 24 carbon atoms, for example, having 10 or fewer carbon atoms (*e.g.*, 1 to 8 or 1 to 6 carbon atoms). A "lower alkylene" group is an alkylene group having from 1 to 4 carbon atoms.

[0323] The term "alkenyl" by itself or as part of another substituent refers to a straight or branched chain hydrocarbon radical having from 2 to 24 carbon atoms and at least one double bond. A typical alkenyl group has from 2 to 10 carbon atoms and at least one double bond. In one embodiment, alkenyl groups have from 2 to 8 carbon atoms or from 2 to 6 carbon atoms and from 1 to 3 double bonds. Exemplary alkenyl groups include vinyl, 2-propenyl, 1-but-3-enyl, crotyl, 2-(butadienyl), 2,4-pentadienyl, 3-(1,4-pentadienyl), 2-isopentenyl, 1-pent-3-enyl, 1-hex-5-enyl and the like.

[0324] The term "alkynyl" by itself or as part of another substituent refers to a straight or branched chain, unsaturated or polyunsaturated hydrocarbon radical having from 2 to 24 carbon atoms and at least one triple bond. A typical "alkynyl" group has from 2 to 10 carbon atoms and at least one triple bond. In one aspect of the disclosure, alkynyl groups have from 2 to 6 carbon atoms and at least one triple bond. Exemplary alkynyl groups include prop-1-ynyl, prop-2-ynyl (*i.e.*, propargyl), ethynyl and 3-butylnyl.

[0325] The terms "alkoxy," "alkylamino" and "alkylthio" (or thioalkoxy) are used in their conventional sense, and refer to alkyl groups that are attached to the remainder of the molecule via an oxygen atom, an amino group, or a sulfur atom, respectively.

[0326] The term "heteroalkyl," by itself or in combination with another term, means a stable, straight or branched chain hydrocarbon radical consisting of the stated number of carbon atoms (*e.g.*, $\text{C}_2\text{-C}_{10}$, or $\text{C}_2\text{-C}_8$) and at least one heteroatom chosen, *e.g.*, from N, O, S, Si, B and P (in one embodiment, N, O and S), wherein the nitrogen, sulfur and phosphorus atoms are optionally oxidized, and the nitrogen atom(s) are optionally quaternized. The heteroatom(s) is/are placed at any interior position of the heteroalkyl group. Examples of heteroalkyl groups include, but are not limited to, $-\text{CH}_2\text{-CH}_2\text{-O-CH}_3$, $-\text{CH}_2\text{-CH}_2\text{-NH-CH}_3$, $-\text{CH}_2\text{-CH}_2\text{-N(CH}_3\text{)-CH}_3$, $-\text{CH}_2\text{-S-CH}_2\text{-CH}_3$, -

CH₂-CH₂-S(O)-CH₃, -CH₂-CH₂-S(O)₂-CH₃, -CH=CH-O-CH₃, -CH₂-Si(CH₃)₃, -CH₂-CH=N-OCH₃, and -CH=CH-N(CH₃)-CH₃. Up to two heteroatoms can be consecutive, such as, for example, -CH₂-NH-OCH₃ and -CH₂-O-Si(CH₃)₃.

[0327] Similarly, the term "heteroalkylene" by itself or as part of another substituent means a divalent radical derived from heteroalkyl, as exemplified, but not limited by, -CH₂-CH₂-S-CH₂-CH₂- and -CH₂-S-CH₂-CH₂-NH-CH₂-. Typically, a heteroalkyl group will have from 3 to 24 atoms (carbon and heteroatoms, excluding hydrogen) (3- to 24-membered heteroalkyl). In another example, the heteroalkyl group has a total of 3 to 10 atoms (3- to 10-membered heteroalkyl) or from 3 to 8 atoms (3- to 8-membered heteroalkyl). The term "heteroalkyl" includes "heteroalkylene" wherever appropriate, *e.g.*, when the formula indicates that the heteroalkyl group is divalent or when substituents are joined to form a ring.

[0328] The term "cycloalkyl" by itself or in combination with other terms, represents a saturated or unsaturated, non-aromatic carbocyclic radical having from 3 to 24 carbon atoms, for example, having from 3 to 12 carbon atoms (*e.g.*, C₃-C₈ cycloalkyl or C₃-C₆ cycloalkyl). Examples of cycloalkyl include, but are not limited to, cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl, 1-cyclohexenyl, 3-cyclohexenyl, cycloheptyl and the like. The term "cycloalkyl" also includes bridged, polycyclic (*e.g.*, bicyclic) structures, such as norbornyl, adamantyl and bicyclo[2.2.1]heptyl. The "cycloalkyl" group can be fused to at least one (*e.g.*, 1 to 3) other ring selected from aryl (*e.g.*, phenyl), heteroaryl (*e.g.*, pyridyl) and non-aromatic (*e.g.*, carbocyclic or heterocyclic) rings. When the "cycloalkyl" group includes a fused aryl, heteroaryl or heterocyclic ring, then the "cycloalkyl" group is attached to the remainder of the molecule via the carbocyclic ring.

[0329] The term "heterocycloalkyl," "heterocyclic," "heterocycle," or "heterocyclyl," by itself or in combination with other terms, represents a carbocyclic, non-aromatic ring (*e.g.*, 3- to 8-membered ring and for example, 4-, 5-, 6- or 7-membered ring) containing at least one and up to 5 heteroatoms selected from, *e.g.*, N, O, S, Si, B and P (for example, N, O and S), wherein the nitrogen, sulfur and phosphorus atoms are optionally oxidized, and the nitrogen atom(s) are optionally quaternized (*e.g.*, from 1 to 4 heteroatoms selected from nitrogen, oxygen and sulfur), or a fused ring system of 4- to 8-membered rings, containing at least one and up to 10 heteroatoms (*e.g.*, from 1 to 5 heteroatoms selected from N, O and S) in stable combinations known to those of skill in the art. Exemplary heterocycloalkyl groups include a fused phenyl ring. When the "heterocyclic" group includes a fused aryl, heteroaryl or cycloalkyl ring, then the "heterocyclic"

group is attached to the remainder of the molecule via a heterocycle. A heteroatom can occupy the position at which the heterocycle is attached to the remainder of the molecule.

[0330] Exemplary heterocycloalkyl or heterocyclic groups of the present disclosure include morpholinyl, thiomorpholinyl, thiomorpholinyl S-oxide, thiomorpholinyl S,S-dioxide, piperazinyl, homopiperazinyl, pyrrolidinyl, pyrrolinyl, imidazolidinyl, tetrahydropyranyl, piperidinyl, tetrahydrofuranyl, tetrahydrothienyl, piperidinyl, homopiperidinyl, homomorpholinyl, homothiomorpholinyl, homothiomorpholinyl S,S-dioxide, oxazolidinonyl, dihydropyrazolyl, dihydropyrrolyl, dihydropyrazolyl, dihydropyridyl, dihydropyrimidinyl, dihydrofuryl, dihydropyranyl, tetrahydrothienyl S-oxide, tetrahydrothienyl S,S-dioxide, homothiomorpholinyl S-oxide, 1-(1,2,5,6-tetrahydropyridyl), 1-piperidinyl, 2-piperidinyl, 3-piperidinyl, 4-morpholinyl, 3-morpholinyl, tetrahydrofuran-2-yl, tetrahydrofuran-3-yl, tetrahydrothien-2-yl, tetrahydrothien-3-yl, 1-piperazinyl, 2-piperazinyl, and the like.

[0331] By "aryl" is meant a 5-, 6- or 7-membered, aromatic carbocyclic group having a single ring (*e.g.*, phenyl) or being fused to other aromatic or non-aromatic rings (*e.g.*, from 1 to 3 other rings). When the "aryl" group includes a non-aromatic ring (such as in 1,2,3,4-tetrahydronaphthyl) or heteroaryl group then the "aryl" group is bonded to the remainder of the molecule via an aryl ring (*e.g.*, a phenyl ring). The aryl group is optionally substituted (*e.g.*, with 1 to 5 substituents described herein). In one example, the aryl group has from 6 to 10 carbon atoms. Non-limiting examples of aryl groups include phenyl, 1-naphthyl, 2-naphthyl, quinoline, indanyl, indenyl, dihydronaphthyl, fluorenyl, tetralinyl, benzo[d][1,3]dioxolyl or 6,7,8,9-tetrahydro-5H-benzo[a]cycloheptenyl. In one embodiment, the aryl group is selected from phenyl, benzo[d][1,3]dioxolyl and naphthyl. The aryl group, in yet another embodiment, is phenyl.

[0332] The term "arylalkyl" or "aralkyl" is meant to include those radicals in which an aryl group or heteroaryl group is attached to an alkyl group to create the radicals -alkyl-aryl and -alkyl-heteroaryl, wherein alkyl, aryl and heteroaryl are defined herein. Exemplary "arylalkyl" or "aralkyl" groups include benzyl, phenethyl, pyridylmethyl and the like.

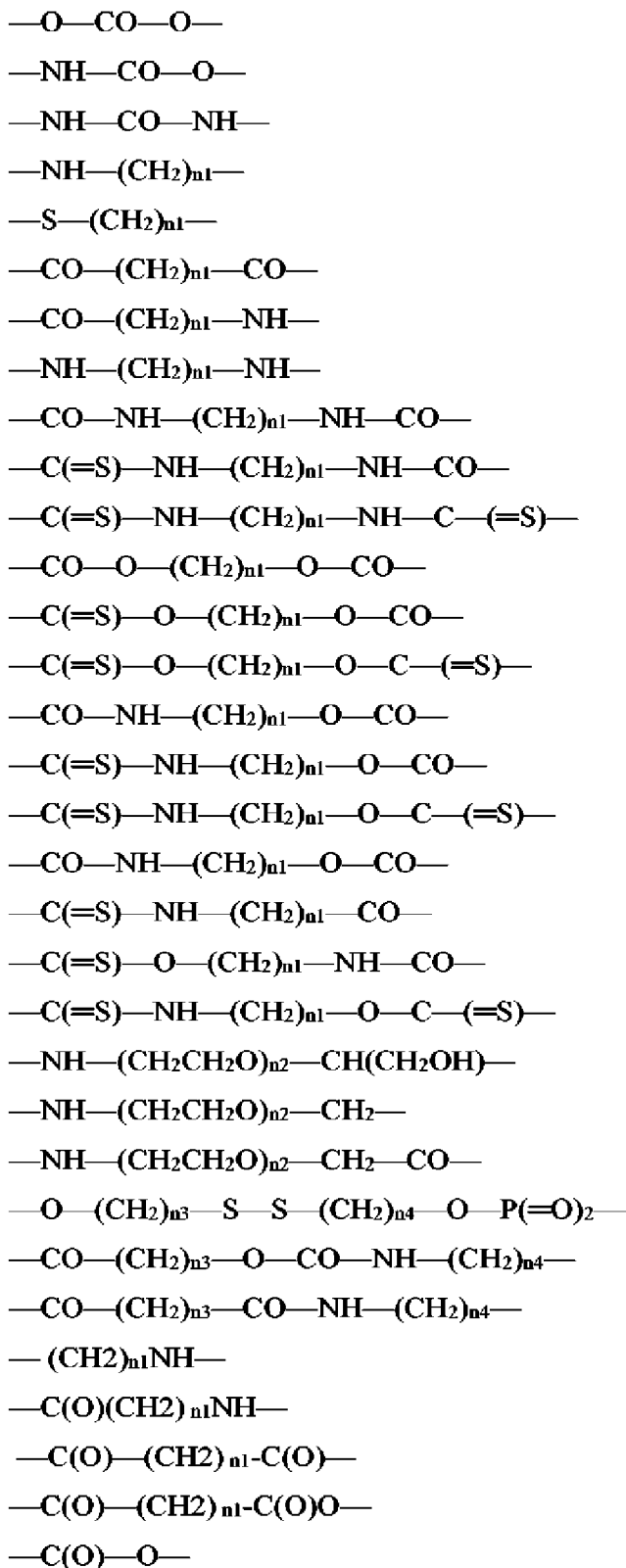
[0333] By "aryloxy" is meant the group -O-aryl, where aryl is as defined herein. In one example, the aryl portion of the aryloxy group is phenyl or naphthyl. The aryl portion of the aryloxy group, in one embodiment, is phenyl.

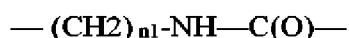
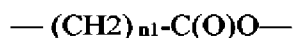
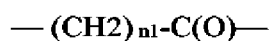
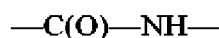
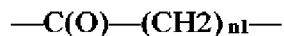
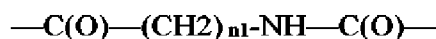
[0334] The term "heteroaryl" or "heteroaromatic" refers to a polyunsaturated, 5-, 6- or 7-membered aromatic moiety containing at least one heteroatom (*e.g.*, 1 to 5 heteroatoms, such as 1-3 heteroatoms) selected from N, O, S, Si and B (for example, N, O and S), wherein the nitrogen and sulfur atoms are optionally oxidized, and the nitrogen atom(s) are optionally quaternized. The

"heteroaryl" group can be a single ring or be fused to other aryl, heteroaryl, cycloalkyl or heterocycloalkyl rings (*e.g.*, from 1 to 3 other rings). When the "heteroaryl" group includes a fused aryl, cycloalkyl or heterocycloalkyl ring, then the "heteroaryl" group is attached to the remainder of the molecule via the heteroaryl ring. A heteroaryl group can be attached to the remainder of the molecule through a carbon- or heteroatom.

[0335] In one example, the heteroaryl group has from 4 to 10 carbon atoms and from 1 to 5 heteroatoms selected from O, S and N. Non-limiting examples of heteroaryl groups include pyridyl, pyrimidinyl, quinolinyl, benzothienyl, indolyl, indolinyl, pyridazinyl, pyrazinyl, isoindolyl, isoquinolyl, quinazolinyl, quinoxalinyl, phthalazinyl, imidazolyl, isoxazolyl, pyrazolyl, oxazolyl, thiazolyl, indoliziny, indazolyl, benzothiazolyl, benzimidazolyl, benzofuranyl, furanyl, thienyl, pyrrolyl, oxadiazolyl, thiadiazolyl, triazolyl, tetrazolyl, isothiazolyl, naphthyridinyl, isochromanyl, chromanyl, tetrahydroisoquinolinyl, isoindolinyl, isobenzotetrahydrofuranly, isobenzotetrahydrothienyl, isobenzothienyl, benzoxazolyl, pyridopyridyl, benzotetrahydrofuranly, benzotetrahydrothienyl, purinyl, benzodioxolyl, triazinyl, pteridinyl, benzothiazolyl, imidazopyridyl, imidazothiazolyl, dihydrobenzisoxazinyl, benzisoxazinyl, benzoxazinyl, dihydrobenzisothiazinyl, benzopyranyl, benzothiopyranyl, chromonyl, chromanonyl, pyridyl-N-oxide, tetrahydroquinolinyl, dihydroquinolinyl, dihydroquinolinonyl, dihydroisoquinolinonyl, dihydrocoumarinyl, dihydroisocoumarinyl, isoindolinonyl, benzodioxanyl, benzoxazolinonyl, pyrrolyl N-oxide, pyrimidinyl N-oxide, pyridazinyl N-oxide, pyrazinyl N-oxide, quinolinyl N-oxide, indolyl N-oxide, indolinyl N-oxide, isoquinolyl N-oxide, quinazolinyl N-oxide, quinoxalinyl N-oxide, phthalazinyl N-oxide, imidazolyl N-oxide, isoxazolyl N-oxide, oxazolyl N-oxide, thiazolyl N-oxide, indoliziny N-oxide, indazolyl N-oxide, benzothiazolyl N-oxide, benzimidazolyl N-oxide, pyrrolyl N-oxide, oxadiazolyl N-oxide, thiadiazolyl N-oxide, triazolyl N-oxide, tetrazolyl N-oxide, benzothiopyranyl S-oxide, benzothiopyranyl S,S-dioxide. Exemplary heteroaryl groups include imidazolyl, pyrazolyl, thiadiazolyl, triazolyl, isoxazolyl, isothiazolyl, imidazolyl, thiazolyl, oxadiazolyl, and pyridyl. Other exemplary heteroaryl groups include 1-pyrrolyl, 2-pyrrolyl, 3-pyrrolyl, 3-pyrazolyl, 2-imidazolyl, 4-imidazolyl, pyrazinyl, 2-oxazolyl, 4-oxazolyl, 2-phenyl-4-oxazolyl, 5-oxazolyl, 3-isoxazolyl, 4-isoxazolyl, 5-isoxazolyl, 2-thiazolyl, 4-thiazolyl, 5-thiazolyl, 2-furyl, 3-furyl, 2-thienyl, 3-thienyl, 2-pyridyl, 3-pyridyl, pyridin-4-yl, 2-pyrimidyl, 4-pyrimidyl, 5-benzothiazolyl, purinyl, 2-benzimidazolyl, 5-indolyl, 1-isoquinolyl, 5-isoquinolyl, 2-quinoxalinyl, 5-quinoxalinyl, 3-quinolyl, and 6-quinolyl. Substituents for each of the above noted aryl and heteroaryl ring systems are selected from the group of acceptable aryl group substituents described below.

[0336] Examples of aliphatic linkers include the following structures:





n_1 is an integer between 1 and 40 (e.g., 2 to 20, or 2 to 12); n_2 is an integer between 1 and 20 (e.g., 1 to 10, or 1 to 6); n_3 and n_4 may be the same or different, and are an integer between 1 and 20 (e.g., 1 to 10, or 1 to 6).

[0337] In some aspects, the linker combination comprises $(C_3)_n$, $(C_4)_n$, $(C_5)_n$, $(C_6)_n$, $(C_7)_n$, or $(C_8)_n$, or a combination thereof, wherein n is an integer between 1 and 50, and each unit is connected, e.g., via a phosphate ester linker, a phosphorothioate ester linkage, or a combination thereof.

III.B.3. Cleavable linkers

[0338] In some aspects, different components of an ASO disclosed herein can be linker by a cleavable linker. The term cleavable linker refers to a linker comprising at least one linkage or chemical bond that can be broken or cleaved. As used herein, the term cleave refers to the breaking of one or more chemical bonds in a relatively large molecule in a manner that produces two or more relatively smaller molecules. Cleavage may be mediated, e.g., by a nuclease, peptidase, protease, phosphatase, oxidase, or reductase, for example, or by specific physicochemical conditions, e.g., redox environment, pH, presence of reactive oxygen species, or specific wavelengths of light.

[0339] In some aspects, the term "cleavable," as used herein, refers, e.g., to rapidly degradable linkers, such as, e.g., phosphodiester and disulfides, while the term "non-cleavable" refers, e.g., to more stable linkages, such as, e.g., nuclease-resistant phosphorothioates.

[0340] In some aspects, the cleavable linker is a dinucleotide or trinucleotide linker, a disulfide, an imine, a thioetal, a val-cit dipeptide, or any combination thereof. In some aspects, the cleavable linker comprises valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate.

III.B.3.a. Redox cleavable linkers

[0341] In some aspects, the linker combination comprises a redox cleavable linker. As a non-limiting example, one type of cleavable linker is a redox cleavable linking group that is cleaved upon reduction or upon oxidation.

[0342] In some aspects, the redox cleavable linker contains a disulfide bond, i.e., it is a disulfide cleavable linker.

[0343] Redox cleavable linkers can be reduced, e.g., by intracellular mercaptans, oxidases, or reductases.

III.B.3.b. Reactive Oxygen Species (ROS) cleavable linkers

[0344] In some aspects, the linker combination can comprise a cleavable linker which may be cleaved by a reactive oxygen species (ROS), such as superoxide (Of) or hydrogen peroxide (H₂O₂), generated, e.g., by inflammation processes such as activated neutrophils. In some aspects, the ROS cleavable linker is a thioketal cleavable linker. See, e.g., U.S. Pat. 8,354,455B2, which is herein incorporated by reference in its entirety.

III.B.3.c. pH dependent cleavable linkers

[0345] In some aspects, the linker is an "acid labile linker" comprising an acid cleavable linking group, which is a linking group that is selectively cleaved under acidic conditions (pH<7).

[0346] As a non-limiting example, the acid cleavable linking group is cleaved in an acidic environment, e.g., about 6.0, 5.5, 5.0 or less. In some aspects, the pH is about 6.5 or less. In some aspects, the linker is cleaved by an agent such as an enzyme that can act as a general acid, e.g., a peptidase (which may be substrate specific) or a phosphatase. Within cells, certain low pH organelles, such as endosomes and lysosomes, can provide a cleaving environment to the acid cleavable linking group. Although the pH of human serum is 7.4, the average pH in cells is slightly lower, ranging from about 7.1 to 7.3. Endosomes also have an acidic pH, ranging from 5.5 to 6.0, and lysosomes are about 5.0 at an even more acidic pH. Accordingly, pH dependent cleavable linkers are sometimes called endosomically labile linkers in the art.

[0347] The acid cleavable group may have the general formula -C = NN-, C (O) O, or -OC (O). In another non-limiting example, when the carbon attached to the ester oxygen (alkoxy group) is attached to an aryl group, a substituted alkyl group, or a tertiary alkyl group such as dimethyl pentyl or t-butyl, for example. Examples of acid cleavable linking groups include, but are not

limited to amine, imine, amino ester, benzoic imine, diortho ester, polyphosphoester, polyphosphazene, acetal, vinyl ether, hydrazone, cis-aconitate, hydrazide, thiocarbamoyl, imizine, azidomethyl-methylmaleic anhydride, thiopropionate, a masked endosomolytic agent, a citraconyl group, or any combination thereof. Disulfide linkages are also susceptible to pH.

[0348] In some aspects, the linker comprises a low pH-labile hydrazone bond. Such acid-labile bonds have been extensively used in the field of conjugates, e.g., antibody-drug conjugates. See, for example, Zhou et al, *Biomacromolecules* 2011, 12, 1460-7; Yuan et al, *Acta Biomater.* 2008, 4, 1024-37; Zhang et al, *Acta Biomater.* 2007, 6, 838-50; Yang et al, *J. Pharmacol. Exp. Ther.* 2007, 321, 462-8; Reddy et al, *Cancer Chemother. Pharmacol.* 2006, 58, 229-36; Doronina et al, *Nature Biotechnol.* 2003, 21, 778-84.

[0349] In certain embodiments, the linker comprises a low pH-labile bond selected from the following: ketals that are labile in acidic environments (e.g., pH less than 7, greater than about 4) to form a diol and a ketone; acetals that are labile in acidic environments (e.g., pH less than 7, greater than about 4) to form a diol and an aldehyde; imines or iminiums that are labile in acidic environments (e.g., pH less than 7, greater than about 4) to form an amine and an aldehyde or a ketone; silicon-oxygen-carbon linkages that are labile under acidic condition; silicon-nitrogen (silazane) linkages; silicon-carbon linkages (e.g., arylsilanes, vinylsilanes, and allylsilanes); maleamates (amide bonds synthesized from maleic anhydride derivatives and amines); ortho esters; hydrazones; activated carboxylic acid derivatives (e.g., esters, amides) designed to undergo acid catalyzed hydrolysis; or vinyl ethers.

[0350] Further examples may be found in U.S. Pat. Nos. 9,790,494B2 and 8,137,695B2, the contents of which are incorporated herein by reference in their entireties.

III.B.3.d. Enzymatic cleavable linkers

[0351] In some aspects, the linker combination can comprise a linker cleavable by intracellular or extracellular enzymes, e.g., proteases, esterases, nucleases, amidases. The range of enzymes that can cleave a specific linker in a linker combination depends on the specific bonds and chemical structure of the linker. Accordingly, peptidic linkers can be cleaved, e.g., by peptidases, linkers containing ester linkages can be cleaved, e.g., by esterases; linkers containing amide linkages can be cleaved, e.g., by amidases; etc.

III.B.3.e. Protease cleavable linkers

[0352] In some aspects, the linker combination comprises a protease cleavable linker, i.e., a linker that can be cleaved by an endogenous protease. Only certain peptides are readily cleaved inside or outside cells. See, e.g., Trout et al., 79 Proc. Natl. Acad. Sci. USA, 626-629 (1982) and Umemoto et al. 43 Int. J. Cancer, 677-684 (1989). Cleavable linkers can contain cleavable sites composed of α -amino acid units and peptidic bonds, which chemically are amide bonds between the carboxylate of one amino acid and the amino group of a second amino acid. Other amide bonds, such as the bond between a carboxylate and the α -amino acid group of lysine, are understood not to be peptidic bonds and are considered non-cleavable.

[0353] In some aspects, the protease-cleavable linker comprises a cleavage site for a protease, e.g., neprilysin (CALLA or CD10), thimet oligopeptidase (TOP), leukotriene A4 hydrolase, endothelin converting enzymes, ste24 protease, neurolysin, mitochondrial intermediate peptidase, interstitial collagenases, collagenases, stromelysins, macrophage elastase, matrilysin, gelatinases, meprins, procollagen C- endopeptidases, procollagen N-endopeptidases, ADAMs and ADAMTs metalloproteinases, myelin associated metalloproteinases, enamelysin, tumor necrosis factor α -converting enzyme, insulysin, nardilysin, mitochondrial processing peptidase, magnolysin, dactylisin-like metalloproteases, neutrophil collagenase, matrix metalloproteinases, membrane-type matrix metalloproteinases, SP2 endopeptidase, prostate specific antigen (PSA), plasmin, urokinase, human fibroblast activation protein (FAP α), trypsin, chymotrypsins, caldecrin, pancreatic elastases, pancreatic endopeptidase, enteropeptidase, leukocyte elastase, myeloblasts, chymases, tryptase, granzyme, stratum corneum chymotryptic enzyme, acrosin, kallikreins, complement components and factors, alternative-complement pathway c3/c5 convertase, mannose- binding protein-associated serine protease, coagulation factors, thrombin, protein c, u and t-type plasminogen activator, cathepsin G, hepsin, prostasin, hepatocyte growth factor-activating endopeptidase, subtilisin/kexin type proprotein convertases, furin, proprotein convertases, prolyl peptidases, acylaminoacyl peptidase, peptidyl-glycaminase, signal peptidase, n-terminal nucleophile aminohydrolases, 20s proteasome, γ -glutamyl transpeptidase, mitochondrial endopeptidase, mitochondrial endopeptidase Ia, htra2 peptidase, matriptase, site 1 protease, legumain, cathepsins, cysteine cathepsins, calpains, ubiquitin isopeptidase T, caspases, glycosylphosphatidylinositolprotein transamidase, cancer procoagulant, prohormone thiol protease, γ -Glutamyl hydrolase, bleomycin hydrolase, seprase, cathepsin B, cathepsin D, cathepsin L, cathepsin M, proteinase K, pepsins, chymosyn, gastricsin, renin, yapsin and/or mapsins,

Prostate-Specific antigen (PSA), or any Asp-N, Glu-C, Lys-C or Arg-C proteases in general. See, *e.g.*, Cancer Res. 77(24):7027-7037 (2017), which is herein incorporated by reference in its entirety.

[0354] In some aspects, the cleavable linker component comprises a peptide comprising one to ten amino acid residues. In these aspects, the peptide allows for cleavage of the linker by a protease, thereby facilitating release of the biologically active molecule upon exposure to intracellular proteases, such as lysosomal enzymes (Doronina et al. (2003) Nat. Biotechnol. 21:778-784). Exemplary peptides include, but are not limited to, dipeptides, tripeptides, tetrapeptides, pentapeptides, and hexapeptides.

[0355] A peptide may comprise naturally-occurring and/or non-natural amino acid residues. The term "naturally-occurring amino acid" refer to Ala, Asp, Cys, Glu, Phe, Gly, His, He, Lys, Leu, Met, Asn, Pro, Gin, Arg, Ser, Thr, Val, Trp, and Tyr. "Non-natural amino acids" (i.e., amino acids do not occur naturally) include, by way of non-limiting example, homoserine, homoarginine, citrulline, phenylglycine, taurine, iodotyrosine, seleno- cysteine, norleucine ("Nle"), norvaline ("Nva"), beta-alanine, L- or D-naphthalanine, ornithine ("Orn"), and the like. Peptides can be designed and optimized for enzymatic cleavage by a particular enzyme, for example, a tumor-associated protease, cathepsin B, C and D, or a plasmin protease.

[0356] Amino acids also include the D-forms of natural and non-natural amino acids. "D-" designates an amino acid having the "D" (dextrorotary) configuration, as opposed to the configuration in the naturally occurring ("L-") amino acids. Natural and non-natural amino acids can be purchased commercially (Sigma Chemical Co., Advanced Chemtech) or synthesized using methods known in the art.

[0357] Exemplary dipeptides include, but are not limited to, valine-alanine, valine-citrulline, phenylalanine-lysine, N-methyl-valine-citrulline, cyclohexylalanine-lysine, and beta-alanine-lysine. Exemplary tripeptides include, but are not limited to, glycine-valine-citrulline (gly-val-cit) and glycine-glycine-glycine (gly-gly-gly).

III.B.3.f. Esterase cleavable linkers

[0358] Some linkers are cleaved by esterases ("esterase cleavable linkers"). Only certain esters can be cleaved by esterases and amidases present inside or outside of cells. Esters are formed by the condensation of a carboxylic acid and an alcohol. Simple esters are esters produced with simple alcohols, such as aliphatic alcohols, and small cyclic and small aromatic alcohols. Examples of ester-based cleavable linking groups include, but are not limited to, esters of alkylene,

alkenylene and alkynylene groups. The ester cleavable linking group has the general formula -C(O) O- or -OC(O)-.

III.B.3.g. Phosphatase cleavable linkers

[0359] In some aspects, a linker combination can includes a phosphate-based cleavable linking group is cleaved by an agent that degrades or hydrolyzes phosphate groups. An example of an agent that cleaves intracellular phosphate groups is an enzyme such as intracellular phosphatase. Examples of phosphate-based linking groups are —O—P(O)(OR_k)—O—, —O—P(S)(OR_k)—O—, —O—P(S)(SR_k)—O—, -S-P(O)(OR_k)-O-, -O-P(O)(OR_k)-S-, -S-P(O)(OR_k)-S-, -O-P(S)(OR_k)-S-, -SP(S)(OR_k)-O-, -OP(O)(R_k)-O-, -OP(S)(R_k)-O-, -SP(O)(R_k)-O-, -SP(S)(R_k)-O-, -SP(O)(R_k)-S-, or -OP(S)(R_k)-S-.

[0360] In various aspects, R_k is any of the following: NH₂, BH₃, CH₃, C₁₋₆ alkyl, C₆₋₁₀ aryl, C₁₋₆ alkoxy and C₆₋₁₀ aryl-oxy. In some aspects, C₁₋₆ alkyl and C₆₋₁₀ aryl are unsubstituted. Further non-limiting examples are -O-P(O)(OH)-O-, -O-P(S)(OH)-O-, -O-P(S)(SH)-O-, -S-P(O)(OH)-O-, -O-P(O)(OH)-S-, -S-P(O)(OH)-S-, -O-P(S)(OH)-S-, -S-P(S)(OH)-O-, -O-P(O)(H)-O-, -O-P(S)(H)-O-, -S-P(O)(H)-O-, -SP(S)(H)-O-, -SP(O)(H)-S-, -OP(S)(H)-S-, or -O-P(O)(OH)-O-.

III.B.3.h. Photoactivated cleavable linkers

[0361] In some aspects, the combination linker comprises a photoactivated cleavable linker, e.g., a nitrobenzyl linker or a linker comprising a nitrobenzyl reactive group.

III.B.3.i. Self-immolative linker

[0362] In some aspects, the linker combination comprises a self-immolative linker. In some aspects, the self-immolative linker in the EV (e.g., exosome) of the present disclosure undergoes 1,4 elimination after the enzymatic cleavage of the protease-cleavable linker. In some aspects, the self-immolative linker in the EV (e.g., exosome) of the present disclosure undergoes 1,6 elimination after the enzymatic cleavage of the protease-cleavable linker. In some aspects, the self-immolative linker is, e.g., a p-aminobenzyl (pAB) derivative, such as a p-aminobenzyl carbamate (pABC), a p-amino benzyl ether (PABE), a p-amino benzyl carbonate, or a combination thereof.

[0363] In certain aspects, the self-immolative linker comprises an aromatic group. In some aspects, the aromatic group is selected from the group consisting of benzyl, cinnamyl, naphthyl,

and biphenyl. In some aspects, the aromatic group is heterocyclic. In other aspects, the aromatic group comprises at least one substituent. In some aspects, the at least one substituent is selected from the group consisting of F, Cl, I, Br, OH, methyl, methoxy, NO₂, NH₂, NO³⁺, NHCOCH₃, N(CH₃)₂, NHCOCF₃, alkyl, haloalkyl, C₁-C₈ alkylhalide, carboxylate, sulfate, sulfamate, and sulfonate. In other aspects, at least one C in the aromatic group is substituted with N, O, or C-R*, wherein R* is independently selected from H, F, Cl, I, Br, OH, methyl, methoxy, NO₂, NH₂, NO³⁺, NHCOCH₃, N(CH₃)₂, NHCOCF₃, alkyl, haloalkyl, C₁-C₈ alkylhalide, carboxylate, sulfate, sulfamate, and sulfonate.

[0364] In some aspects, the self-immolative linker comprises an aminobenzyl carbamate group (e.g., para-aminobenzyl carbamate), an aminobenzyl ether group, or an aminobenzyl carbonate group. In one aspect, the self-immolative linker is p-amino benzyl carbamate (pABC).

[0365] pABC is the most efficient and most widespread connector linkage for self-immolative site-specific prodrug activation (see, e.g., Carl *et al.* J. Med. Chem. 24:479-480 (1981); WO 1981/001145; Rautio *et al.*, Nature Reviews Drug Discovery 7:255-270 (2008); Simplicio *et al.*, Molecules 13:519-547 (2008)).

[0366] In some aspects, the self-immolative linker connects a biologically active molecule (e.g., an ASO) to a protease-cleavable substrate (e.g., Val-Cit). In specific aspects, the carbamate group of a pABC self-immolative linker is connected to an amino group of a biologically active molecule (e.g., ASO), and the amino group of the pABC self-immolative linker is connected to a protease-cleavable substrate.

[0367] The aromatic ring of the aminobenzyl group can optionally be substituted with one or more (e.g., R₁ and/or R₂) substituents on the aromatic ring, which replace a hydrogen that is otherwise attached to one of the four non-substituted carbons that form the ring. As used herein, the symbol "R_x" (e.g., R₁, R₂, R₃, R₄) is a general abbreviation that represents a substituent group as described herein.

[0368] Substituent groups can improve the self-immolative ability of the p-aminobenzyl group (Hay *et al.*, J. Chem Soc., Perkin Trans. 1:2759-2770 (1999); see also, Sykes *et al.* J. Chem. Soc., Perkin Trans. 1:1601-1608 (2000)).

[0369] Self-immolative elimination can take place, e.g., via 1,4 elimination, 1,6 elimination (e.g., pABC), 1,8 elimination (e.g., p-amino-cinnamyl alcohol), β-elimination, cyclisation-elimination (e.g., 4-aminobutanol ester and ethylenediamines),

cyclization/lactonization, cyclization/lactolization, *etc.* See, *e.g.*, Singh *et al.* *Curr. Med. Chem.* 15:1802-1826 (2008); Greenwald *et al.* *J. Med. Chem.* 43:475-487 (2000).

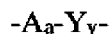
[0370] In some aspects, the self-immolative linker can comprise, *e.g.*, cinnamyl, naphthyl, or biphenyl groups (see, *e.g.*, Blencowe *et al.* *Polym. Chem.* 2:773-790 (2011)). In some aspects, the self-immolative linker comprises a heterocyclic ring (see, *e.g.*, U.S. Patent Nos. 7,375,078; 7,754,681). Numerous homoaromatic (see, *e.g.*, Carl *et al.* *J. Med. Chem.* 24:479 (1981); Senter *et al.* *J. Org. Chem.* 55:2975 (1990); Taylor *et al.* *J. Org. Chem.* 43:1197 (1978); Andrianomenjanahary *et al.* *Bioorg. Med. Chem. Lett.* 2:1903 (1992)), and coumarin (see, *e.g.*, Weinstein *et al.* *Chem. Commun.* 46:553 (2010)), furan, thiophene, thiazole, oxazole, isoxazole, pyrrole, pyrazole (see, *e.g.*, Hay *et al.* *J. Med. Chem.* 46:5533 (2003)), pyridine (see, *e.g.*, Perry-Feigenbaum *et al.* *Org. Biomol. Chem.* 7:4825 (2009)), imidazone (see, *e.g.*, Nailor *et al.* *Bioorg. Med. Chem. Lett.* 12:1267 (1999); Hay and Denny, *Tetrahedron Lett.* 38:8425 (1997)), and triazole (see, *e.g.*, Bertrand and Gesson, *J. Org. Chem.* 72:3596 (2007)) based heteroaromatic groups that are self-immolative under both aqueous and physiological conditions are known in the art. See also, U.S. Pat. Nos. 7,691,962; 7,091,186; U.S. Pat. Publ. Nos. US2006/0269480; US2010/0092496; US2010/0145036; US2003/0130189; US2005/0256030)

[0371] In some aspects, a linker combination disclosed herein comprises more than one self-immolative linker in tandem, *e.g.*, two or more pABC units. See, *e.g.*, de Groot *et al.* *J. Org. Chem.* 66:8815-8830 (2001). In some aspects, a linker combination disclosed herein can comprise a self-immolative linker (*e.g.*, a p-aminobenzylalcohol or a hemithioaminal derivative of p-carboxybenzaldehyde or glyoxilic acid) linked to a fluorogenic probe (see, *e.g.*, Meyer *et al.* *Org. Biomol. Chem.* 8:1777-1780 (2010)).

[0372] Where substituent groups in the self-immolative linker s are specified by their conventional chemical formulae, written from left to right, they equally encompass the chemically identical substituents, which would result from writing the structure from right to left. For example, "-CH₂O-" is intended to also recite "-OCH₂-".

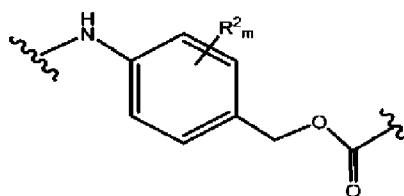
[0373] Substituent groups in self-immolative, for example, R₁ and/or R₂ substituents in a p-aminobenzyl self-immolative linker as discuss above can include, *e.g.*, alkyl, alkylene, alkenyl, alkynyl, alkoxy, alkylamino, alkylthio, heteroalkyl, cycloalkyl, heterocycloalkyl, aryl, arylalkyl, aryloxy, heteroaryl, *etc.* When a compound of the present disclosure includes more than one substituent, then each of the substituents is independently chosen.

[0374] In some specific aspects, the self-immolative linker is attached to cleavable peptide linker has the following formula, the combination having the following formula:



wherein each $-A-$ is independently an amino acid unit, a is independently an integer from 1 to 12; and $-Y-$ is a self-immolative spacer, and y is 1, or 2. In some aspects, $-A_a-$ is a dipeptide, a tripeptide, a tetrapeptide, a pentapeptide, or a hexapeptide. In some aspects, $-A_a-$ is selected from the group consisting of valine-alanine, valine-citrulline, phenylalanine-lysine, N-methylvaline-citrulline, cyclohexylalanine-lysine, and beta-alanine-lysine. In some aspects, $-A_a-$ is valine-alanine or valine-citrulline.

[0375] In some aspects, the self-immolative linker $-Y_y-$ has the following formula:



wherein each R^2 is independently C_{1-8} alkyl, $-O-(C_{1-8}$ alkyl), halogen, nitro, or cyano; and m is an integer from 0 to 4. In some aspects, m is 0, 1, or 2. In some aspects, m is 0.

[0376] In some aspects, the cleavable linker is valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate.

III.B.4. Reactive moieties (RM)

[0377] The ASOs of the present disclosure are generated either via chemical synthesis or via chemical reaction between their components. For example, in some aspects, an anchoring moiety comprising a reactive group (e.g., maleimide) can react with an ASO comprising a maleimide-reacting group, to yield a hydrophobically modified ASO of the present disclosure, where the anchoring moiety may insert into the lipid bilayer of the membrane of an exosome, thereby attaching the ASO to the surface of the exosome.

[0378] Any component or group of components of a hydrophobically modified ASO of the present disclosure can comprise at least a RG and/or an RM, which would allow the attachment of the components through one reaction or series of reactions, to yield a hydrophobically modified ASO of the present disclosure. Exemplary synthesis schemas for the production of hydrophobically modified ASOs include:





wherein [AM] is an anchoring moiety, [ASO] is an antisense oligonucleotide, [L] is a linker or linker combination, /RM/ is a reactive moiety, and /RG/ is a reactive group. In any of the schematic representations provided, the ASO can be attached, e.g., via its 5' end or 3' end.

[0379] Exemplary synthesis schemas for the production of intermediates in the synthesis of ASOs include:



wherein [AM] is an anchoring moiety, [ASO] is an antisense oligonucleotide, [L] is a linker or linker combination, /RM/ is a reactive moiety, and /RG/ is a reactive group. In any of the schematic representations provided, the ASO can be attached, e.g., via its 5' end or 3' end.

[0380] In some aspects, the reactive group “/RG/” can be, e.g., an amino group, a thiol group, a hydroxyl group, a carboxylic acid group, or an azide group. Specific reactive moieties “/RM/” that can react with these reactive groups are described in more detail below.



[0382] Any of the anchoring moieties, linker or linker combinations, or ASO disclosed herein can be conjugated to a reactive moiety, e.g., an amino reactive moiety (e.g., NHS-ester, p-nitrophenol, isothiocyanate, isocyanate, or aldehyde), a thiol reactive moiety (e.g., acrylate, maleimide, or pyridyl disulfide), a hydroxy reactive moiety (e.g., isothiocyanate or isocyanate), a carboxylic acid reactive moiety (e.g., epoxyde), or an azide reactive moiety (e.g., alkyne).

