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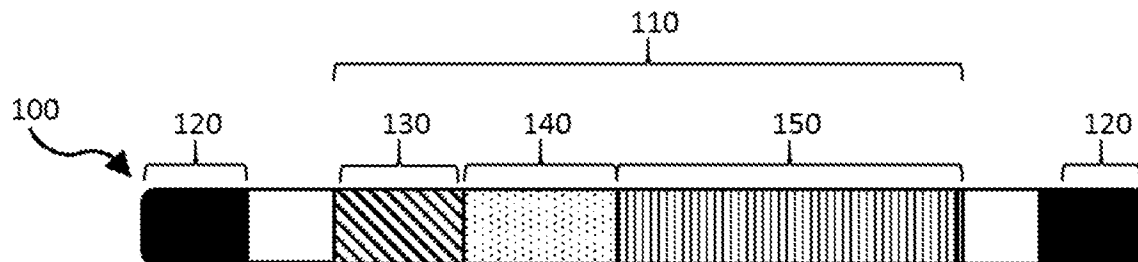
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(54) Titre : POLYNUCLEOTIDES AADC POUR LE TRAITEMENT DE LA MALADIE DE PARKINSON
(54) Title: AADC POLYNUCLEOTIDES FOR THE TREATMENT OF PARKINSON'S DISEASE

FIG. 1



(57) **Abrégé/Abstract:**

The invention relates to compositions and methods for the preparation, manufacture and therapeutic use of polynucleotides encoding AADC for the treatment of Parkinson's Disease.

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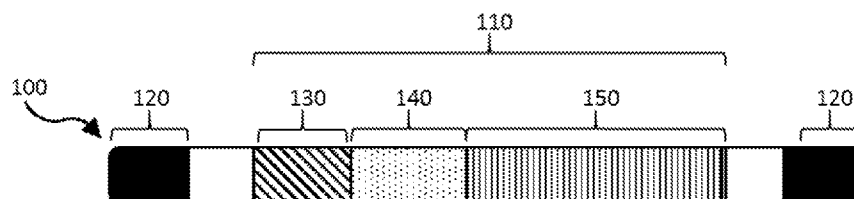
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(54) Title: AADC POLYNUCLEOTIDES FOR THE TREATMENT OF PARKINSON'S DISEASE

FIG. 1



(57) **Abstract:** The invention relates to compositions and methods for the preparation, manufacture and therapeutic use of polynucleotides encoding AADC for the treatment of Parkinson's Disease.

AADC POLYNUCLEOTIDES FOR THE TREATMENT OF PARKINSON'S DISEASE

REFERENCE TO SEQUENCE LISTING

[0001] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing file, entitled 14482-022-228_Sequence_Listing.txt, was created on June 10, 2018, and is 6,461,106 bytes in size. The information in electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] The invention relates to compositions, particularly nucleic acid molecules, e.g., polynucleotides encoding AADC, for use in the treatment of Parkinson's disease. In some embodiments such AADC polynucleotides may be encoded by or within recombinant adeno-associated viruses (AAVs).

BACKGROUND OF THE INVENTION

[0003] Aromatic L-amino acid decarboxylase (AADC) is a homodimeric pyridoxal phosphate-dependent enzyme responsible for the synthesis of dopamine and serotonin. The encoded protein catalyzes the decarboxylation of L-3,4-dihydroxyphenylalanine (L-DOPA or levodopa) to dopamine; L-5-hydroxytryptophan to serotonin; and L-tryptophan to tryptamine. Defects in this gene are the cause of aromatic L-amino-acid decarboxylase deficiency (AADCD), which is an inborn error in neurotransmitter metabolism leading to combined serotonin and catecholamine deficiency that results in severe motor and autonomic dysfunctions.

[0004] Parkinson's Disease (PD) is a progressive neurodegenerative disease of the central nervous system (CNS) producing sensory and motor symptoms. Dopamine replacement (i.e., levodopa) has been the standard pharmacotherapy for motor impairment in PD. However, the benefit of dopamine therapy becomes less marked over time, due, in part, to the progressive death of dopamine-generating cells and corresponding loss of AADC activity. Furthermore, systemic administration of high-dose dopamine is complicated by side effects, such as fluctuations in motor performance, dyskinesias, and hallucinations, resulting from dopaminergic stimulation of the mesolimbic system. One strategy to restore dopaminergic function and minimize side effects is the use of gene therapy to deliver AADC directly to a targeted region of the CNS.