[0383] Exemplary reactive moieties that can be used to covalent bind two components disclosed herein (e.g., an anchoring moiety and an ASO, or an anchoring moiety and a linker, or an anchoring moiety and a linker, or two linkers, or a linker and an ASO, or a two anchoring

moieties) include, e.g., N-succinimidyl-3-(2-pyridyldithio)propionate, N-4-maleimide butyric acid, S-(2-pyridyldithio)cysteamine, iodoacetoxysuccinimide, N-(4-maleimidebutyryl oxy)succinimide, N-[5-(3'-maleimide propylamide)-1-carboxypentyl]iminodiacetic acid, N-(5-aminopentyl)iminodiacetic acid, and 1'-[(2-cyanoethyl)-(N,N-diisopropyl)}-phosphoramidite). Bifunctional linkers (linkers containing two functional groups) are also usable.

[0384] In some aspects, an anchoring moiety, linker, or ASO can comprise a terminal oxyamino group, e.g., —ONH₂, an hydrazino group, —NHNH₂, a mercapto group (i.e., SH or thiol), or an olefin (e.g., CH=CH₂). In some aspects, an anchoring moiety, linker, or ASO can comprise an electrophilic moiety, e.g., at a terminal position, e.g., an aldehyde, alkyl halide, mesylate, tosylate, nosylate, or brosylate, or an activated carboxylic acid ester, e.g. an NHS ester, a phosphoramidite, or a pentafluorophenyl ester. In some aspects, a covalent bond can be formed by coupling a nucleophilic group of a ligand, e.g., a hydroxyl, a thiol or amino group, with an electrophilic group.

[0385] The present invention is amenable to all manner of reactive groups and reactive moieties including but not limited to those known in the art.

[0386] The term "protecting group," as used herein, refers to a labile chemical moiety which is known in the art to protect reactive groups including without limitation, hydroxyl, amino and thiol groups, against undesired reactions during synthetic procedures. Protecting groups are typically used selectively and/or orthogonally to protect sites during reactions at other reactive sites and can then be removed to leave the unprotected group as is or available for further reactions. Protecting groups as known in the art are described generally in Greene and Wuts, *Protective Groups in Organic Synthesis*, 3rd edition, John Wiley & Sons, New York (1999).

[0387] Additionally, the various synthetic steps may be performed in an alternate sequence or order to give the desired compounds. Synthetic chemistry transformations and protecting group methodologies (protection and deprotection) useful in synthesizing the compounds described herein are known in the art and include, for example, those such as described in R. Larock, *Comprehensive Organic Transformations*, VCH Publishers (1989); T. W. Greene and P. G. M. Wuts, *Protective Groups in Organic Synthesis*, 2d. Ed., John Wiley and Sons (1991); L. Fieser and M. Fieser, *Fieser and Fieser's Reagents for Organic Synthesis*, John Wiley and Sons (1994); and L. Paquette, ed., *Encyclopedia of Reagents for Organic Synthesis*, John Wiley and Sons (1995), and subsequent editions thereof.

[0388] Solid phase synthesis known in the art may additionally or alternatively be employed. Suitable solid phase techniques, including automated synthesis techniques, are

described in F. Eckstein (ed.), *Oligonucleotides and Analogues, a Practical Approach*, Oxford University Press, New York (1991) and Toy, P.H.; Lam, Y (ed.), *Solid-Phase Organic synthesis, concepts, Strategies, and Applications*, John Wiley & Sons, Inc. New Jersey (2012).

[0389] In some aspects, the reactive group can alternatively react with more than one of the reactive moieties described below.

III.B.4.a. Amine reactive moieties

[0390] In some aspects, the reactive moiety is an amine reactive moiety. As used herein the term "amine reactive moiety" refers to a chemical groups which can react with a reactive group having an amino moiety, e.g., primary amines. Exemplary amine reactive moieties are N-hydroxysuccinimide esters (NHS-ester), p-nitrophenol, isothiocyanate, isocyanate, and aldehyde. Alternative reactive moieties that react with primary amines are also well known in the art. In some aspects, an amine reactive moiety can be attached to a terminal position of an anchoring moiety, linker combination, or ASO of the present disclosure.

[0391] In some aspects, the amine reactive moiety is a NHS-ester. Typically, a NHS-ester reactive moiety reacts with a primary amine of a reactive group to yield a stable amide bond and N-hydroxysuccinimide (NHS).

[0392] In some aspects, the amine reactive moiety is a p-nitrophenol group. Typically, a p-nitrophenol reactive moiety is an activated carbamate that reacts with a primary amine of a reactive group to yield a stable carbamate moiety and p-nitrophenol.

[0393] In some aspects, the amine reactive moiety is an isothiocyanate. Typically, a isothiocyanate reacts with a primary amine of a reactive group to yield a stable thiourea moiety.

[0394] In some aspects, the amine reactive moiety is an isocyanate. Typically, a isocyanate reacts with a primary amine of a reactive group to yield a stable urea moiety.

[0395] In some aspects, amine the reactive moiety is an aldehyde. Typically, aldehydes react with primary amines to form Schiff bases which can be further reduced to form a covalent bond through reductive amination.

III.B.4.b. Thiol reactive moieties

[0396] In some aspects, the reactive moiety is a thiol reactive moiety. As used herein the term "thiol reactive moiety" refers to a chemical groups which can react with a reactive group having a thiol moiety (or mercapto group). Exemplary thiol reactive moieties are acrylates,

maleimides, and pyridyl disulfides. Alternative reactive moieties that react with thiols are also well known in the art. In some aspects, a thiol reactive moiety can be attached to a terminal position of an anchoring moiety, linker combination, or ASO of the present disclosure.

[0397] In some aspects, the thiol reactive moiety is an acrylate. Typically, acrylates react with thiols at the carbon β to the carbonyl of the acrylate to form a stable sulfide bond.

[0398] In some aspects, the thiol reactive moiety is a maleimide. Typically, maleimides react with thiols at either of at the carbon β the to the carbonyls to form a stable sulfide bond.

[0399] In some aspects, the thiol reactive moiety is a pyridyl disulfide. Typically, pyridyl disulfides react with thiols at the sulfur atom β to the pyridyl to form a stable disulfide bond and pyridine-2-thione.

III.B.4.c. Hydroxy reactive moieties

[0400] In some aspects, the reactive moiety is a hydroxyl reactive moiety. As used herein the term "hydroxyl reactive moiety" refers to a chemical group which can react with a reactive group having an hydroxyl moiety. Exemplary hydroxyl reactive moieties are isothiocyanates and isocyanates. Alternative reactive moieties that react with hydroxyl moieties are also well known in the art. In some aspects, a hydroxyl reactive moiety can be attached to a terminal position of an anchoring moiety, linker combination, or ASO of the present disclosure.

[0401] In some aspects, the hydroxyl reactive moiety is an isothiocyanate. Typically, an isothiocyanate reacts with a hydroxyl of a reactive group to yield a stable carbamothioate moiety.

[0402] In some aspects, amine the reactive moiety is a isocyanate. Typically, an isocyanate reacts with a hydroxyl of a reactive group to yield a stable carbamate moiety.

III.B.4.d. Carboxylic acid reactive moieties

[0403] In some aspects, the reactive moiety is a carboxylic acid reactive moiety. As used herein the term "carboxylic acid reactive moiety" refers to a chemical groups which can react with a reactive group having an carboxylic acid moiety. An exemplary carboxylic acid reactive moieties is an epoxide. Alternative reactive moieties that react with carboxylic acid moieties are also well known in the art. In some aspects, an carboxylic acid reactive moiety can be attached to a terminal position of an anchoring moiety, linker combination, or ASO of the present disclosure.

[0404] In some aspects, the carboxylic acid reactive moiety is an epoxide. Typically, an epoxide reacts with the carboxylic acid of a reactive group at either of the carbon atoms of the epoxide to form a 2-hydroxyethyl acetate moiety.

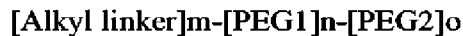
III.B.4.e. Azide reactive moieties

[0405] In some aspects, the reactive moiety is an azide reactive moiety. As used herein the term "azide reactive moiety" refers to a chemical groups which can react with a reactive group having an azide moiety. An exemplary azide reactive moieties is an alkyne. Alternative reactive moieties that react with azide moieties are also well known in the art. In some aspects, a carboxylic acid reactive moiety can be attached to a terminal position of an anchoring moiety, linker combination, or ASO of the present disclosure.

[0406] In some aspects, the azide reactive moiety is an alkyne. Typically, an alkyne reacts with the azide of a reactive group through a 1,3-dipolar cycloaddition reaction, also referred to "click chemistry," to form a 1,2,3-triazole moiety.

III.B.5. Specific examples and topologies

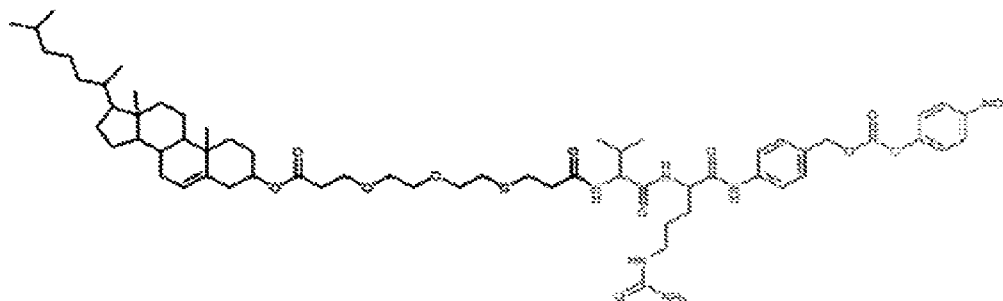
[0407] In specific aspects of the present disclosure, the linker combination consists of a linker of formula



wherein m, n, and o are 0 or 1, and at least one of m, n, or o is not zero. Exemplary linker combinations according to such formula are C6-TEG-HEG, C6-HEG, C6-TEG, C6, TEG-HEG, TEG, C8-TEG-HEG, C8-HEG, C8-TEG, and C8.

[0408] In some aspects, the linker combination comprises a non-cleavable linker (e.g., TEG or HEG) in combination with one or more cleavable linkers, e.g., an enzymatic cleavable linker and a self immolative linker.

[0409] In a specific aspect, the linker combination the linker combination comprises the linker combination TEG (non-cleavable linker)-Val-Cit(cleavable linker)-pAB(self-immolative linker), as shown below



[0410] Specific combinations of anchoring moieties and linker combinations are illustrated in the tables below.

Anchoring moiety	Linker combination		
	1 st Linker	2 nd Linker	3 rd Linker
Cholesterol	C6	TEG	HEG
Cholesterol	C6	HEG	No
Cholesterol	C6	TEG	No
Cholesterol	C6	No	No
Cholesterol	TEG	HEG	No
Cholesterol	TEG	No	No
Tocopherol	C8	TEG	HEG
Tocopherol	C8	HEG	No
Tocopherol	C8	TEG	No
Tocopherol	C8	No	No
Tocopherol	TEG	HEG	No
Tocopherol	HEG	No	No
Tocopherol	TEG	No	No
Tocopherol	No	No	No
Palmitate	C6	TEG	HEG
Palmitate	C6	HEG	No

Palmitate	C6	TEG	No
Palmitate	C6	No	No
Cholesterol	TEG	Glycerol	HEG

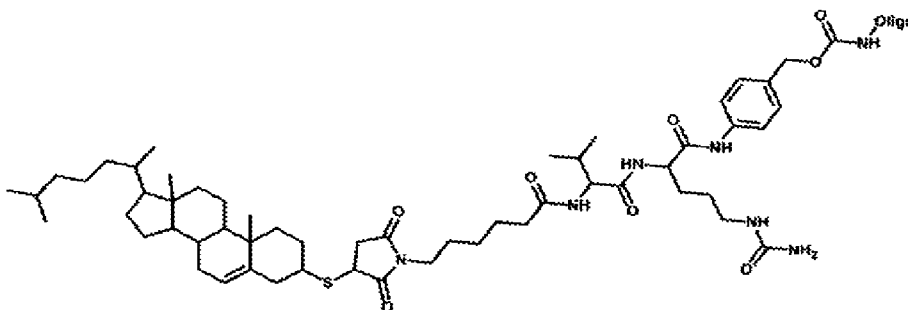
Linker Combination		
Linker 1	Cleavable Linker 2	Linker 3
C6	Disulfide Imine Thioketal Tri/Dinucleotide Val-Cit	C6
None		None
TEG		TEG
HEG		HEG
TEG-HEG		TEG-HEG

[0411] Specific oligonucleotides such as ASOs of the present disclosure are exemplified below

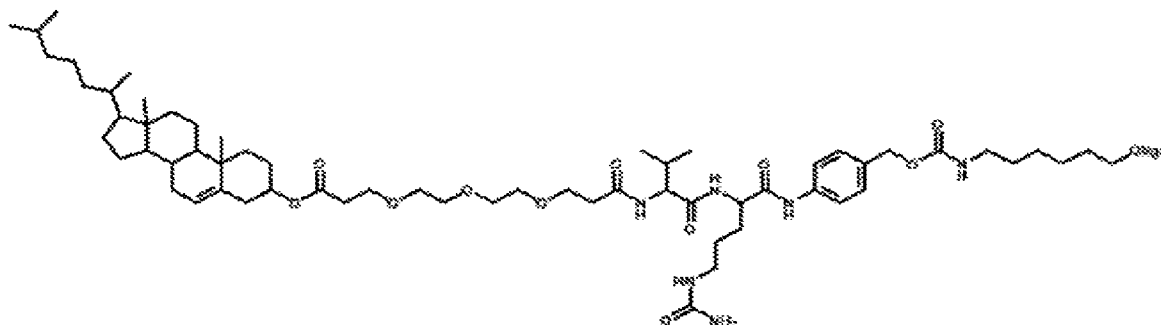
[Cholesterol]-[TEG]-[HEG]-[ASO]



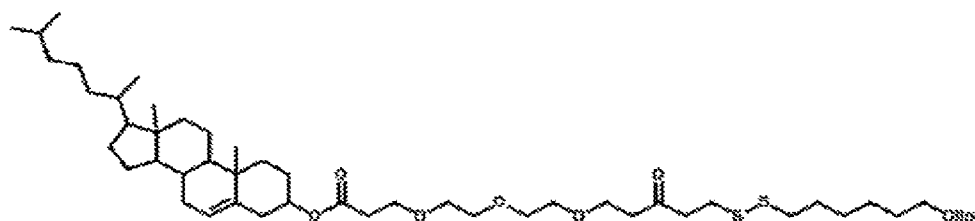
[Cholesterol]-[SMal]-[Val-Cit]-[pAB]-[ASO]



[Cholesterol]-[TEG]-[Val-Cit]-[C6]-[ASO]



[Cholesterol]-[TEG]-[SS]-[C6]-[ASO]



wherein [Cholesterol] is a cholesterol anchoring moiety, [TEG] is a TEG non-cleavable linker, [HEG] is a HEG non-cleavable linker, [SS] is a disulfide redox cleavable linker, [C6] is an alkyl non-cleavable linker, [SMal] is S-maleimide, [Val-Cit] is a valine-citrulline cleavable linker, [pAB] is a pAB self-immolative linker. In some aspects, an ASO of the present disclosure has a structure according to the exemplary structures provided above, in which one or more components has been replaced by a component in the same class as those depicted in the example. For example, the [cholesterol] anchoring moiety can be substituted by another anchoring moiety disclosed herein, a [TEG] can be substituted by another polymeric non-cleavable linker disclosed herein (e.g., HEG, PEG, PG), [Val-Cit] can be replaced by another peptidase cleavable linker, or [pAB] can be substituted by another self-immolative linker.

III.B.6 Scaffold Moieties

[0412] One or more scaffold moieties can be expressed in the EVs. In some aspects, one or more scaffold moieties are used to anchor an ASO to the EV of the present disclosure. In other aspects, one or more scaffold moieties are used to anchor a protein or a molecule to the EVs in addition to the ASOs. Therefore, an EV of the present disclosure comprises an anchoring moiety linking an ASO and a scaffold moiety linking a protein or a molecule, e.g., a targeting moiety. In some aspects, the ASO is linked to the scaffold moiety. In some aspects, the EV comprises more

than one scaffold moiety. In some aspects, a first ASO is linked to a first scaffold moiety and a second ASO is linked to a second scaffold moiety. In some aspects, the first scaffold moiety and the second scaffold moiety are the same type of scaffold moiety, *e.g.*, the first and second scaffold moieties are both a Scaffold X protein. In some aspects, the first scaffold moiety and the second scaffold moiety are different types of scaffold moiety, *e.g.*, the first scaffold moiety is a Scaffold Y protein and the second scaffold moiety is a Scaffold X protein. In some aspects, the first scaffold moiety is a Scaffold Y, disclosed herein. In some aspects, the first scaffold moiety is a Scaffold X, disclosed herein. In some aspects, the second scaffold moiety is a Scaffold Y, disclosed herein. In some aspects, the second scaffold moiety is a Scaffold X, disclosed herein.

[0413] In some aspects, the EV comprises one or more scaffold moieties, which are capable of anchoring an ASO to the EV, *e.g.*, exosome, (*e.g.*, either on the luminal surface or on the exterior surface). In certain aspects, the scaffold moiety is a polypeptide ("scaffold protein"). In certain aspects, the scaffold protein comprises an exosome protein or a fragment thereof. In other aspects, scaffold moieties are non-polypeptide moieties. In some aspects, scaffold proteins include various membrane proteins, such as transmembrane proteins, integral proteins and peripheral proteins, enriched on the exosome membranes. They can include various CD proteins, transporters, integrins, lectins, and cadherins. In certain aspects, a scaffold moiety (*e.g.*, scaffold protein) comprises Scaffold X. In other aspects, a scaffold moiety (*e.g.*, exosome protein) comprises Scaffold Y. In further aspects, a scaffold moiety (*e.g.*, exosome protein) comprises both a Scaffold X and a Scaffold Y.

III.C.1. Scaffold X-Engineered EVs, *e.g.*, Exosomes

[0414] In some aspects, EVs, *e.g.*, exosomes, of the present disclosure comprise a membrane modified in its composition. For example, their membrane compositions can be modified by changing the protein, lipid, or glycan content of the membrane.

[0415] In some aspects, the surface-engineered EVs, *e.g.*, exosomes, are generated by chemical and/or physical methods, such as PEG-induced fusion and/or ultrasonic fusion. In other aspects, the surface-engineered EVs, *e.g.*, exosomes, are generated by genetic engineering. EVs, *e.g.*, exosomes, produced from a genetically-modified producer cell or a progeny of the genetically-modified cell can contain modified membrane compositions. In some aspects, surface-engineered EVs, *e.g.*, exosomes, have scaffold moiety (*e.g.*, exosome protein, *e.g.*, Scaffold X) at a higher or lower density (*e.g.*, higher number) or include a variant or a fragment of the scaffold moiety.

[0416] For example, surface (*e.g.*, Scaffold X)-engineered EVs, can be produced from a cell (*e.g.*, HEK293 cells) transformed with an exogenous sequence encoding a scaffold moiety (*e.g.*, exosome proteins, *e.g.*, Scaffold X) or a variant or a fragment thereof. EVs including scaffold moiety expressed from the exogenous sequence can include modified membrane compositions.

[0417] Various modifications or fragments of the scaffold moiety can be used for the aspects of the present disclosure. For example, scaffold moiety modified to have enhanced affinity to a binding agent can be used for generating surface-engineered EV that can be purified using the binding agent. Scaffold moieties modified to be more effectively targeted to EVs and/or membranes can be used. Scaffold moieties modified to comprise a minimal fragment required for specific and effective targeting to exosome membranes can be also used.

[0418] Scaffold moieties can be engineered to be expressed as a fusion molecule, *e.g.*, fusion molecule of Scaffold X to an ASO. For example, the fusion molecule can comprise a scaffold moiety disclosed herein (*e.g.*, Scaffold X, *e.g.*, PTGFRN, BSG, IGSF2, IGSF3, IGSF8, ITGB1, ITGA4, SLC3A2, ATP transporter, or a fragment or a variant thereof) linked to an ASO.

[0419] In some aspects, the surface (*e.g.*, Scaffold X)-engineered EVs described herein demonstrate superior characteristics compared to EVs known in the art. For example, surface (*e.g.*, Scaffold X)-engineered contain modified proteins more highly enriched on their surface than naturally occurring EVs or the EVs produced using conventional exosome proteins. Moreover, the surface (*e.g.*, Scaffold X)-engineered EVs of the present disclosure can have greater, more specific, or more controlled biological activity compared to naturally occurring EVs or the EVs produced using conventional exosome proteins.

[0420] In some aspects, the Scaffold X comprises Prostaglandin F2 receptor negative regulator (the PTGFRN polypeptide). The PTGFRN protein can be also referred to as CD9 partner 1 (CD9P-1), Glu-Trp-Ile EWI motif-containing protein F (EWI-F), Prostaglandin F2-alpha receptor regulatory protein, Prostaglandin F2-alpha receptor-associated protein, or CD315. The full length amino acid sequence of the human PTGFRN protein (Uniprot Accession No. Q9P2B2) is shown at Table 2 as SEQ ID NO: 301. The PTGFRN polypeptide contains a signal peptide (amino acids 1 to 25 of SEQ ID NO: 301), the extracellular domain (amino acids 26 to 832 of SEQ ID NO: 301), a transmembrane domain (amino acids 833 to 853 of SEQ ID NO: 301), and a cytoplasmic domain (amino acids 854 to 879 of SEQ ID NO: 301). The mature PTGFRN polypeptide consists of SEQ ID NO: 301 without the signal peptide, *i.e.*, amino acids 26 to 879 of SEQ ID NO: 301. In some aspects, a PTGFRN polypeptide fragment useful for the present disclosure comprises a transmembrane domain of the PTGFRN polypeptide. In other aspects, a

PTGFRN polypeptide fragment useful for the present disclosure comprises the transmembrane domain of the PTGFRN polypeptide and (i) at least five, at least 10, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, at least 70, at least 80, at least 90, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150 amino acids at the N terminus of the transmembrane domain, (ii) at least five, at least 10, at least 15, at least 20, or at least 25 amino acids at the C terminus of the transmembrane domain, or both (i) and (ii).

[0421] In some aspects, the fragments of PTGFRN polypeptide lack one or more functional or structural domains, such as IgV.

[0422] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 26 to 879 of SEQ ID NO: 301. In other aspects, the Scaffold X comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 302. In other aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 302, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any combination thereof. In some aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 302 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NO: 302.

[0423] In other aspects, the Scaffold X comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, or 318. In other aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, or 318, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any

combination thereof. In some aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, or 318 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NO: 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, or 318.

Table 1A. Exemplary Scaffold X Protein Sequences

Protein	Sequence
The PTGFRN Protein (SEQ ID NO: 301)	MGRLASRPLLLALLSLALCRGRVVRVPTATLVRVVGTELVIPCNVSDYDGPSEQNFDWSFS SLGSSFVELASTWEVGFPAPQLYQERLQGEILLRRTANDAVELHIKNVQPSDQGHYKCSTP STDATVQGNIEDTVQVKVLADSLHVGPSARPPPSLSLREGEPPFELRCTAASASPLHHTHAL LWEVHRGPARRSVLALTHEGRFHPGLGYEQRYHSGDVRLDTVGSDAYRLSVSRALSADQGS YRCIVSEWIAEQGNWQEIQEKAVEVATVVIQPSVLRAAVPKNVSAEGKELDLTCNITTD ADDVRPEVTWSFSRMPDSTLPGSRVLARLDRDSLHSSPHVALSHVDARSYHLLVRDVSKE NSGYYYCHVSLWAPGHNRSWHKVAEAVSSPAGVGVTWLEPDYQVYLNASKVPGFADDPTEL ACRVVDTKSGEANVRFTVSWYYRMNRRSDNVVTSELLAVMDGDWTLKYGERSKQRAQDGD IFSKEHTDTFNFRIQRTTEEDRGNYYCVVSAWTKQRNNSWVKS KDVFSKPVNI FWALED SVLVVKARQPKPFPAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGDLSSPNETKYIIISLDQ DSVVKLENWTDASRV DGVVLEKVQEDEFYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREA ATSLSNPIEIDFQTSGPIFNASVHSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWF AVHSFGLDKAPVLLSSLDKGI VTTSRRDWKS DLSLERSVLEFLLQVHGSEDQDFGNYYC SVTPWVKSP TGSWQKEABIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIGLLSCLIGYCS SHWCKKEVQETRRERRRLMSMEMD
The PTGFRN protein Fragment (SEQ ID NO: 302)	GPIFNASVHSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLS SLDRKGIVTTSRRDWKSDLSLERSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQK EABIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIGLLSCLIGYCSSHWCKKEVQETRRE RRRLMSMEM 687-878 of SEQ ID NO: 301

[0424] In other aspects, the Scaffold X comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 319, 320, 321, 322, 323, 323, or 325. In other aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 319, 320, 321, 322, 323, 323, or 325, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any combination thereof.

In some aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 319, 320, 321, 322, 323, 323, or 325 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NO: 319, 320, 321, 322, 323, 323, or 325.

Table 1B. Exemplary Scaffold X Protein Sequences

Protein	Sequence
PTGFRN Protein Fragment #1 (SEQ ID NO: 319)	PSARPPPSLSLREGEPPFELRCTAASASPLHHLALLWEVHRGPARRSVLALTHEGRFHPG LGYEQRYHSGDVRLDTVGSDAYRLSVSRALSADQGSYRCIVSEWIAEQGNWQEIQEKAVE VATVVIQPSVLRAAVPKNVSVAEKGELDLTCNITTDRAADDVRPEVTWSFSRMPDSTLPGS RVLARLDRDSLHSSPHVALSHVDARSYHLLVRDVS KENSGY YCHVSLWAPGHNRSWHK VAEAVSSPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWY YRMNRRSDNVVTSELLAVMDGDWTLKYGERSKQRAQDGD F IFSKEHTDTFNFRIQRTTEE DRGNYYCVVSAWTKQRNNSWVKS KDVFSKPVNIFWALEDSVLVVKARQPKPFFAAGNTFE MTCKVSSKNIKSPRYSVLIMAEKPVGDLS SPNETKY I IISLDQDSVVKLENWTDASRVDGV VLEKQVEDEFYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGP IFNASVHSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSS LDRKGIVTTSRRDWKSDLSLERSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQK EAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIGLLSCLIGYCSSHWCCKKEVQETR ERRRLMSMEMD
PTGFRN Protein Fragment #2 (SEQ ID NO: 320)	VATVVIQPSVLRAAVPKNVSVAEKGELDLTCNITTDRAADDVRPEVTWSFSRMPDSTLPGS RVLARLDRDSLHSSPHVALSHVDARSYHLLVRDVS KENSGY YCHVSLWAPGHNRSWHK VAEAVSSPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWY YRMNRRSDNVVTSELLAVMDGDWTLKYGERSKQRAQDGD F IFSKEHTDTFNFRIQRTTEE DRGNYYCVVSAWTKQRNNSWVKS KDVFSKPVNIFWALEDSVLVVKARQPKPFFAAGNTFE MTCKVSSKNIKSPRYSVLIMAEKPVGDLS SPNETKY I IISLDQDSVVKLENWTDASRVDGV VLEKQVEDEFYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGP IFNASVHSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSS LDRKGIVTTSRRDWKSDLSLERSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQK EAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIGLLSCLIGYCSSHWCCKKEVQETR ERRRLMSMEMD
PTGFRN Protein Fragment #3 (SEQ ID NO: 321)	SPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWYYRMNRR SDNVVTSELLAVMDGDWTLKYGERSKQRAQDGD F IFSKEHTDTFNFRIQRTTEEDRGNY CVVSAWTKQRNNSWVKS KDVFSKPVNIFWALEDSVLVVKARQPKPFFAAGNTFEMTCKVS SKNIKSPRYSVLIMAEKPVGDLS SPNETKY I IISLDQDSVVKLENWTDASRVDGVVLEKQ EDEFYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASV HSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSLDKGI VTTSRRDWKSDLSLERSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQKEAEIHS KPVFITVKMDVLNAFKYPLLIGVGLSTVIGLLSCLIGYCSSHWCCKKEVQETRERRRLM SMEMD
PTGFRN Protein Fragment #4 (SEQ ID NO: 322)	KPVNIFWALEDSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGD LSPNETKY I IISLDQDSVVKLENWTDASRVDGVVLEKQVEDEFYRMYQTQVSDAGLYRCM VTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASVHSDTPSVIRGDLIKLFCIITVE GAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSLDKGI VTTSRRDWKSDLSLERSVLEF LLQVHGSEDQDFGNYYCSVTPWVKSP TGSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIG VGLSTVIGLLSCLIGYCSSHWCCKKEVQETRERRRLMSMEMD
PTGFRN Protein Fragment #5 (SEQ ID NO: 323)	VRGSLWREAATSLSNPIEIDFQTSGPIFNASVHSDTPSVIRGDLIKLFCIITVEGAALDP DDMAFDVSWFAVHSFGLDKAPVLLSSLDKGI VTTSRRDWKSDLSLERSVLEFLLQVHG SEDQDFGNYYCSVTPWVKSP TGSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTV IGLLSCLIGYCSSHWCCKKEVQETRERRRLMSMEMD

PTGFRN Protein Fragment #6 (SEQ ID NO: 324)	SKPVFITVKMDVLNAFKYPLLIQVGLSTVIGLLSCLIGYCSSHWCCKKEVQETRERRRL MSMEMD
PTGFRN Protein - Signal Peptide (SEQ ID NO: 325)	MGRLASRPILLALLSLALCRG

[0425] In some aspects, a Scaffold X comprises Basigin (the BSG protein), represented by SEQ ID NO: 303. The BSG protein is also known as 5F7, Collagenase stimulatory factor, Extracellular matrix metalloproteinase inducer (EMMPRIN), Leukocyte activation antigen M6, OK blood group antigen, Tumor cell-derived collagenase stimulatory factor (TCSF), or CD147. The Uniprot number for the human BSG protein is P35613. The signal peptide of the BSG protein is amino acid 1 to 21 of SEQ ID NO: 303. Amino acids 138-323 of SEQ ID NO: 303 is the extracellular domain, amino acids 324 to 344 is the transmembrane domain, and amino acids 345 to 385 of SEQ ID NO: 303 is the cytoplasmic domain.

[0426] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 22 to 385 of SEQ ID NO: 303. In some aspects, the fragments of BSG polypeptide lack one or more functional or structural domains, such as IgV, *e.g.*, amino acids 221 to 315 of SEQ ID NO: 303. In other aspects, the Scaffold X comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 326, 327, or 328. In other aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 326, 327, or 328, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any combination thereof. In some aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 326, 327, or 328 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids,

19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NO: 326, 327, or 328.

[0427] In some aspects, a Scaffold X comprises Immunoglobulin superfamily member 8 (IgSF8 or the IGSF8 protein), which is also known as CD81 partner 3, Glu-Trp-Ile EWI motif-containing protein 2 (EWI-2), Keratinocytes-associated transmembrane protein 4 (KCT-4), LIR-D1, Prostaglandin regulatory-like protein (PGRL) or CD316. The full length human IGSF8 protein is accession no. Q969P0 in Uniprot and is shown as SEQ ID NO: 304 herein. The human IGSF8 protein has a signal peptide (amino acids 1 to 27 of SEQ ID NO: 304), an extracellular domain (amino acids 28 to 579 of SEQ ID NO: 304), a transmembrane domain (amino acids 580 to 600 of SEQ ID NO: 304), and a cytoplasmic domain (amino acids 601 to 613 of SEQ ID NO: 304).

[0428] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 28 to 613 of SEQ ID NO: 304. In some aspects, the IGSF8 protein lack one or more functional or structural domains, such as IgV. In other aspects, the Scaffold X comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 330, 331, 332, or 333. In other aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 330, 331, 332, or 333, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any combination thereof. In some aspects, the Scaffold X comprises the amino acid sequence of SEQ ID NO: 330, 331, 332, or 333 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NO: 330, 331, 332, or 333.

[0429] In some aspects, a Scaffold X for the present disclosure comprises Immunoglobulin superfamily member 3 (IgSF3 or the IGSF3 protein), which is also known as Glu-Trp-Ile EWI motif-containing protein 3 (EWI-3), and is shown as the amino acid sequence of SEQ ID NO: 309. The human IGSF3 protein has a signal peptide (amino acids 1 to 19 of SEQ ID NO: 309), an extracellular domain (amino acids 20 to 1124 of SEQ ID NO: 309), a transmembrane domain

(amino acids 1125 to 1145 of SEQ ID NO: 309), and a cytoplasmic domain (amino acids 1146 to 1194 of SEQ ID NO: 309).

[0430] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 28 to 613 of SEQ ID NO: 309. In some aspects, the IGSF3 protein lack one or more functional or structural domains, such as IgV.

[0431] In some aspects, a Scaffold X for the present disclosure comprises Integrin beta-1 (the ITGB1 protein), which is also known as Fibronectin receptor subunit beta, Glycoprotein IIa (GPIIA), VLA-4 subunit beta, or CD29, and is shown as the amino acid sequence of SEQ ID NO: 305. The human ITGB1 protein has a signal peptide (amino acids 1 to 20 of SEQ ID NO: 305), an extracellular domain (amino acids 21 to 728 of SEQ ID NO: 305), a transmembrane domain (amino acids 729 to 751 of SEQ ID NO: 305), and a cytoplasmic domain (amino acids 752 to 798 of SEQ ID NO: 305).

[0432] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 21 to 798 of SEQ ID NO: 305. In some aspects, the ITGB1 protein lack one or more functional or structural domains, such as IgV.

[0433] In other aspects, the Scaffold X comprises the ITGA4 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 306 without the signal peptide (amino acids 1 to 33 of SEQ ID NO: 306). In some aspects, the ITGA4 protein lacks one or more functional or structural domains, such as IgV.

[0434] In other aspects, the Scaffold X comprises the SLC3A2 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 307 without the signal peptide. In some aspects, the SLC3A2 protein lacks one or more functional or structural domains, such as IgV.

[0435] In other aspects, the Scaffold X comprises the ATP1A1 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about

85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 310 without the signal peptide. In some aspects, the ATP1A1 protein lacks one or more functional or structural domains, such as IgV.

[0436] In other aspects, the Scaffold X comprises the ATP1A2 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 311 without the signal peptide. In some aspects, the ATP1A2 protein lacks one or more functional or structural domains, such as IgV.

[0437] In other aspects, the Scaffold X comprises the ATP1A3 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 312 without the signal peptide. In some aspects, the ATP1A3 protein lacks one or more functional or structural domains, such as IgV.

[0438] In other aspects, the Scaffold X comprises the ATP1A4 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 313 without the signal peptide. In some aspects, the ATP1A4 protein lacks one or more functional or structural domains, such as IgV.

[0439] In other aspects, the Scaffold X comprises the ATP2B1 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 314 without the signal peptide. In some aspects, the ATP2B1 protein lacks one or more functional or structural domains, such as IgV.

[0440] In other aspects, the Scaffold X comprises the ATP2B2 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 315 without the signal peptide.

In some aspects, the ATP2B2 protein lacks one or more functional or structural domains, such as IgV.

[0441] In other aspects, the Scaffold X comprises the ATP2B3 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 316 without the signal peptide. In some aspects, the ATP2B3 protein lacks one or more functional or structural domains, such as IgV.

[0442] In other aspects, the Scaffold X comprises the ATP2B4 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 317 without the signal peptide. In some aspects, the ATP2B4 protein lacks one or more functional or structural domains, such as IgV.

[0443] In other aspects, the Scaffold X comprises the IGSF2 protein, which comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 318 without the signal peptide. In some aspects, the IGSF2 protein lacks one or more functional or structural domains, such as IgV.

[0444] Non-limiting examples of other Scaffold X proteins can be found at US Patent No. US10195290B1, issued Feb. 5, 2019, which is incorporated by reference in its entirety.

[0445] In some aspects, the sequence encodes a fragment of the scaffold moiety lacking at least 5, 10, 50, 100, 200, 300, 400, 500, 600, 700, or 800 amino acids from the N-terminus of the native protein. In some aspects, the sequence encodes a fragment of the scaffold moiety lacking at least 5, 10, 50, 100, 200, 300, 400, 500, 600, 700, or 800 amino acids from the C-terminus of the native protein. In some aspects, the sequence encodes a fragment of the scaffold moiety lacking at least 5, 10, 50, 100, 200, 300, 400, 500, 600, 700, or 800 amino acids from both the N-terminus and C-terminus of the native protein. In some aspects, the sequence encodes a fragment of the scaffold moiety lacking one or more functional or structural domains of the native protein.

[0446] In some aspects, the scaffold moieties, *e.g.*, Scaffold X, *e.g.*, a PTGFRN protein, are linked to one or more heterologous proteins. The one or more heterologous proteins can be linked to the N-terminus of the scaffold moieties. The one or more heterologous proteins can be linked to the C-terminus of the scaffold moieties. In some aspects, the one or more heterologous

proteins are linked to both the N-terminus and the C-terminus of the scaffold moieties. In some aspects, the heterologous protein is a mammalian protein. In some aspects, the heterologous protein is a human protein.

[0447] In some aspects, Scaffold X can be used to link any moiety, *e.g.*, an ASO, to the luminal surface and on the exterior surface of the EV, *e.g.*, exosome, at the same time. For example, the PTGFRN polypeptide can be used to link an ASO inside the lumen (*e.g.*, on the luminal surface) in addition to the exterior surface of the EV, *e.g.*, exosome. Therefore, in certain aspects, Scaffold X can be used for dual purposes, *e.g.*, an ASO on the luminal surface and an ASO on the exterior surface of the EV, *e.g.*, exosome. In some aspects, Scaffold X is a scaffold protein that is capable of anchoring the ASO on the luminal surface of the EV and/or on the exterior surface of the EV.

III.C.2. Scaffold Y-Engineered EVs, *e.g.*, Exosomes

[0448] In some aspects, EVs, *e.g.*, exosomes, of the present disclosure comprise an internal space (*i.e.*, lumen) that is different from that of the naturally occurring EVs. For example, the EV can be changed such that the composition in the luminal surface of the EV, *e.g.*, exosome has the protein, lipid, or glycan content different from that of the naturally-occurring exosomes.

[0449] In some aspects, engineered EVs, *e.g.*, exosomes, can be produced from a cell transformed with an exogenous sequence encoding a scaffold moiety (*e.g.*, exosome proteins, *e.g.*, Scaffold Y) or a modification or a fragment of the scaffold moiety that changes the composition or content of the luminal surface of the EV, *e.g.*, exosome. Various modifications or fragments of the exosome protein that can be expressed on the luminal surface of the EV, *e.g.*, exosome, can be used for the aspects of the present disclosure.

[0450] In some aspects, the exosome proteins that can change the luminal surface of the EVs, *e.g.*, exosomes, include, but are not limited to, the myristoylated alanine rich Protein Kinase C substrate (MARCKS) protein, the myristoylated alanine rich Protein Kinase C substrate like 1 (MARCKSL1) protein, the brain acid soluble protein 1 (BASP1) protein, or any combination thereof.

[0451] In some aspects, Scaffold Y comprises the MARCKS protein (Uniprot accession no. P29966). The MARCKS protein is also known as protein kinase C substrate, 80 kDa protein, light chain. The full-length human MARCKS protein is 332 amino acids in length and comprises a calmodulin-binding domain at amino acid residues 152-176. In some aspects, Scaffold Y comprises the MARCKSL1 protein (Uniprot accession no. P49006). The MARCKSL1 protein is also known as MARCKS-like protein 1, and macrophage myristoylated alanine-rich C kinase

substrate. The full-length human MARCKSL1 protein is 195 amino acids in length. The MARCKSL1 protein has an effector domain involved in lipid-binding and calmodulin-binding at amino acid residues 87-110. In some aspects, the Scaffold Y comprises the BASP1 protein (Uniprot accession number P80723). The BASP1 protein is also known as 22 kDa neuronal tissue-enriched acidic protein or neuronal axonal membrane protein NAP-22. The full-length human BASP1 protein sequence (isomer 1) is 227 amino acids in length. An isomer produced by an alternative splicing is missing amino acids 88 to 141 from SEQ ID NO: 403 (isomer 1).

Table 2. Exemplary Scaffold Y Protein Sequences

Protein	Sequence
The BASP1 protein (SEQ ID NO: 403)	MGGKLSKKKKGYNVNDEKAKEKDKKAEGAATEEEGTPKRSEPQAAAEPAEAKGKE KPDQDAEGKAEKEGEKDAAAAKEEAPKAEPEKTEGAABAKAEPPKAPEQEQAAPG PAAGGEAPKAAEAAAAPAESAAPAAGEEPSKEEGEPKKTEAPAAPAAQETKSDGAP ASDSKPGSSEAAPSSKETPAATEAPSSSTPKAQGPAASAEPPKPV EAPAA NSDQTVT VKE

[0452] The mature BASP1 protein sequence is missing the first Met from SEQ ID NO: 403 and thus contains amino acids 2 to 227 of SEQ ID NO: 403. Similarly, the mature MARCKS and MARCKSL1 proteins also lack the first Met from SEQ ID NOs: 401 and 402, respectively. Accordingly, the mature MARCKS protein contains amino acids 2 to 332 of SEQ ID NO: 401. The mature MARCKSL1 protein contains amino acids 2 to 227 of SEQ ID NO: 402.