[0005] The adeno-associated virus (AAV) has emerged as an attractive vector for gene therapy due to its long-term gene expression, the inability to autonomously replicate without a helper virus,

the ability to transduce dividing and non-dividing cells, and the lack of pathogenicity from wild-type infections (See e.g., Hadaczek et al. Mol. Ther. 18(8), 1458-1461, Aug. 2010). AAV is a helper-dependent DNA parvovirus which belongs to the genus *Dependovirus*.

[0006] The present invention provides such improved nucleic acid constructs, e.g., polynucleotides, for use with AAV-derived vectors comprising dopa carboxylase (“DDC”) gene sequence which encodes a full-length AADC protein for the purpose of gene therapy in the treatment of Parkinson’s Disease.

[0007] The nucleic acid constructs described herein comprise at least a 5’-ITR and a 3’-ITR, each or both of which may be derived from an AAV, positioned about a *DDC gene* sequence, as well as additional components required for gene expression and clone selection.

SUMMARY OF THE INVENTION

[0008] Described herein are compositions, methods, processes, kits and devices for the design, preparation, manufacture and/or formulation of AADC polynucleotides.

[0009] In some embodiments such AADC polynucleotides may be encoded by or contained within plasmids or vectors or recombinant adeno-associated viruses (AAV).

[00010] The details of various embodiments of the invention are set forth in the description below. Other features, objects, and advantages of the invention will be apparent from the description and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[00011] The foregoing and other objects, features and advantages will be apparent from the following description of particular embodiments of the invention, as illustrated in the accompanying drawings. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of various embodiments of the invention.

[00012] FIG. 1 is a schematic of a viral genome of the invention.

DETAILED DESCRIPTION

I. Compositions of the Invention

Adeno-associated viruses (AAVs) and AAV particles

[00013] Viruses of the Parvoviridae family are small non-enveloped icosahedral capsid viruses characterized by a single stranded DNA genome. Parvoviridae family viruses consist of two subfamilies: Parvovirinae, which infect vertebrates, and Densovirinae, which infect invertebrates. Due to its relatively simple structure, easily manipulated using standard molecular biology

techniques, this virus family is useful as a biological tool. The genome of the virus may be modified to contain a minimum of components for the assembly of a functional recombinant virus, or viral particle, which is loaded with or engineered to express or deliver a desired payload, which may be delivered to a target cell, tissue, organ, or organism.

[00014] The parvoviruses and other members of the Parvoviridae family are generally described in Kenneth I. Berns, “Parvoviridae: The Viruses and Their Replication,” Chapter 69 in *FIELDS VIROLOGY* (3d Ed. 1996), the contents of which are incorporated by reference in their entirety.

[00015] The Parvoviridae family comprises the Dependovirus genus which includes adeno-associated viruses (AAV) capable of replication in vertebrate hosts including, but not limited to, human, primate, bovine, canine, equine, and ovine species.

[00016] The vector genome is a linear, single-stranded DNA (ssDNA) molecule approximately 5,000 nucleotides (nt) in length. The AAV viral genome can comprise a payload region and at least one inverted terminal repeat (ITR) or ITR region. ITRs traditionally flank the coding nucleotide sequences for the non-structural proteins (encoded by Rep genes) and the structural proteins (encoded by capsid genes or Cap genes). While not wishing to be bound by theory, an AAV viral genome typically comprises two ITR sequences. The vector genome comprises a characteristic T-shaped hairpin structure defined by the self-complementary terminal 145 nt of the 5' and 3' ends of the ssDNA which form an energetically stable double stranded region. The double stranded hairpin structures comprise multiple functions including, but not limited to, acting as an origin for DNA replication by functioning as primers for the endogenous DNA polymerase complex of the host viral replication cell.