[0453] In other aspects, Scaffold Y useful for the present disclosure comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 2 to 227 of SEQ ID NO: 403. In other aspects, the Scaffold Y comprises an amino acid sequence at least about at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to any one of SEQ ID NOs: 404-567. In other aspects, a Scaffold Y useful for the present disclosure comprises the amino acid sequence of SEQ ID NO: 403, except one amino acid mutation, two amino acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. In other aspects, a Scaffold Y useful for the present disclosure comprises the amino acid sequence of SEQ ID NO: 403 without Met at amino acid residue 1 of the SEQ ID NO: 403, except one amino acid mutation, two amino

acid mutations, three amino acid mutations, four amino acid mutations, five amino acid mutations, six amino acid mutations, or seven amino acid mutations. The mutations can be a substitution, an insertion, a deletion, or any combination thereof. In some aspects, a Scaffold Y useful for the present disclosure comprises the amino acid sequence of any one of SEQ ID NOs: 404-567 and 1 amino acid, two amino acids, three amino acids, four amino acids, five amino acids, six amino acids, seven amino acids, eight amino acids, nine amino acids, ten amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids or longer at the N terminus and/or C terminus of SEQ ID NOs: 404-567.

[0454] In some aspects, the protein sequence of any of SEQ ID NOs: 404-567 is sufficient to be a Scaffold Y for the present disclosure (*e.g.*, scaffold moiety linked to an ASO).

[0455] In some aspects, a Scaffold Y useful for the present disclosure comprises a peptide with the GXKLSKKK, where X is alanine or any other amino acid (SEQ ID NO: 404). In some aspects, an EV, *e.g.*, exosome, comprises a peptide with sequence of (G)(π)(ξ)(Φ/π)(S/A/G/N)(+)(+), wherein each parenthetical position represents an amino acid, and wherein π is any amino acid selected from the group consisting of (Pro, Gly, Ala, Ser), ξ is any amino acid selected from the group consisting of (Asn, Gln, Ser, Thr, Asp, Glu, Lys, His, Arg), Φ is any amino acid selected from the group consisting of (Val, Ile, Leu, Phe, Trp, Tyr, Met), and (+) is any amino acid selected from the group consisting of (Lys, Arg, His); and wherein position five is not (+) and position six is neither (+) nor (Asp or Glu). In further aspects, an exosome described herein (*e.g.*, engineered exosome) comprises a peptide with sequence of (G)(π)(X)(Φ/π)(π)(+)(+), wherein each parenthetical position represents an amino acid, and wherein π is any amino acid selected from the group consisting of (Pro, Gly, Ala, Ser), X is any amino acid, Φ is any amino acid selected from the group consisting of (Val, Ile, Leu, Phe, Trp, Tyr, Met), and (+) is any amino acid selected from the group consisting of (Lys, Arg, His); and wherein position five is not (+) and position six is neither (+) nor (Asp or Glu). See Aasland et al., FEBS Letters 513 (2002) 141-144 for amino acid nomenclature.

[0456] In other aspects, the Scaffold X comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to any one of SEQ ID NO: 404-567.

[0457] Scaffold Y-engineered EVs, *e.g.*, exosomes described herein can be produced from a cell transformed with a sequence set forth in SEQ ID NOs: 404-567.

[0458] In some aspects, the Scaffold Y protein useful for the present disclosure comprises an "N-terminus domain" (ND) and an "effector domain"(ED), wherein the ND and/or the ED are associated with the luminal surface of the EV, *e.g.*, an exosome. In some aspects, the Scaffold Y protein useful for the present disclosure comprises an intracellular domain, a transmembrane domain, and an extracellular domain; wherein the intracellular domain comprises an "N-terminus domain" (ND) and an "effector domain" (ED), wherein the ND and/or the ED are associated with the luminal surface of the EV, *e.g.*, an exosome. As used herein the term "associated with" refers to the interaction between a scaffold protein with the luminal surface of the EV, *e.g.*, and exosome, that does not involve covalent linking to a membrane component. For example, the scaffolds useful for the present disclosure can be associated with the luminal surface of the EV, *e.g.*, via a lipid anchor (*e.g.*, myristic acid), and/or a polybasic domain that interacts electrostatically with the negatively charged head of membrane phospholipids. In other aspects, the Scaffold Y protein comprises an N-terminus domain (ND) and an effector domain (ED), wherein the ND is associated with the luminal surface of the EV and the ED are associated with the luminal surface of the EV by an ionic interaction, wherein the ED comprises at least two, at least three, at least four, at least five, at least six, or at least seven contiguous basic amino acids, *e.g.*, lysines (Lys), in sequence.

[0459] In other aspects, the Scaffold Y protein comprises an N-terminus domain (ND) and an effector domain (ED), wherein the ND is associated with the luminal surface of the EV, *e.g.*, exosome, and the ED is associated with the luminal surface of the EV by an ionic interaction, wherein the ED comprises at least two, at least three, at least four, at least five, at least six, or at least seven contiguous basic amino acids, *e.g.*, lysines (Lys), in sequence.

[0460] In some aspects, the ND is associated with the luminal surface of the EV, *e.g.*, an exosome, via lipidation, *e.g.*, via myristoylation. In some aspects, the ND has Gly at the N terminus. In some aspects, the N-terminal Gly is myristoylated.

[0461] In some aspects, the ED is associated with the luminal surface of the EV, *e.g.*, an exosome, by an ionic interaction. In some aspects, the ED is associated with the luminal surface of the EV, *e.g.*, an exosome, by an electrostatic interaction, in particular, an attractive electrostatic interaction.

[0462] In some aspects, the ED comprises (i) a basic amino acid (*e.g.*, lysine), or (ii) two or more basic amino acids (*e.g.*, lysine) next to each other in a polypeptide sequence. In some aspects, the basic amino acid is lysine (Lys; K), arginine (Arg, R), or Histidine (His, H). In some aspects, the basic amino acid is (Lys)_n, wherein n is an integer between 1 and 10.

[0463] In other aspects, the ED comprises at least a lysine and the ND comprises a lysine at the C terminus if the N terminus of the ED is directly linked to lysine at the C terminus of the ND, *i.e.*, the lysine is in the N terminus of the ED and is fused to the lysine in the C terminus of the ND. In other aspects, the ED comprises at least two lysines, at least three lysines, at least four lysines, at least five lysines, at least six lysines, or at least seven lysines when the N terminus of the ED is linked to the C terminus of the ND by a linker, *e.g.*, one or more amino acids.

[0464] In some aspects, the ED comprises K, KK, KKK, KKKK (SEQ ID NO: 405), KKKKK (SEQ ID NO: 406), R, RR, RRR, RRRR (SEQ ID NO: 407); RRRRR (SEQ ID NO: 408), KR, RK, KKR, KRK, RKK, KRR, RRR, (K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 409), (K/R)(K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 410), or any combination thereof. In some aspects, the ED comprises KK, KKK, KKKK (SEQ ID NO: 405), KKKKK (SEQ ID NO: 406), or any combination thereof. In some aspects, the ND comprises the amino acid sequence as set forth in G:X2:X3:X4:X5:X6, wherein G represents Gly; wherein "." represents a peptide bond; wherein each of the X2 to the X6 independently represents an amino acid; and wherein the X6 represents a basic amino acid. In some aspects, the X6 amino acid is selected from the group consisting of Lys, Arg, and His. In some aspects, the X5 amino acid is selected from the group consisting of Pro, Gly, Ala, and Ser. In some aspects, the X2 amino acid is selected from the group consisting of Pro, Gly, Ala, and Ser. In some aspects, the X4 is selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln, and Met.

[0465] In some aspects, the Scaffold Y protein comprises an N-terminus domain (ND) and an effector domain (ED), wherein the ND comprises the amino acid sequence as set forth in G:X2:X3:X4:X5:X6, wherein G represents Gly; wherein "." represents a peptide bond; wherein each of the X2 to the X6 is independently an amino acid; wherein the X6 comprises a basic amino acid, and wherein the ED is linked to X6 by a peptide bond and comprises at least one lysine at the N terminus of the ED.

[0466] In some aspects, the ND of the Scaffold Y protein comprises the amino acid sequence of G:X2:X3:X4:X5:X6, wherein G represents Gly; "." represents a peptide bond; the X2 represents an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; the X3 represents any amino acid; the X4 represents an amino acid selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln, and Met; the X5 represents an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; and the X6 represents an amino acid selected from the group consisting of Lys, Arg, and His.

[0467] In some aspects, the X3 amino acid is selected from the group consisting of Asn, Gln, Ser, Thr, Asp, Glu, Lys, His, and Arg.

[0468] In some aspects, the ND and ED are joined by a linker. In some aspects, the linker comprises one or more amino acids. In some aspects, the term "linker" refers to a peptide or polypeptide sequence (*e.g.*, a synthetic peptide or polypeptide sequence) or to a non-polypeptide, *e.g.*, an alkyl chain. In some aspects, two or more linkers can be linked in tandem. Generally, linkers provide flexibility or prevent/ameliorate steric hindrances. Linkers are not typically cleaved; however, in certain aspects, such cleavage can be desirable. Accordingly, in some aspects a linker can comprise one or more protease-cleavable sites, which can be located within the sequence of the linker or flanking the linker at either end of the linker sequence. When the ND and ED are joined by a linker, the ED comprise at least two lysines, at least three lysines, at least four lysines, at least five lysines, at least six lysines, or at least seven lysines.

[0469] In some aspects, the linker is a peptide linker. In some aspects, the peptide linker can comprise at least about two, at least about three, at least about four, at least about five, at least about 10, at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, or at least about 100 amino acids.

[0470] In some aspects, the linker is a glycine/serine linker. In some aspects, the peptide linker is glycine/serine linker according to the formula $[(\text{Gly})_n\text{-Ser}]_m$ where n is any integer from 1 to 100 and m is any integer from 1 to 100. In other aspects, the glycine/serine linker is according to the formula $[(\text{Gly})_x\text{-Sery}]_z$ wherein x is an integer from 1 to 4, y is 0 or 1, and z is an integer from 1 to 50. In some aspects, the peptide linker comprises the sequence Gn , where n can be an integer from 1 to 100. In some aspects, the peptide linker can comprise the sequence $(\text{GlyAla})_n$, wherein n is an integer between 1 and 100. In other aspects, the peptide linker can comprise the sequence $(\text{GlyGlySer})_n$, wherein n is an integer between 1 and 100.

[0471] In some aspects, the peptide linker is synthetic, *i.e.*, non-naturally occurring. In one aspect, a peptide linker includes peptides (or polypeptides) (*e.g.*, natural or non-naturally occurring peptides) which comprise an amino acid sequence that links or genetically fuses a first linear sequence of amino acids to a second linear sequence of amino acids to which it is not naturally linked or genetically fused in nature. For example, in one aspect the peptide linker can comprise non-naturally occurring polypeptides which are modified forms of naturally occurring polypeptides (*e.g.*, comprising a mutation such as an addition, substitution or deletion).

[0472] In other aspects, the peptide linker can comprise non-naturally occurring amino acids. In yet other aspects, the peptide linker can comprise naturally occurring amino acids occurring in a linear sequence that does not occur in nature. In still other aspects, the peptide linker can comprise a naturally occurring polypeptide sequence.

[0473] The present disclosure also provides an isolated extracellular vesicle (EV), *e.g.*, an exosome, comprising an ASO linked to a Scaffold Y protein, wherein the Scaffold Y protein comprises ND—ED, wherein: ND comprises G:X2:X3:X4:X5:X6; wherein: G represents Gly; ":" represents a peptide bond; X2 represents an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; X3 represents any amino acid; X4 represents an amino acid selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Glu, and Met; X5 represents an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; X6 represents an amino acid selected from the group consisting of Lys, Arg, and His; "—" represents an optional linker; and ED is an effector domain comprising (i) at least two contiguous lysines (Lys), which is linked to the X6 by a peptide bond or one or more amino acids or (ii) at least one lysine, which is directly linked to the X6 by a peptide bond.

[0474] In some aspects, the X2 amino acid is selected from the group consisting of Gly and Ala. In some aspects, the X3 amino acid is Lys. In some aspects, the X4 amino acid is Leu or Glu. In some aspects, the X5 amino acid is selected from the group consisting of Ser and Ala. In some aspects, the X6 amino acid is Lys. In some aspects, the X2 amino acid is Gly, Ala, or Ser; the X3 amino acid is Lys or Glu; the X4 amino acid is Leu, Phe, Ser, or Glu; the X5 amino acid is Ser or Ala; and X6 amino acid is Lys. In some aspects, the "—" linker comprises a peptide bond or one or more amino acids.

[0475] In some aspects, the ED in the scaffold protein comprises Lys (K), KK, KKK, KKKK (SEQ ID NO: 405), KKKKK (SEQ ID NO: 406), Arg (R), RR, RRR, RRRR (SEQ ID NO: 407), RRRRR (SEQ ID NO: 408), KR, RK, KKR, KRK, RKK, KRR, RRK, (K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 409), (K/R)(K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 410), or any combination thereof.

[0476] In some aspects, the Scaffold Y protein comprises an amino acid sequence selected from the group consisting of (i) GGKLSKK (SEQ ID NO: 411), (ii) GAKLSKK (SEQ ID NO: 412), (iii) GGKQSKK (SEQ ID NO: 413), (iv) GGKLAKK (SEQ ID NO: 414), or (v) any combination thereof.

[0477] In some aspects, the ND in the Scaffold Y protein comprises an amino acid sequence selected from the group consisting of (i) GGKLSK (SEQ ID NO: 415), (ii) GAKLSK

(SEQ ID NO: 416), (iii) GGKQSK (SEQ ID NO: 417), (iv) GGKLAK (SEQ ID NO: 418), or (v) any combination thereof and the ED in the scaffold protein comprises K, KK, KKK, KKKG (SEQ ID NO: 419), KKKGY (SEQ ID NO: 420), KKKGYN (SEQ ID NO: 421), KKKGYNV (SEQ ID NO: 422), KKKGYNVN (SEQ ID NO: 423), KKKGYS (SEQ ID NO: 424), KKKGYG (SEQ ID NO: 425), KKKGYGG (SEQ ID NO: 426), KKKGS (SEQ ID NO: 427), KKKGSG (SEQ ID NO: 428), KKKGSGS (SEQ ID NO: 429), KKKS (SEQ ID NO: 430), KKKSG (SEQ ID NO: 431), KKKSGG (SEQ ID NO: 432), KKKSGGS (SEQ ID NO: 433), KKKSGGSG (SEQ ID NO: 434), KKSGGSGG (SEQ ID NO: 435), KKKSGGSGGS (SEQ ID NO: 436), KRFSFKKS (SEQ ID NO: 437).

[0478] In some aspects, the polypeptide sequence of a Scaffold Y protein useful for the present disclosure consists of an amino acid sequence selected from the group consisting of (i) GGKLSKK (SEQ ID NO: 411), (ii) GAKLSKK (SEQ ID NO: 412), (iii) GGKQSKK (SEQ ID NO: 413), (iv) GGKLAKK (SEQ ID NO: 414), or (v) any combination thereof.

[0479] In some aspects, the Scaffold Y protein comprises an amino acid sequence selected from the group consisting of (i) GGKLSKKK (SEQ ID NO: 438), (ii) GGKLSKKS (SEQ ID NO: 439), (iii) GAKLSKKK (SEQ ID NO: 440), (iv) GAKLSKKS (SEQ ID NO: 441), (v) GGKQSKKK (SEQ ID NO: 442), (vi) GGKQSKKS (SEQ ID NO: 443), (vii) GGKLAKKK (SEQ ID NO: 444), (viii) GGKLAKKS (SEQ ID NO: 445), and (ix) any combination thereof.

[0480] In some aspects, the polypeptide sequence of a Scaffold Y protein useful for the present disclosure consists of an amino acid sequence selected from the group consisting of (i) GGKLSKKK (SEQ ID NO: 438), (ii) GGKLSKKS (SEQ ID NO: 439), (iii) GAKLSKKK (SEQ ID NO: 440), (iv) GAKLSKKS (SEQ ID NO: 441), (v) GGKQSKKK (SEQ ID NO: 442), (vi) GGKQSKKS (SEQ ID NO: 443), (vii) GGKLAKKK (SEQ ID NO: 444), (viii) GGKLAKKS (SEQ ID NO: 445), and (ix) any combination thereof.

[0481] In some aspects, the Scaffold Y protein is at least about 8, at least about 9, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 26, at least about 27, at least about 28, at least about 29, at least about 30, at least about 31, at least about 32, at least about 33, at least about 34, at least about 35, at least about 36, at least about 37, at least about 38, at least about 39, at least about 39, at least about 40, at least about 41, at least about 42, at least about 43, at least about 44, at least about 50, at least about 46, at least about 47, at least about 48, at least about 49, at least about 50, at least about 55, at least about 60, at least about 65,

at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, at least about 100, at least about 105, at least about 110, at least about 115, at least about 120, at least about 125, at least about 130, at least about 135, at least about 140, at least about 145, at least about 150, at least about 155, at least about 160, at least about 165, at least about 170, at least about 175, at least about 180, at least about 185, at least about 190, at least about 195, at least about 200, at least about 205, at least about 210, at least about 215, at least about 220, at least about 225, at least about 230, at least about 235, at least about 240, at least about 245, at least about 250, at least about 255, at least about 260, at least about 265, at least about 270, at least about 275, at least about 280, at least about 285, at least about 290, at least about 295, at least about 300, at least about 305, at least about 310, at least about 315, at least about 320, at least about 325, at least about 330, at least about 335, at least about 340, at least about 345, or at least about 350 amino acids in length.

[0482] In some aspects, the Scaffold Y protein is between about 5 and about 10, between about 10 and about 20, between about 20 and about 30, between about 30 and about 40, between about 40 and about 50, between about 50 and about 60, between about 60 and about 70, between about 70 and about 80, between about 80 and about 90, between about 90 and about 100, between about 100 and about 110, between about 110 and about 120, between about 120 and about 130, between about 130 and about 140, between about 140 and about 150, between about 150 and about 160, between about 160 and about 170, between about 170 and about 180, between about 180 and about 190, between about 190 and about 200, between about 200 and about 210, between about 210 and about 220, between about 220 and about 230, between about 230 and about 240, between about 240 and about 250, between about 250 and about 260, between about 260 and about 270, between about 270 and about 280, between about 280 and about 290, between about 290 and about 300, between about 300 and about 310, between about 310 and about 320, between about 320 and about 330, between about 330 and about 340, or between about 340 and about 350 amino acids in length.

[0483] In some aspects, the Scaffold Y protein comprises (i) GGKLSKKKKGYNVN (SEQ ID NO: 446), (ii) GAKLSKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKKGYS GG (SEQ ID NO: 450), (vi) GGKLSKKKKKSGGGS (SEQ ID NO: 451), (vii) GGKLSKKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 484), (x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456).

[0484] In some aspects, the polypeptide sequence of a Scaffold Y protein useful for the present disclosure consists of (i) GGKLSKKKKGYNVN (SEQ ID NO: 446), (ii) GAKLSKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKGYSGG (SEQ ID NO: 450), (vi) GGKLSKKKKKSGGS (SEQ ID NO: 451), (vii) GGKLSKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 454), (x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456).

[0485] Non-limiting examples of the Scaffold Y protein useful for the present disclosure are listed below. In some aspects, the Scaffold Y protein comprises an amino acid sequence any one of SEQ ID NOs: 411, 438, 446-567. In some aspects, the Scaffold Y protein consists of an amino acid sequence any one of SEQ ID NOs: 411, 438, 446-567.

[0486] In some aspects, the Scaffold Y protein useful for the present disclosure does not contain an N-terminal Met. In some aspects, the Scaffold Y protein comprises a lipidated amino acid, *e.g.*, a myristoylated amino acid, at the N-terminus of the scaffold protein, which functions as a lipid anchor. In some aspects, the amino acid residue at the N-terminus of the scaffold protein is Gly. The presence of an N-terminal Gly is an absolute requirement for N-myristoylation. In some aspects, the amino acid residue at the N-terminus of the scaffold protein is synthetic. In some aspects, the amino acid residue at the N-terminus of the scaffold protein is a glycine analog, *e.g.*, allylglycine, butylglycine, or propargylglycine.

[0487] Non-limiting examples of scaffold proteins can be found at WO/2019/099942, published May 23, 2019 and WO/2020/101740, published May 22, 2020, which are incorporated herein by reference in their entireties.

III.D. Targeting Moiety

[0488] In some aspects, the EV, *e.g.*, exosome, comprises a targeting moiety, *e.g.*, an exogenous targeting moiety. In some aspects, the targeting moiety comprises a peptide, an antibody or an antigen-binding fragment thereof, a chemical compound, or any combination thereof. In some aspects, the targeting moiety comprises a microprotein, a designed ankyrin repeat protein (darpin), an anticalin, an adnectin, an aptamer, a peptide mimetic molecule, a natural ligand for a receptor, a camelid nanobody, or any combination thereof. In some aspects, the targeting moiety comprises the exogenous targeting moiety comprises a full-length antibody, a single domain antibody, a heavy chain only antibody (VHH), a single chain antibody, a shark heavy chain only antibody (VNAR), an scFv, a Fv, a Fab, a Fab', a F(ab')₂, or any combination thereof. In some aspects, the antibody is a single chain antibody.

[0489] In some aspects, the targeting moiety targets the exosome to the liver, heart, lungs, brain, kidneys, central nervous system, peripheral nervous system, muscle, bone, joint, skin, intestine, bladder, pancreas, lymph nodes, spleen, or any combination thereof. In some aspects, the targeting moiety targets the exosome to a tumor cell, dendritic cell, T cell, B cell, macrophage, neuron, hepatocyte, Kupffer cell, a myeloid-lineage cell (*e.g.*, neutrophil, monocyte, or macrophage), hematopoietic stem cell, or any combination thereof.

[0490] In some aspects, the targeting moiety is linked to the EV, *e.g.*, the exosome, by a scaffold protein. In some aspects, the scaffold protein is any scaffold protein disclosed herein. In some aspects, the scaffold protein is a Scaffold X. In some aspects, the scaffold protein is a Scaffold Y.

III.E. Linkers

[0491] As described *supra*, extracellular vesicles (EVs) of the present disclosure (*e.g.*, exosomes and nanovesicles) can comprise one or more linkers that link a molecule of interest (*e.g.*, an ASO) to the EVs (*e.g.*, to the exterior surface or on the luminal surface). In some aspects, an ASO is linked to the EVs directly or via a scaffold moiety (*e.g.*, Scaffold X or Scaffold Y). In certain aspects, the ASO is linked to the scaffold moiety by a linker. In certain aspects, the ASO is linked to the second scaffold moiety by a linker.

[0492] In certain aspects, an ASO is linked to the exterior surface of an exosome via Scaffold X. In further aspects, an ASO is linked to the luminal surface of an exosome via Scaffold X or Scaffold Y. The linker can be any chemical moiety known in the art.

[0493] As used herein, the term "linker" refers to a peptide or polypeptide sequence (*e.g.*, a synthetic peptide or polypeptide sequence) or to a non-polypeptide, *e.g.*, an alkyl chain. In some aspects, two or more linkers can be linked in tandem. When multiple linkers are present, each of the linkers can be the same or different. Generally, linkers provide flexibility or prevent/ameliorate steric hindrances. Linkers are not typically cleaved; however, in certain aspects, such cleavage can be desirable. Accordingly, in some aspects, a linker can comprise one or more protease-cleavable sites, which can be located within the sequence of the linker or flanking the linker at either end of the linker sequence.

[0494] In some aspects, the linker is a peptide linker. In some aspects, the peptide linker can comprise at least about two, at least about three, at least about four, at least about five, at least about 10, at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least

about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, or at least about 100 amino acids.

[0495] In some aspects, the peptide linker is synthetic, *i.e.*, non-naturally occurring. In one aspect, a peptide linker includes peptides (or polypeptides) (*e.g.*, natural or non-naturally occurring peptides) which comprise an amino acid sequence that links or genetically fuses a first linear sequence of amino acids to a second linear sequence of amino acids to which it is not naturally linked or genetically fused in nature. For example, in one aspect the peptide linker can comprise non-naturally occurring polypeptides which are modified forms of naturally occurring polypeptides (*e.g.*, comprising a mutation such as an addition, substitution or deletion).

[0496] Linkers can be susceptible to cleavage ("cleavable linker") thereby facilitating release of the biologically active molecule (*e.g.*, an ASO).

[0497] In some aspects, the linker is a "reduction-sensitive linker." In some aspects, the reduction-sensitive linker contains a disulfide bond. In some aspects, the linker is an "acid labile linker." In some aspects, the acid labile linker contains hydrazone. Suitable acid labile linkers also include, for example, a cis-aconitic linker, a hydrazide linker, a thiocarbamoyl linker, or any combination thereof.

[0498] In some aspects, the linker comprises a non-cleavable linker.

[0499] In some aspects, the linker comprises acrylic phosphoramidite (*e.g.*, ACRYDITE™), adenylation, azide (NHS Ester), digoxigenin (NHS Ester), cholesterol-TEG, I-LINKER™, an amino modifier (*e.g.*, amino modifier C6, amino modifier C12, amino modifier C6 dT, or Uni-Link™ amino modifier), alkyne, 5' Hexynyl, 5-Octadiynyl dU, biotinylation (*e.g.*, biotin, biotin (Azide), biotin dT, biotin-TEG, dual biotin, PC biotin, or desthiobiotin), thiol modification (thiol modifier C3 S-S, dithiol or thiol modifier C6 S-S), or any combination thereof.

[0500] In some aspects, the linker comprises a terpene such as nerolidol, farnesol, limonene, linalool, geraniol, carvone, fenchone, or menthol; a lipid such as palmitic acid or myristic acid; cholesterol; oleyl; retinyl; cholesteryl residues; cholic acid; adamantane acetic acid; 1-pyrene butyric acid; dihydrotestosterone; 1,3-Bis-O(hexadecyl)glycerol; geranyloxyhexyl group; hexadecylglycerol; borneol; 1,3-propanediol; heptadecyl group; O3-(oleoyl)lithocholic acid; O3-(oleoyl)cholenic acid; dimethoxytrityl; phenoxazine, a maleimide moiety, a glucorinidase type, a CL2A-SN38 type, folic acid; a carbohydrate; vitamin A; vitamin E; vitamin K, or any combination thereof.

III.F. Modified EVs Comprising Tropism Moieties

[0501] In some aspects, an EV, *e.g.*, exosome, disclosed herein can be surface engineered to adjust its properties, *e.g.*, biodistribution, *e.g.*, via incorporation of immuno-affinity ligands or cognate receptor ligands. For example, EV, *e.g.*, exosomes, disclosed herein can be surface engineered to direct them to a specific cellular type, *e.g.*, Schwann cells, sensory neurons, motor neurons, meningeal macrophages, a tumor cell, or can be surface engineered to enhance their migration to a specific compartment, *e.g.*, to the CNS (in order to improve intrathecal compartment retention) or to a tumor microenvironment.

[0502] In some aspects, an EV, *e.g.*, exosome, comprises (i) an ASO disclosed herein and (ii) a bio-distribution modifying agent or targeting moiety. In some aspects, the bio-distribution modifying agent or targeting moiety comprises a single-domain antigen-binding moiety, *e.g.*, a VHH and/or a vNAR. As used here, the terms "bio-distribution modifying agent" and "targeting moiety" are used interchangeably and refer to an agent that can modify the distribution of extracellular vesicles (*e.g.*, exosomes, nanovesicles) *in vivo* or *in vitro* (*e.g.*, in a mixed culture of cells of different varieties). In some aspects, the targeting moiety alters the tropism of the EV (*e.g.*, exosome), *i.e.*, the target moiety is a "tropism moiety". As used herein, the term "tropism moiety" refers to a targeting moiety that when expressed on an EV (*e.g.*, exosome) alters and/or enhances the natural movement of the EV. For example, in some aspects, a tropism moiety can promote the EV (*e.g.*, exosome) to be taken up by a particular cell, tissue, or organ.

[0503] EVs, *e.g.*, exosomes, exhibit preferential uptake in discrete cell types and tissues, and their tropism can be directed by adding proteins to their surface that interact with receptors on the surface of target cells. The tropism moiety can comprise a biological molecule, such as a protein, a peptide, a lipid, or a carbohydrate, or a synthetic molecule. For example, in some aspects the tropism moiety can comprise an affinity ligand, *e.g.*, an antibody (such as an anti-CD19 nanobody, an anti-CD22 nanobody, an anti-CLEC9A nanobody, or an anti-CD3 nanobody), a VHH domain, a phage display peptide, a fibronectin domain, a camelid nanobody, and/or a vNAR. In some aspects, the tropism moiety can comprise, *e.g.*, a synthetic polymer (*e.g.*, PEG), a natural ligand/molecule (*e.g.*, CD40L, albumin, CD47, CD24, CD55, CD59), and/or a recombinant protein (*e.g.*, XTEN).

[0504] In some aspects, a tropism moiety can increase uptake of the EV, *e.g.*, an exosome, by a cell. In some aspects, the tropism moiety that can increase uptake of the EV, *e.g.*, an exosome, by a cell comprises a lymphocyte antigen 75 (also known as DEC205 or CD205), C-type lectin domain family 9 member A (CLEC9A), C-type lectin domain family 6 (CLEC6), C-type lectin

domain family 4 member A (also known as DCIR or CLEC4A), Dendritic Cell-Specific Intercellular adhesion molecule-3-Grabbing Non-integrin (also known as DC-SIGN or CD209), lectin-type oxidized LDL receptor 1(LOX-1), macrophage receptor with collagenous structure (MARCO), C-type lectin domain family 12 member A (CLEC12A), C-type lectin domain family 10 member A (CLEC10A), DC-asialoglycoprotein receptor (DC-ASGPR), DC immunoreceptor 2 (DCIR2), Dectin-1, macrophage mannose receptor (MMR), BDCA-2 (CD303, CLEC4C), Dectin-2, BST-2 (CD317), Langerin, CD206, CD11b, CD11c, CD123, CD304, XCR1, AXL, SIGLEC 6, CD209, SIRPA, CX3CR1, GPR182, CD14, CD16, CD32, CD34, CD38, CD10, anti-CD3 antibody, or any combination thereof.

[0505] In some aspects, when tropism to the central nervous system is desired, an EV, *e.g.*, exosome, of the present disclosure can comprise a tissue or cell-specific target ligand, which increases EV, *e.g.*, exosome, tropism to a specific central nervous system tissue or cell. In some aspects, the cell is a glial cell. In some aspects, the glial cell is an oligodendrocyte, an astrocyte, an ependymal cell, a microglia cell, a Schwann cell, a satellite glial cell, an olfactory ensheathing cell, or a combination thereof. In some aspects, the cell is a neural stem cell. In some aspects, the cell-specific target ligand, which increases EV, *e.g.*, exosome, tropism to a Schwann cells binds to a Schwann cell surface marker such as Myelin Basic Protein (MBP), Myelin Protein Zero (P0), P75NTR, NCAM, PMP22, or any combination thereof. In some aspects, the cell-specific tropism moiety comprises an antibody or an antigen-binding portion thereof, an aptamer, or an agonist or antagonist of a receptor expressed on the surface of the Schwann cell.

[0506] In some aspects, the bio-distribution modifying agent or targeting moiety comprises an antigen-binding moiety that binds an antigen expressed on a tumor cell. In some aspects, the bio-distribution modifying agent or targeting moiety comprises an antigen-binding moiety that binds an antigen expressed in a tumor microenvironment. In some aspects, the bio-distribution modifying agent or targeting moiety comprises an antigen-binding moiety that binds mesothelin or a fragment thereof. Any antigen-binding moiety known in the art that is capable of binding mesothelin or a fragment thereof can be used in the EVs disclosed herein. In some aspects, bio-distribution modifying agent or targeting moiety comprises an antigen-binding moiety that binds CD33 or a fragment thereof. Any antigen-binding moiety known in the art that is capable of binding CD33 or a fragment thereof can be used in the EVs disclosed herein. In certain aspects, the antigen-binding moiety that binds CD33 or a fragment thereof is selected from the anti-CD33 binding moieties disclosed in US Patent No. 5,877,296, which is incorporated by reference herein in its entirety. CD33 is a transmembrane receptor expressed on both myeloid and lymphoid cells. It binds

sialic acid, and therefore, is a member of the sialic acid-binding immunoglobulin-type lectin (SIGLEC) family. CD33 plays a role in mediating cell-cell interactions and in maintaining immune cells in a resting state. Upon binding, the immunoreceptor tyrosine-based inhibition motif (ITIM) of CD33, present on the cytosolic portion of the protein, is phosphorylated and acts as a docking site for Src homology 2 (SH2) domain-containing proteins like SHP phosphatases. This can result in a cascade that inhibits phagocytosis in the cell. Structurally, the extracellular portion of CD33 contains two immunoglobulin domains, and the intracellular portion contains the ITIM. Synonyms of CD33 include, but are not limited to, sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, and p67.

[0507] Sequences for CD33 are also known in the art. The canonical amino acid sequence for human CD33 is set forth in SEQ ID NO: 900 (UniProt Identifier: P20138-1). Isoforms of human CD33, resulting from alternative splicing, are known: (i) Isoform 2 (UniProt Identifier: P20138-3; SEQ ID NO: 901); (ii) Isoform 3 (UniProt Identifier: P20138-2; SEQ ID NO: 902); (iii) Isoform X1 (GenBank Accession No. XP_011525833.1; SEQ ID NO: 903); (iv) Isoform X2 (GenBank Accession No. XP_016882998.1; SEQ ID NO: 904); and (v) Isoform X4 (GenBank Accession No. XP_016882999.1; SEQ ID NO: 905). In some aspects, a targeting moiety disclosed herein is capable of binding to one or more of the human CD33 proteins disclosed herein.

[0508] In principle, the EVs, *e.g.*, exosomes of the present disclosure comprising at least one tropism moiety that can direct the EV, *e.g.*, exosome, to a specific target cell or tissue (*e.g.*, a cell in the CNS or a Schwann cell in peripheral nerves) can be administered using any suitable administration method known in the art (*e.g.*, intravenous injection or infusion) since the presence of the tropism moiety (alone or in combination with the presence of an antiphagocytic signal such as CD47 and the use of a specific administration route) will induce a tropism of the EVs, *e.g.*, exosomes, towards the desired target cell or tissue.

[0509] In certain aspects, the tropism moiety is linked, *e.g.*, chemically linked via a maleimide moiety, to a scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof, on the exterior surface of the EV, *e.g.*, exosome. Tropism can be further improved by the attachment of an anti-phagocytic signal (*e.g.*, CD47 and/or CD24), a half-life extension moiety (*e.g.*, albumin or PEG), or any combination thereof to the external surface of an EV, *e.g.*, exosome of the present disclosure. In certain aspects, the anti-phagocytic signal is linked, *e.g.*, chemically linked via a maleimide moiety, to a scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof, on the exterior surface of the EV, *e.g.*, exosome.

[0510] Pharmacokinetics, biodistribution, and in particular tropism and retention in the desired tissue or anatomical location can also be accomplished by selecting the appropriate administration route (e.g., intrathecal administration or intraocular administration to improve tropism to the central nervous system).

[0511] In some aspects, the EV, *e.g.*, exosome, comprises at least two different tropism moieties. In some aspects, the EV, *e.g.*, exosome, comprises three different tropism moieties. In some aspects, the EV, *e.g.*, exosome, comprises four different tropism moieties. In some aspects, the EV, *e.g.*, exosome, comprises five or more different tropism moieties. In some aspects, one or more of the tropism moieties increases uptake of the EV, *e.g.*, exosome, by a cell. In some aspects, each tropism moiety is attached to a scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof. In some aspects, multiple tropism moieties can be attached to the same scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof. In some aspects, several tropism moieties can be attached in tandem to a scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof. In some aspects, a tropism moiety disclosed herein or a combination thereof is attached to a scaffold moiety, *e.g.*, a Scaffold X protein or a fragment thereof, via a linker or spacer. In some aspects, a linker or spacer or a combination thereof is interposed between two tropism moieties disclosed herein.

[0512] Non-limiting examples of tropism moieties capable of directing EVs, *e.g.*, exosomes, of the present disclosure to different nervous system cell types are disclosed below.

III.F.1. Tropism moieties targeting Schwann cells

[0513] In some aspects, a tropism moiety can target a Schwann cell. In some aspects, the tropism moiety that directs an EV, *e.g.*, exosome, disclosed herein to a Schwann cell targets, *e.g.*, a transferrin receptor (TfR), apolipoprotein D (ApoD), Galectin 1 (LGALS1), Myelin proteolipid protein (PLP), Glypican 1, or Syndecan 3. In some aspects, the tropism moiety directing an EV, *e.g.*, exosome, of the present disclosure to a Schwann cell is a transferrin, or a fragment, variant or derivative thereof.

[0514] In some aspects, a tropism moiety of the present disclosure targets a transferrin receptor (TfR). Transferrin receptors, *e.g.*, TfR1 or TfR2, are carrier proteins for transferrin. Transferrin receptors import iron by internalizing the transferrin-iron complex through receptor-mediated endocytosis.

[0515] TfR1 (*see, e.g.*, UniProt P02786 TFR1_Human) or transferrin receptor 1 (also known as cluster of differentiation 71 or CD71) is expressed on the endothelial cells of the blood-brain barrier (BBB). TfR1 is known to be expressed in a variety of cells such as red blood cells,

monocytes, hepatocytes, intestinal cells, and erythroid cells, and is upregulated in rapidly dividing cells such as tumor cells (non small cell lung cancer, colon cancer, and leukemia) as well as in tissue affected by disorders such as acute respiratory distress syndrome (ARDS). TfR2 is primarily expressed in liver and erythroid cells, is found to a lesser extent in lung, spleen and muscle, and has a 45% identity and 66% similarity with TfR1. TfR1 is a transmembrane receptor that forms a homodimer of 760 residues with disulfide bonds and a molecular weight of 90 kDa. Affinity for transferrin varies between the two receptor types, with the affinity for TfR1 being at least 25-30 fold higher than that of TfR2.

[0516] Binding to TfR1 allows the transit of large molecules, *e.g.*, antibodies, into the brain. Some TfR1-targeting antibodies have been shown to cross the blood-brain barrier, without interfering with the uptake of iron. Amongst those are the mouse anti rat-TfR antibody OX26 and the rat anti mouse-TfR antibody 8D3. The affinity of the antibody-TfR interaction is important to determine the success of transcytotic transport over endothelial cells of the BBB. Monovalent TfR interaction favors BBB transport due to altered intracellular sorting pathways. Avidity effects of bivalent interactions redirecting transport to the lysosome. Also, reducing TfR binding affinity directly promote dissociation from the TfR which increase brain parenchymal exposure of the TfR binding antibody. *See, e.g.*, U.S. Patent No. 8,821,943, which is herein incorporated by reference in its entirety. Accordingly, in some aspects, a tropism moiety of the present disclosure can comprise a ligand that can target TfR, *e.g.*, target TfR1, such as transferrin, or an antibody or other binding molecule capable of specifically binding to TfR. In some aspects, the antibody targeting a transferrin receptor is a low affinity anti-transferring receptor antibody (*see, e.g.*, US20190202936A1 which is herein incorporated by reference in its entirety).

[0517] In some aspects, the tropism moiety comprises all or a portion (*e.g.*, a binding portion) of a ligand for a transferrin receptor, for example a human transferrin available in GenBank as Accession numbers NM001063, XM002793, XM039847, NM002343 or NM013900, among others, or a variant, fragment, or derivative thereof.

[0518] In some aspects, the tropism moiety comprises a transferrin-receptor-targeting moiety, *i.e.*, a targeting moiety directed to a transferrin receptor. Suitable transferrin-receptor-targeting moieties include a transferrin or transferrin variant, such as, but not limited to, a serum transferrin, lacto transferrin (lactoferrin) ovotransferrin, or melanotransferrin. Transferrins are a family of nonheme iron-binding proteins found in vertebrates, including serum transferrins, lacto transferrins (lactoferrins), ovotransferrins, and melanotransferrins. Serum transferrin is a glycoprotein with a molecular weight of about 80 kDa, comprising a single polypeptide chain with

two N-linked polysaccharide chains that are branched and terminate in multiple antennae, each with terminal sialic acid residues. There are two main domains, the N domain of about 330 amino acids, and the C domain of about 340 amino acids, each of which is divided into two subdomains, N1 and N2, and C1 and C2. Receptor binding of transferrin occurs through the C domain, regardless of glycosylation.

[0519] In some aspects, the tropism moiety is a serum transferrin or transferrin variant such as, but not limited to a hexasialo transferrin, a pentasialo transferrin, a tetrasialo transferrin, a trisialo transferrin, a disialo transferrin, a monosialo transferrin, or an asialo transferrin, or a carbohydrate-deficient transferrin (CDT) such as an asialo, monosialo or disialo transferrin, or a carbohydrate-free transferrin (CFT) such as an asialo transferrin. In some aspects, the tropism moiety is a transferrin variant having the N-terminal domain of transferrin, the C-terminal domain of transferrin, the glycosylation of native transferrin, reduced glycosylation as compared to native (wild-type) transferrin, no glycosylation, at least two N terminal lobes of transferrin, at least two C terminal lobes of transferrin, at least one mutation in the N domain, at least one mutation in the C domain, a mutation wherein the mutant has a weaker binding avidity for transferrin receptor than native transferrin, and/or a mutation wherein the mutant has a stronger binding avidity for transferrin receptor than native transferrin, or any combination of the foregoing.

[0520] In some aspects, the tropism moiety targeting a transferrin receptor comprises an anti-transferrin receptor variable new antigen receptor (vNAR), *e.g.*, a binding domain with a general motif structure (FW1-CDR1-FW2-3-CDR3-FW4). *See, e.g.*, U.S. 2017-0348416, which is herein incorporated by reference in its entirety. vNARs are key component of the adaptive immune system of sharks. At only 11 kDa, these single-domain structures are the smallest IgG-like proteins in the animal kingdom and provide an excellent platform for molecular engineering and biologics drug discovery. vNAR attributes include high affinity for target, ease of expression, stability, solubility, multi-specificity, and increased potential for solid tissue penetration. *See Ubah et al. Biochem. Soc. Trans. (2018) 46(6):1559-1565.*

[0521] In some aspects, the tropism moiety comprises a vNAR domain capable of specifically binding to TfR1, wherein the vNAR domain comprises or consists essentially of a vNAR scaffold with any one CDR1 peptide in Table 1 of U.S. 2017-0348416 in combination with any one CDR3 peptide in Table 1 of U.S. 2017-0348416.