[00017] In addition to the encoded heterologous payload, AAV particles may comprise the viral genome, in whole or in part, of any naturally occurring and/or recombinant AAV serotype nucleotide sequence or variant. AAV variants may have sequences of significant homology at the nucleic acid (genome or capsid) and amino acid levels (capsids), to produce constructs which are generally physical and functional equivalents, replicate by similar mechanisms, and assemble by similar mechanisms. Chiorini et al., *J. Vir.* 71: 6823-33(1997); Srivastava et al., *J. Vir.* 45:555-64 (1983); Chiorini et al., *J. Vir.* 73:1309-1319 (1999); Rutledge et al., *J. Vir.* 72:309-319 (1998); and Wu et al., *J. Vir.* 74: 8635-47 (2000), the contents of each of which are incorporated herein by reference in their entirety.

[00018] In one embodiment, AAV particles of the present invention are recombinant AAV particles which are replication defective, lacking sequences encoding functional Rep and Cap proteins within their viral genome. These defective AAV particles may lack most or all parental coding sequences and essentially carry only one or two AAV ITR sequences and the nucleic acid of interest for delivery to a cell, a tissue, an organ or an organism.

[00019] In one embodiment, the viral genome of the AAV particles of the present invention comprise at least one control element which provides for the replication, transcription and translation of a coding sequence encoded therein. Not all of the control elements need always be present as long as the coding sequence is capable of being replicated, transcribed and/or translated in an appropriate host cell. Non-limiting examples of expression control elements include sequences for transcription initiation and/or termination, promoter and/or enhancer sequences, efficient RNA processing signals such as splicing and polyadenylation signals, sequences that stabilize cytoplasmic mRNA, sequences that enhance translation efficacy (e.g., Kozak consensus sequence), sequences that enhance protein stability, and/or sequences that enhance protein processing and/or secretion.

[00020] According to the present invention, AAV particles for use in therapeutics and/or diagnostics comprise a virus that has been distilled or reduced to the minimum components necessary for transduction of a nucleic acid payload or cargo of interest. In this manner, AAV particles are engineered as vehicles for specific delivery while lacking the deleterious replication and/or integration features found in wild-type viruses.

[00021] AAV particles of the present invention may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. As used herein, a “vector” is any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule such as the nucleic acids described herein.

[00022] In addition to single stranded AAV particles (e.g., ssAAVs), the present invention also provides for self-complementary AAV (scAAVs) particles. scAAV particles contain DNA strands which anneal together to form double stranded DNA. By skipping second strand synthesis, scAAVs allow for rapid expression in the cell.

[00023] In one embodiment, the AAV particle of the present invention is an scAAV.

[00024] In one embodiment, the AAV particle of the present invention is an ssAAV.

[00025] Methods for producing and/or modifying AAV particles are disclosed in the art such as pseudotyped AAV particles (PCT Patent Publication Nos. WO200028004; WO200123001;

WO2004112727; WO 2005005610 and WO 2005072364, the content of each of which is incorporated herein by reference in its entirety).

[00026] AAV particles may be modified to enhance the efficiency of delivery. Such modified AAV particles can be packaged efficiently and be used to successfully infect the target cells at high frequency and with minimal toxicity. In some embodiments the capsids of the AAV particles are engineered according to the methods described in US Publication Number US 20130195801, the contents of which are incorporated herein by reference in their entirety.

[00027] In one embodiment, the AAV particles comprising a payload region encoding the polypeptides of the invention may be introduced into mammalian cells.

AAV serotypes

[00028] AAV particles of the present invention may comprise or be derived from any natural or recombinant AAV serotype. According to the present invention, the AAV particles may utilize or be based on a serotype selected from any of the following PHP.B, PHP.A, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/rh.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-

10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAV, BAAV, caprine AAV, bovine AAV, ovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T, AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101, AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2, AAV Shuffle 100-1, AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8, AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10,

AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV CLv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV CLv1-7, AAV CLv1-8, AAV CLv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, AAVF9/HSC9, PHP.B (AAV-PHP.B), PHP.A (AAV.PHP.A), G2B-26, G2B-13, TH1.1-32, TH1.1-35, AAVPHP.B2, AAVPHP.B3, AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3, AAVG2B4, and/or AAVG2B5, and variants thereof.

[00029] In some embodiments, the AAV serotype may be, or have, a modification as described in United States Publication No. US 20160361439, the contents of which are herein incorporated by reference in their entirety, such as but not limited to, Y252F, Y272F, Y444F, Y500F, Y700F, Y704F, Y730F, Y275F, Y281F, Y508F, Y576F, Y612G, Y673F, and Y720F of the wild-type AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, and hybrids thereof.

[00030] In some embodiments, the AAV serotype may be, or have, a mutation as described in United States Patent No. US 9546112, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, at least two, but not all the F129L, D418E, K531E, L584F, V598A and H642N mutations in the sequence of AAV6 (SEQ ID NO:4 of US 9546112), AAV1 (SEQ ID NO:6 of US 9546112), AAV2, AAV3, AAV4, AAV5, AAV7, AAV9, AAV10 or AAV11 or derivatives thereof. In yet another embodiment, the AAV serotype may be, or have, an AAV6 sequence comprising the K531E mutation (SEQ ID NO:5 of US 9546112).

[00031] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV1 sequence, as described in United States Publication No. US 20130224836, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, at least one of the surface-exposed tyrosine residues, preferably, at positions 252, 273, 445, 701, 705 and 731 of AAV1 (SEQ ID NO: 2 of US 20130224836) substituted with another amino acid, preferably with a phenylalanine residue. In one embodiment, the AAV serotype may be, or have, a mutation in the AAV9 sequence, such as, but not limited to, at least one of the surface-exposed tyrosine residues, preferably, at positions 252, 272, 444, 500, 700, 704 and 730 of AAV2 (SEQ ID NO: 4 of US 20130224836) substituted with another amino acid, preferably with a phenylalanine residue. In one embodiment, the tyrosine residue at position 446 of AAV9 (SEQ ID NO: 6 US 20130224836) is substituted with a phenylalanine residue.

[00032] In some embodiments, the serotype may be AAV2 or a variant thereof, as described in International Publication No. WO2016130589, herein incorporated by reference in its entirety. The amino acid sequence of AAV2 may comprise N587A, E548A, or N708A mutations. In one embodiment, the amino acid sequence of any AAV may comprise a V708K mutation.

[00033] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20030138772, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV1 (SEQ ID NO: 6 and 64 of