[0522] In some aspects, a tropism moiety of the present disclosure targets ApoD. Unlike other lipoproteins, which are mainly produced in the liver, apolipoprotein D is mainly produced in the brain, cerebellum, and peripheral nerves. ApoD is 169 amino acids long, including a secretion

peptide signal of 20 amino acids. It contains two glycosylation sites (asparagines 45 and 78) and the molecular weight of the mature protein varies from 20 to 32 kDa. ApoD binds steroid hormones such as progesterone and pregnenolone with a relatively strong affinity, and to estrogen with a weaker affinity. Arachidonic acid (AA) is an ApoD ligand with a much better affinity than that of progesterone or pregnenolone. Other ApoD ligands include E-3-methyl-2-hexenoic acid, retinoic acid, sphingomyelin and sphingolipids. Accordingly, in some aspects, a tropism moiety of the present disclosure comprises a ligand that can target ApoD, *e.g.*, an antibody or other binding molecule capable of specifically binding to ApoD.

[0523] In some aspects, a tropism moiety of the present disclosure targets Galectin 1. The galectin-1 protein is 135 amino acids in length. Accordingly, in some aspects, a tropism moiety of the present disclosure comprises a ligand that can target Galectin 1, *e.g.*, an antibody or other binding molecule capable of specifically binding to Galectin 1.

[0524] In some aspects, a tropism moiety of the present disclosure targets PLP. PLP is the major myelin protein from the CNS. It plays an important role in the formation or maintenance of the multilamellar structure of myelin. The myelin sheath is a multi-layered membrane, unique to the nervous system that functions as an insulator to greatly increase the efficiency of axonal impulse conduction. PLP is a highly conserved hydrophobic protein of 276 to 280 amino acids which contains four transmembrane segments, two disulfide bonds and which covalently binds lipids (at least six palmitate groups in mammals). Accordingly, in some aspects, a tropism moiety of the present disclosure comprises a ligand that can target PLP, *e.g.*, an antibody or other binding molecule capable of specifically binding to PLP.

[0525] In some aspects, a tropism moiety of the present disclosure targets Glypican 1. Accordingly, in some aspects, a tropism moiety of the present disclosure comprises a ligand that can target Glypican 1, *e.g.*, an antibody or other binding molecule capable of specifically binding to Glypican 1. In some aspects, a tropism moiety of the present disclosure targets Syndecan 3. Accordingly, in some aspects, a tropism moiety of the present disclosure comprises a ligand that can target Syndecan 3, *e.g.*, an antibody or other binding molecule capable of specifically binding to Syndecan 3.

III.F.2. Tropism moieties targeting sensory neurons

[0526] In some aspects, a tropism moiety disclosed herein can direct an EV, *e.g.*, exosome, disclosed herein to a sensory neuron. In some aspects, the tropism moiety that directs an EV, *e.g.*,

exosome, disclosed herein to a sensory neuron targets a Trk receptor, *e.g.*, TrkA, TrkB, TrkC, or a combination thereof.

[0527] Trk (tropomyosin receptor kinase) receptors are a family of tyrosine kinases that regulates synaptic strength and plasticity in the mammalian nervous system. The common ligands of Trk receptors are neurotrophins, a family of growth factors critical to the functioning of the nervous system. The binding of these molecules is highly specific. Each type of neurotrophin has different binding affinity toward its corresponding Trk receptor. Accordingly, in some aspects, the tropism moiety directing an EV, *e.g.*, exosome, disclosed herein to a sensory neuron, comprises a neurotrophin.

[0528] Neurotrophins bind to Trk receptors as homodimers. Accordingly, in some aspects, the tropism moiety comprises at least two neurotrophins disclosed herein, *e.g.*, in tandem. In some aspects, the tropism moiety comprises at least two neurotrophins disclosed herein, *e.g.*, in tandem, that are attached to a scaffold protein, for example, Protein X, via a linker. In some aspects, the linker connecting the scaffold protein, *e.g.*, Protein X, to the neurotrophin (*e.g.*, a neurotrophin homodimer) has a length of at least 10 amino acids. In some aspects, the linker connecting the scaffold protein, *e.g.*, Protein X, to the neurotrophin (*e.g.*, a neurotrophin homodimer) has a length of at least about 25 amino acids, about 30 amino acids, about 35 amino acids, about 40 amino acids, about 45 amino acids, or about 50 amino acids.

[0529] In some aspects, the neurotrophin is a neurotrophin precursor, *i.e.*, a proneurotrophin, which is later cleaved to produce a mature protein.

[0530] Nerve growth factor (NGF) is the first identified and probably the best characterized member of the neurotrophin family. It has prominent effects on developing sensory and sympathetic neurons of the peripheral nervous system. Brain-derived neurotrophic factor (BDNF) has neurotrophic activities similar to NGF, and is expressed mainly in the CNS and has been detected in the heart, lung, skeletal muscle and sciatic nerve in the periphery (Leibrock, J. et al., *Nature*, 341:149-152 (1989)). Neurotrophin-3 (NT-3) is the third member of the NGF family and is expressed predominantly in a subset of pyramidal and granular neurons of the hippocampus, and has been detected in the cerebellum, cerebral cortex and peripheral tissues such as liver and skeletal muscles (Ernfors, P. et al., *Neuron* 1: 983-996 (1990)). Neurotrophin-4 (also called NT-4) is the most variable member of the neurotrophin family. Neurotrophin-6 (NT-6) was found in teleost fish and binds to p75 receptor.

[0531] In some aspects, the neurotrophin targeting TrkB comprises, *e.g.*, NT-4 or BDNF, or a fragment, variant, or derivative thereof. In some aspects, the neurotrophin targeting TrkA

comprises, *e.g.*, NGF or a fragment, variant, or derivative thereof. In some aspects, the neurotrophin targeting TrkC comprises, *e.g.*, NT-3 or a fragment, variant, or derivative thereof.

[0532] In some aspects, the tropism moiety comprises brain derived neurotrophic factor (BDNF). In some aspects, the BDNF is a variant of native BDNF, such as a two amino acid carboxyl-truncated variant. In some aspects, the tropism moiety comprises the full-length 119 amino acid sequence of BDNF (HSDPARRGELSVCDSSISEWVTAADKKTAVDMSGGTVTVLEKVPVSKGQLKQYFYETK CNPMGYTKEGCRGIDKRHWNSQCRTTQSYVRALTMDSKKRIGWRFIRIDTSCVCTLTIK RGR; SEQ ID NO: 711). In some aspects, a one amino-acid carboxy-truncated variant of BDNF is utilized (amino acids 1-118 of SEQ ID NO: 711).

[0533] In some aspects, the tropism moiety comprises a carboxy-truncated variant of the native BDNF, *e.g.*, a variant in which 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10 amino acids are absent from the carboxy-terminus of the BDNF. BDNF variants include the complete 119 amino acid BDNF, the 117 or 118 amino acid variant with a truncated carboxyl terminus, variants with a truncated amino terminus, or variants with up to about 20%, about 30, or about 40% change in amino acid composition, as long as the protein variant still binds to the TrkB receptor with high affinity.

[0534] In some aspects, the tropism moiety comprises a two amino-acid carboxy-truncated variant of BDNF (amino acids 1-117 of SEQ ID NO: 711). In some aspects, the tropism moiety comprises a three amino-acid carboxy-truncated variant of BDNF (amino acids 1-116 of SEQ ID NO: 711). In some aspects, the tropism moiety comprises a four amino-acid carboxy-truncated variant of BDNF (amino acids 1-115 of SEQ ID NO: 711). In some aspects, the tropism moiety comprises a five amino-acid carboxy-truncated variant of BDNF (amino acids 1-114 of SEQ ID NO: 711). In some aspects, the tropism moiety comprises a BDNF that is at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, or about 100% identical with the sequence of SEQ ID NO: 711, or a truncated version thereof, *e.g.*, the 117 or 118 amino acid variant with a one- or two-amino acid truncated carboxyl terminus, or variants with a truncated amino terminus. See, *e.g.*, U.S. Pat. No. 8,053,569B2, which is herein incorporated by reference in its entirety.

[0535] In some aspects, the tropism moiety comprises nerve growth factor (NGF). In some aspects, the NGF is a variant of native NGF, such as a truncated variant. In some aspects, the tropism moiety comprises the 26-kDa beta subunit of protein, the only component of the 7S NGF complex that is biologically active. In some aspects, the tropism moiety comprises the full-length

120 amino acid sequence of beta NGF (SSSHPIFHRGEFSVCDSVSVWVGDKTTATDIKGKEVMVLGEVNINNSVFKQYFFETKCRDPNPVDSGCRGIDSKHWNSYCTTTHTFVKALTMGKQAAWRFIRIDTACVCVLSRKAVRRA; SEQ ID NO: 712). In some aspects, the tropism moiety comprises a carboxy-truncated variant of the native NGF, e.g., a variant in which 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10 amino acids are absent from the carboxy-terminus of NGF. NGF variants include the complete 120 amino acid NGF, the shorter amino acid variants with a truncated carboxyl terminus, variants with a truncated amino terminus, or variants with up to about 20%, about 30%, or about 40% change in amino acid composition, as long as the tropism moiety still binds to the TrkB receptor with high affinity. In some aspects, the tropism moiety comprises an NGF that is at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, or about 100% identical with the sequence of SEQ ID NO: 712, or a truncated version thereof.

[0536] In some aspects, the tropism moiety comprises neurotrophin-3 (NT-3). In some aspects, the NT-3 is a variant of native NT-3, such as a truncated variant. In some aspects, the tropism moiety comprises the full-length 119 amino acid sequence of NT-3 (YAEHKSHRGEYSVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTGNSPVKQYFYETRCKE ARPVKNGCRGIDDKHWNSQCKTSQTYVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT; SEQ ID NO: 713). In some aspects, the tropism moiety comprises a carboxy-truncated variant of the native NT-3, e.g., a variant in which 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10 amino acids are absent from the carboxy-terminus of NT-3. NT-3 variants include the complete 119 amino acid NT-3, the shorter amino acid variants with a truncated carboxyl terminus, variants with a truncated amino terminus, or variants with up to about 20%, about 30%, or about 40% change in amino acid composition, as long as the tropism moiety still binds to the TrkC receptor with high affinity. In some aspects, the tropism moiety comprises an NT-3 that is at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, or about 100% identical with the sequence of SEQ ID NO: 713, or a truncated version thereof.

[0537] In some aspects, the tropism moiety comprises neurotrophin-4 (NT-4). In some aspects, the NT-4 is a variant of native NT-4, such as a truncated variant. In some aspects, the tropism moiety comprises the full-length 130 amino acid sequence of NT-4 (GVSETAPASRRGELAVCDAVSGWVTDRTAVDLRGREVEVLGEVPAAGGSPLRQYFFE TRCKADNAEEGGPGAGGGGCRGVDRRHVVSECKAKQSYVRALTADAQGRVGRWIR

IDTACVCTLLSRTGRA; SEQ ID NO: 714). In some aspects, the tropism moiety comprises a carboxy-truncated variant of the native NT-4, e.g., a variant in which 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more than 10 amino acids are absent from the carboxy-terminus of NT-4. NT-4 variants include the complete 130 amino acid NT-4, the shorter amino acid variants with a truncated carboxyl terminus, variants with a truncated amino terminus, or variants with up to about 20%, about 30%, or about 40% change in amino acid composition, as long as the tropism moiety still binds to the TrkB receptor with high affinity. In some aspects, the tropism moiety comprises an NT-4 that is at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, or about 100% identical with the sequence of SEQ ID NO: 714, or a truncated version thereof.

[0538] Structure/function relationship studies of NGF and NGF-related recombinant molecules demonstrated that mutations in NGF region 25-36, along with other β -hairpin loop and non-loop regions, significantly influenced NGF/NGF-receptor interactions (Ibanez et al., EMBO J., 10, 2105-2110, (1991)). Small peptides derived from this region have been demonstrated to mimic NGF in binding to Mock receptor and affecting biological responses (LeSauter et al. J. Biol. Chem. 270, 6564-6569, 1995). Dimers of cyclized peptides corresponding to β -loop regions of NGF were found to act as partial NGF agonists in that they had both survival-promoting and NGF-inhibiting activity while monomer and linear peptides were inactive (Longo et al., J. Neurosci. Res., 48, 1-17, 1997). Accordingly, in some aspects, a tropism moiety of the present disclosure comprises such peptides.

[0539] Cyclic peptides have also been designed and synthesized to mimic the β -loop regions of NGF, BDNF, NT3 and NT-4/5. Certain monomers, dimers or polymers of these cyclic peptides can have a three-dimensional structure, which binds to neurotrophin receptors under physiological conditions. All of these structural analogs of neurotrophins that bind to nerve cell surface receptors and are internalized can serve as the binding agent B of the compound according to the present disclosure to deliver the conjugated therapeutic moiety TM to the nervous system. Accordingly, in some aspects, a tropism moiety of the present disclosure comprises such cyclic peptides or combinations thereof.

[0540] In some aspects, antibodies against nerve cell surface receptors that are capable of binding to the receptors and being internalized can also serve as tropism moieties binding to a Trk receptor. For example, monoclonal antibody (MAb) 5C3 is specific for the NGF docking site of the human p140 TrkA receptor, with no cross-reactivity with human TrkB receptor. MAb 5C3 and its Fab mimic the effects of NGF in vitro, and image human Trk-A positive tumors in vivo (Kramer

et al., Eur. J. Cancer, 33, 2090-2091, (1997)). Molecular cloning, recombination, mutagenesis and modeling studies of Mab 5C3 variable region indicated that three or less of its complementarity determining regions (CDRs) are relevant for binding to TrkA. Assays with recombinant CDRs and CDR-like synthetic polypeptides demonstrated that they had agonistic bioactivities similar to intact Mab 5C3. Monoclonal antibody MC192 against p75 receptor has also been demonstrated to have neurotrophic effects. Therefore, these antibodies and their functionally equivalent fragments can also serve as tropism moieties of the present disclosure.

[0541] In some aspects, peptidomimetics that are synthesized by incorporating unnatural amino acids or other organic molecules can also serve tropism moieties of the present disclosure.

[0542] Other neurotrophins are known in the art. Accordingly, in some aspects, the target moiety comprises a neurotrophin selected from the group consisting of fibroblast growth factor (FGF)-2 and other FGFs, erythropoietin (EPO), hepatocyte growth factor (HGF), epidermal growth factor (EGF), transforming growth factor (TGF)- α , TGF- β , vascular endothelial growth factor (VEGF), interleukin-1 receptor antagonist (IL-1ra), ciliary neurotrophic factor (CNTF), glial-derived neurotrophic factor (GDNF), neurturin, platelet-derived growth factor (PDGF), heregulin, neuregulin, artemin, persephin, interleukins, granulocyte-colony stimulating factor (CSF), granulocyte-macrophage-CSF, netrins, cardiotrophin-1, hedgehogs, leukemia inhibitory factor (LIF), midline, pleiotrophin, bone morphogenetic proteins (BMPs), netrins, saposins, semaphorins, and stem cell factor (SCF).

[0543] In some aspects, the tropism moiety directing an EV, e.g., exosome, disclosed herein to a sensory neuron, comprises a varicella zoster virus (VZV) peptide.

III.F.3. Tropism moieties targeting motor neurons

[0544] In some aspects, a tropism moiety disclosed herein can direct an EV, e.g., exosome, disclosed herein to a motor neuron. In some aspects, the tropism moiety that directs an EV, e.g., exosome, disclosed herein to a motor comprises a Rabies Virus Glycoprotein (RVG) peptide, a Targeted Axonal Import (TaxI) peptide, a P75R peptide, or a Tet-C peptide.

[0545] In some aspects, the tropism moiety comprises a Rabies Virus Glycoprotein (RVG) peptide. See, e.g., U.S. Pat. App. Publ. 2014-00294727, which is herein incorporated by reference in its entirety. In some aspects, the RVG peptide comprises amino acid residues 173-202 of the RVG (YTIWMPENPRPGTPCDIFTNSRGKRASNG; SEQ ID NO: 601) or a variant, fragment, or derivative thereof. In some aspects, the tropism moiety is a fragment of SEQ ID NO: 601. Such a fragment of SEQ ID NO: 601 can have, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids

deleted from the N-terminal and/or the C-terminal of SEQ ID NO: 601. A functional fragment derived from SEQ ID NO: 601 can be identified by sequentially deleting N- and/or C-terminal amino acids from SEQ ID NO: 601 and assessing the function of the resulting peptide fragment, such as function of the peptide fragment to bind acetylcholine receptor and/or ability to transmit through the blood brain barrier. In some aspects, the tropism moiety comprises a fragment of SEQ ID NO: 601 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16 or 15 amino acids in length. In some aspects, the tropism moiety comprises a fragment of SEQ ID NO: 601 less than 15 peptides in length.

[0546] A “variant” of a RGV peptide, for example SEQ ID NO: 601, is meant to refer to a molecule substantially similar in structure and function, i.e., where the function is the ability to pass or transit through the BBB, to either the entire molecule, or to a fragment thereof. A variant of an RVG peptide can contain a mutation or modification that differs from a reference amino acid in SEQ ID NO: 601. In some aspects, a variant of SEQ ID NO: 601 is a fragment of SEQ ID NO: 601 as disclosed herein. In some aspects, an RVG variant can be a different isoform of SEQ ID NO: 601 or can comprise different isomer amino acids. Variants can be naturally-occurring, synthetic, recombinant, or chemically modified polynucleotides or polypeptides isolated or generated using methods well known in the art. RVG variants can include conservative or non-conservative amino acid changes. See, e.g., U.S. Pat. No. 9,757,470, which is herein incorporated by reference in its entirety.

[0547] In some aspects, the tropism moiety comprises a Targeted Axonal Import (TAXI) peptide. In some aspects, the TAXI peptide is cyclized TAXI peptide of sequence SACQSQSQMRCGGG (SEQ ID NO: 602). See, e.g., Sellers et al. (2016) Proc. Natl. Acad. Sci. USA 113:2514-2519, and U.S. Pat. No. 9,056,892, which are herein incorporated by reference in their entireties. TAXI transport peptides as described herein may be of any length. Typically, the transport peptide will be between 6 and 50 amino acids in length, more typically between 10 and 20 amino acids in length. In some aspects, the TAXI transport peptide comprises the amino acid sequence QSQSQMR (SEQ ID NO: 603), ASGAQAR (SEQ ID NO: 604), PF, or TSTAPHLRLRLTSR (SEQ ID NO: 605). Optionally, the TAXI transport peptide further includes a flanking sequence to facilitate incorporation into a delivery construct or carrier, e.g., a linker. In one aspect, the peptide is flanked with cysteines. In some aspects, the TAXI transport peptide further comprises additional sequence selected to facilitate delivery into nuclei. For example, a peptide that facilitates nuclear delivery is a nuclear localizing signal (NLS). Typically, this signal consists of a few short sequences of positively charged lysines or arginines, such as PPKKRKV

(SEQ ID NO: 606). In one aspect, the NLS has the amino acid sequence PKKRKV (SEQ ID NO: 607).

[0548] In some aspects, a tropism moiety of the present disclosure comprises a peptide BBB shuttle disclosed in the table below. See, e.g., Oller-Salvia et al. (2016) Chem. Soc. Rev. 45, 4690-4707, and Jafari et al. (2019) Expert Opinion on Drug Delivery 16:583-605 which are herein incorporated by reference in their entireties.

SEQ ID NO	Peptide	Sequence
608	Angiopep-2	TFFYGGSRGKRNNFKTEEY-OH
609	ApoB (3371-3409)	SSVIDALQYKLEGTTTLTRK-RGLKLATALSLSNKFVEGS
610	ApoE (159-167) ₂	(LRKLKRLL) ₂
611	Peptide-22	Ac-C(&)MPRLRGC(&)-NH ₂
612	THR	THRPPMWSPVWP-NH ₂
613	THR retro-enantio	pwvpswmpprht-NH ₂
614	CRT	C(&)RTIGPSVC(&)
615	Leptin30	YQQILTSMPSRNVIQISND-LENLRDLLHVL
616	RVG29	YTIWMPENPRPGTPCDIFT-NSRGKRASNG-OH
617	⁰ CDX	GreirtGraerwsekf-OH
618	Apamin	C(& ₁)NC(& ₂)KAPETALC(& ₁)-AR-RC(& ₂)QQH-NH ₂
619	MiniAp-4	[Dap](&)KAPETALD(&)
620	GSH	γ-L-glutamyl-CG-OH
621	G23	HLNILSTLWKYRC
622	g7	GFtGFLS(O-β-Glc)-NH ₂
623	TGN	TGNYKALHPHNG
624	TAT (47-57)	YGRKKRRQRRR-NH ₂
625	SynB1	RGGRLSYSRRRFSTSTGR
626	Diketopiperazines	&(N-MePhe)-(N-MePhe)Diketo-piperazines
627	PhPro	(Phenylproline) ₄ -NH ₂

Nomenclature for cyclic peptides (&) is adapted to the 3-letter amino acid code from the one described by Spengler *et al.* *Pept. Res.*, 2005, 65, 550-555

[Dap] stands for diaminopropionic acid.

III.G. Anti-phagocytic Signal

[0549] Clearance of administered EVs, e.g., exosomes, by the body's immune system can reduce the efficacy of an administered EV, e.g., exosome, therapy. In some aspects, the surface of the EV, e.g., exosome, is modified to limit or block uptake of the EV, e.g., exosome, by cells of the immune system, e.g., macrophages. In some aspects, the surface of the EV, e.g., exosome, is modified to express one or more surface antigen that inhibits uptake of the EV, e.g., exosome, by a macrophage. In some aspects, the surface antigen is associated with the exterior surface of the EV, (e.g., exosome).

[0550] Surface antigens useful in the present disclosure include, but are not limited to, antigens that label a cell as a "self" cell. In some aspects, the surface antigen comprises an anti-phagocytic signal. In some aspects, the anti-phagocytic signal is selected from CD47, CD24, a fragment thereof, and any combination thereof. In certain aspects, the anti-phagocytic signal comprises CD24, e.g., human CD24. In some aspects, the anti-phagocytic signal comprises a fragment of CD24, e.g., human CD24. In certain aspects, the EV, e.g., exosome, is modified to express CD47 or a fragment thereof on the exterior surface of the EV, e.g., exosome.

[0551] CD47, also referred to as leukocyte surface antigen CD47 and integrin associated protein (IAP), as used herein, is a transmembrane protein that is found on many cells in the body. CD47 is often referred to as the "don't eat me" signal, as it signals to immune cells, in particular myeloid cells, that a particular cell expressing CD47 is not a foreign cell. CD47 is the receptor for SIRPA, binding to which prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells. Interaction of CD47 with SIRPG mediates cell-cell adhesion, enhances superantigen-dependent T-cell-mediated proliferation and costimulates T-cell activation. CD47 is also known to have a role in both cell adhesion by acting as an adhesion receptor for THBS1 on platelets, and in the modulation of integrins. CD47 also plays an important role in memory formation and synaptic plasticity in the hippocampus (by similarity). In addition, CD47 can play a role in membrane transport and/or integrin dependent signal transduction, prevent premature elimination of red blood cells, and be involved in membrane permeability changes induced following virus infection.

[0552] In some aspects, an EV, e.g., exosome, disclosed herein is modified to express a human CD47 on the surface of the EV, e.g., exosome. The canonical amino acid sequence for human CD47 and various known isoforms are shown in Table 3 (UniProtKB - Q08722; SEQ ID NOs: 629-632). In some aspects, the EV, e.g., exosome, is modified to express a polypeptide

comprising the amino acid sequence set forth in SEQ ID NO: 629 or a fragment thereof. In some aspects, the EV, e.g., exosome, is modified to express a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 630 or a fragment thereof. In some aspects, the EV, e.g., exosome, is modified to express a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 631 or a fragment thereof. In some aspects, the EV, e.g., exosome, is modified to express a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 632 or a fragment thereof.

Table 3: Human CD47 Amino Acid Sequences

Canonical CD47	MWPLVAALLLGSACCGSAQLLFNKTKSVEFTFCNDTVVIPCFTVNMEAQNTTEVYVKW KFKGRDIYTFDGALNKSTVPTDFSSAKIEVSQLLKGDASLKMDKSDAVSHTGNYTCEV TELTREGETIIEELKYRVVSWFSPNENILIVIFPIFAILLFWGQFGIKTLKYRSGGMDE KTIALLVAGLVITVIVIVGAILFVFPGEYSLKNATGLGLIVTSTGILILLHHYYVFSTAI GLTSFVIAILVIQVIAYILAVVGLSLCIAACIPMHGPLLISGLSILALAQLLGLVYMK FVASNQKTIQPPRKAVEEPLNAFKESKGMNDE (SEQ ID NO: 629)
CD47 HUMAN Isoform OA3-293	MWPLVAALLLGSACCGSAQLLFNKTKSVEFTFCNDTVVIPCFTVNMEAQNTTEVYVKW KFKGRDIYTFDGALNKSTVPTDFSSAKIEVSQLLKGDASLKMDKSDAVSHTGNYTCEV TELTREGETIIEELKYRVVSWFSPNENILIVIFPIFAILLFWGQFGIKTLKYRSGGMDE KTIALLVAGLVITVIVIVGAILFVFPGEYSLKNATGLGLIVTSTGILILLHHYYVFSTAI GLTSFVIAILVIQVIAYILAVVGLSLCIAACIPMHGPLLISGLSILALAQLLGLVYMK FV (SEQ ID NO: 630)
CD47 HUMAN Isoform OA3-305	MWPLVAALLLGSACCGSAQLLFNKTKSVEFTFCNDTVVIPCFTVNMEAQNTTEVYVKW KFKGRDIYTFDGALNKSTVPTDFSSAKIEVSQLLKGDASLKMDKSDAVSHTGNYTCEV TELTREGETIIEELKYRVVSWFSPNENILIVIFPIFAILLFWGQFGIKTLKYRSGGMDE KTIALLVAGLVITVIVIVGAILFVFPGEYSLKNATGLGLIVTSTGILILLHHYYVFSTAI GLTSFVIAILVIQVIAYILAVVGLSLCIAACIPMHGPLLISGLSILALAQLLGLVYMK FVASNQKTIQPPRNN (SEQ ID NO: 631)
CD47 HUMAN Isoform OA3-312	MWPLVAALLLGSACCGSAQLLFNKTKSVEFTFCNDTVVIPCFTVNMEAQNTTEVYVKW KFKGRDIYTFDGALNKSTVPTDFSSAKIEVSQLLKGDASLKMDKSDAVSHTGNYTCEV TELTREGETIIEELKYRVVSWFSPNENILIVIFPIFAILLFWGQFGIKTLKYRSGGMDE KTIALLVAGLVITVIVIVGAILFVFPGEYSLKNATGLGLIVTSTGILILLHHYYVFSTAI GLTSFVIAILVIQVIAYILAVVGLSLCIAACIPMHGPLLISGLSILALAQLLGLVYMK FVASNQKTIQPPRKAVEEPLN (SEQ ID NO: 632)

[0553] In some aspects, the EV, e.g., exosome, is modified to express full length CD47 on the surface of the EV, e.g., exosome. In some aspects, the EV, e.g., exosome, is modified to express a fragment of CD47 on the surface of the EV, e.g., exosome, wherein the fragment comprises the extracellular domain of CD47, e.g., human CD47. Any fragment of CD47 that retains an ability to block and/or inhibit phagocytosis by a macrophage can be used in the EVs, e.g., exosomes, disclosed herein. In some aspects, the fragment comprises amino acids 19 to about 141 of the canonical human CD47 sequence (e.g., amino acids 19-141 of SEQ ID NO: 629). In some aspects, the fragment comprises amino acids 19 to about 135 of the canonical human CD47 sequence (e.g., amino acids 19-135 of SEQ ID NO: 629). In some aspects, the fragment comprises amino acids 19

to about 130 of the canonical human CD47 sequence (e.g., amino acids 19-130 of SEQ ID NO: 629). In some aspects, the fragment comprises amino acids 19 to about 125 of the canonical human CD47 sequence (e.g., amino acids 19-125 of SEQ ID NO: 629).

[0554] In some aspects, the EV, e.g., exosome, is modified to express a polypeptide having at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to amino acids 19 to about 141 of the canonical human CD47 sequence (e.g., amino acids 19-141 of SEQ ID NO: 629). In some aspects, the EV, e.g., exosome, is modified to express a polypeptide having at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to amino acids 19 to about 135 of the canonical human CD47 sequence (e.g., amino acids 19-135 of SEQ ID NO: 629). In some aspects, the EV, e.g., exosome, is modified to express a polypeptide having at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to amino acids 19 to about 130 of the canonical human CD47 sequence (e.g., amino acids 19-130 of SEQ ID NO: 629). In some aspects, the EV, e.g., exosome, is modified to express a polypeptide having at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity to amino acids 19 to about 125 of the canonical human CD47 sequence (e.g., amino acids 19-125 of SEQ ID NO: 629).

[0555] In some aspects, the CD47 or the fragment thereof is modified to increase the affinity of CD47 and its ligand SIRP α . In some aspects, the fragment of CD47 comprises a Velcro-CD47 (see, e.g., Ho et al., JBC 290:12650-63 (2015), which is incorporated by reference herein in its entirety). In some aspects, the Velcro-CD47 comprises a C15S substitution relative to the wild-type human CD47 sequence (SEQ ID NO: 629).

[0556] In some aspects, the EV, e.g., exosome, comprises a CD47 or a fragment thereof expressed on the surface of the EV, e.g., exosome, at a level that is higher than an unmodified EV, e.g., exosome. In some aspects, the CD47 or the fragment thereof is fused with a scaffold protein. Any scaffold protein disclosed herein can be used to express the CD47 or the fragment thereof on the surface of the EV, e.g., exosome. In some aspects, the EV, e.g., exosome, is modified to express a fragment of CD47 fused to the N-terminus of a Scaffold X protein. In some aspects, the EV, e.g., exosome, is modified to express a fragment of CD47 fused to the N-terminus of PTGFRN.

exosome. In some aspects, the EV, e.g., exosome, comprises at least about 400 molecules of CD47 on the surface of the EV, e.g., exosome. In some aspects, the EV, e.g., exosome, comprises at least about 500 molecules of CD47 on the surface of the EV, e.g., exosome. In some aspects, the EV, e.g., exosome, comprises at least about 1000 molecules of CD47 on the surface of the EV, e.g., exosome.

[0559] In some aspects, expression CD47 or a fragment thereof on the surface of the EV, e.g., exosome, results in decreased uptake of the EV, e.g., exosome, by myeloid cells as compared to an EV, e.g., exosome, not expressing CD47 or a fragment thereof. In some aspects, uptake by myeloid cells of the EV, e.g., exosome, expressing CD47 or a fragment thereof is decreased by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95%, relative to uptake by myeloid cells of EVs, e.g., exosomes, that do not express CD47 or a fragment thereof.

[0560] In some aspects, expression CD47 or a fragment thereof on the surface of the EV, e.g., exosome, results in decreased localization of the EV, e.g., exosome, to the liver, as compared to an EV, e.g., exosome, not expressing CD47 or a fragment thereof. In some aspects, localization to the liver of EVs, e.g., exosomes, expressing CD47 or a fragment thereof is decreased by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95%, relative to the localization to the liver of EVs, e.g., exosomes, not expressing CD47 or a fragment thereof.

[0561] In some aspects, the in vivo half-life of an EV, e.g., exosome, expressing CD47 or a fragment thereof is increased relative to the in vivo half-life of an EV, e.g., exosome, that does not express CD47 or a fragment thereof. In some aspects, the in vivo half-life of an EV, e.g., exosome, expressing CD47 or a fragment thereof is increased by at least about 1.5-fold, at least about 2-fold, at least about 2.5-fold, at least about 3-fold, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 6-fold, at least about 7-fold, at least about 8-fold, at least about 9-fold, or at least about 10-fold, relative to the in vivo half-life of an EV, e.g., exosome, that does not express CD47 or a fragment thereof.

[0562] In some aspects, an EV, e.g., exosome, expressing CD47 or a fragment thereof has an increased retention in circulation, e.g., plasma, relative to the retention of an EV, e.g., exosome,

that does not express CD47 or a fragment thereof in circulation, e.g., plasma. In some aspects, retention in circulation, e.g., plasma, of an EV, e.g., exosome, expressing CD47 or a fragment thereof is increased by at least about 1.5-fold, at least about 2-fold, at least about 2.5-fold, at least about 3-fold, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 6-fold, at least about 7-fold, at least about 8-fold, at least about 9-fold, or at least about 10-fold, relative to the retention in circulation, e.g., plasma, of an EV, e.g., exosome, that does not express CD47 or a fragment thereof.

[0563] In some aspects, an EV, e.g., exosome, expressing CD47 or a fragment thereof has an altered biodistribution when compared with an exosome that does not express CD47 or a fragment. In some aspects, the altered biodistribution leads to increased uptake into endothelial cells, T cells, or increased accumulation in various tissues, including, but not limited to skeletal muscle, cardiac muscle, diaphragm, kidney, bone marrow, central nervous system, lungs, cerebral spinal fluid (CSF), or any combination thereof.

IV. Producer Cell for Production of Engineered Exosomes

[0564] EVs, e.g., exosomes, of the present disclosure can be produced from a cell grown *in vitro* or a body fluid of a subject. When exosomes are produced from *in vitro* cell culture, various producer cells, e.g., HEK293 cells, CHO cells, and MSCs, can be used. In certain aspects, a producer cell is not a dendritic cell, macrophage, B cell, mast cell, neutrophil, Kupffer-Browicz cell, cell derived from any of these cells, or any combination thereof.

[0565] Human embryonic kidney 293 cells, also often referred to as HEK 293, HEK-293, 293 cells, or less precisely as HEK cells, are a specific cell line originally derived from human embryonic kidney cells grown in tissue culture. HEK 293 cells were generated in 1973 by transfection of cultures of normal human embryonic kidney cells with sheared adenovirus 5 DNA in Alex van der Eb's laboratory in Leiden, the Netherlands. The cells were cultured and transfected by adenovirus. Subsequent analysis has shown that the transformation was brought about by inserting ~4.5 kilobases from the left arm of the viral genome, which became incorporated into human chromosome 19. A comprehensive study of the genomes and transcriptomes of HEK 293 and five derivative cell lines compared the HEK 293 transcriptome with that of human kidney, adrenal, pituitary and central nervous tissue. The HEK 293 pattern most closely resembled that of adrenal cells, which have many neuronal properties. HEK 293 cells have a complex karyotype, exhibiting two or more copies of each chromosome and with a modal chromosome number of 64. They are described as hypotriploid, containing less than three times the number of chromosomes

of a haploid human gamete. Chromosomal abnormalities include a total of three copies of the X chromosome and four copies of chromosome 17 and chromosome 22. Variants of HEK293 cells useful to produce EVs include, but are not limited to, HEK 293F, HEK 293FT, and HEK 293T.

[0566] The producer cell can be genetically modified to comprise exogenous sequences encoding an ASO to produce EVs described herein. The genetically-modified producer cell can contain the exogenous sequence by transient or stable transformation. The exogenous sequence can be transformed as a plasmid. In some aspects, the exogenous sequence is a vector. The exogenous sequences can be stably integrated into a genomic sequence of the producer cell, at a targeted site or in a random site. In some aspects, a stable cell line is generated for production of lumen-engineered exosomes.

[0567] The exogenous sequences can be inserted into a genomic sequence of the producer cell, located within, upstream (5'-end) or downstream (3'-end) of an endogenous sequence encoding an exosome protein. Various methods known in the art can be used for the introduction of the exogenous sequences into the producer cell. For example, cells modified using various gene editing methods (*e.g.*, methods using a homologous recombination, transposon-mediated system, loxP-Cre system, CRISPR/Cas9 or TALEN) are within the scope of the present disclosure.

[0568] The exogenous sequences can comprise a sequence encoding a scaffold moiety disclosed herein or a fragment or variant thereof. An extra copy of the sequence encoding a scaffold moiety can be introduced to produce an exosome described herein (*e.g.*, having a higher density of a scaffold moiety on the surface or on the luminal surface of the EV, *e.g.*, exosome). An exogenous sequence encoding a modification or a fragment of a scaffold moiety can be introduced to produce a lumen-engineered and/or surface-engineered exosome containing the modification or the fragment of the scaffold moiety.

[0569] In some aspects, a producer cell can be modified, *e.g.*, transfected, with one or more vectors encoding a scaffold moiety linked to an ASO.

[0570] In some aspects, EVs, *e.g.*, exosomes, of the present disclosure (*e.g.*, surface-engineered and/or lumen-engineered exosomes) can be produced from a cell transformed with a sequence encoding a full-length, mature scaffold moiety disclosed herein or a scaffold moiety linked to an ASO. Any of the scaffold moieties described herein can be expressed from a plasmid, an exogenous sequence inserted into the genome or other exogenous nucleic acid, such as a synthetic messenger RNA (mRNA).

V. Pharmaceutical Compositions

[0571] Provided herein are pharmaceutical compositions comprising an EV, *e.g.*, exosome, of the present disclosure having the desired degree of purity, and a pharmaceutically acceptable carrier or excipient, in a form suitable for administration to a subject. Pharmaceutically acceptable excipients or carriers can be determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions comprising a plurality of extracellular vesicles. (*See, e.g.*, Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa. 21st ed. (2005)). The pharmaceutical compositions are generally formulated sterile and in full compliance with all Good Manufacturing Practice (GMP) regulations of the U.S. Food and Drug Administration.

[0572] In some aspects, a pharmaceutical composition comprises one or more therapeutic agents and an exosome described herein. In certain aspects, the EVs, *e.g.*, exosomes, are co-administered with one or more additional therapeutic agents in a pharmaceutically acceptable carrier. In some aspects, the ASO and the one or more additional therapeutic agents for the present disclosure can be administered in the same EV. In other aspects, the ASO and the one or more additional therapeutic agents for the present disclosure are administered in different EVs. For example, the present disclosure includes a pharmaceutical composition comprising an EV comprising an ASO and an EV comprising an additional therapeutic agent. In some aspects, the pharmaceutical composition comprising the EV, *e.g.*, exosome, is administered prior to administration of the additional therapeutic agent(s). In other aspects, the pharmaceutical composition comprising the EV, *e.g.*, exosome, is administered after the administration of the additional therapeutic agent(s). In further aspects, the pharmaceutical composition comprising the EV, *e.g.*, exosome, is administered concurrently with the additional therapeutic agent(s).

[0573] Acceptable carriers, excipients, or stabilizers are nontoxic to recipients (*e.g.*, animals or humans) at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids

such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[0574] Examples of carriers or diluents include, but are not limited to, water, saline, Ringer's solutions, dextrose solution, and 5% human serum albumin. The use of such media and compounds for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or compound is incompatible with the extracellular vesicles described herein, use thereof in the compositions is contemplated. Supplementary therapeutic agents can also be incorporated into the compositions. Typically, a pharmaceutical composition is formulated to be compatible with its intended route of administration. The EVs, *e.g.*, exosomes, can be administered by parenteral, topical, intravenous, oral, subcutaneous, intra-arterial, intradermal, transdermal, rectal, intracranial, intraperitoneal, intranasal, intratumoral, intramuscular route or as inhalants. In certain aspects, the pharmaceutical composition comprising exosomes is administered intravenously, *e.g.* by injection. The EVs, *e.g.*, exosomes, can optionally be administered in combination with other therapeutic agents that are at least partly effective in treating the disease, disorder or condition for which the EVs, *e.g.*, exosomes, are intended.

[0575] Solutions or suspensions can include the following components: a sterile diluent such as water, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial compounds such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating compounds such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and compounds for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[0576] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (if water soluble) or dispersions and sterile powders. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). The composition is generally sterile and fluid to the extent that easy syringeability exists. The carrier can be a solvent or dispersion medium containing, *e.g.*, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, *e.g.*, by

the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal compounds, *e.g.*, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. If desired, isotonic compounds, *e.g.*, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride can be added to the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition a compound which delays absorption, *e.g.*, aluminum monostearate and gelatin.

[0577] Sterile injectable solutions can be prepared by incorporating the EVs, *e.g.*, exosomes, in an effective amount and in an appropriate solvent with one or more ingredients enumerated herein or known in the art, as desired. Generally, dispersions are prepared by incorporating the EVs, *e.g.*, exosomes, into a sterile vehicle that contains a basic dispersion medium and any desired other ingredients. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The EVs, *e.g.*, exosomes, can be administered in the form of a depot injection or implant preparation which can be formulated in such a manner to permit a sustained or pulsatile release of the EV, *e.g.*, exosome.

[0578] Systemic administration of compositions comprising exosomes can also be by transmucosal means. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, *e.g.*, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of, *e.g.*, nasal sprays.

[0579] In certain aspects the pharmaceutical composition comprising EVs, *e.g.*, exosomes is administered intravenously into a subject that would benefit from the pharmaceutical composition. In certain other aspects, the composition is administered to the lymphatic system, *e.g.*, by intralymphatic injection or by intranodal injection (*see e.g.*, Senti *et al.*, PNAS 105(46): 17908 (2008)), or by intramuscular injection, by subcutaneous administration, by intratumoral injection, by direct injection into the thymus, or into the liver.

[0580] In certain aspects, the pharmaceutical composition comprising exosomes is administered as a liquid suspension. In certain aspects, the pharmaceutical composition is administered as a formulation that is capable of forming a depot following administration. In certain preferred aspects, the depot slowly releases the EVs, *e.g.*, exosomes, into circulation, or remains in depot form.

[0581] Typically, pharmaceutically-acceptable compositions are highly purified to be free of contaminants, are biocompatible and not toxic, and are suited to administration to a subject. If water is a constituent of the carrier, the water is highly purified and processed to be free of contaminants, *e.g.*, endotoxins.