US20030138772), AAV2 (SEQ ID NO: 7 and 70 of US20030138772), AAV3 (SEQ ID NO: 8 and 71 of US20030138772), AAV4 (SEQ ID NO: 63 of US20030138772), AAV5 (SEQ ID NO: 114 of US20030138772), AAV6 (SEQ ID NO: 65 of US20030138772), AAV7 (SEQ ID NO: 1-3 of US20030138772), AAV8 (SEQ ID NO: 4 and 95 of US20030138772), AAV9 (SEQ ID NO: 5 and 100 of US20030138772), AAV10 (SEQ ID NO: 117 of US20030138772), AAV11 (SEQ ID NO: 118 of US20030138772), AAV12 (SEQ ID NO: 119 of US20030138772), AAVrh10 (amino acids 1 to 738 of SEQ ID NO: 81 of US20030138772), AAV16.3 (US20030138772 SEQ ID NO: 10), AAV29.3/bb.1 (US20030138772 SEQ ID NO: 11), AAV29.4 (US20030138772 SEQ ID NO: 12), AAV29.5/bb.2 (US20030138772 SEQ ID NO: 13), AAV1.3 (US20030138772 SEQ ID NO: 14), AAV13.3 (US20030138772 SEQ ID NO: 15), AAV24.1 (US20030138772 SEQ ID NO: 16), AAV27.3 (US20030138772 SEQ ID NO: 17), AAV7.2 (US20030138772 SEQ ID NO: 18), AAVC1 (US20030138772 SEQ ID NO: 19), AAVC3 (US20030138772 SEQ ID NO: 20), AAVC5 (US20030138772 SEQ ID NO: 21), AAVF1 (US20030138772 SEQ ID NO: 22), AAVF3 (US20030138772 SEQ ID NO: 23), AAVF5 (US20030138772 SEQ ID NO: 24), AAVH6 (US20030138772 SEQ ID NO: 25), AAVH2 (US20030138772 SEQ ID NO: 26), AAV42-8 (US20030138772 SEQ ID NO: 27), AAV42-15 (US20030138772 SEQ ID NO: 28), AAV42-5b (US20030138772 SEQ ID NO: 29), AAV42-1b (US20030138772 SEQ ID NO: 30), AAV42-13 (US20030138772 SEQ ID NO: 31), AAV42-3a (US20030138772 SEQ ID NO: 32), AAV42-4 (US20030138772 SEQ ID NO: 33), AAV42-5a (US20030138772 SEQ ID NO: 34), AAV42-10 (US20030138772 SEQ ID NO: 35), AAV42-3b (US20030138772 SEQ ID NO: 36), AAV42-11 (US20030138772 SEQ ID NO: 37), AAV42-6b (US20030138772 SEQ ID NO: 38), AAV43-1 (US20030138772 SEQ ID NO: 39), AAV43-5 (US20030138772 SEQ ID NO: 40), AAV43-12 (US20030138772 SEQ ID NO: 41), AAV43-20 (US20030138772 SEQ ID NO: 42), AAV43-21 (US20030138772 SEQ ID NO: 43), AAV43-23 (US20030138772 SEQ ID NO: 44), AAV43-25 (US20030138772 SEQ ID NO: 45), AAV44.1 (US20030138772 SEQ ID NO: 46), AAV44.5 (US20030138772 SEQ ID NO: 47), AAV223.1 (US20030138772 SEQ ID NO: 48), AAV223.2 (US20030138772 SEQ ID NO: 49), AAV223.4 (US20030138772 SEQ ID NO: 50), AAV223.5 (US20030138772 SEQ ID NO: 51), AAV223.6 (US20030138772 SEQ ID NO: 52), AAV223.7 (US20030138772 SEQ ID NO: 53), AAVA3.4 (US20030138772 SEQ ID NO: 54), AAVA3.5 (US20030138772 SEQ ID NO: 55), AAVA3.7 (US20030138772 SEQ ID NO: 56), AAVA3.3 (US20030138772 SEQ ID NO: 57), AAV42.12 (US20030138772 SEQ ID NO: 58), AAV44.2

(US20030138772 SEQ ID NO: 59), AAV42-2 (US20030138772 SEQ ID NO: 9), or variants thereof.

[00034] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20150159173, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV2 (SEQ ID NO: 7 and 23 of US20150159173), rh20 (SEQ ID NO: 1 of US20150159173), rh32/33 (SEQ ID NO: 2 of US20150159173), rh39 (SEQ ID NO: 3, 20 and 36 of US20150159173), rh46 (SEQ ID NO: 4 and 22 of US20150159173), rh73 (SEQ ID NO: 5 of US20150159173), rh74 (SEQ ID NO: 6 of US20150159173), AAV6.1 (SEQ ID NO: 29 of US20150159173), rh.8 (SEQ ID NO: 41 of US20150159173), rh.48.1 (SEQ ID NO: 44 of US20150159173), hu.44 (SEQ ID NO: 45 of US20150159173), hu.29 (SEQ ID NO: 42 of US20150159173), hu.48 (SEQ ID NO: 38 of US20150159173), rh54 (SEQ ID NO: 49 of US20150159173), AAV2 (SEQ ID NO: 7 of US20150159173), cy.5 (SEQ ID NO: 8 and 24 of US20150159173), rh.10 (SEQ ID NO: 9 and 25 of US20150159173), rh.13 (SEQ ID NO: 10 and 26 of US20150159173), AAV1 (SEQ ID NO: 11 and 27 of US20150159173), AAV3 (SEQ ID NO: 12 and 28 of US20150159173), AAV6 (SEQ ID NO: 13 and 29 of US20150159173), AAV7 (SEQ ID NO: 14 and 30 of US20150159173), AAV8 (SEQ ID NO: 15 and 31 of US20150159173), hu.13 (SEQ ID NO: 16 and 32 of US20150159173), hu.26 (SEQ ID NO: 17 and 33 of US20150159173), hu.37 (SEQ ID NO: 18 and 34 of US20150159173), hu.53 (SEQ ID NO: 19 and 35 of US20150159173), rh.43 (SEQ ID NO: 21 and 37 of US20150159173), rh2 (SEQ ID NO: 39 of US20150159173), rh.37 (SEQ ID NO: 40 of US20150159173), rh.64 (SEQ ID NO: 43 of US20150159173), rh.48 (SEQ ID NO: 44 of US20150159173), ch.5 (SEQ ID NO 46 of US20150159173), rh.67 (SEQ ID NO: 47 of US20150159173), rh.58 (SEQ ID NO: 48 of US20150159173), or variants thereof including, but not limited to Cy5R1, Cy5R2, Cy5R3, Cy5R4, rh.13R, rh.37R2, rh.2R, rh.8R, rh.48.1, rh.48.2, rh.48.1.2, hu.44R1, hu.44R2, hu.44R3, hu.29R, ch.5R1, rh64R1, rh64R2, AAV6.2, AAV6.1, AAV6.12, hu.48R1, hu.48R2, and hu.48R3.