[0582] The pharmaceutically-acceptable carrier can be lactose, dextrose, sucrose, sorbitol, mannitol, starch, gum acacia, calcium phosphate, alginates, gelatin, calcium silicate, micro-crystalline cellulose, polyvinylpyrrolidone, cellulose, water, syrup, methyl cellulose, methylhydroxy benzoate, propylhydroxy benzoate, talc, magnesium stearate, and/or mineral oil, but is not limited thereto. The pharmaceutical composition can further include a lubricant, a wetting agent, a sweetener, a flavor enhancer, an emulsifying agent, a suspension agent, and/or a preservative.

[0583] The pharmaceutical compositions described herein comprise the EVs, *e.g.*, exosomes, described herein and optionally a pharmaceutically active or therapeutic agent. The therapeutic agent can be a biological agent, a small molecule agent, or a nucleic acid agent. In some aspects, the additional therapeutic agent is an additional STAT3 antagonist. In some aspects, the STAT3 antagonist is any STAT3 antagonist disclosed herein. In some aspects, the additional STAT3 antagonist is an anti-STAT3 antibody. In some aspects, the additional STAT3 antagonist is a small molecule. In certain aspects, the additional therapeutic agent is an anti-cancer therapy. Non-limiting example of such anti-cancer therapies include a surgical therapy, chemotherapy, radiation therapy, cryotherapy, hormonal therapy, immunotherapy, or combinations thereof.

[0584] In some aspects, the additional STAT3 antagonist comprises an ASO. In some aspects, the additional STAT3 antagonist comprises any ASO described herein.

[0585] Dosage forms are provided that comprise a pharmaceutical composition comprising the EVs, *e.g.*, exosomes, described herein. In some aspects, the dosage form is formulated as a liquid suspension for intravenous injection. In some aspects, the dosage form is formulated as a liquid suspension for intratumoral injection.

[0586] In certain aspects, the preparation of exosomes is subjected to radiation, *e.g.*, X rays, gamma rays, beta particles, alpha particles, neutrons, protons, elemental nuclei, UV rays in order to damage residual replication-competent nucleic acids.

[0587] In certain aspects, the preparation of exosomes is subjected to gamma irradiation using an irradiation dose of more than 1, 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, or more than 100 kGy.

[0588] In certain aspects, the preparation of exosomes is subjected to X-ray irradiation using an irradiation dose of more than 0.1, 0.5, 1, 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, or greater than 10000 mSv.

VI. Kits

[0589] Also provided herein are kits comprising one or more exosomes described herein. In some aspects, provided herein is a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions described herein, such as one or more exosomes provided herein, optional an instruction for use. In some aspects, the kits contain a pharmaceutical composition described herein and any prophylactic or therapeutic agent, such as those described herein. In some aspects, the kit further comprises instructions to administer the EV according to any method disclosed herein. In some aspects, the kit is for use in the treatment of a disease or condition associated with hematopoiesis.

VII. Methods of Producing EVs

[0590] In some aspects, the present disclosure is also directed to methods of producing EVs described herein. In some aspects, the method comprises: obtaining the EV, *e.g.*, exosome from a producer cell, wherein the producer cell contains one or more components of the EV, *e.g.*, exosome (*e.g.*, an ASO); and optionally isolating the obtained EV, *e.g.*, exosome. In some aspects, the method comprises: modifying a producer cell by introducing one or more components of an EV disclosed herein (*e.g.*, an ASO); obtaining the EV, *e.g.*, exosome, from the modified producer cell; and optionally isolating the obtained EV, *e.g.*, exosome. In further aspects, the method comprises: obtaining an EV from a producer cell; isolating the obtained EV; and modifying the isolated EV. In certain aspects, the method further comprises formulating the isolated EV into a pharmaceutical composition.

VIIA. Methods of Modifying a Producer Cell

[0591] As described *supra*, in some aspects, a method of producing an EV comprises modifying a producer cell with one or more moieties (*e.g.*, an ASO). In certain aspects, the one or more moieties comprise an ASO. In some aspects, the one or more moieties further comprise a scaffold moiety disclosed herein (*e.g.*, Scaffold X or Scaffold Y).

[0592] In some aspects, the producer cell can be a mammalian cell line, a plant cell line, an insect cell line, a fungi cell line, or a prokaryotic cell line. In certain aspects, the producer cell is a mammalian cell line. Non-limiting examples of mammalian cell lines include: a human embryonic kidney (HEK) cell line, a Chinese hamster ovary (CHO) cell line, an HT-1080 cell line, a HeLa cell line, a PERC-6 cell line, a CEVEC cell line, a fibroblast cell line, an amniocyte cell line, an epithelial cell line, a mesenchymal stem cell (MSC) cell line, and combinations thereof. In certain aspects, the mammalian cell line comprises HEK-293 cells, BJ human foreskin fibroblast cells, fHDF fibroblast cells, AGE.HN[®] neuronal precursor cells, CAP[®] amniocyte cells, adipose mesenchymal stem cells, RPTEC/TERT1 cells, or combinations thereof. In some aspects, the producer cell is a primary cell. In certain aspects, the primary cell can be a primary mammalian cell, a primary plant cell, a primary insect cell, a primary fungi cell, or a primary prokaryotic cell.

[0593] In some aspects, the producer cell is not an immune cell, such as an antigen presenting cell, a T cell, a B cell, a natural killer cell (NK cell), a macrophage, a T helper cell, or a regulatory T cell (Treg cell). In other aspects, the producer cell is not an antigen presenting cell (e.g., dendritic cells, macrophages, B cells, mast cells, neutrophils, Kupffer-Browicz cell, or a cell derived from any such cells).

[0594] In some aspects, the one or more moieties can be a transgene or mRNA, and introduced into the producer cell by transfection, viral transduction, electroporation, extrusion, sonication, cell fusion, or other methods that are known to the skilled in the art.

[0595] In some aspects, the one or more moieties is introduced to the producer cell by transfection. In some aspects, the one or more moieties can be introduced into suitable producer cells using synthetic macromolecules, such as cationic lipids and polymers (Papapetrou *et al.*, *Gene Therapy* 12: S118-S130 (2005)). In some aspects, the cationic lipids form complexes with the one or more moieties through charge interactions. In some of these aspects, the positively charged complexes bind to the negatively charged cell surface and are taken up by the cell by endocytosis. In some other aspects, a cationic polymer can be used to transfect producer cells. In some of these aspects, the cationic polymer is polyethylenimine (PEI). In certain aspects, chemicals such as calcium phosphate, cyclodextrin, or polybrene, can be used to introduce the one or more moieties to the producer cells. The one or more moieties can also be introduced into a producer cell using a physical method such as particle-mediated transfection, "gene gun", biolistics, or particle bombardment technology (Papapetrou *et al.*, *Gene Therapy* 12: S118-S130 (2005)). A reporter gene such as, for example, beta-galactosidase, chloramphenicol acetyltransferase, luciferase, or green fluorescent protein can be used to assess the transfection efficiency of the producer cell.

[0596] In certain aspects, the one or more moieties are introduced to the producer cell by viral transduction. A number of viruses can be used as gene transfer vehicles, including moloney murine leukemia virus (MMLV), adenovirus, adeno-associated virus (AAV), herpes simplex virus (HSV), lentiviruses, and spumaviruses. The viral mediated gene transfer vehicles comprise vectors based on DNA viruses, such as adenovirus, adeno-associated virus and herpes virus, as well as retroviral based vectors.

[0597] In certain aspects, the one or more moieties are introduced to the producer cell by electroporation. Electroporation creates transient pores in the cell membrane, allowing for the introduction of various molecules into the cell. In some aspects, DNA and RNA as well as polypeptides and non-polypeptide therapeutic agents can be introduced into the producer cell by electroporation.

[0598] In certain aspects, the one or more moieties introduced to the producer cell by microinjection. In some aspects, a glass micropipette can be used to inject the one or more moieties into the producer cell at the microscopic level.

[0599] In certain aspects, the one or more moieties are introduced to the producer cell by extrusion.

[0600] In certain aspects, the one or more moieties are introduced to the producer cell by sonication. In some aspects, the producer cell is exposed to high intensity sound waves, causing transient disruption of the cell membrane allowing loading of the one or more moieties.

[0601] In certain aspects, the one or more moieties are introduced to the producer cell by cell fusion. In some aspects, the one or more moieties are introduced by electrical cell fusion. In other aspects, polyethylene glycol (PEG) is used to fuse the producer cells. In further aspects, sendai virus is used to fuse the producer cells.

[0602] In some aspects, the one or more moieties are introduced to the producer cell by hypotonic lysis. In such aspects, the producer cell can be exposed to low ionic strength buffer causing them to burst allowing loading of the one or more moieties. In other aspects, controlled dialysis against a hypotonic solution can be used to swell the producer cell and to create pores in the producer cell membrane. The producer cell is subsequently exposed to conditions that allow resealing of the membrane.

[0603] In some aspects, the one or more moieties are introduced to the producer cell by detergent treatment. In certain aspects, producer cell is treated with a mild detergent which transiently compromises the producer cell membrane by creating pores allowing loading of the one

or more moieties. After producer cells are loaded, the detergent is washed away thereby resealing the membrane.

[0604] In some aspects, the one or more moieties introduced to the producer cell by receptor mediated endocytosis. In certain aspects, producer cells have a surface receptor which upon binding of the one or more moieties induces internalization of the receptor and the associated moieties.

[0605] In some aspects, the one or more moieties are introduced to the producer cell by filtration. In certain aspects, the producer cells and the one or more moieties can be forced through a filter of pore size smaller than the producer cell causing transient disruption of the producer cell membrane and allowing the one or more moieties to enter the producer cell.

[0606] In some aspects, the producer cell is subjected to several freeze thaw cycles, resulting in cell membrane disruption allowing loading of the one or more moieties.

VII.B. Methods of Modifying EV, e.g., Exosome

[0607] In some aspects, a method of producing an EV, e.g., exosome, comprises modifying the isolated EV by directly introducing one or more moieties into the EVs. In certain aspects, the one or more moieties comprise an ASO. In some aspects, the one or more moieties comprise a scaffold moiety disclosed herein (e.g., Scaffold X or Scaffold Y).

[0608] In certain aspects, the one or more moieties are introduced to the EV by transfection. In some aspects, the one or more moieties can be introduced into the EV using synthetic macromolecules such as cationic lipids and polymers (Papapetrou *et al.*, Gene Therapy 12: S118-S130 (2005)). In certain aspects, chemicals such as calcium phosphate, cyclodextrin, or polybrene, can be used to introduce the one or more moieties to the EV.

[0609] In certain aspects, the one or more moieties are introduced to the EV by electroporation. In some aspects, EVs are exposed to an electrical field which causes transient holes in the EV membrane, allowing loading of the one or more moieties.

[0610] In certain aspects, the one or more moieties are introduced to the EV by microinjection. In some aspects, a glass micropipette can be used to inject the one or more moieties directly into the EV at the microscopic level.

[0611] In certain aspects, the one or more moieties are introduced to the EV by extrusion.

[0612] In certain aspects, the one or more moieties are introduced to the EV by sonication. In some aspects, EVs are exposed to high intensity sound waves, causing transient disruption of the EV membrane allowing loading of the one or more moieties.

[0613] In some aspects, one or more moieties can be conjugated to the surface of the EV. Conjugation can be achieved chemically or enzymatically, by methods known in the art.

[0614] In some aspects, the EV comprises one or more moieties that are chemically conjugated. Chemical conjugation can be accomplished by covalent bonding of the one or more moieties to another molecule, with or without use of a linker. The formation of such conjugates is within the skill of artisans and various techniques are known for accomplishing the conjugation, with the choice of the particular technique being guided by the materials to be conjugated. In certain aspects, polypeptides are conjugated to the EV. In some aspects, non-polypeptides, such as lipids, carbohydrates, nucleic acids, and small molecules, are conjugated to the EV.

[0615] In some aspects, the one or more moieties are introduced to the EV by hypotonic lysis. In such aspects, the EVs can be exposed to low ionic strength buffer causing them to burst allowing loading of the one or more moieties. In other aspects, controlled dialysis against a hypotonic solution can be used to swell the EV and to create pores in the EV membrane. The EV is subsequently exposed to conditions that allow resealing of the membrane.

[0616] In some aspects, the one or more moieties are introduced to the EV by detergent treatment. In certain aspects, extracellular vesicles are treated with a mild detergent which transiently compromises the EV membrane by creating pores allowing loading of the one or more moieties. After EVs are loaded, the detergent is washed away thereby resealing the membrane.

[0617] In some aspects, the one or more moieties are introduced to the EV by receptor mediated endocytosis. In certain aspects, EVs have a surface receptor which upon binding of the one or more moieties induces internalization of the receptor and the associated moieties.

[0618] In some aspects, the one or more moieties are introduced to the EV by mechanical firing. In certain aspects, extracellular vesicles can be bombarded with one or more moieties attached to a heavy or charged particle such as gold microcarriers. In some of these aspects, the particle can be mechanically or electrically accelerated such that it traverses the EV membrane.

[0619] In some aspects, extracellular vesicles are subjected to several freeze thaw cycles, resulting in EV membrane disruption allowing loading of the one or more moieties.

VII.C. Methods of Isolating EV, e.g., Exosome

[0620] In some aspects, methods of producing EVs disclosed herein comprises isolating the EV from the producer cells. In certain aspects, the EVs released by the producer cell into the cell culture medium. It is contemplated that all known manners of isolation of EVs are deemed suitable for use herein. For example, physical properties of EVs can be employed to separate them

from a medium or other source material, including separation on the basis of electrical charge (*e.g.*, electrophoretic separation), size (*e.g.*, filtration, molecular sieving, *etc.*), density (*e.g.*, regular or gradient centrifugation), Svedberg constant (*e.g.*, sedimentation with or without external force, *etc.*). Alternatively, or additionally, isolation can be based on one or more biological properties, and include methods that can employ surface markers (*e.g.*, for precipitation, reversible binding to solid phase, FACS separation, specific ligand binding, non-specific ligand binding, affinity purification *etc.*).

[0621] Isolation and enrichment can be done in a general and non-selective manner, typically including serial centrifugation. Alternatively, isolation and enrichment can be done in a more specific and selective manner, such as using EV or producer cell-specific surface markers. For example, specific surface markers can be used in immunoprecipitation, FACS sorting, affinity purification, and magnetic separation with bead-bound ligands.

[0622] In some aspects, size exclusion chromatography can be utilized to isolate the EVs. Size exclusion chromatography techniques are known in the art. Exemplary, non-limiting techniques are provided herein. In some aspects, a void volume fraction is isolated and comprises the EVs of interest. Further, in some aspects, the EVs can be further isolated after chromatographic separation by centrifugation techniques (of one or more chromatography fractions), as is generally known in the art. In some aspects, for example, density gradient centrifugation can be utilized to further isolate the extracellular vesicles. In certain aspects, it can be desirable to further separate the producer cell-derived EVs from EVs of other origin. For example, the producer cell-derived EVs can be separated from non-producer cell-derived EVs by immunosorbent capture using an antigen antibody specific for the producer cell.

[0623] In some aspects, the isolation of EVs can involve combinations of methods that include, but are not limited to, differential centrifugation, size-based membrane filtration, immunoprecipitation, FACS sorting, and magnetic separation.

VILD. Methods of Using

[0624] Present disclosure also provides methods of preventing and/or treating a disease or disorder in a subject in need thereof, comprising administering an EV (*e.g.*, exosome) disclosed herein (*e.g.*, comprising an ASO of the present disclosure) to the subject. Present disclosure further provides methods (*in vitro* or *in vivo*) of reducing and/or inhibiting STAT3 protein expression in a cell (*e.g.*, tumor cell). In certain aspects, an *in vitro* method of reducing and/or inhibiting STAT3 protein expression comprises contacting an EV, ASO, conjugate, or pharmaceutical composition

disclosed herein to a cell expressing STAT3 protein. In certain aspects, an *in vivo* method of reducing and/or inhibiting STAT3 protein expression comprises administering the EV, ASO, conjugate, or pharmaceutical composition of the present disclosure to a subject in need thereof.

[0625] In some aspects, contacting a cell or administering to a subject results in reduction and/or inhibition of *STAT3* mRNA and/or STAT3 protein expression. In certain aspects, *STAT3* mRNA is reduced by at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% after the administration compared to *STAT3* mRNA expression in a cell not exposed to the ASO. In some aspects, STAT3 protein is reduced by at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% after the administration compared to the expression of STAT3 protein in a cell not exposed to the ASO. As described herein, the STAT3 mRNA and/or STAT3 protein can be wild-type or a variant thereof.

[0626] ASOs useful for the present disclosure can specifically hybridize to one or more regions of a *STAT3* transcript (*e.g.*, pre-mRNA or mRNA), resulting in reduction and/or inhibition of STAT3 protein expression in a cell. Accordingly, EVs (*e.g.*, exosomes) comprising such an ASO (*e.g.*, EVs disclosed herein) can be useful for preventing and/or treating any disease or disorder associated with increased expression of a STAT3 protein.

[0627] In some aspects, a disease or disorder that can be treated with the present methods comprises a cancer. In certain aspects, the cancer is associated with increased expression of a STAT3 protein. Non-limiting examples of cancers that can be treated with the present disclosure include a colorectal cancer, lung cancer (*e.g.*, non-small cell lung cancer (NSCLC)), pancreatic cancer, leukemia, uterine cancer, ovarian cancer, bladder cancer, bile duct cancer, gastric cancer, or any combination thereof. Other examples include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell cancer, squamous cell cancer of the head and neck cancer, colorectal cancer, lymphoma, leukemia, liver cancer, glioblastoma, melanoma, myeloma basal cell cancer, adenocarcinoma, sweat gland cancer, sebaceous gland cancer, papillary cancer, papillary adenocarcinomas, cystadenocarcinoma, medullary cancer, bronchogenic cancer, renal cell cancer, hepatoma, bile duct cancer, choriocarcinoma, seminoma, embryonal cancer, Wilms' tumor, cervical cancer, testicular cancer, lung cancer, small cell lung cancer, bladder cancer, epithelial

cancer, glioma, glioblastoma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma, acute myeloid leukemia, hepatocellular carcinoma, and any combination thereof.

[0628] When administered to a subject with a cancer, in certain aspects, EVs (*e.g.*, exosome) of the present disclosure can up-regulate an immune response and enhance the tumor targeting of the subject's immune system. In some aspects, the cancer being treated is characterized by infiltration of leukocytes (T-cells, B-cells, macrophages, dendritic cells, monocytes) into the tumor microenvironment, or so-called "hot tumors" or "inflammatory tumors". In some aspects, the cancer being treated is characterized by low levels or undetectable levels of leukocyte infiltration into the tumor microenvironment, or so-called "cold tumors" or "non-inflammatory tumors". In some aspects, an EV is administered in an amount and for a time sufficient to convert a "cold tumor" into a "hot tumor", *i.e.*, said administering results in the infiltration of leukocytes (such as T-cells) into the tumor microenvironment. In certain aspects, cancer comprises bladder cancer, cervical cancer, renal cell cancer, testicular cancer, colorectal cancer, lung cancer, head and neck cancer, and ovarian, lymphoma, liver cancer, glioblastoma, melanoma, myeloma, leukemia, pancreatic cancers, or combinations thereof. In other term, "distal tumor" or "distant tumor" refers to a tumor that has spread from the original (or primary) tumor to distant organs or distant tissues, *e.g.*, lymph nodes. In some aspects, the EVs of the disclosure treats a tumor after the metastatic spread.

[0629] In some aspects, the EVs (*e.g.*, exosomes) are administered intravenously to the circulatory system of the subject. In some aspects, the EVs are infused in suitable liquid and administered into a vein of the subject.

[0630] In some aspects, the EVs (*e.g.*, exosomes) are administered intra-arterially to the circulatory system of the subject. In some aspects, the EVs are infused in suitable liquid and administered into an artery of the subject.

[0631] In some aspects, the EVs (*e.g.*, exosomes) are administered to the subject by intrathecal administration. In some aspects, the EVs (*e.g.*, exosomes) are administered by intrathecal administration, followed by application of a mechanical convective force to the torso. See, *e.g.*, Verma et al., *Alzheimer's Dement.* 12:e12030 (2020); which is incorporated by reference herein in its entirety). As such, certain aspects of the present disclosure are directed to methods of administering an EV, *e.g.*, an exosome, to a subject in need thereof, comprising administering the EV, *e.g.*, exosome, to the subject by intrathecal injection, followed by applying a mechanical

convective force to the torso of the subject. In some aspects, the mechanical convective force is achieved using a high frequency chest wall or lumbothoracic oscillating respiratory clearance device (*e.g.*, a Smart Vest or Smart Wrap, ELECTROMED INC, New Prague, MN, USA). In some aspects, the mechanical convective force, *e.g.*, the oscillating vest, facilitates spread of the intrathecally dosed EVs, *e.g.*, exosomes, further down the nerve thus allowing for better EV, *e.g.*, exosome, delivery to nerves.

[0632] In some aspects, the intra- and trans-compartmental biodistribution of exosomes can be manipulated by exogenous extracorporeal forces acting upon a subject after compartmental delivery of exosomes. This includes the application of mechanical convection, for example by way of applying percussion, vibration, shaking, or massaging of a body compartment or the entire body. Following intrathecal dosing for example, the application of chest wall vibrations by several means including an oscillating mechanical jacket can spread the biodistribution of exosomes along the neuraxis or along cranial and spinal nerves, which can be helpful in the treatment of nerve disorders by drug carrying exosomes.

[0633] In some aspects, the application of external mechanical convective forces via an oscillating jacket or other similar means can be used to remove exosomes and other material from the cerebrospinal fluid of the intrathecal space and out to the peripheral circulation. This aspect can help remove endogenous toxic exosomes and other deleterious macromolecules such as beta-amyloid, tau, alpha-synuclein, TDP43, neurofilament and excessive cerebrospinal fluid from the intrathecal space to the periphery for elimination.

[0634] In some aspects, exosomes delivered via the intracerebroventricular route can be made to translocate throughout the neuraxis by simultaneously incorporating a lumbar puncture and allowing for ventriculo-lumbar perfusion wherein additional fluid is infused into the ventricles after exosome dosing, while allowing the existing neuraxial column of CSF to exit is the lumbar puncture. Ventriculo-lumbar perfusion can allow ICV dosed exosome to spread along the entire neuraxis and completely cover the subarachnoid space in order to treat leptomeningeal cancer and other diseases.

[0635] In some aspects, the application of external extracorporeal focused ultrasound, thermal energy (heat) or cold may be used to manipulate the compartmental pharmacokinetics and drug release properties of exosomes engineered to be sensitive to these phenomena.

[0636] In some aspects, the intracompartmental behavior and biodistribution of exosomes engineered to contain paramagnetic material can be manipulated by the external application of magnets or a magnetic field.

[0637] In some aspects, the EVs are administered *via* an injection into the spinal canal, or into the subarachnoid space so that it reaches the cerebrospinal fluid (CSF).

[0638] In some aspects, the EVs (*e.g.*, exosomes) are administered intratumorally into one or more tumors of the subject.

[0639] In some aspects, the EVs (*e.g.*, exosomes) are administered to the subject by intranasal administration. In some aspects, the EVs can be insufflated through the nose in a form of either topical administration or systemic administration. In certain aspects, the EVs are administered as nasal spray.

[0640] In some aspects, the EVs (*e.g.*, exosomes) are administered to the subject by intraperitoneal administration. In some aspects, the EVs are infused in suitable liquid and injected into the peritoneum of the subject. In some aspects, the intraperitoneal administration results in distribution of the EVs to the lymphatics. In some aspects, the intraperitoneal administration results in distribution of the EVs to the thymus, spleen, and/or bone marrow. In some aspects, the intraperitoneal administration results in distribution of the EVs to one or more lymph nodes. In some aspects, the intraperitoneal administration results in distribution of the EVs to one or more of the cervical lymph node, the inguinal lymph node, the mediastinal lymph node, or the sternal lymph node. In some aspects, the intraperitoneal administration results in distribution of the EVs to the pancreas.

[0641] In some aspects, the EVs, *e.g.*, exosomes, are administered to the subject by periocular administration. In some aspects, the s are injected into the periocular tissues. Periocular drug administration includes the routes of subconjunctival, anterior sub-Tenon's, posterior sub-Tenon's, and retrobulbar administration.

VIII.A. Methods of Treating a brain tumor

[0642] Certain aspects of the present disclosure are directed to methods of treating a brain tumor in a subject in need thereof. In some aspects, the method comprises administering to the subject a therapeutically effective amount of an EV, *e.g.*, exosome, comprising an ASO, as disclosed herein. In some aspects, the EV, *e.g.*, exosome, is capable of targeted delivery of a therapeutic agent, *e.g.*, an ASO, as disclosed herein, to the CNS to treat the brain tumor. In some aspects, the EV, *e.g.*, exosome, is capable of up-regulating an immune response in the subject, thereby enhancing the subject's immune response against the neuroimmunological disorder. In some aspects, the composition is administered intratumorally or intrathecally to the subject.

[0643] Also provided herein are methods of preventing metastasis of a brain tumor in a subject. The method comprises administering to the subject a therapeutically effective amount of the compositions disclosed herein, wherein the composition is capable of preventing a brain tumor at one location in the subject from promoting the growth of one or more tumors at another location in the subject. In some aspects, the composition is administered intratumorally or intrathecally in a first tumor in one location, and the composition administered in a first tumor prevents metastasis of one or more tumors at a second location.

[0644] In some aspects, administering an EV, e.g., exosome, disclosed herein inhibits and/or reduces growth of a brain tumor in a subject. In some aspects, the growth of a brain tumor (e.g., tumor volume or weight) is reduced by at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% compared to a reference (e.g., tumor volume in a corresponding subject after administration of an EV, e.g., exosome, without the ASO).

[0645] As used herein, the term "brain tumor" refers to an abnormal growth of cells within the brain (e.g., within the meninges). Brain tumors can be categorized as primary or secondary brain tumor. "Primary brain tumor" refers to brain tumors that originate within the brain. "Secondary brain tumor" refers to brain tumors that are the result of cancer cells originating at primary sites outside the brain that have metastasized (*i.e.*, spread) to the brain. Unless specified otherwise, the term brain tumor can refer to both primary and secondary brain tumors.

[0646] In some aspects, a brain tumor that can be treated with the present disclosure comprises an acoustic neuroma, choroid plexus carcinoma, craniopharyngioma, embryonal tumor, glioma, medulloblastoma, meningioma, pediatric brain tumor, pineoblastoma, pituitary tumor, or combinations thereof.

[0647] In certain aspects, a brain tumor that can be treated with the present disclosure comprises a glioma. As used herein, the term "glioma" refers to a type of tumor that starts in the glial cells of the brain or the spine. In some aspects, a glioma can be classified by specific type of cells with which they share histological features. Accordingly, a glioma that can be treated with EVs (e.g., exosomes) disclosed herein can be classified as an ependymoma (ependymal cells), astrocytoma (astrocytes), oligodendroglioma (oligodendrocytes), brainstem glioma (e.g., diffuse intrinsic pontine glioma), optic nerve glioma, mixed glioma, oligoastrocytoma, or any combination thereof. In certain aspects, an astrocytoma comprises glioblastoma multiforme (GBM).

[0648] Gliomas disclosed herein can be further categorized according to their grade, which is determined by pathologic evaluation of the tumor. In some aspects, the neuropathological

evaluation and diagnostics of brain tumor specimens is performed according to WHO Classification of Tumours of the Central Nervous System. In some aspects, a glioma that can be treated with the present disclosure comprises a low-grade glioma. A "low-grade glioma" [WHO grade II] are well-differentiated (not anaplastic) and tend to exhibit benign tendencies and portend a better prognosis for the patient. However, in some aspects, low-grade gliomas can have a uniform rate of recurrence and increase in grade over time, so should be classified as malignant. In some aspects, a glioma that can be treated comprises a high grade glioma. A "high-grade glioma" [WHO grades III–IV] gliomas are undifferentiated or anaplastic and are malignant and carry a worse prognosis. Of numerous grading systems in use, the most common is the World Health Organization (WHO) grading system for astrocytoma, under which tumors are graded from I (least advanced disease—best prognosis) to IV (most advanced disease—worst prognosis). Non-limiting examples of high-grade gliomas include anaplastic astrocytomas and glioblastoma multiforme.

[0649] In some aspects, an EV (*e.g.*, exosome) disclosed herein can be used to treat a glioma grade I, grade II, grade III, grade IV, or combinations thereof, as determined under the WHO grading system. In certain aspects, an EV (*e.g.*, exosome) disclosed herein can be used to treat any type of gliomas.

[0650] In some aspects, the glioma treatable by the present methods is a diffuse intrinsic pontine glioma (DIPG), a type of brainstem glioma. Diffuse intrinsic pontine glioma primarily affects children, usually between the ages of 5 and 7. The median survival time with DIPG is under 12 months. Surgery to attempt tumor removal is usually not possible or advisable for DIPG. By their very nature, these tumors invade diffusely throughout the brain stem, growing between normal nerve cells.

[0651] In other aspects, the glioma treatable by the present methods is an IDH1 and IDH2-mutated glioma. Patients with glioma carrying mutations in either IDH1 or IDH2 have a relatively favorable survival, compared with patients with glioma with wild-type IDH1/2 genes. In WHO grade III glioma, IDH1/2-mutated glioma have a median prognosis of ~3.5 years, whereas IDH1/2 wild-type glioma perform poor with a median overall survival of 1.5 years. In glioblastoma, the difference is larger.

[0652] In some aspects, a neuroimmunological disorder that can be treated with the present disclosure comprises a neoplastic meningitis. As used herein, "neoplastic meningitis" refers to a tumor which has spread from the original tumor site into the dural and leptomeninges, which are thin tissue membranes covering the brain and spinal cord. In some aspects, connective tissue nerve sheaths that extend from the meninges onto and into nerves can also become involved. Neoplastic

meningitis is also known as carcinomatous meningitis, leptomeningeal carcinoma, leptomeningeal carcinomatosis, leptomeningeal metastasis, leptomeningeal disease (LMD), leptomeningeal cancer, meningeal carcinomatosis, and meningeal metastasis. In certain aspects, a neoplastic meningitis is caused by leukemia. In some aspects, a neoplastic meningitis is caused by melanoma, breast, lung, gastrointestinal cancer, or combinations thereof. In certain aspects, a neoplastic meningitis is caused by a glioma.

[0653] The practice of the present disclosure will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See*, for example, Sambrook *et al.*, ed. (1989) *Molecular Cloning A Laboratory Manual* (2nd ed.; Cold Spring Harbor Laboratory Press); Sambrook *et al.*, ed. (1992) *Molecular Cloning: A Laboratory Manual*, (Cold Springs Harbor Laboratory, NY); D. N. Glover ed., (1985) *DNA Cloning*, Volumes I and II; Gait, ed. (1984) *Oligonucleotide Synthesis*; Mullis *et al.* U.S. Pat. No. 4,683,195; Hames and Higgins, eds. (1984) *Nucleic Acid Hybridization*; Hames and Higgins, eds. (1984) *Transcription And Translation*; Freshney (1987) *Culture Of Animal Cells* (Alan R. Liss, Inc.); *Immobilized Cells And Enzymes* (IRL Press) (1986); Perbal (1984) *A Practical Guide To Molecular Cloning*; the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); Miller and Calos eds. (1987) *Gene Transfer Vectors For Mammalian Cells*, (Cold Spring Harbor Laboratory); Wu *et al.*, eds., *Methods In Enzymology*, Vols. 154 and 155; Mayer and Walker, eds. (1987) *Immunochemical Methods In Cell And Molecular Biology* (Academic Press, London); Weir and Blackwell, eds., (1986) *Handbook Of Experimental Immunology*, Volumes I-IV; *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986);); Crooke, *Antisense drug Technology: Principles, Strategies and Applications*, 2nd Ed. CRC Press (2007) and in Ausubel *et al.* (1989) *Current Protocols in Molecular Biology* (John Wiley and Sons, Baltimore, Md.).

[0654] All of the references cited above, as well as all references cited herein, are incorporated herein by reference in their entireties.

[0655] The following examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1: Analysis of STAT3 mRNA Expression

[0656] Exemplary ASOs disclosed herein were designed to specifically target *STAT3* transcript encoding the STAT3 protein. See FIG. 1. The ASOs of the present disclosure were tested for their ability to reduce *STAT3* mRNA expression in IL-6 stimulated PANC-1 cells. The PANC-1 cells were grown in cell culture media and seeded onto a 96 well plate at a density of 20,000 cells/well. ASOs were tested in two separate cohorts: 2 doses or 5 doses were given to the PANC-1 cells (See Table 4) at final concentrations of 20nM and 2nM, respectively. The assay used Lipofectamine2000 transfection and a 48hr treatment cycle, with incubation at 37°C and 5% CO₂. Analysis of the mRNA expression was then carried out using a branched DNA assay.

[0657] Generally, each of the ASOs tested was able to reduce *STAT3* mRNA expression in the PANC-1 cells with minimal effect on *GADPH* mRNA expression. (see Table 4, FIGs. 2A-2N, and FIG. 3)

Table 4. Summary of *STAT3* mRNA expression

SEQ ID NO:	starting base	length	5 point DR data		2 point DR data			Notes
			STAT3 PANC 1 IC50 Prism	STAT3 Max inhibition 24nM	STAT3 Inhibition 20nM	STAT3 Inhibition 2nM	GAPDH Inhibition 20nM	
103	1046	15	0.465	89.93	95.8	82.5	10.00	1 CpG, 7x1mm, 261x2mm hits
115	2267	15	0.796	78.99	90.8	65.2	3.00	rat, 2 CpG, 3x1mm, 143x2mm hits
138	1238	16	1.306	85.33	86.8	53.0	9.00	2 CpG, 51x2mm hits
112	1482	16	1.041	86.32	91.0	70.0	-25.00	1 CpG, 1 GGGG, 90x2mm hits
105	450	20	1.471	85.61	91.6	79.4	13.00	1 CpG
137	516	20	1.803	79.46	87.4	53.0	-2.00	1 CpG
124	995	20	1.597	86.46	83.3	62.6	13.00	1 CpG
114	2262	20	0.814	84.94	87.0	66.4	10.00	rat, 2 CpG
102	2557	20	0.473	78.02	89.5	82.7	16.00	2 CpG, 1 GGGG
107	2558	20	0.037	70.92	87.7	79.0	8.00	2 CpG, 1 GGGG
116	411	20	1.854	69.78	85.5	64.5	16.00	1 CpG
120	525	20	2.054	87.43	93.4	62.8	12.00	2 CpG
130	458	20	1.677	72.16	80.7	59.3	13.00	1 CpG
134	1039	20	2.127	77.94	82.8	54.3	10.00	1 CpG

135	1238	20	1.046	78.59	84.2	53.9	4.00	2 CpG
133	2274	20	2.243	81.73	90.7	55.9	14.00	1 CpG
125	2263	20	2.296	81.67	85.1	61.7	14.00	2 CpG
126	511	20	2.783	87.71	90.7	61.4	13.00	1 CpG
131	894	17	2.825	75.20	90.7	58.9	12.00	2 CpG, 9x2mm hits
145	2273	20	3.063	85.73	89.2	50.2	17.00	1 CpG
128	1043	20	3.565	79.56	81.1	61.1	19.00	1 CpG
139	1034	20	4.023	72.50	83.4	52.8	10.00	1 CpG
Control	1286	20	4.103	81.62	84.5	49.6	15.00	no cyno, 9x2mm hits
142	1484	20	6.757	76.10	80.0	51.7	9.00	1 CpG, 1 GGGG

EXAMPLE 2: Construction of an Exosome

[0658] To generate exosomes described herein, human embryonic kidney (HEK) cell line (*e.g.*, HEK293SF) will be used. The cells will be stably transfected with Scaffold X, Scaffold Y, and/or anchoring moiety linked to an agent of interest.

[0659] Upon transfection, HEK cells will be grown to high density in chemically defined medium for 7 days. Conditioned cell culture media will be then collected and centrifuged at 300 – 800 x g for 5 minutes at room temperature to remove cells and large debris. Media supernatant will be supplemented with 1000 U/L BENZONASE® and incubated at 37 °C for 1 hour in a water bath. Supernatant will be collected and centrifuged at 16,000 x g for 30 minutes at 4 °C to remove residual cell debris and other large contaminants. Supernatant will then be ultracentrifuged at 133,900 x g for 3 hours at 4 °C to pellet the exosomes. Supernatant will be discarded and any residual media will be aspirated from the bottom of the tube. The pellet will be resuspended in 200 – 1000 µL PBS (-Ca -Mg).

[0660] To further enrich exosome populations, the pellet will be processed via density gradient purification (sucrose or OPTIPREP™).

[0661] The gradient will be spun at 200,000 x g for 16 hours at 4 °C in a 12 mL Ultra-Clear (344059) tube placed in a SW 41 Ti rotor to separate the exosome fraction.

[0662] The exosome layer will then be gently removed from the top layer and diluted in ~32.5 mL PBS in a 38.5 mL Ultra-Clear (344058) tube and ultracentrifuged again at 133,900 x g for 3 hours at 4 °C to pellet the purified exosomes. The resulting pellet will be resuspended in a minimal volume of PBS (~200 µL) and stored at 4 °C.

[0663] For OPTIPREP™ gradient, a 3-tier sterile gradient will be prepared with equal volumes of 10%, 30%, and 45% OPTIPREP™ in a 12 mL Ultra-Clear (344059) tube for a SW 41

Ti rotor. The pellet will be added to the OPTIPREP™ gradient and ultracentrifuged at 200,000 x g for 16 hours at 4 °C to separate the exosome fraction. The exosome layer will then be gently collected from the top ~3 mL of the tube.

[0664] The exosome fraction will be diluted in ~32 mL PBS in a 38.5 mL Ultra-Clear (344058) tube and ultracentrifuged at 133,900 x g for 3 hours at 4 °C to pellet the purified exosomes. The pelleted exosomes will then be resuspended in a minimal volume of PBS (~200 µL) and stored at 4°C until ready to be used.

EXAMPLE 3: *Treatment of a Tumor Model Using Exo-STAT3-ASO*

[0665] Tumor cells were implanted subcutaneously into the flanks of BALB/c mice. Six days after implantation, mice were treated intratumorally with Exo-STAT3-ASO (*i.e.*, free STAT3-ASO (*i.e.*, not associated with an EV), or PBS. The mice received a single dose of the treatment for six consecutive days (*i.e.*, treated from days 6-12 post tumor inoculation). Then, tumor volume was assessed in the animals at various time points.

[0666] As shown in FIGs. 4A-4C, mice treated with Exo-STAT3-ASO-MOE and free STAT3 ASO MOE had reduced tumor growth through 13 days post implantation compared to PBS control treated mice. These results suggest that EVs (*e.g.*, exosomes) disclosed herein can effectively deliver the STAT3-specific ASOs to tumor cells, and thereby, reduce tumor growth.

EXAMPLE 4: *Analysis of STAT3 Gene Expression in Exo-STAT3-ASO treated mice*

[0667] To further characterize the knockdown efficiency of the EVs (*e.g.*, exosomes) described herein (*i.e.*, comprising a STAT3-specific ASO), cells were treated with one of the following: (i) PBS; (2) native EVs ("HEK Exo"); (3) EVs comprising a scramble control ASO ("Scramble Exo ASO"); (4) C188-9 (100 mg/kg); (5) EVs comprising a STAT3-specific ASO ("Stat 3 Exo ASO"); (6) STAT3-specific ASO alone (*i.e.*, not linked to an EV) at a dose of 4 µg ("Stat 3 Free ASO"); and (7) STAT3-specific ASO alone at a dose of 8 µg ("Stat 3 Free ASO 2x").

[0668] As shown in FIG. 5, in STAT3-Exo-ASO treated cells, there was approximately a 40% knockdown in *STAT3* mRNA expression compared to the PBS-treated control. In contrast, even at the higher dose (*i.e.*, 8 µg), *STAT3* mRNA expression in cells treated with STAT3-specific ASO alone was reduced by at most about 25% compared to the PBS control. These results suggest that the EVs disclosed herein could improve the ability of the STAT3-specific ASOs to reduce and/or inhibit *STAT3* mRNA expression in target cells.

[0669] Next, to further understand the anti-tumor efficacy of the EVs disclosed herein (*i.e.*, comprising a STAT3-specific ASO), animals from Example 3 were sacrificed and the infiltration of the following cell populations were assessed in the tumors: (i) total CD45⁺ cells; (ii) CD45⁺ macrophages (CD11b^{High} F40/80^{High}/CD45), and (iii) myeloid-derived suppressor cells (MDSCs) (Ly6G^{High} CD11b^{High}/IA/IE^{Low}). As shown in FIGs. 6A-6C, a significant increase in both percentage of infiltrating CD45⁺ cells and MDSCs/CD45⁺ cells was observed between PBS and Exo-STAT3-ASO-MOE treatments. The observed increase was associated with a corresponding decrease in the percentage of macrophages within the population of CD45⁺ cells (*see* FIG. 6B). In contrast, treating the tumor mice with STAT3-specific ASO alone (*i.e.*, not linked to an EV) had minimal effect on the infiltration of the different cell populations assessed.

[0670] Moreover, as shown in FIGs. 7A and 7B, the increased infiltration of the MDSCs was largely due to an increase in the population of granulocytic (gMDSCs). In fact, tumors from mice treated with EVs comprising STAT3-specific ASO (*i.e.*, Exo-STAT3-ASO-MOE) had decreased population of monocytic MDSCs (*see* FIG. 7B).

[0671] Lastly, to confirm that the above-described results were associated with the EVs disclosed herein (*i.e.*, comprising a STAT3-specific ASO), *STAT3* mRNA expression, was assessed in the tumors of animals from the different treatment groups. As shown in FIG. 8, *STAT3* mRNA was significantly decreased in Exo-STAT-3ASO treated mice compared to both PBS and Scrambled Exo-ASO controls (FIG.8).

[0672] Collectively, the above results demonstrate that the EVs (*e.g.*, exosomes) described herein can effectively deliver STAT3-specific ASOs to target cells *in vivo*, resulting in the successful knockdown of *STAT3* transcript in the target cells. The data further demonstrates that the reduction in *STAT3* expression is associated with an increased anti-tumor immune response (*e.g.*, decreased tumor volume, increased infiltration of CD45⁺ cells, including granulocytic MDSCs, and decreased infiltration of macrophages and monocytic MDSCs).

EXAMPLE 5: Exo-STAT3 Are Capable of Repolarizing M2 Macrophages

[0673] Monocytes isolated from PBMCs were cultured and differentiated into M2 macrophages and treated with increasing concentrations of Exo-STAT3-ASO for 48 hours. Cells treated with (i) an EV (*e.g.*, exosome) comprising a scramble control ASO ("Scramble") or (ii) STAT3-specific ASO alone (*i.e.*, not associated with an EV) ("Free ASO") were used as controls. In the "Free ASO" group, the ASO was used at the highest concentration of the STAT3-specific ASOs present on the EVs (*i.e.*, 1.25×10^5 nM).

[0674] *In vitro* treatment of these primary human M2 macrophages with Exo-STAT3-ASO induced a dose-dependent knockdown of *STAT3* mRNA measured by qPCR. (FIG. 12A). Exo-STAT3-ASO treatment led to greater level of knockdown than with equivalent dose of free ASO in the primary human macrophages.

[0675] Next, to assess whether the reduced *STAT3* mRNA expression had any effect on the polarization of macrophages, proinflammatory cytokine responses were measured in LPS-stimulated human primary macrophages after treatment with an EV disclosed herein (*i.e.*, comprising a STAT3-specific ASO) or STAT3-specific ASO alone. Macrophages were cultured and treated for 48 hours and cytokines were detected from the media. As shown in FIGs. 12B-12D, Exo-STAT3 treatment resulted in a dose-dependent increase in TNF- α (2X), IL-23 (5X), and IL-12p40 (37X) compared to the control groups (*i.e.*, untreated and treated with EVs comprising the scramble control ASO).

[0676] Collectively, the above results demonstrate that the EVs (*e.g.*, exosomes) described herein can effectively deliver STAT3-specific ASOs to macrophages, resulting in the successful knockdown of *STAT3* transcript and repolarize M2 macrophages into a more pro-inflammatory phenotype.

EXAMPLE 6: Exo-STAT3-ASO Knockdown in Hep3B Liver Cells

[0677] To assess whether the EVs disclosed herein (*i.e.*, comprising a STAT3-specific ASO) could be useful in treating liver cancers, Hep3B liver cells were treated with increasing concentrations of Exo-STAT3-ASO (*i.e.*, comprising a STAT3-specific ASO linked to the exterior surface of the EV). About 48 hours after treatment, *STAT3* and *mcl1* (a STAT3 downstream target gene) mRNA expression was measured by qPCR. STAT3 protein expression was also assessed using AlphaLISA surefire Ultra kit.

[0678] As shown in FIG. 13A, for all cells treated with the Exo-STAT3-ASO, there was significant reduction in *STAT3* mRNA expression (approximately 60% knockdown) compared to the control cells. The reduced *STAT3* mRNA expression was associated with decreased expression of both *mcl1* mRNA (35-65% inhibition) (FIG. 13B) and STAT3 protein (35% inhibition) (FIG. 13C).

[0679] These results confirm that the EVs disclosed herein (*i.e.*, comprising a STAT3-specific ASO) can be effective in reducing *STAT3* expression in various cell types, including liver cells.

EXAMPLE 7: Treatment of a Liver Cancer Mouse Model Using Exo-STAT3-ASO

[0680] Further to the *in vitro* data provided above in Example 6, the anti-tumor effects of the EVs disclosed herein were assessed in an animal model of human liver cancer. Briefly, Hep3B human liver cancer cells were implanted subcutaneously into the flanks of mice. After implantation, mice were treated intratumorally with Exo-STAT3-ASO (*i.e.*, comprising a STAT3-specific ASO fused to a Scaffold X (PTGFRN) linked to the exterior surface) three times every two days. Control animals were treated with one of the following: (i) native EVs; (ii) STAT3-specific ASO only (*i.e.*, not linked to an EV); and (iii) native EVs comprising only the STAT3-specific ASO (*i.e.*, not fused to Scaffold X). Then, *STAT3* mRNA expression was assessed in the tumor lysates from the animals.

[0681] As shown in FIG. 14, the greatest knockdown was observed in animals where the STAT3-specific ASOs were delivered using an EV. Treatment Exo-STAT3-ASO resulted in a 35% knockdown of human STAT3 within tumor lysates after 3 treatments of 3 µg STAT3 ASO (FIG. 14).

[0682] The above results demonstrate that the EVs (*e.g.*, exosomes) described herein can effectively deliver STAT3-specific ASOs to target cells *in vivo*, resulting in the successful knockdown of *STAT3* transcript in the target cells and can provide an effective treatment in diseases associated with abnormal STAT3 activity, such as cancers, particularly liver cancers.

EXAMPLE 8: Treatment of a Hepatocarcinoma Mouse-Model Using Exo-STAT3-ASO

[0683] Hepa1-6 mice will be used to test the *in vivo* efficacy of Exo-STAT3-ASO for treating a tumor. The Hepa1-6 line is an orthotopic mouse model of hepatocarcinoma. The Hepa1-6 mouse liver cancer models will be used to assess intravenous delivery of Exo-STAT3-ASO administration for the reduction of liver tumor growth rate.

EXAMPLE 9: Treatment of a Colon Carcinoma Mouse-Model Using Exo-STAT3-ASO

[0684] A subcutaneous CT26 mouse colorectal cancer model which is IL-6 driven and macrophage rich will be used to show STAT3 knockdown in macrophages drives anti-tumor efficacy. CT26 tumor cells will be subcutaneously implanted into the flanks of BALB/c mice. Eight days after implantation mice will be treated intratumorally with exo-STAT3-ASO or free STAT3 ASO or intraperitoneally with an anti-PD1 antibody or an anti-CSF1R antibody (n=10 mice per group). As controls, two groups of mice will be treated with either exoASO-scramble or PBS. Geometric means of the tumor volumes will be analyzed.

EXAMPLE 10: *Increased Uptake of CD33 Targeted Exosomes in AML cells*

[0685] As described herein, EVs (*e.g.*, exosomes) can be modified to comprise a targeting moiety, which can alter and/or enhance the tropism of the EVs to specific cells. To assess whether EVs (*e.g.*, exosomes) can be modified to target CD33⁺ cells, an anti-CD33 targeting moiety fused to a Scaffold X (PTGFRN) was linked to the exterior surface of the EV and their uptake by different AML cells was assessed.

[0686] First, using an ALFA Nb-anti-CD33 antibody (*e.g.*, hP67.6-AF568) (*See* US 5,877,296, which is incorporated herein by reference in its entirety), CD33 expression on the AML cells was determined. MV4-11 and KG1 cells were determined to contain 204,000 and 76,000 CD33 per cell, respectively.

[0687] Next, using Octet, the ability of EVs (*e.g.*, exosomes) comprising anti-CD33 targeting moiety to bind CD33 was confirmed. As shown in FIG. 15, among the different EVs (*e.g.*, exosomes) tested, EVs comprising anti-CD33 targeting moiety fused to Scaffold X and linked to the exterior surface of the EVs exhibited the greatest binding (*see* "PrX" and "PrX-AF568" in FIG. 15).

[0688] Then, to assess the uptake of the EVs comprising anti-CD33 targeting moiety in the AML cells, ALFA plug-and-play system was used to externally load anti-CD33 ALFA tagged antibody onto ALFA Nb exosomes. 100k cells/well were incubated overnight with NHS-Alexa Fluor 568 labeled exosomes at MOIs ranging from 1.0e6 to 1.56e4 in duplicate prior to flow cytometry readout. Increased uptake was observed for anti-CD33 Ab-coupled ALFA Nb exosomes in high CD33 expressing MV4-11 AML cells (FIG. 16A) compared to KG1 cells which express lower levels of CD33 (FIG. 16B). RAW264.7 cells were used as a positive control (FIG. 16C). Increased uptake was observed for CD33-targeted exosomes, with higher fold-changes at lower MOIs (FIGs. 16E-16G).

[0689] The above results confirm that linking an anti-CD33 antibody to the exterior surface of EVs (*e.g.*, exosomes) can enhance the tropism of the EVs to CD33⁺ cells, such as AML cells.

[0690] Throughout this application, various publications are referenced in parentheses by author name and date, or by Patent No. or Patent Publication No. The disclosures of these publications are hereby incorporated in their entireties by reference into this application in order to more fully describe the state of the art as known to those skilled therein as of the date of the

disclosure described and claimed herein. However, the citation of a reference herein should not be construed as an acknowledgement that such reference is prior art to the present disclosure.

WHAT IS CLAIMED IS:

1. An extracellular vesicle comprising an antisense oligonucleotide (ASO) which is an antagonist and comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within a *STAT3* transcript (SEQ ID NO: 1 or SEQ ID NO: 3).
2. The extracellular vesicle of claim 1, wherein the ASO is not TAAGCTGATAATTCAACTCA (SEQ ID NO: 5).
3. The extracellular vesicle of claim 1 or 2, which targets a macrophage.
4. The extracellular vesicle of any one of claims 1 to 3, wherein the ASO comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within nucleotides 1 to 56982 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 57003 to 75171 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 1 to 1287 of a *STAT3* transcript corresponding to SEQ ID NO: 3, or nucleotides 1306 to 2787 of a *STAT3* transcript corresponding to SEQ ID NO: 3.
5. The extracellular vesicle of claim 4, wherein the contiguous nucleotide sequence is at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% complementary to the nucleic acid sequence within the *STAT3* transcript.
6. The extracellular vesicle of any one of claims 1 to 5, wherein the ASO is capable of reducing STAT3 protein expression in a human cell (*e.g.*, HEK293 cell), wherein the human cell expresses the STAT3 protein.
7. The extracellular vesicle of claim 6, wherein the STAT3 protein expression is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to STAT3 protein expression in a human cell that is not exposed to the ASO.

8. The extracellular vesicle of any one of claims 4 to 7, wherein the ASO is capable of reducing a level of *STAT3* mRNA in a human cell (*e.g.*, HEK293 cell), wherein the human cell expresses the *STAT3* mRNA.
9. The extracellular vesicle of claim 8, wherein the level of *STAT3* mRNA is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to the level of the *STAT3* mRNA in a human cell that is not exposed to the ASO.
10. The extracellular vesicle of any one of claims 1 to 9, wherein the ASO is a gapmer, a mixmer, or a totalmer.
11. The extracellular vesicle of any one of claims 1 to 10, wherein the ASO comprises one or more nucleoside analogs.
12. The extracellular vesicle of claim 11, wherein one or more of the nucleoside analogs comprises a 2'-O-alkyl-RNA; 2'-O-methyl RNA (2'-OMe); 2'-alkoxy-RNA; 2'-O-methoxyethyl-RNA (2'-MOE); 2'-amino-DNA; 2'-fluoro-RNA; 2'-fluoro-DNA; arabino nucleic acid (ANA); 2'-fluoro-ANA; or bicyclic nucleoside analog.
13. The extracellular vesicle of claim 11 or 12, wherein one or more of the nucleoside analogs is a sugar modified nucleoside.
14. The extracellular vesicle of claim 13, wherein the sugar modified nucleoside is an affinity enhancing 2' sugar modified nucleoside.
15. The extracellular vesicle of any one of claims 11 to 14, wherein one or more of the nucleoside analogs comprises a nucleoside comprising a bicyclic sugar.
16. The extracellular vesicle of any one of claims 11 to 14, wherein one or more of the nucleoside analogs comprises an LNA.
17. The extracellular vesicle of any one of claims 11 to 16, wherein one or more of the nucleotide analogs is selected from the group consisting of constrained ethyl nucleoside (cEt), 2',4'-

constrained 2'-O-methoxyethyl (cMOE), α -L-LNA, β -D-LNA, 2'-O,4'-C-ethylene-bridged nucleic acids (ENA), amino-LNA, oxy-LNA, thio-LNA, and any combination thereof.

18. The extracellular vesicle of any one of claims 1 to 17, wherein the ASO comprises one or more 5'-methyl-cytosine nucleobases.
19. The extracellular vesicle of any one of claims 10 to 18, wherein the contiguous nucleotide sequence is complementary to a nucleic acid sequence within (i) a 5' untranslated region (UTR); (ii) a coding region; or (iii) a 3' UTR of the *STAT3* transcript.
20. The extracellular vesicle of any one of claims 1 to 19, wherein the contiguous nucleotide sequence in the ASO is complementary to a nucleic acid sequence comprising (i) nucleotides 151 – 745 of SEQ ID NO: 3; (ii) nucleotides 642-1331 of SEQ ID NO: 3; (iii) nucleotides 1031 - 1704 of SEQ ID NO: 3; (iv) nucleotides 1521 – 2335 of SEQ ID NO: 3; (v) 2062 – 2776 of SEQ ID NO: 3, (vi) nucleotides 251 – 645 of SEQ ID NO: 3; (vii) nucleotides 742-1231 of SEQ ID NO: 3; (viii) nucleotides 1131 - 1604 of SEQ ID NO: 3; (ix) nucleotides 1621 – 2235 of SEQ ID NO: 3; (x) 2162 – 2676 of SEQ ID NO: 3; (xi) nucleotides 301 - 595 of SEQ ID NO: 3; (xii) nucleotides 792 - 1181 of SEQ ID NO: 3; (xiii) nucleotides 1181 - 1554 of SEQ ID NO: 3; (xiv) nucleotides 1671 - 2185 of SEQ ID NO: 3; (xv) 2212 - 2626 of SEQ ID NO: 3; (xvi) nucleotides 341 - 555 of SEQ ID NO: 3; (xvii) nucleotides 832 - 1141 of SEQ ID NO: 3; (xviii) nucleotides 1221 - 1514 of SEQ ID NO: 3; (xix) nucleotides 1711 - 2145 of SEQ ID NO: 3; or (xx) 2252 - 2586 of SEQ ID NO: 3.
21. The extracellular vesicle of any one of claims 1 to 20, wherein the contiguous nucleotide sequence is complementary to a nucleic acid sequence within (i) nucleotides 351 - 545 of SEQ ID NO: 3; (ii) nucleotides 842 - 1131 of SEQ ID NO: 3; (iii) nucleotides 1231 - 1504 of SEQ ID NO: 3; (iv) nucleotides 1721 - 2135 of SEQ ID NO: 3; or (v) 2262 - 2576 of SEQ ID NO: 3.
22. The extracellular vesicle of any one of claims 1 to 21, wherein the contiguous nucleotide sequence comprises a nucleotide sequence complementary to a sequence selected from the sequences in FIG. 1.
23. The extracellular vesicle of any one of claims 10 to 22, wherein the continuous nucleotide sequence is fully complementary to a nucleotide sequence within the *STAT3* transcript.

24. The extracellular vesicle of any one of claims 13 to 23, wherein the ASO comprises a nucleotide sequence selected from SEQ ID NOs: 100-199, with one or two mismatches.
25. The extracellular vesicle of any one of claims 1 to 24, wherein the ASO has a design selected from the group consisting of the designs in FIG. 1, wherein the upper case letter is a sugar modified nucleoside and the lower case letter is DNA.
26. The extracellular vesicle of any one of claims 1 to 25, wherein the ASO is from 14 to 20 nucleotides in length.
27. The extracellular vesicle of any one of claims 10 to 26, wherein the contiguous nucleotide sequence comprises one or more modified internucleoside linkages.
28. The extracellular vesicle of claim 27, wherein the one or more modified internucleoside linkages is a phosphorothioate linkage.
29. The extracellular vesicle of claim 27 or 28, wherein at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of internucleoside linkages are modified.
30. The extracellular vesicle of claim 29, wherein each of the internucleoside linkages in the ASO is a phosphorothioate linkage.
31. The extracellular vesicle of any one of claims 1 to 30, which further comprises an anchoring moiety.
32. The extracellular vesicle of claim 31, wherein the STAT3 antagonist is linked to the anchoring moiety.
33. The extracellular vesicle of any one of claims 1 to 32, further comprising an exogenous targeting moiety.
34. The extracellular vesicle of claim 33, wherein the exogenous targeting moiety comprises a peptide, an antibody or an antigen-binding fragment thereof, a chemical compound, or any combination thereof.
35. The extracellular vesicle of claim 33 or 34, wherein the exogenous targeting moiety comprises a peptide.

36. The extracellular vesicle of any one of claims 33 to 35, wherein the exogenous targeting moiety comprises a microprotein, a designed ankyrin repeat protein (darpin), an anticalin, an adnectin, an aptamer, a peptide mimetic molecule, a natural ligand for a receptor, a camelid nanobody, or any combination thereof.
37. The extracellular vesicle of any one of claims 33 to 36, wherein the exogenous targeting moiety comprises a full-length antibody, a single domain antibody, a heavy chain only antibody (VHH), a single chain antibody, a shark heavy chain only antibody (VNAR), an scFv, a Fv, a Fab, a Fab', a F(ab')₂, or any combination thereof.
38. The extracellular vesicle of claim 37, wherein the antibody is a single chain antibody.
39. The extracellular vesicle of any one of claims 33 to 36, wherein the exogenous targeting moiety targets the exosome to the liver, heart, lungs, brain, kidneys, central nervous system, peripheral nervous system, muscle, bone, or any combination thereof.
40. The extracellular vesicle of any one of claims 33 to 39, wherein the exogenous targeting moiety targets the exosome to a tumor cell, dendritic cell, T cell, B cell, macrophage, neuron, hepatocyte, hematopoietic stem cell, or any combination thereof.
41. The extracellular vesicle of any one of claims 33 to 40, wherein the exogenous targeting moiety binds to CD33 or a fragment thereof.
42. The extracellular vesicle of any one of claims 33 to 41, wherein the EV comprises a scaffold moiety linking the exogenous targeting moiety to the EV.
43. The extracellular vesicle of any one of claims 31 to 42, wherein the anchoring moiety and/or the scaffold moiety is a Scaffold X.
44. The extracellular vesicle of any one of claims 31 to 42, wherein the anchoring moiety and/or the scaffold moiety is a Scaffold Y.
45. The extracellular vesicle of claim 43, wherein the Scaffold X is a scaffold protein that is capable of anchoring the STAT3 antagonist on the luminal surface of the EV and/or on the exterior surface of the EV.

46. The extracellular vesicle of claim 43 or 45, wherein the Scaffold X is selected from the group consisting of prostaglandin F2 receptor negative regulator (the PTGFRN protein); basigin (the BSG protein); immunoglobulin superfamily member 2 (the IGSF2 protein); immunoglobulin superfamily member 3 (the IGSF3 protein); immunoglobulin superfamily member 8 (the IGSF8 protein); integrin beta-1 (the ITGB1 protein); integrin alpha-4 (the ITGA4 protein); 4F2 cell-surface antigen heavy chain (the SLC3A2 protein); a class of ATP transporter proteins (the ATP1A1, ATP1A2, ATP1A3, ATP1A4, ATP1B3, ATP2B1, ATP2B2, ATP2B3, ATP2B4 proteins); a functional fragment thereof; and any combination thereof.
47. The extracellular vesicle of any one of claims 31 to 46, wherein the anchoring moiety and/or the scaffold moiety is PTGFRN protein or a functional fragment thereof.
48. The extracellular vesicle of any one of claims 31 to 47, wherein the anchoring moiety and/or the scaffold moiety comprises an amino acid sequence as set forth in SEQ ID NO: 302.
49. The extracellular vesicle of any one of claims 31 to 48, wherein the anchoring moiety and/or the scaffold moiety comprises an amino acid sequence at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or about 100% identical to SEQ ID NO: 301.
50. The extracellular vesicle of claim 44, wherein the Scaffold Y is a scaffold protein that is capable of anchoring the STAT3 antagonist on the luminal surface of the EV and/or on the exterior surface of the EV.
51. The extracellular vesicle of claim 44 or 50, wherein the Scaffold Y is selected from the group consisting of myristoylated alanine rich Protein Kinase C substrate (the MARCKS protein), myristoylated alanine rich Protein Kinase C substrate like 1 (the MARCKSL1 protein), brain acid soluble protein 1 (the BASP1 protein), a functional fragment thereof, and any combination thereof.
52. The extracellular vesicle of any one of claims 44, 50, and 51, wherein the Scaffold Y is a BASP1 protein or a functional fragment thereof.

53. The extracellular vesicle of any one of claims 44 and 50 to 52, wherein the Scaffold Y comprises an N terminus domain (ND) and an effector domain (ED), wherein the ND and/or the ED are associated with the luminal surface of the EV.
54. The extracellular vesicle of claim 53, wherein the ND is associated with the luminal surface of the exosome via myristoylation.
55. The extracellular vesicle of claim 53 or 54, wherein the ED is associated with the luminal surface of the exosome by an ionic interaction.
56. The extracellular vesicle of any one of claims 53 to 55, wherein the ED comprises (i) a basic amino acid or (ii) two or more basic amino acids in sequence, wherein the basic amino acid is selected from the group consisting of Lys, Arg, His, and any combination thereof.
57. The extracellular vesicle of claim 56, wherein the basic amino acid is (Lys)_n, wherein n is an integer between 1 and 10.
58. The extracellular vesicle of any one of claims 53 to 57, wherein the ED comprises Lys (K), KK, KKK, KKKK (SEQ ID NO: 405), KKKKK (SEQ ID NO: 406), Arg (R), RR, RRR, RRRR (SEQ ID NO: 407); RRRRR (SEQ ID NO: 408), KR, RK, KKR, KRK, RKK, KRR, RRK, (K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 409), (K/R)(K/R)(K/R)(K/R)(K/R) (SEQ ID NO: 410), or any combination thereof.
59. The extracellular vesicle of any one of claims 53 to 58, wherein the ND comprises the amino acid sequence as set forth in G:X₂:X₃:X₄:X₅:X₆, wherein G represents Gly; wherein ":" represents a peptide bond, wherein each of the X₂ to the X₆ is independently an amino acid, and wherein the X₆ comprises a basic amino acid.
60. The extracellular vesicle of claim 59, wherein:
- (i) the X₂ is selected from the group consisting of Pro, Gly, Ala, and Ser;
 - (ii) the X₄ is selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln and Met;
 - (iii) the X₅ is selected from the group consisting of Pro, Gly, Ala, and Ser;

- (iv) the X6 is selected from the group consisting of Lys, Arg, and His; or
 - (v) any combination of (i)–(iv).
61. The extracellular vesicle of any one of claims 53 to 60, wherein the ND comprises the amino acid sequence of G:X2:X3:X4:X5:X6, wherein
- (i) G represents Gly;
 - (ii) ":" represents a peptide bond;
 - (iii) the X2 is an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser;
 - (iv) the X3 is an amino acid;
 - (v) the X4 is an amino acid selected from the group consisting of Pro, Gly, Ala, Ser, Val, Ile, Leu, Phe, Trp, Tyr, Gln and Met;
 - (vi) the X5 is an amino acid selected from the group consisting of Pro, Gly, Ala, and Ser; and
 - (vii) the X6 is an amino acid selected from the group consisting of Lys, Arg, and His.
62. The extracellular vesicle of any one of claims 59 to 61, wherein the X3 is selected from the group consisting of Asn, Gln, Ser, Thr, Asp, Glu, Lys, His, and Arg.
63. The extracellular vesicle of any one of claims 53 to 62, wherein the ND and the ED are joined by a linker.
64. The extracellular vesicle of claim 63, wherein the linker comprises one or more amino acids.
65. The method of any one of claims 53 to 64, wherein the ND comprises an amino acid sequence selected from the group consisting of (i) GGKLSKK (SEQ ID NO: 411), (ii) GAKLSKK (SEQ ID NO: 412), (iii) GGKQSKK (SEQ ID NO: 413), (iv) GGKLAKK (SEQ ID NO: 414), (v) GGKLSK (SEQ ID NO: 415), or (vi) any combination thereof.
66. The extracellular vesicle of claim 65, wherein the ND comprises an amino acid sequence selected from the group consisting of (i) GGKLSKKK (SEQ ID NO: 438), (ii) GGKLSKKS

(SEQ ID NO: 439), (iii) GAKLSKKK (SEQ ID NO: 440), (iv) GAKLSKKS (SEQ ID NO: 441), (v) GGKQSKKK (SEQ ID NO: 442), (vi) GGKQSKKS (SEQ ID NO: 443), (vii) GGKLAKKK (SEQ ID NO: 444), (viii) GGKLAKKS (SEQ ID NO: 445), and (ix) any combination thereof.

67. The extracellular vesicle of any one of claims 53 to 66, wherein the ND comprises the amino acid sequence GGKLSKK (SEQ ID NO: 411).
68. The extracellular vesicle of any one of claims 43 and 50 to 67, wherein the Scaffold Y is at least about 8, at least about 9, at least about 10, at least about 11, at least about 12, at least about 13, at least about 14, at least about 15, at least about 16, at least about 17, at least about 18, at least about 19, at least about 20, at least about 21, at least about 22, at least about 23, at least about 24, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 55, at least about 60, at least about 65, at least about 70, at least about 75, at least about 80, at least about 85, at least about 90, at least about 95, at least about 100, at least about 105, at least about 110, at least about 120, at least about 130, at least about 140, at least about 150, at least about 160, at least about 170, at least about 180, at least about 190, or at least about 200 amino acids in length.
69. The extracellular vesicle of claims 44 and 50 to 68, wherein the Scaffold Y comprises (i) GGKLSKKKKKGYNVN (SEQ ID NO: 446), (ii) GAKLSKKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKKGYS GG (SEQ ID NO: 450), (vi) GGKLSKKKKKSGGGS (SEQ ID NO: 451), (vii) GGKLSKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 454), (x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456).
70. The extracellular vesicle of claims 44 and 50 to 69, wherein the Scaffold Y consists of (i) GGKLSKKKKKGYNVN (SEQ ID NO: 446), (ii) GAKLSKKKKKGYNVN (SEQ ID NO: 447), (iii) GGKQSKKKKGYNVN (SEQ ID NO: 448), (iv) GGKLAKKKKGYNVN (SEQ ID NO: 449), (v) GGKLSKKKKKGYS GG (SEQ ID NO: 450), (vi) GGKLSKKKKKSGGGS (SEQ ID NO: 451), (vii) GGKLSKKKKSGGSG (SEQ ID NO: 452), (viii) GGKLSKKKSGGSGG (SEQ ID NO: 453), (ix) GGKLSKKSGGSGGS (SEQ ID NO: 454),

(x) GGKLSKSGGSGGSV (SEQ ID NO: 455), or (xi) GAKKSKKRFSFKKS (SEQ ID NO: 456).

71. The extracellular vesicle of claim 44 and 50 to 70, wherein the Scaffold Y does not comprise Met at the N terminus.
72. The extracellular vesicle of any one of claims 44 and 50 to 71, wherein the Scaffold Y comprises a myristoylated amino acid residue at the N terminus of the scaffold protein.
73. The extracellular vesicle of claim 72, wherein the amino acid residue at the N terminus of the Scaffold Y is Gly.
74. The extracellular vesicle of any one of claims 31 to 73, wherein the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety on the exterior of the EV.
75. The extracellular vesicle of any one of claims 31 to 74, wherein the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety on the luminal surface of the EV.
76. The extracellular vesicle of any one of claims 31 to 75, wherein the anchoring moiety comprises sterol, GM1, a lipid, a vitamin, a small molecule, a peptide, or a combination thereof.
77. The extracellular vesicle of any one of claims 31 to 75, wherein the anchoring moiety comprises cholesterol.
78. The extracellular vesicle of any one of claims 31 to 75, wherein the anchoring moiety comprises a phospholipid, a lysophospholipid, a fatty acid, a vitamin (e.g., vitamin D and/or vitamin E), or any combination thereof.
79. The extracellular vesicle of any one of claims 31 to 78, wherein the STAT3 ASO is linked to the anchoring moiety and/or the scaffold moiety by a linker.
80. The extracellular vesicle of any one of claims 1 to 79, wherein the STAT3 ASO is linked to the EV by a linker.
81. The extracellular vesicle of claim 79 or 80, wherein the linker is a polypeptide.
82. The extracellular vesicle of claim 79 or 80, wherein the linker is a non-polypeptide moiety.

83. The extracellular vesicle of claim 79 or claim 80, wherein the linker comprises ethylene glycol.
84. The extracellular vesicle of claim 79 or claim 80, wherein the linker comprises HEG, TEG, PEG, or any combination thereof.
85. The extracellular vesicle of claim 79 or 80, wherein the linker comprises acrylic phosphoramidite (e.g., ACRYDITE™), adenylation, azide (NHS Ester), digoxigenin (NHS Ester), cholesterol-TEG, I-LINKER™, an amino modifier (e.g., amino modifier C6, amino modifier C12, amino modifier C6 dT, or Uni-Link™ amino modifier), alkyne, 5' Hexynyl, 5-Octadiynyl dU, biotinylation (e.g., biotin, biotin (Azide), biotin dT, biotin-TEG, dual biotin, PC biotin, or desthiobiotin), thiol modification (thiol modifier C3 S-S, dithiol or thiol modifier C6 S-S), or any combination thereof.
86. The extracellular vesicle of any one of claims 79 to 85, wherein the linker is a cleavable linker.
87. The extracellular vesicle of claim 86, wherein the linker comprises valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate.
88. The extracellular vesicle of any one of claims 76 to 87, wherein the linker comprises (i) a maleimide moiety and (ii) valine-alanine-p-aminobenzylcarbamate or valine-citrulline-p-aminobenzylcarbamate.
89. The extracellular vesicle of any one of claims 1 to 88, wherein the EV is an exosome.
90. An antisense oligonucleotide (ASO) comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length that is complementary to a nucleic acid sequence within nucleotides 1 to 56982 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 57003 to 75171 of a *STAT3* transcript corresponding to SEQ ID NO: 1, nucleotides 1 to 1287 of a *STAT3* transcript corresponding to SEQ ID NO: 3, or nucleotides 1306 to 2787 of a *STAT3* transcript corresponding to SEQ ID NO: 3.
91. The ASO of claim 90, wherein the contiguous nucleotide sequence thereof is at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% complementary to the nucleic acid sequence within the *STAT3* transcript.

92. The ASO of claim 90 or 91, which is capable of reducing STAT3 protein expression in a human cell (*e.g.*, HEK293 cell), wherein the human cell expresses the STAT3 protein.
93. The ASO of claim 92, wherein the STAT3 protein expression is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to STAT3 protein expression in a human cell that is not exposed to the ASO.
94. The ASO of any one of claims 90 to 93, which is capable of reducing a level of STAT3 mRNA in a human cell (*e.g.*, HEK293 cell), wherein the human cell expresses the *STAT3* mRNA.
95. The ASO of claim 94, wherein the level of *STAT3* mRNA is reduced by at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100% compared to the level of the *STAT3* mRNA in a human cell that is not exposed to the ASO.
96. The ASO of any one of claims 90 to 95, which is a gapmer, a mixmer, or a totalmer.
97. The ASO of any one of claims 90 to 95, which comprises one or more nucleoside analogs.
98. The ASO of claim 97, wherein one or more of the nucleoside analogs comprises a 2'-O-alkyl-RNA; 2'-O-methyl RNA (2'-OMe); 2'-alkoxy-RNA; 2'-O-methoxyethyl-RNA (2'-MOE); 2'-amino-DNA; 2'-fluoro-RNA; 2'-fluoro-DNA; arabino nucleic acid (ANA); 2'-fluoro-ANA; or bicyclic nucleoside analog (LNA).
99. The ASO of claim 97 or 98, wherein one or more of the nucleoside analogs is a sugar modified nucleoside.
100. The ASO of claim 99, wherein the sugar modified nucleoside is an affinity enhancing 2' sugar modified nucleoside.
101. The ASO of any one of claims 97 to 100, wherein one or more of the nucleoside analogs comprises a nucleoside comprising a bicyclic sugar.

102. The ASO of any one of claims 97 to 100, wherein one or more of the nucleoside analogs comprises an LNA.
103. The ASO of claim 102, wherein the LNA is selected from the group consisting of constrained ethyl nucleoside (cEt), 2',4'-constrained 2'-O-methoxyethyl (cMOE), α -L-LNA, β -D-LNA, 2'-O,4'-C-ethylene-bridged nucleic acids (ENA), amino-LNA, oxy-LNA, thio-LNA, and any combination thereof.
104. The ASO of any one of claims 90 to 103, which comprises one or more 5'-methyl-cytosine nucleobases.
105. The ASO of any one of claims 90 to 104, wherein the ASO comprises any one of SEQ ID NO: 100 to SEQ ID NO: 199.
106. The ASO of any one of claims 90 to 105, wherein the ASO has a design selected from the group consisting of the designs in FIs. 1, wherein the upper letter is a sugar modified nucleoside and the lower case letter is DNA.
107. The ASO of any one of claims 90 to 106, wherein the ASO is from 14 to 20 nucleotides in length.
108. The ASO of any one of claims 90 to 107, wherein the contiguous nucleotide sequence comprises one or more modified internucleoside linkages.
109. The ASO of claim 108, wherein the one or more modified internucleoside linkages is a phosphorothioate linkage.
110. The ASO of claim 108 or 109, wherein at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of internucleoside linkages are modified.
111. The ASO of claim 110, wherein each of the internucleoside linkages in the ASO is a phosphorothioate linkage.
112. A conjugate comprising the ASO of any one of claims 90 to 111, wherein the ASO is covalently attached to at least one non-nucleotide or non-polynucleotide moiety.

113. The conjugate of claim 112, wherein the non-nucleotide or non-polynucleotide moiety comprises a protein, a fatty acid chain, a sugar residue, a glycoprotein, a polymer, or any combinations thereof.
114. An extracellular vesicle comprising the ASO of any one of claims 90 to 111 or the conjugate of claim 112 or 113.
115. A pharmaceutical composition comprising the extracellular vesicle of any one of claims 1 to 89 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 113, and a pharmaceutically acceptable diluent, carrier, salt, or adjuvant.
116. The pharmaceutical composition of claim 115, wherein the pharmaceutically acceptable salt comprises a sodium salt, a potassium salt, an ammonium salt, or any combination thereof.
117. The pharmaceutical composition of claim 115 or 116, which further comprises at least one additional therapeutic agent.
118. The pharmaceutical composition of claim 117, wherein the additional therapeutic agent is an STAT3 antagonist.
119. The pharmaceutical composition of claim 118, wherein the STAT3 antagonist is a chemical compound, an siRNA, an shRNA, an antisense oligonucleotide, a protein, or any combination thereof.
120. The pharmaceutical composition of claim 118 or 119, wherein the STAT3 antagonist is an anti- STAT3 antibody or fragment thereof.
121. A kit comprising the extracellular vesicle of any one of claims 1 to 89 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 113, or a pharmaceutical composition of any one of claims 115 to 120, and instructions for use.
122. A diagnostic kit comprising the extracellular vesicle of any one of claims 1 to 90 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 113, or a pharmaceutical composition of any one of claims 115 to 120, and instructions for use.
123. A method of inhibiting or reducing STAT3 protein expression in a cell, comprising administering the extracellular vesicle of any one of claims 1 to 89 and 114, the ASO of any

one of claims 90 to 111, or the conjugate of claim 112 or 113, or a pharmaceutical composition of any one of claims 115 to 120 to the cell expressing STAT3 protein, wherein the STAT3 protein expression in the cell is inhibited or reduced after the administration.

124. The method of claim 123, wherein the ASO inhibits or reduces expression of *STAT3* or mRNA in the cell after the administration.
125. The method of claim 124, wherein a level of *STAT3* mRNA is reduced by at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or about 100% after the administration compared to the level of *STAT3* mRNA in a cell not exposed to the ASO.
126. The method of any one of claims 123 to 125, wherein the expression of STAT3 or protein is reduced by at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% after the administration compared to the expression of STAT3 protein in a cell not exposed to the ASO.
127. A method of treating a cancer in a subject in need thereof, comprising administering an effective amount of the extracellular vesicle of any one of claims 1 to 89 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 114, or a pharmaceutical composition of any one of claims 115 to 120 to the subject.
128. Use of the extracellular vesicle of any one of claims 1 to 89 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 113, or a pharmaceutical composition of any one of claims 115 to 120 in the manufacture of a medicament for the treatment of a cancer in a subject in need thereof.
129. The extracellular vesicle of any one of claims 1 to 90 and 114, the ASO of any one of claims 90 to 111, or the conjugate of claim 112 or 113, or a pharmaceutical composition of any one of claims 115 to 120 for use in the treatment of a cancer in a subject in need thereof.
130. The method of any one of claims 122 to 127, the use of claim 128, or the composition for use of claim 129, wherein the extracellular vesicle, the ASO, the conjugate, or the pharmaceutical

composition is administered intracardially, orally, parenterally, intrathecally, intracerebroventricularly, pulmorarily, topically, or intraventricularly.

131. The method of claim 127, the use of claim 128, or the composition for use of claim 136, wherein the cancer is selected from the group consisting of fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell cancer, squamous cell cancer of the head and neck cancer, colorectal cancer, lymphoma, leukemia, liver cancer, glioblastoma, melanoma, myeloma basal cell cancer, adenocarcinoma, sweat gland cancer, sebaceous gland cancer, papillary cancer, papillary adenocarcinomas, cystadenocarcinoma, medullary cancer, bronchogenic cancer, renal cell cancer, hepatoma, bile duct cancer, choriocarcinoma, seminoma, embryonal cancer, Wilms' tumor, cervical cancer, testicular cancer, lung cancer, small cell lung cancer, bladder cancer, epithelial cancer, glioma, glioblastoma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma, acute myeloid leukemia, hepatocellular carcinoma, and any combination thereof.