[00035] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 7198951, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 1-3 of US 7198951), AAV2 (SEQ ID NO: 4 of US 7198951), AAV1 (SEQ ID NO: 5 of US 7198951), AAV3 (SEQ ID NO: 6 of US 7198951), and AAV8 (SEQ ID NO: 7 of US7198951).

[00036] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV9 sequence as described by N Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011), herein incorporated by reference in its entirety), such as but not limited to, AAV9.9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84.

[00037] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 6156303, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV3B (SEQ ID NO: 1 and 10 of US 6156303), AAV6 (SEQ ID NO: 2, 7 and 11 of US 6156303), AAV2 (SEQ ID NO: 3 and 8 of US 6156303), AAV3A (SEQ ID NO: 4 and 9, of US 6156303), or derivatives thereof.

[00038] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20140359799, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV8 (SEQ ID NO: 1 of US20140359799), AAVDJ (SEQ ID NO: 2 and 3 of US20140359799), or variants thereof.

[00039] In some embodiments, the serotype may be AAVDJ or a variant thereof, such as AAVDJ8 (or AAV-DJ8), as described by Grimm et al. (Journal of Virology 82(12): 5887-5911 (2008), herein incorporated by reference in its entirety). The amino acid sequence of AAVDJ8 may comprise two or more mutations in order to remove the heparin binding domain (HBD). As a non-limiting example, the AAV-DJ sequence described as SEQ ID NO: 1 in US Patent No. 7,588,772, the contents of which are herein incorporated by reference in their entirety, may comprise two mutations: (1) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (2) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr). As another non-limiting example, may comprise three mutations: (1) K406R where lysine (K; Lys) at amino acid 406 is changed to arginine (R; Arg), (2) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (3) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr).

[00040] In some embodiments, the AAV serotype may be, or have, a sequence of AAV4 as described in International Publication No. WO1998011244, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV4 (SEQ ID NO: 1-20 of WO1998011244).

[00041] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV2 sequence to generate AAV2G9 as described in International Publication No. WO2014144229 and herein incorporated by reference in its entirety.