FIG. 1

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Mb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51545	ASO-STAT3 - 2559	GGTAGGCGCCTCAGTCG	100	17	2559	2576	GbsCbsTbsdAsdGsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsTbsCbsGb
X51613	ASO-STAT3 - 2556	GGTAGGCGCCTCAGTCG TAT	101	20	2556	2576	GbsCbsTbsAmsGmsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsdTsCmsGm sTbsAbsTb
X51614	ASO-STAT3 - 2557	AGGTAGGCGCCTCAGTC GTA	102	20	2557	2577	AbsCbsGbsTmsAmsdGsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsTmsCm sGbsTbsAb
X51518	ASO-STAT3 - 1046	ATTGTGTGACGGGTC	103	15	1046	1061	AbsTbsTbsdTsdGsdTsdTsdGsdAs (5MdC) sdGsdGsGbsTbsCb
X51546	ASO-STAT3 - 351	GATTCTTTGCTGGCCGC ATA	104	20	351	371	GbsAbsTbsTmsCmsdTsdTsdTsdGs (5MdC) sdTsdGsdGs (5MdC) s (5MdC) sGmsCmsAbs TbsAb
X51549	ASO-STAT3 - 450	CGTAGATTGTGCTGATA GAG	105	20	450	470	CbsCbsTbsAmsGmsdAsdTsdTsdGsdTsdGs (5MdC) sdTsdGsdAsTmsAmsGbsAbsGb
X51544	ASO-STAT3 - 2558	GTAGGCGCCTCAGTCGT	106	17	2558	2575	GbsTbsAbsdGsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsdTsCbsGbsTb
X51615	ASO-STAT3 - 2558	CAGGTAGGCGCCTCAGT CGT	107	20	2558	2578	CbsAbsGbsGmsTmsdAsdGsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsGmsTm sCbsGbsTb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51565	ASO-STAT3-865	CGCCAGCTCACTCACGA TGC	108	20	865	885	CbsGbsCbsCmsAmsdGs (5MdC) sdTs (5MdC) sdAs (5MdC) sG msAmsTbsGbsCb
X51529	ASO-STAT3-894	CGTACTCCATCGCTGA	109	16	894	910	CbsGbsTbsdAs (5MdC) sdTs (5MdC) s (5MdC) sdAsdTs (5MdC) sdGs (5MdC) sTbsGbsA
X51596	ASO-STAT3-1778	TAGTCAGCTGCTCGATG CTC	110	20	1778	1798	TbsAbsGbsTmsCmsdAsdGs (5MdC) sdTsdGs s (5MdC) sdTs (5MdC) sdGsdsAsTmsGmsCbs TbsCb
X51536	ASO-STAT3-2558	TAGCGCCTCAGTCGT	111	16	2558	2574	TbsAbsGbsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAedGsdTsCbsGbsTb
X51535	ASO-STAT3-1482	CACAATTGGCTCGGCC	112	16	1482	1498	CbsAbsCbsdAsdAsdTsdsdGsdGs (5MdC) sdTs (5MdC) sdGsGbsCbsCb
X51571	ASO-STAT3-892	CACGTACTCCATCGCTG ACA	113	20	892	912	CbsAbsCbsGmsTmsdAs (5MdC) sdTs (5MdC) s (5MdC) sdAsdTs (5MdC) sdGs (5MdC) sT msGmsAbsCbsAb
X51602	ASO-STAT3-2262	CGACAATACTTTCCGAA TGC	114	20	2262	2282	CbsGbsAbsCmsAmsdAsdTsds (5MdC) sdT sdTsdTs (5MdC) s (5MdC) sdGsAmsAmsTbs GbsCb
X51525	ASO-STAT3-2267	CGACAATACTTTCCG	115	15	2267	2282	CbsGbsAbs (5MdC) sdAsdAsdTsds (5MdC)) sdTsdTsdsCbsCbsGb
X51548	ASO-STAT3-411	AAGCGGCTATACTGCTG GTC	116	20	411	431	AbsAbsGbsCmsGmsdGs (5MdC) sdTsdAsdT sdAs (5MdC) sdTsdsGs (5MdC) sTmsGmsGbs TbsCb
X51542	ASO-STAT3-2267	GCCGACAATACTTTCCG	117	17	2267	2284	GbsCbsCbsdGsdAs (5MdC) sdAsdAsdTsdA s (5MdC) sdTsdTsdsCbsCbsGb
X51516	ASO-STAT3-896	ACGTACTCCATCGCT	118	15	896	911	AbsCbsGbsdTsds (5MdC) sdTs (5MdC) s (5MdC) sdAsdTs (5MdC) sGbsCbsTb
X51612	ASO-STAT3-2555	GTAGGCGCCTCAGTCGT ATC	119	20	2555	2575	GbsTbsAbsGmsGms (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsdTs (5MdC) sG msTmsAbsTbsCb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51562	ASO-STAT3-525	AGGCACCGGGCCACAAT CCG	120	20	525	545	AbsGbsGbsCmsAms (5MdC) s (5MdC) sdGsdGsdGs (5MdC) s (5MdC) sdAs (5MdC) sdAsAmsTmsCbsCbsGb
X51595	ASO-STAT3-1766	CGATGCTCAGTCTCGC TTG	121	20	1766	1786	CbsGbsAbsTmsGms (5MdC) sdTs (5MdC) sdA sdGsdTs (5MdC) s (5MdC) sdTs (5MdC) sGmsCmsTbsTbsGb
X51531	ASO-STAT3-1114	ATCGGCGGCTGCTGTA	122	16	1114	1130	AbsTbsCbsdGsdGs (5MdC) s (5MdC) sdGsdGsdTs (5MdC) s (5MdC) sdTsGbsTbsAb
X51543	ASO-STAT3-2557	TAGGCGCCTCAGTCGTA	123	17	2557	2574	TbsAbsGbsdGs (5MdC) sdGs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsdTs (5MdC) sGbsTbsAb
X51576	ASO-STAT3-995	AGTTTCTAGCCGATCT AGG	124	20	995	1015	AbsGbsTbsTmsTmsdTs (5MdC) sdTsAdsdGs (5MdC) s (5MdC) sdGsdAsdTsCmsTmsAbsGb sGb
X51603	ASO-STAT3-2263	CCGACAATACTTTCCGA ATG	125	20	2263	2283	CbsCbsGbsAmsCmsdAsdAsdTsdsAs (5MdC) s dTsAdTs (5MdC) s (5MdC) sGmsAmsAbsTb sGb
X51553	ASO-STAT3-511	AATCCGGGCAATCTCCA TTG	126	20	511	531	AbsAbsTbsCmsCmsdGsdGsdGs (5MdC) sdAs dAsdTs (5MdC) sdTs (5MdC) sCmsAmsTbsTb sGb
X51528	ASO-STAT3-511	CGGGCAATCTCCATTG	127	16	511	527	CbsGbsGbsdGs (5MdC) sdAsdAsdTs (5MdC) sdTs (5MdC) s (5MdC) sdAsTbsTbsGb
X51579	ASO-STAT3-1043	TAATTGTTGACGGGTC TGA	128	20	1043	1063	TbsAbsAbsTmsTmsdTsAdTsAdTsAdTsAdTsAdTs (5MdC) sdGsdGsdGsTmsCmsTbsGbsAb
X51598	ASO-STAT3-1780	TGTAGTCAGCTGCTCGA TGC	129	20	1780	1800	TbsGbsTbsAmsGmsdTs (5MdC) sdAsdGs (5MdC) sdTs (5MdC) sGmsAmsTbsGbsCb
X51550	ASO-STAT3-458	TGATTTCTTCGTAGATTG TGC	130	20	458	478	TbsGbsAbsTmsTms (5MdC) sdTsAdTs (5MdC) sdGsdTsAdGsAdTsTmsGmsTbsGbsCb
X51538	ASO-STAT3-894	ACGTACTCCATCGCTGA	131	17	894	911	AbsCbsGbsdTsdsAs (5MdC) sdTs (5MdC) s (5MdC) sdAsdTs (5MdC) sdGs (5MdC) sTbsGbsAb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51597	ASO-STAT3-1779	GTAGTCAGCTGCTCGAT GCT	132	20	1779	1799	GbsTbsAbsGmsTms (5MdC) sdAsdGs (5MdC) sdTsdGs (5MdC) sdTs (5MdC) sdGsAmsTmsGbsCbsTb
X51609	ASO-STAT3-2274	TGGCTCTCTGGCCGACA ATA	133	20	2274	2294	TbsGbsGbsCmsTms (5MdC) sdTs (5MdC) sdTsdGs (5MdC) s (5MdC) sdGsdAsCmsAmsAbsTbsAb
X51578	ASO-STAT3-1039	TTGTTGACGGTCTGAA GTT	134	20	1039	1059	TbsTbsGbsTmsTmsdGsdAs (5MdC) sdGsdGs dGsdTs (5MdC) sdTsdGsAmsAmsGbsTbsTb
X51588	ASO-STAT3-1238	TAGTGAACCTGACGCCG GTC	135	20	1238	1258	TbsAbsGbsTmsGmsdAsdAs (5MdC) sdTsdGs dGsdAs (5MdC) sdGs (5MdC) sCmsGmsGbsTb sCb
X51589	ASO-STAT3-1239	GTAGTGAACCTGGACGCC GGT	136	20	1239	1259	GbsTbsAbsGmsTmsdGsdAsdAs (5MdC) sdTs dGsdGsdAs (5MdC) sdGsCmsCmsGbsTb
X51555	ASO-STAT3-516	GCCACAATCCGGGCAAT CTC	137	20	516	536	GbsCbsCbsAmsCmsdAsdAsdTs (5MdC) s (5MdC) sdGsdGsdGs (5MdC) sdAsAmsTmsCbsTb sCb
X51534	ASO-STAT3-1238	GAACTGGACGCCGGTC	138	16	1238	1254	GbsAbsAbs (5MdC) sdTsdGsdGsdAs (5MdC) sdGs (5MdC) s (5MdC) sdGsGbsTbsCb
X51577	ASO-STAT3-1034	GACGGGTCTGAAGTTGA GAT	139	20	1034	1054	GbsAbsCbsGmsGmsdGsdTs (5MdC) sdTsdGs dAsdAsdGsdTsdTsGmsAmsGbsAbsTb
X51524	ASO-STAT3-1239	GAACTGGACGCCGGT	140	15	1239	1254	GbsAbsAbs (5MdC) sdTsdGsdGsdAs (5MdC) sdGs (5MdC) s (5MdC) sGbsGbsTb
X51539	ASO-STAT3-1113	ATCGGCCGGTCTGTGTAC	141	17	1113	1130	AbsTbsCbsdGsdGs (5MdC) s (5MdC) sdGsdGsdTs (5MdC) sdTsdGsTbsAbsCb
X51593	ASO-STAT3-1484	AAGCATCACAAATTGGCT CGG	142	20	1484	1504	AbsAbsGbsCmsAmsdTs (5MdC) sdAs (5MdC) sdAsdAsdTsTsdGsdGsCmsTmsCbsGbsGb
X51526	ASO-STAT3-2556	GCGCCTCAGTCGTAT	143	15	2556	2571	GbsCbsGbs (5MdC) s (5MdC) sdTs (5MdC) sdAsdGsTs (5MdC) sdGsTbsAbsTb
X51551	ASO-STAT3-461	GCTTGATTCCTCGTAGA TTG	144	20	461	481	GbsCbsTbsTmsGmsdAsdTs (5MdC) sdTs dTs (5MdC) sdGsdTsdAsGmsAmsTbsTbsGb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51608	ASO-STAT3-2273	GGCTCTCTGCGGACAA TAC	145	20	2273	2293	GbsGbsCbsTmsCmsdTts (5MdC) sdTsdGsdGs (5MdC) s (5MdC) sdGsdAs (5MdC) sAmsAmst bsAbsCb
X51599	ASO-STAT3-1783	CAGTGTAGTCAGCTGCT CGA	146	20	1783	1803	CbsAbsGbsTmsGmsdTsdAsdGsdTts (5MdC) s dAsdGs (5MdC) sdTsdGsCmsTmsCbsGbsAb
X51570	ASO-STAT3-891	ACGTACTCCATCGCTGA CAA	147	20	891	911	AbsCbsGbsTmsAms (5MdC) sdTts (5MdC) s (5MdC) sdAsdTts (5MdC) sdGs (5MdC) sdTtsGms AmsCbsAbsAb
X51552	ASO-STAT3-510	ATCGGGCAATCTCCAT TGG	148	20	510	530	AbsTbsCbsCmsGmsdGsdGs (5MdC) sdAsdAs dTts (5MdC) sdTts (5MdC) s (5MdC) sAmsTmsT bsgbsGb
X51601	ASO-STAT3-2115	GGTTCACGACTGGAT CTG	149	20	2115	2135	GbsGbsTbsTmsCms (5MdC) sdAs (5MdC) sdG sdGsdAs (5MdC) sdTsdGsdGsAmsTmsCbsTb sGb
X51592	ASO-STAT3-1482	GCATCACAAATTGGCTCG GCC	150	20	1482	1502	GbsCbsAbsTmsCmsdAs (5MdC) sdAsdAsdTts dTsdGsdGs (5MdC) sdTtsCmsGmsCbsCbsCb
X51575	ASO-STAT3-986	GCCGATCTAGCAGATG TTG	151	20	986	1006	GbsCbsCbsGmsAmsdTts (5MdC) sdTsdAsdGs dGs (5MdC) sdAsdGsdAsTmsGmsTbsTbsGb
X51572	ASO-STAT3-893	GCACGTACTCCATCGCT GAC	152	20	893	913	GbsCbsAbsCmsGmsdTsdAs (5MdC) sdTts (5MdC) s (5MdC) sdAsdTts (5MdC) sdGsCmsTmsG bsAbsCb
X51522	ASO-STAT3-1237	ACTGGACGCGGTCT	153	15	1237	1252	AbsCbsTbsdGsdGsdAs (5MdC) sdGs (5MdC) s (5MdC) sdGsdGsTbsCbsTb
X51585	ASO-STAT3-1111	CATCGCCCGTGCTGTA CAA	154	20	1111	1131	CbsAbsTbsCmsGmsdGs (5MdC) s (5MdC) sdG sdGsdTsdGs (5MdC) sdTsdGsTmsAmsCbsAb sAb
X51532	ASO-STAT3-1236	ACTGGACGCGGTCTT	155	16	1236	1252	AbsCbsTbsdGsdGsdAs (5MdC) sdGs (5MdC) s (5MdC) sdGsdGsdTtsCbsTbsTb
X51527	ASO-STAT3-2557	GGCGCCTCAGTCGTA	156	15	2557	2572	GbsGbsCbsdGs (5MdC) s (5MdC) sdTts (5MdC) sdAsdGsdTts (5MdC) sGbsTbsAb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51604	ASO-STAT3-2264	GCCGACAAATACTTCCG AAT	157	20	2264	2284	GbsCbsCbsGmsAms (5MdC) sdAsdAsdTsdAs (5MdC) sdTsdTsdTs (5MdC) sCmsGmsAbsAb sTb
X51520	ASO-STAT3-1234	GGACGCCGGTCTTGA	158	15	1234	1249	GbsGbsAbs (5MdC) sdGs (5MdC) s (5MdC) sdGsdsTs (5MdC) sdTsTbsGbsAb
X51541	ASO-STAT3-1241	TAGTGAACCTGACGCCG	159	17	1241	1258	TbsAbsGbsdTsdGsdAsdAs (5MdC) sdTsdGs dGsdAs (5MdC) sdGsCbsCbsGb
X51561	ASO-STAT3-524	GGACCCGGGCCACAATC CGG	160	20	524	544	GbsGbsCbsAmsCms (5MdC) sdGsdsGs (5MdC) s (5MdC) sdAs (5MdC) sdAsdAsTmsCmsCbsGb
X51569	ASO-STAT3-890	CGTACTCCATCGCTGAC AAA	161	20	890	910	CbsGbsTbsAmsCmsdTts (5MdC) s (5MdC) sdA sdTs (5MdC) sdGs (5MdC) sdTsdGsAmsCmsA bsaAbsAb
X51540	ASO-STAT3-1114	CATCGCCCGTGCTGTA	162	17	1114	1131	CbsAbsTbs (5MdC) sdGsdsGs (5MdC) s (5MdC)) sdGsdsTsdsGs (5MdC) sdTsCbsTbsAb
X51583	ASO-STAT3-1108	CGGCCGGTGCTGTACAA TGG	163	20	1108	1128	CbsGbsGbsCmsCmsdsGsdTsdsGs (5MdC) s dTsdGsdsTsdsAs (5MdC) sAmsAmsTbsGbsGb
X51547	ASO-STAT3-409	GCGGCTATACTGCTGGT CAA	164	20	409	429	GbsCbsGbsGmsCmsdTsdAsdTsdAs (5MdC) s dTsdGs (5MdC) sdTsdGsGmsTmsCbsAbsAb
X51590	ASO-STAT3-1356	ATGTTAAATTCGGGA TCC	165	20	1356	1376	AbdTbsGbsTmsTmsdsAsdAsdTsdTsdsTs (5MdC) s (5MdC) sdGsdsGmsAmsTbsCbsCb
X51519	ASO-STAT3-1231	CGCCGGTCTTGATGA	166	15	1231	1246	CbsGbsCbs (5MdC) sdGsdsGsdsTs (5MdC) sdTsdGsdsAsTbsGbsAb
X51607	ASO-STAT3-2267	CTGGCCGACAATACTTT CCG	167	20	2267	2287	CbsTbsGbsGmsCms (5MdC) sdGsdsAs (5MdC) sdAsdTsdAs (5MdC) sdTsTmsTmsCbsCb sGb
X51523	ASO-STAT3-1238	AACTGGACGCCGGTC	168	15	1238	1253	AbdAbsCbsdTsdGsdsAs (5MdC) sdGs (5MdC) s (5MdC) sdGsCbsTbsCb
X51533	ASO-STAT3-1237	AACTGGACGCCGGTCT	169	16	1237	1253	AbdAbsCbsdTsdGsdsAs (5MdC) sdGs (5MdC) s (5MdC) sdGsdsTsCbsTb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51560	ASO-STAT3-522	CACCGGGCCACAATCCG GGC	170	20	522	542	CbsAbsCbsCmsGmsdGsdGs (5MdC) s (5MdC) sdAs (5MdC) sdAsdAsTs (5MdC) sCmsGmsGbsCbsCb
X51606	ASO-STAT3-2266	TGGCCGACAATACTTTC CGA	171	20	2266	2286	TbsGbsGbsCmsCmsdGsdAs (5MdC) sdAsdAs dTsAs (5MdC) sdTsTsTmsCmsCbsGbsAb
X51600	ASO-STAT3-1998	GTGCTCAAGATGGCCCG CTC	172	20	1998	2018	GbsTbsGbsCmsTms (5MdC) sdAsdAsdGsdAs dTsGsdGs (5MdC) s (5MdC) sCmsGmsCbsTbs sCb
X51566	ASO-STAT3-881	TCGCTGACAAAAGCCCC GCC	173	20	881	901	TbsCbsGbsCmsTmsdGsdAs (5MdC) sdAsdAs dAsdAsdGs (5MdC) s (5MdC) sCmsCmsGbsCb sCb
X51554	ASO-STAT3-513	ACAATCCGGGCAATCTC CAT	174	20	513	533	AbsCbsAbsAmsTms (5MdC) s (5MdC) sdGsdGsdGs (5MdC) sdAsdAsTs (5MdC) sTmsCmsCbsAbsTbs
X51582	ASO-STAT3-1107	GGCCGGTGTCTGTACAAT GGG	175	20	1107	1127	GbsCbsCbsCmsGmsdGsdTsGds (5MdC) sdTs dGsdTsAs (5MdC) sdAsAmsTmsCbsGbsGb
X51521	ASO-STAT3-1235	TGGACGCCGCTCTTG	176	15	1235	1250	TbsGbsGbsdAs (5MdC) sdGs (5MdC) s (5MdC) sdGsdGsdTs (5MdC) sTbsTbsGb
X51567	ASO-STAT3-882	ATCGCTGACAAAAGCCCC CGC	177	20	882	902	AbsTbsCbsGmsCmsdTsGsdAs (5MdC) sdAs dAsdAsdAsdGs (5MdC) sCmsCmsCbsGbsCb
X51586	ASO-STAT3-1112	GCATCGCCGGTGTGTGT ACA	178	20	1112	1132	GbsCbsAbsTmsCmsdGsdGs (5MdC) s (5MdC) sdGsdGsdTsGds (5MdC) sdTsGmsTmsAbsCb sAb
X51559	ASO-STAT3-521	ACCGGGCCACAATCCCG GCA	179	20	521	541	AbsCbsCbsGmsGmsdGs (5MdC) s (5MdC) sdAs (5MdC) sdAsdAsTs (5MdC) s (5MdC) sGms GmsCbsCbsAb
X51584	ASO-STAT3-1110	ATCGCCGGTGTGTGTAC AAT	180	20	1110	1130	AbsTbsCbsGmsGms (5MdC) s (5MdC) sdGsdGsdTsGds (5MdC) sdTsGsdTsAmsCmsAbsAb sTb
X51591	ASO-STAT3-1475	AATTGGCTCGGCCCCCA TTC	181	20	1475	1495	AbsAbsTbsTmsGmsdGs (5MdC) sdTs (5MdC) sdGsdGs (5MdC) s (5MdC) sCmsAmsTbsTbsCb

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51573	ASO-STAT3-894	TGCACGTA CCAATCGC TGA	182	20	894	914	TbsGbsCbsAmsCmsdGsdTsdAs (5MdC) sdTs (5MdC) s (5MdC) sdAsdTts (5MdC) sGmsCmsTbsGbsAb
X51557	ASO-STAT3-519	CGGGCCACAATCCGGC AAT	183	20	519	539	CbsGbsGbsGmsCms (5MdC) sdAs (5MdC) sdA sdAsdTts (5MdC) s (5MdC) sdGsdGsgmsCmsA bsAbbsTb
X51611	ASO-STAT3-2553	AGCGCCTCAGTCGTAT CTT	184	20	2553	2573	AbsGbsGbsCmsGms (5MdC) s (5MdC) sdTs (5MdC) sdAsdTts (5MdC) sdGsdTtsAmsTmsC bsTbsTb
X51610	ASO-STAT3-2552	GGCGCCTCAGTCGTATC TTT	185	20	2552	2572	CbsGbsCbsGmsCms (5MdC) sdTs (5MdC) sdA sdGsdTs (5MdC) sdGsdTsdAsTmsCmsTbsTb sTb
X51568	ASO-STAT3-883	CATCGCTGACAAAAGCC CCG	186	20	883	903	CbsAbbsTbsCmsGms (5MdC) sdTsdGsdAs (5MdC) sdAsdTtsAmsdTtsCmsCbsCbsGbs
X51563	ASO-STAT3-842	TCCGCATCTGGTCCAGC GCA	187	20	842	862	TbsCbsCbsGmsCmsdAsdTts (5MdC) sdTsdGsdGsdTs (5MdC) s (5MdC) sdAsGmsCmsGbsCb sAb
X51564	ASO-STAT3-851	CGATGCTTCGCGCATC TGG	188	20	851	871	CbsGbsAbsTmsGms (5MdC) sdTsdTs (5MdC) sdTs (5MdC) s (5MdC) sdGs (5MdC) sdAsTmsCmsTbsGbsGbs
X51605	ASO-STAT3-2265	GGCCGACATACTTTCC GAA	189	20	2265	2285	GbsGbsCbsCmsGmsdAs (5MdC) sdAsdTts dAs (5MdC) sdTsdTtsCmsCmsGbsAbsAb
X51558	ASO-STAT3-520	CCGGGCCACAATCCGGG CAA	190	20	520	540	CbsCbsGbsGmsGms (5MdC) s (5MdC) sdAs (5MdC) sdAsdTts (5MdC) s (5MdC) sdGsGmsGmsCbsAbsAb
X51574	ASO-STAT3-985	CCGATCTAGCAGATGT TGG	191	20	985	1005	CbsCbsGbsAmsTms (5MdC) sdTsdAsdTtsGsdGs (5MdC) sdAsdTtsGmsTmsTbsGbsGbs
X51537	ASO-STAT3-524	ACGGGCCACAATCCGGG	192	17	524	541	AbsCbsCbsdTsdGsdGs (5MdC) s (5MdC) sdA s (5MdC) sdAsdTts (5MdC) sCbsGbsGbs

FIG. 1 (Cont'd)

ID	Description	Sequence	SEQ ID NO	Length (NT)	mRNA Position (SEQ ID NO: 3)		ASO Chemical Structure (Nb - LNA, dN - DNA, (5MdC) - 5-Methyl-dC, Nm - MOE, s - phosphorothioate)
					Start	End	
X51581	ASO-STAT3-1106	GCGGTGCTGTACAATG GGG	193	20	1106	1126	GbsCbsCbsGmsGmsdTsdGs (5MdC) sdTsdGsdTsdAs (5MdC) sdAsdTsdGsGbsGbsG
X51556	ASO-STAT3-517	GGCCACAATCCGGCAA TCT	194	20	517	537	GbsGbsCbsCmsAms (5MdC) sdAsdTsdTs (5MdC) s (5MdC) sdGsdGsdGs (5MdC) sAmsAm sTbsCbsTb
X51594	ASO-STAT3-1721	GGACCTCGGCCACTTGA TCC	195	20	1721	1741	GbsGbsAbsCmsCmsdTds (5MdC) sdGsdGs (5MdC) s (5MdC) sdAs (5MdC) sdTsdTsGmsAm sTbsCbsCb
X51587	ASO-STAT3-1113	AGCATCGGCCGGTGCTG TAC	196	20	1113	1133	AbbsGbsCbsAmsTms (5MdC) sdGsdGs (5MdC) s (5MdC) sdGsdGsdTsds (5MdC) sTmsGm sTbsAbsCb
X51530	ASO-STAT3-992	TAGCCGATCTAGGCAG	197	16	992	1008	TbsAbsGbs (5MdC) s (5MdC) sdGsdAsdTds (5MdC) sdTsdAsdTsdGsCbsAbsGb
X51517	ASO-STAT3-993	TAGCCGATCTAGGCA	198	15	993	1008	TbsAbsGbs (5MdC) s (5MdC) sdGsdAsdTds (5MdC) sdTsdAsdTsdGsCbsAbs
X51580	ASO-STAT3-1104	CGGTGCTGTACAATGGG GTC	199	20	1104	1124	CbsGbsGbsTmsGms (5MdC) sdTsdGsdTsda s (5MdC) sdAsdTsdGsGmsGmsCbsTbsC

10/30

FIG. 2B

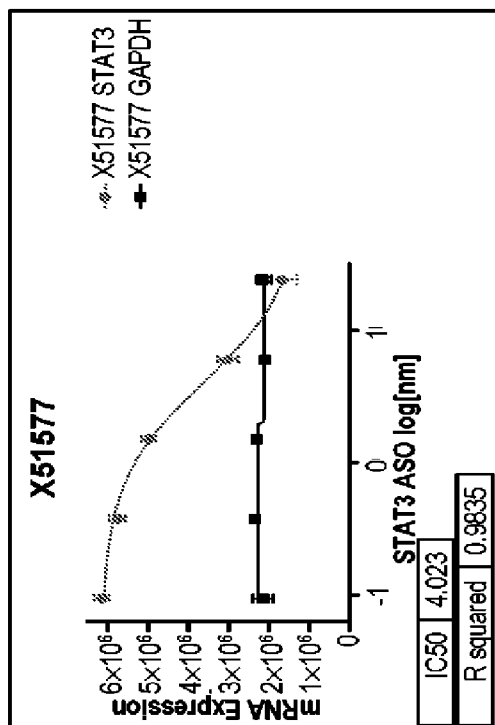


FIG. 2D

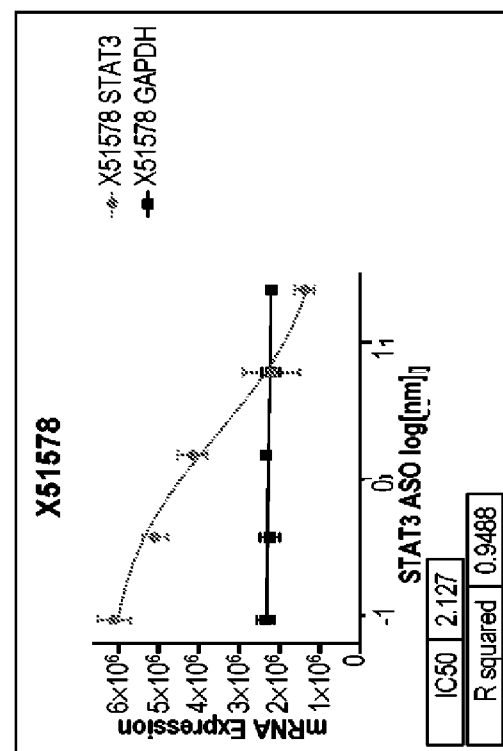


FIG. 2A

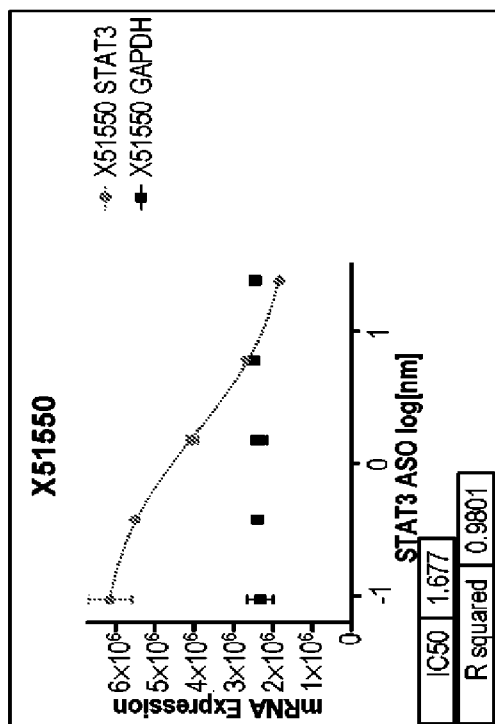


FIG. 2C

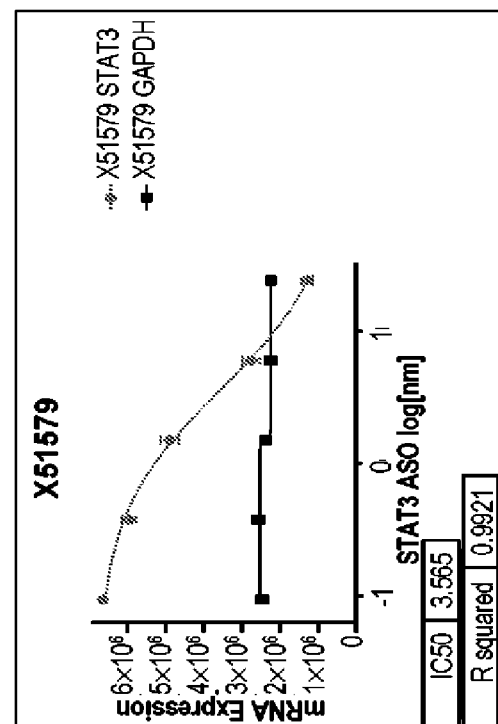


FIG. 2F

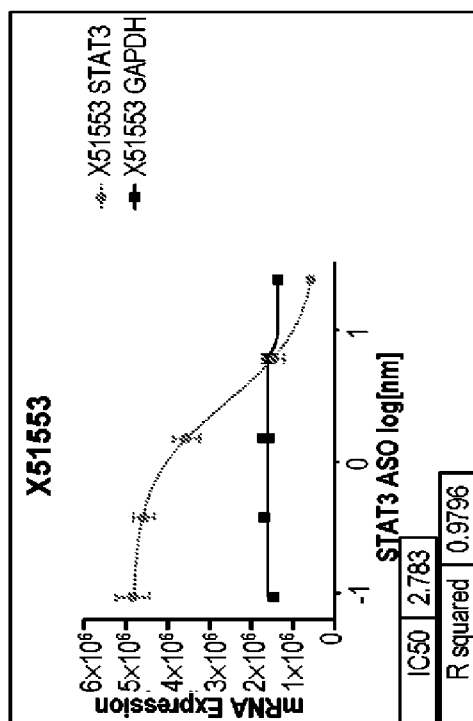


FIG. 2H

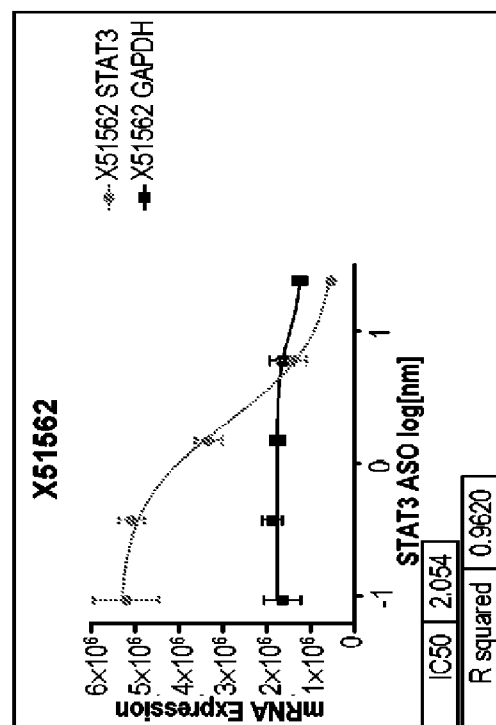


FIG. 2E

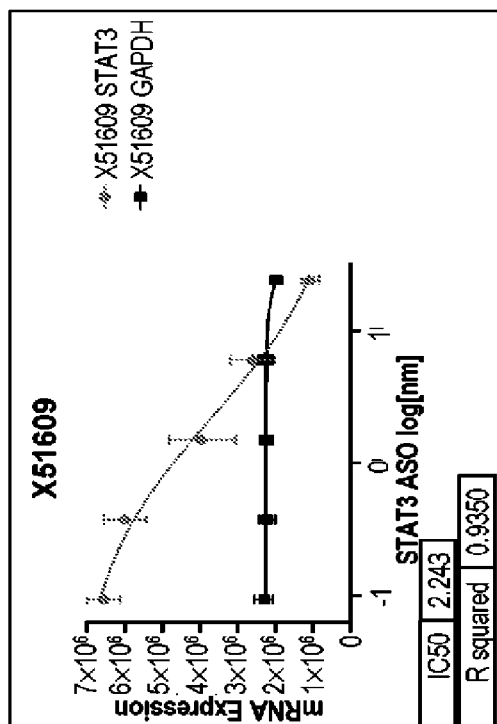


FIG. 2G

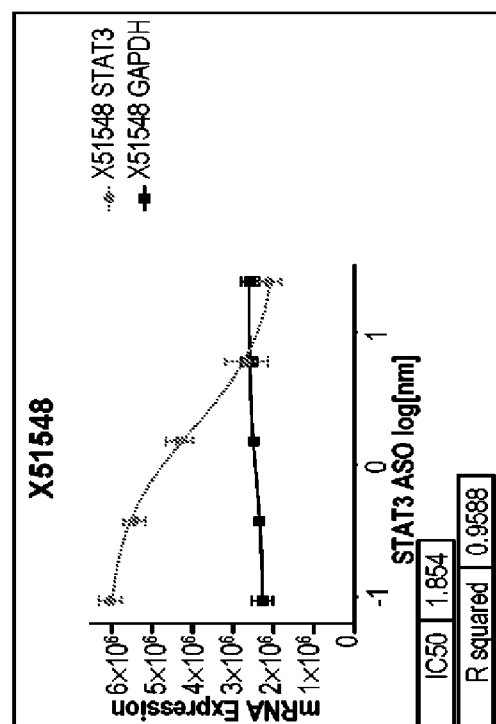


FIG. 2J

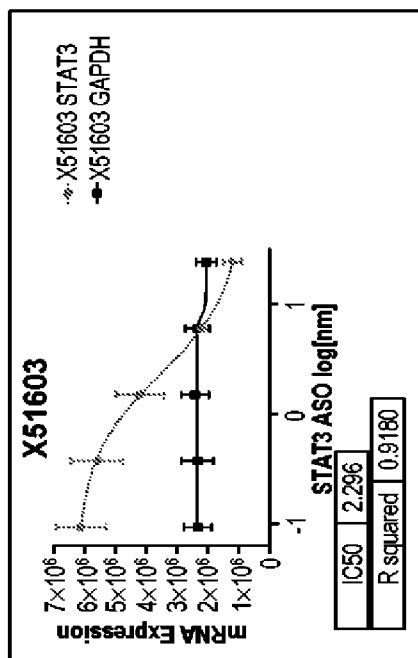


FIG. 2L

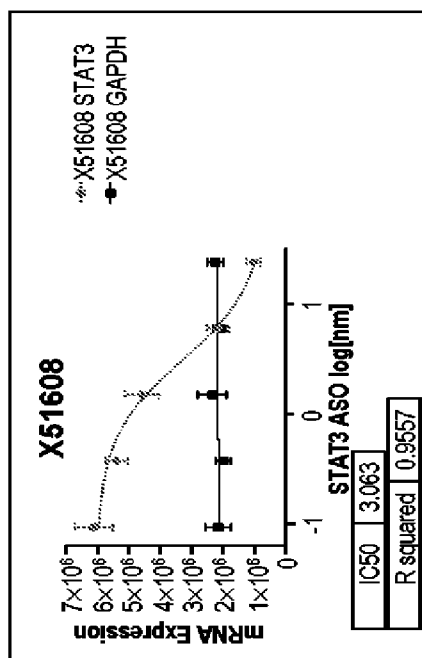


FIG. 2N

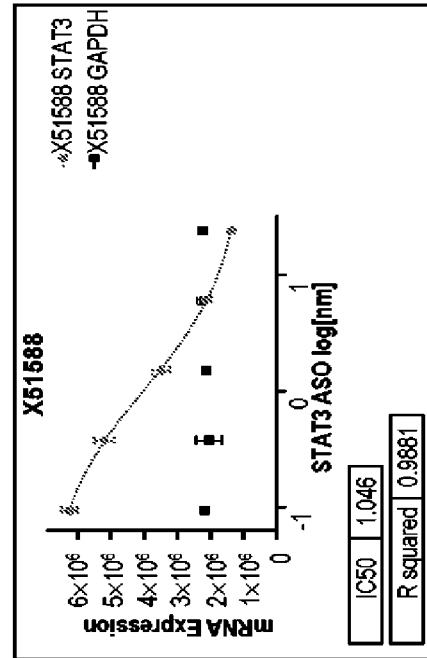


FIG. 2I

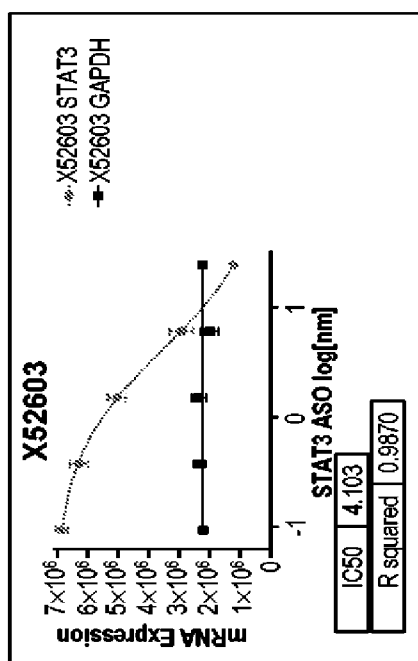


FIG. 2K

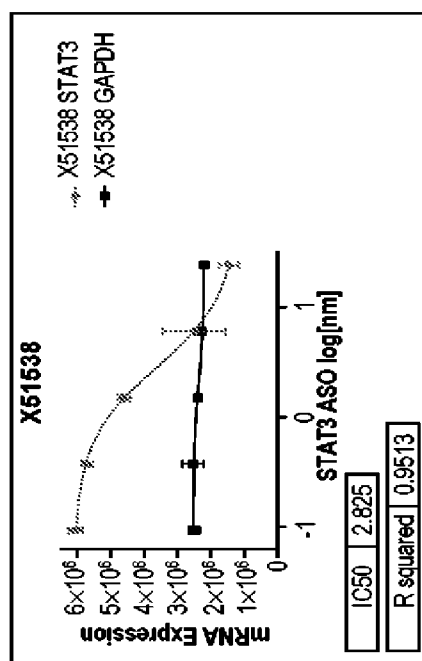


FIG. 2M

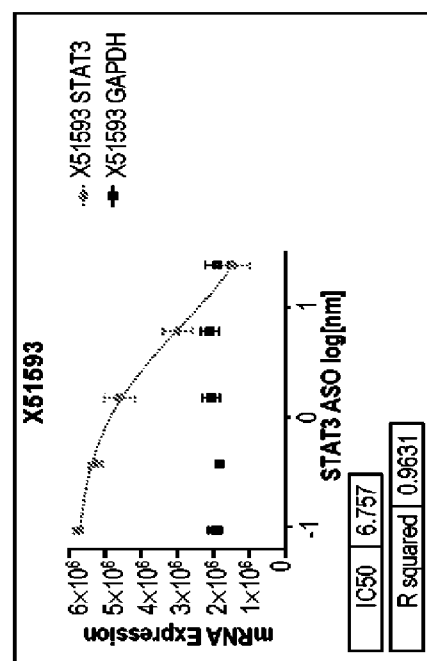


FIG. 3

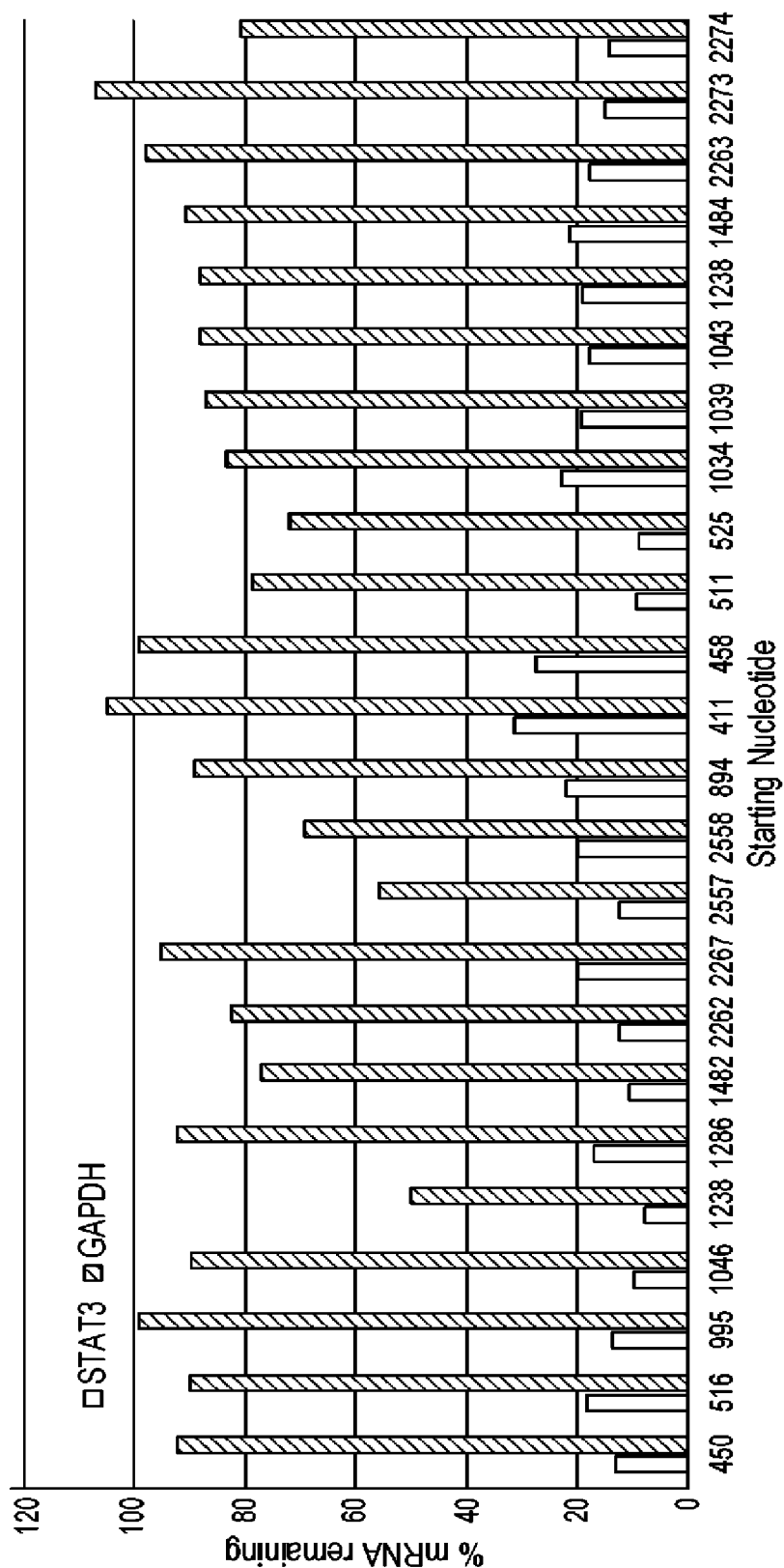


FIG. 4B

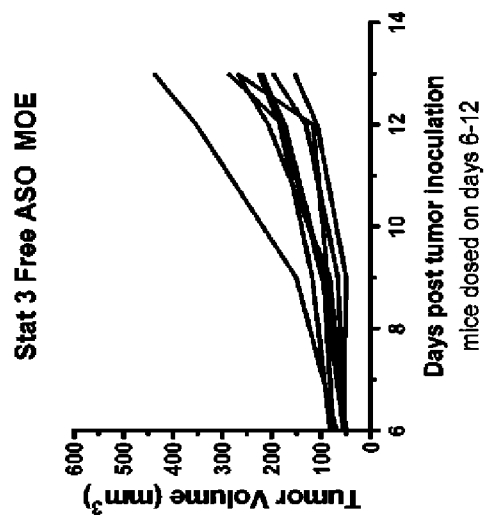


FIG. 4A

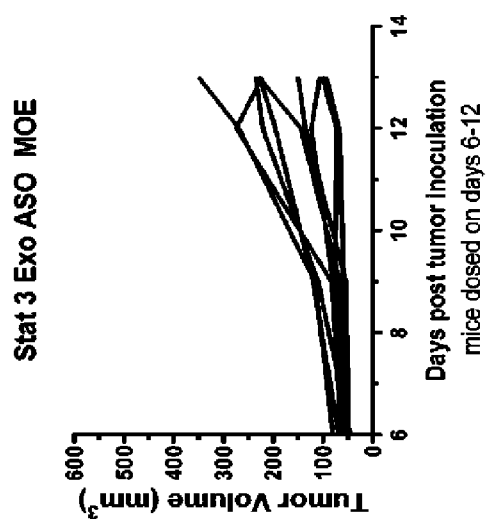
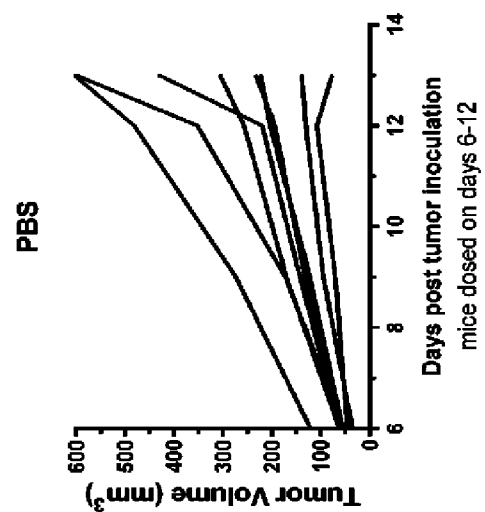


FIG. 4C



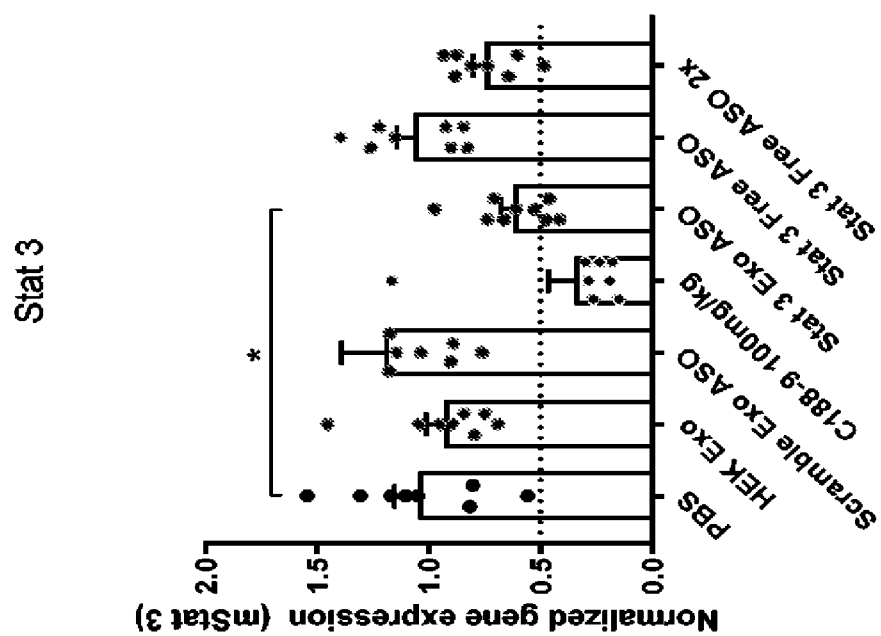


FIG. 5

FIG. 6B

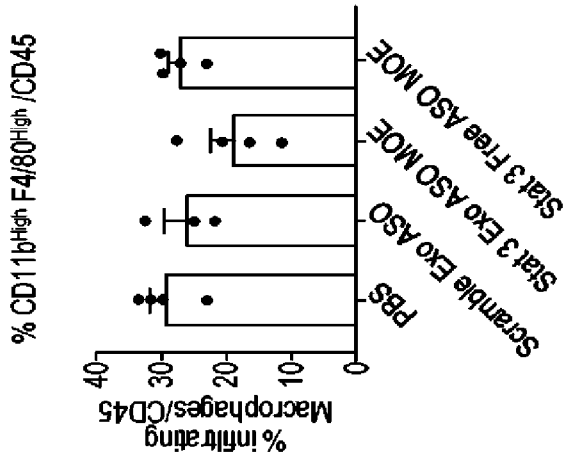


FIG. 6A

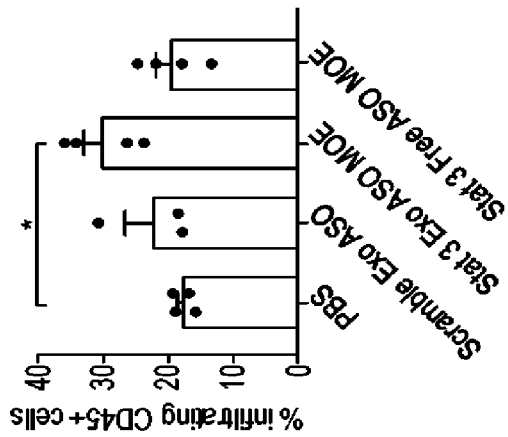


FIG. 6C

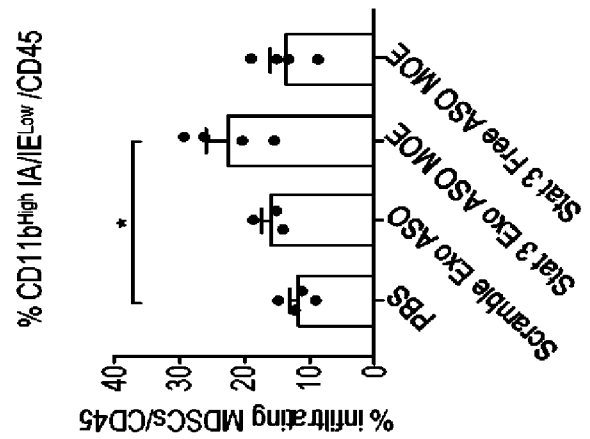


FIG. 7B

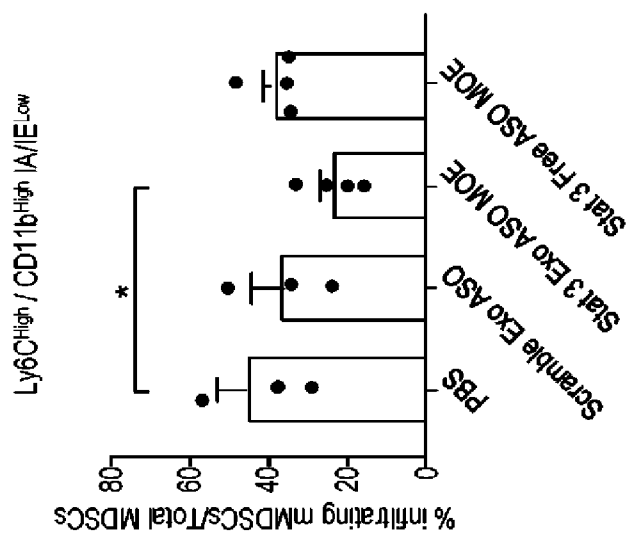


FIG. 7A

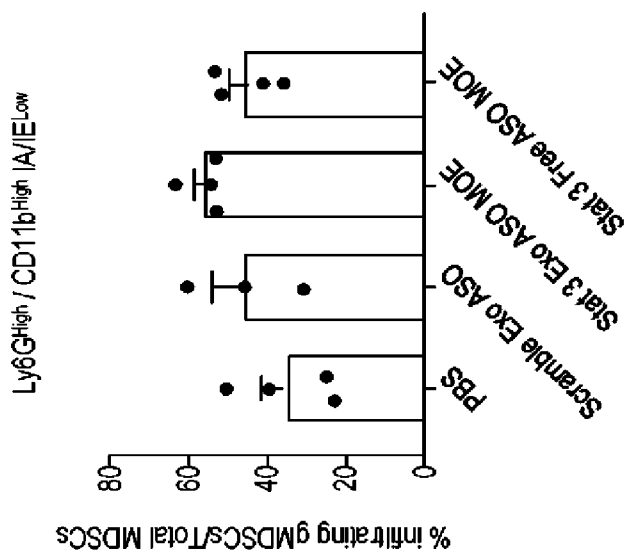


FIG. 8

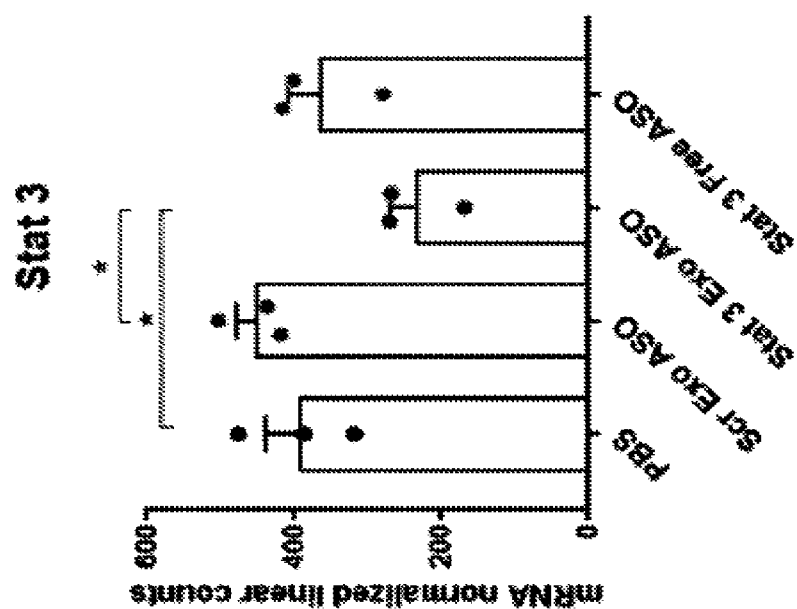


FIG. 9A

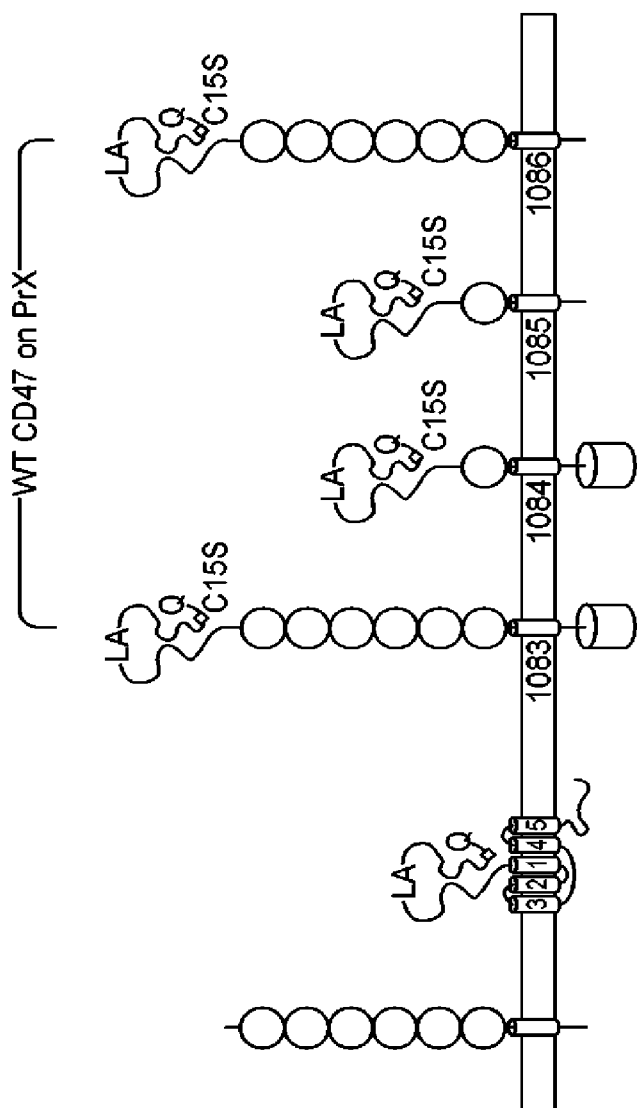


FIG. 9B

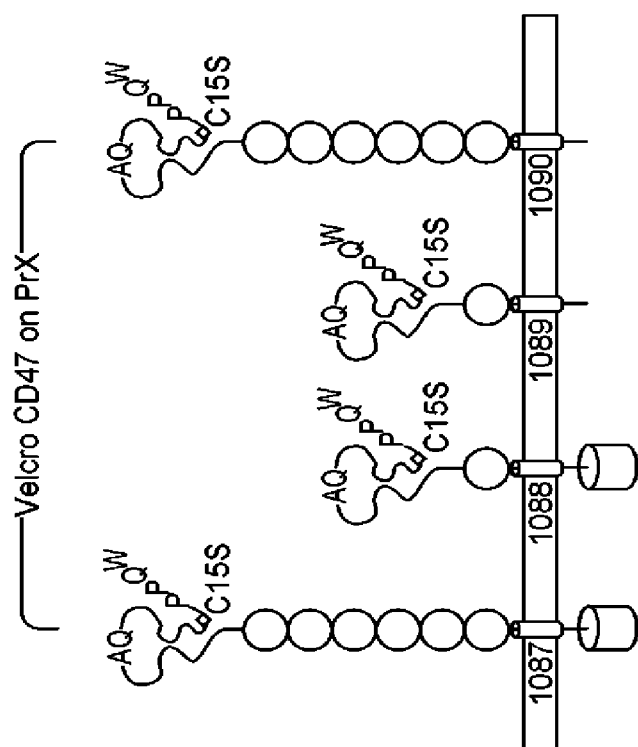


FIG. 9C

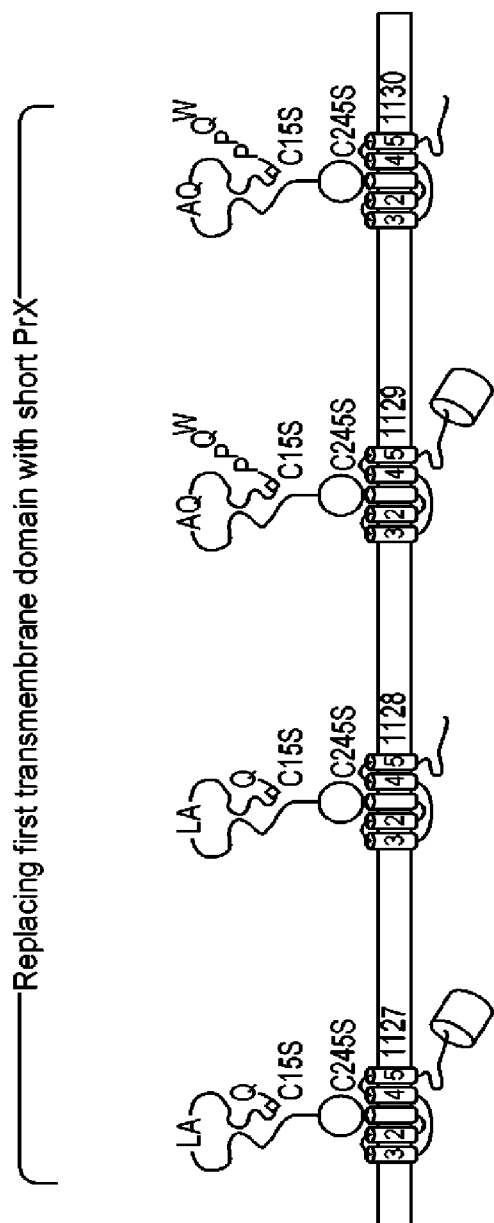


FIG. 9D

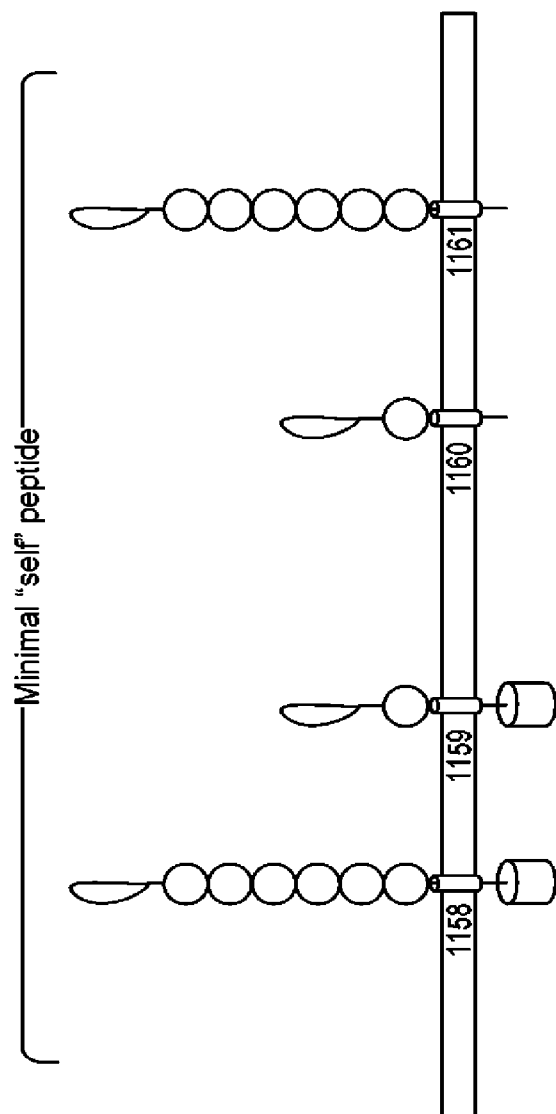
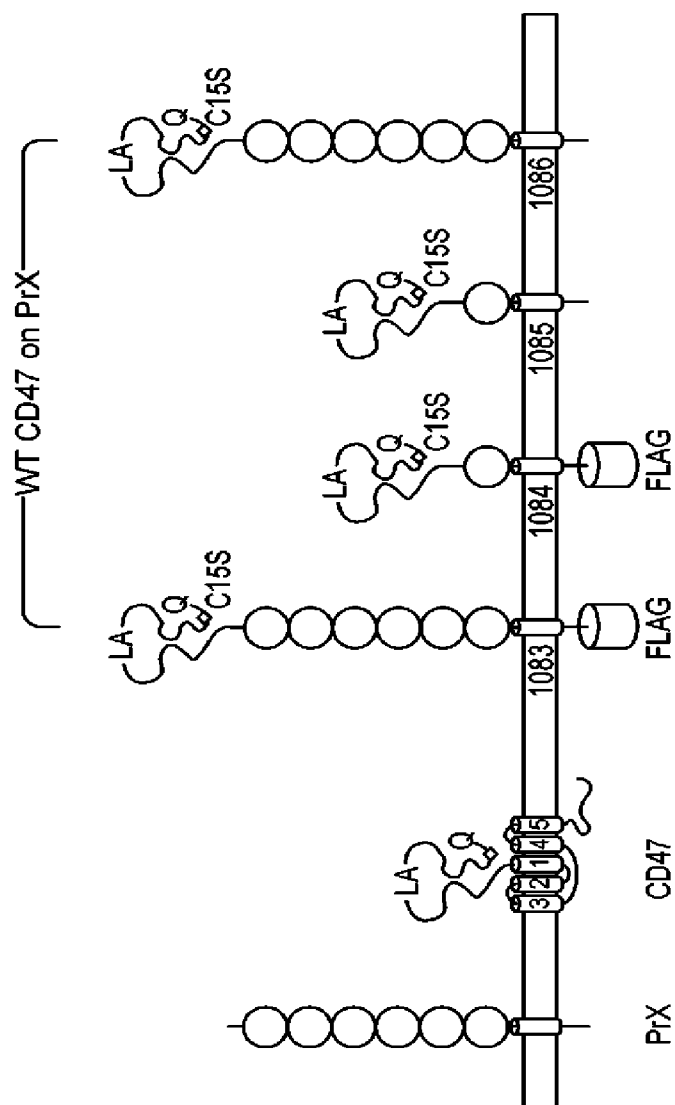


FIG. 10



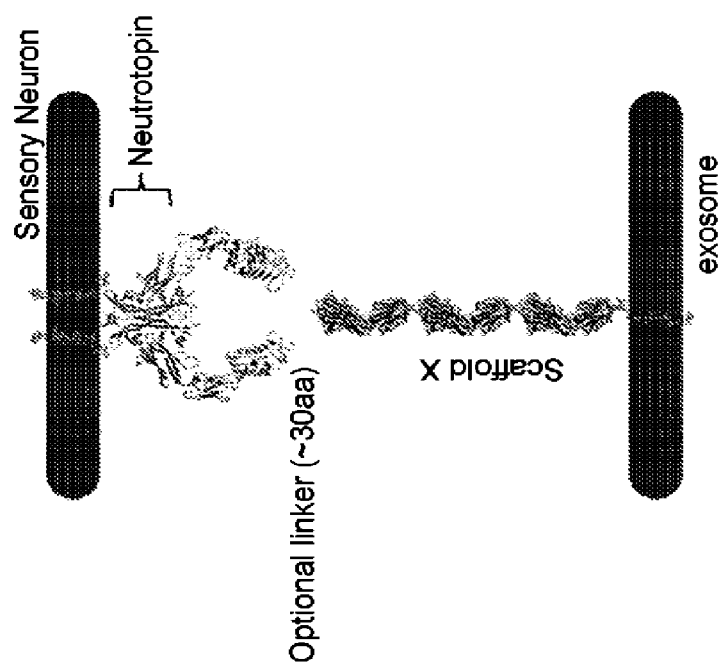
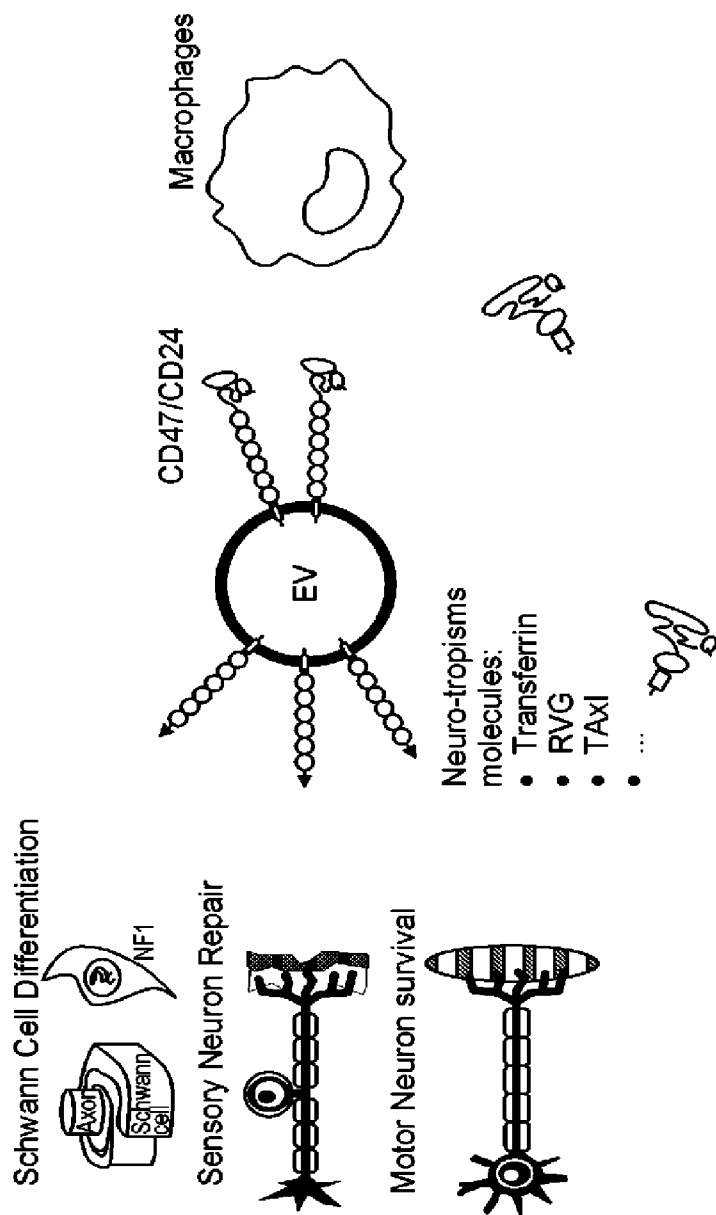


FIG. 11A

FIG. 11B



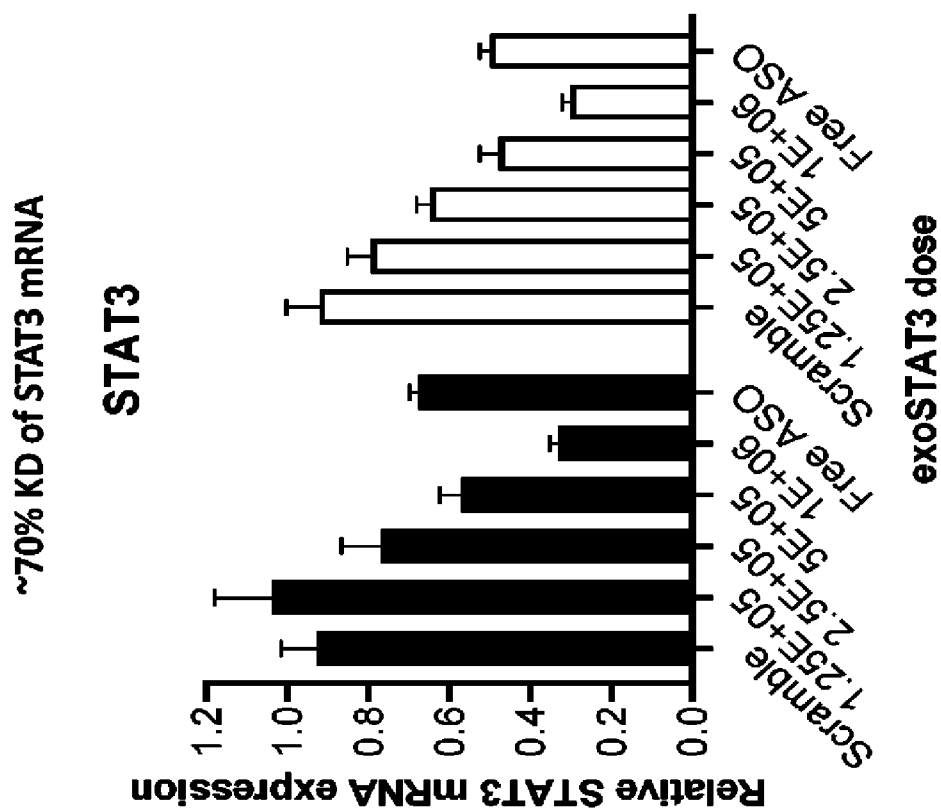


FIG. 12A

FIG. 12D

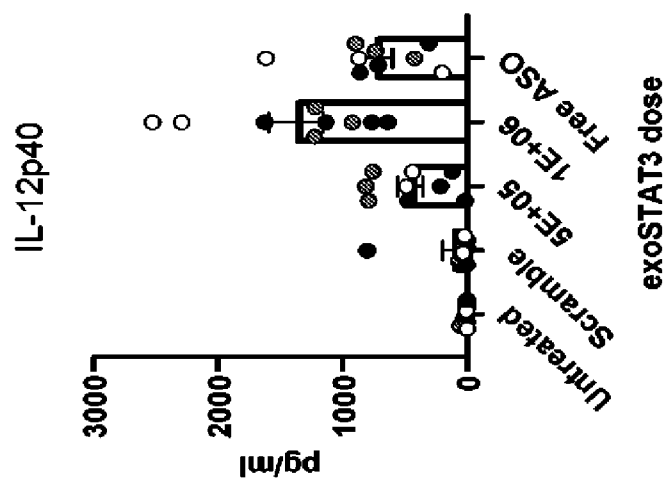


FIG. 12C

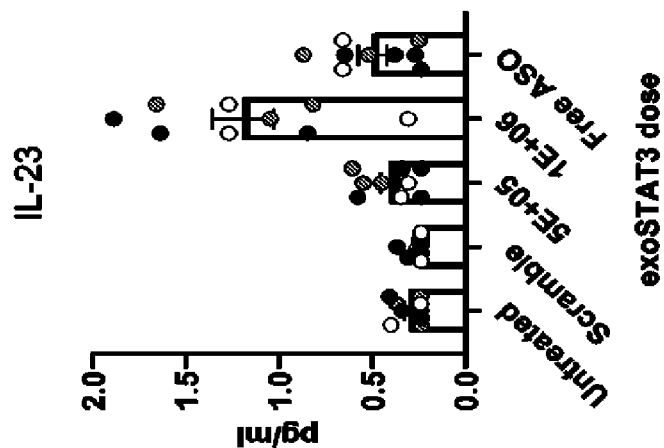


FIG. 12B

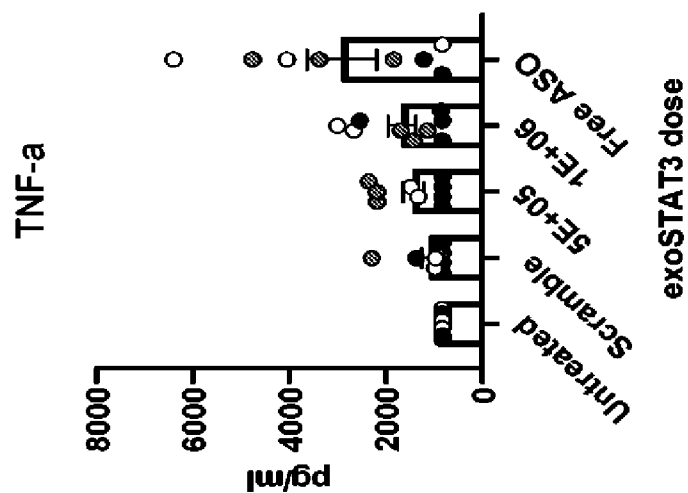


FIG. 13C

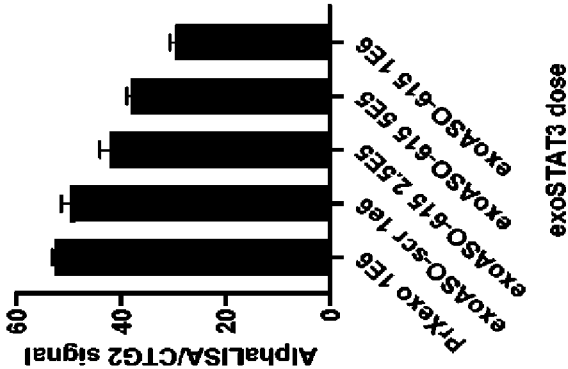


FIG. 13B

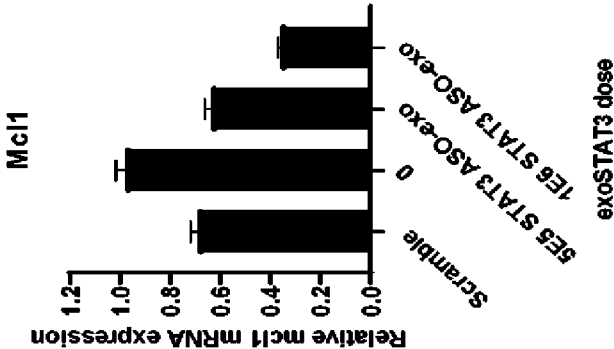
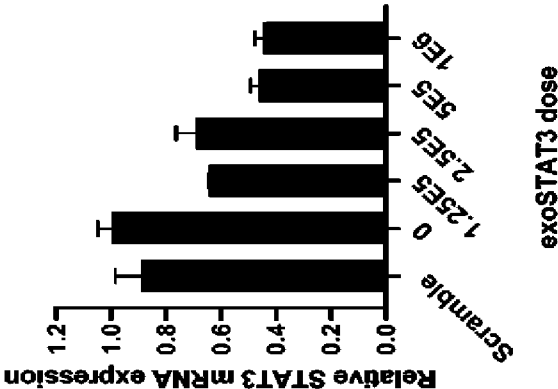


FIG. 13A



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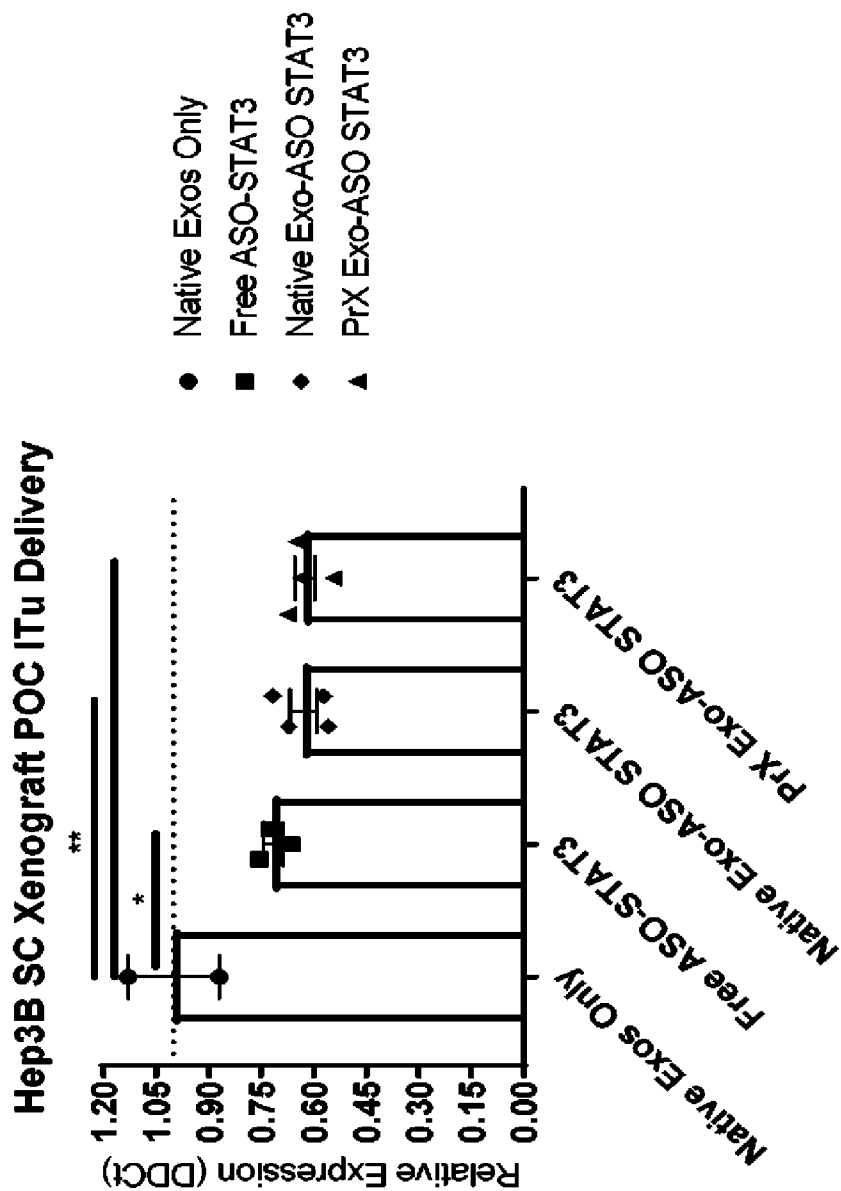


FIG. 14

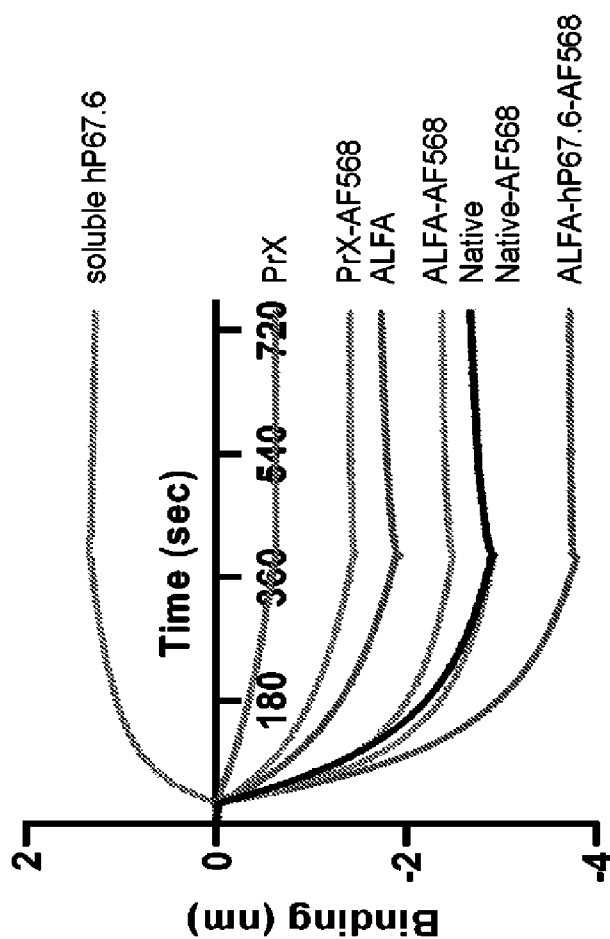


FIG. 15

FIG. 16A

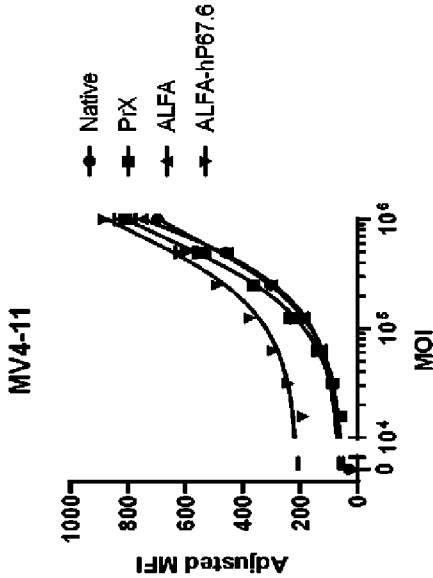


FIG. 16B

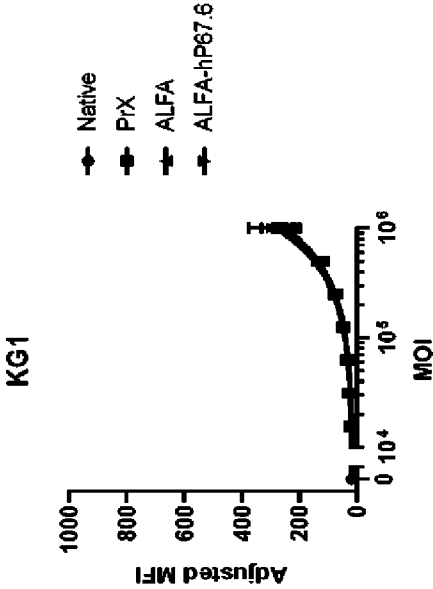


FIG. 16C

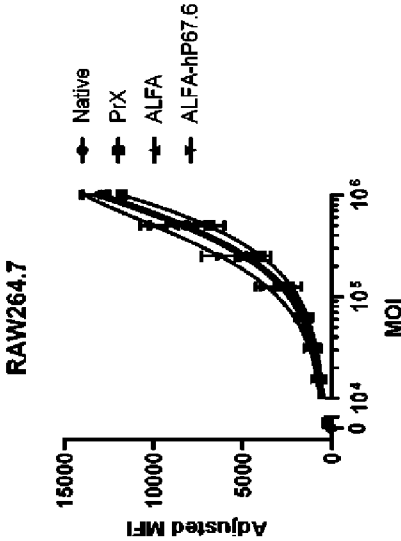


FIG. 16D

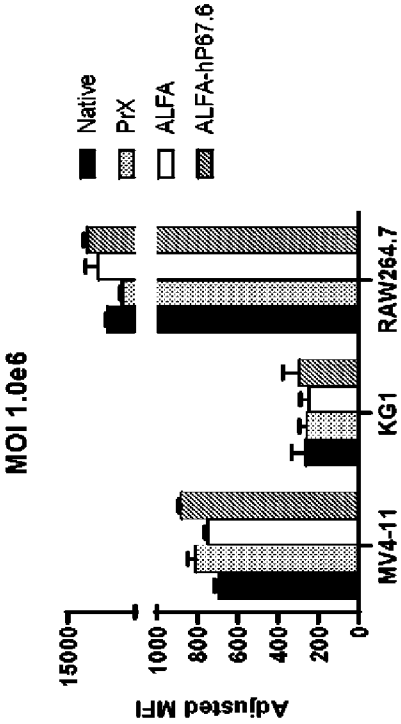


FIG. 16E

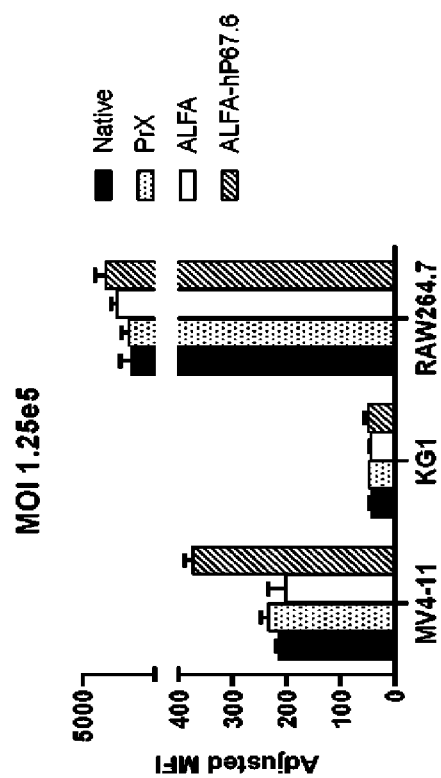


FIG. 16F