[00042] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2005033321, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV3-3 (SEQ ID NO: 217 of WO2005033321), AAV1 (SEQ ID NO: 219 and 202 of WO2005033321), AAV106.1/hu.37 (SEQ ID No: 10 of WO2005033321), AAV114.3/hu.40 (SEQ ID No: 11 of WO2005033321), AAV127.2/hu.41 (SEQ ID NO:6 and 8 of WO2005033321), AAV128.3/hu.44 (SEQ ID No: 81 of WO2005033321), AAV130.4/hu.48 (SEQ ID NO: 78 of WO2005033321), AAV145.1/hu.53 (SEQ ID No: 176 and 177 of WO2005033321), AAV145.6/hu.56 (SEQ ID NO: 168 and 192 of WO2005033321), AAV16.12/hu.11 (SEQ ID NO: 153 and 57 of WO2005033321), AAV16.8/hu.10 (SEQ ID NO: 156 and 56 of WO2005033321), AAV161.10/hu.60 (SEQ ID No: 170 of WO2005033321), AAV161.6/hu.61 (SEQ ID No: 174 of WO2005033321), AAV1-7/rh.48 (SEQ ID NO: 32 of WO2005033321), AAV1-8/rh.49 (SEQ ID NOs: 103 and 25 of WO2005033321), AAV2 (SEQ ID NO: 211 and 221 of WO2005033321), AAV2-15/rh.62 (SEQ ID No: 33 and 114 of WO2005033321), AAV2-3/rh.61 (SEQ ID NO: 21 of WO2005033321), AAV2-4/rh.50 (SEQ ID No: 23 and 108 of WO2005033321), AAV2-5/rh.51 (SEQ ID NO: 104 and 22 of WO2005033321), AAV3.1/hu.6 (SEQ ID NO: 5 and 84 of WO2005033321), AAV3.1/hu.9 (SEQ ID NO: 155 and 58 of WO2005033321), AAV3-11/rh.53 (SEQ ID NO: 186 and 176 of WO2005033321), AAV3-3 (SEQ ID NO: 200 of WO2005033321), AAV33.12/hu.17 (SEQ ID NO:4 of WO2005033321), AAV33.4/hu.15 (SEQ ID No: 50 of WO2005033321), AAV33.8/hu.16 (SEQ ID No: 51 of WO2005033321), AAV3-9/rh.52 (SEQ ID NO: 96 and 18 of WO2005033321), AAV4-19/rh.55 (SEQ ID NO: 117 of WO2005033321), AAV4-4 (SEQ ID NO: 201 and 218 of WO2005033321), AAV4-9/rh.54 (SEQ ID NO: 116 of WO2005033321), AAV5 (SEQ ID NO: 199 and 216 of WO2005033321), AAV52.1/hu.20 (SEQ ID NO: 63 of WO2005033321), AAV52/hu.19 (SEQ ID NO: 133 of WO2005033321), AAV5-22/rh.58 (SEQ ID No: 27 of WO2005033321), AAV5-3/rh.57 (SEQ ID NO: 105 of WO2005033321), AAV5-3/rh.57 (SEQ ID No: 26 of WO2005033321), AAV58.2/hu.25 (SEQ ID No: 49 of WO2005033321), AAV6 (SEQ ID NO: 203 and 220 of WO2005033321), AAV7 (SEQ ID NO: 222 and 213 of WO2005033321), AAV7.3/hu.7 (SEQ ID No: 55 of WO2005033321), AAV8 (SEQ ID NO: 223 and 214 of WO2005033321),

AAVH-1/hu.1 (SEQ ID No: 46 of WO2005033321), AAVH-5/hu.3 (SEQ ID No: 44 of WO2005033321), AAVhu.1 (SEQ ID NO: 144 of WO2005033321), AAVhu.10 (SEQ ID NO: 156 of WO2005033321), AAVhu.11 (SEQ ID NO: 153 of WO2005033321), AAVhu.12 (WO2005033321 SEQ ID NO: 59), AAVhu.13 (SEQ ID NO: 129 of WO2005033321), AAVhu.14/AAV9 (SEQ ID NO: 123 and 3 of WO2005033321), AAVhu.15 (SEQ ID NO: 147 of WO2005033321), AAVhu.16 (SEQ ID NO: 148 of WO2005033321), AAVhu.17 (SEQ ID NO: 83 of WO2005033321), AAVhu.18 (SEQ ID NO: 149 of WO2005033321), AAVhu.19 (SEQ ID NO: 133 of WO2005033321), AAVhu.2 (SEQ ID NO: 143 of WO2005033321), AAVhu.20 (SEQ ID NO: 134 of WO2005033321), AAVhu.21 (SEQ ID NO: 135 of WO2005033321), AAVhu.22 (SEQ ID NO: 138 of WO2005033321), AAVhu.23.2 (SEQ ID NO: 137 of WO2005033321), AAVhu.24 (SEQ ID NO: 136 of WO2005033321), AAVhu.25 (SEQ ID NO: 146 of WO2005033321), AAVhu.27 (SEQ ID NO: 140 of WO2005033321), AAVhu.29 (SEQ ID NO: 132 of WO2005033321), AAVhu.3 (SEQ ID NO: 145 of WO2005033321), AAVhu.31 (SEQ ID NO: 121 of WO2005033321), AAVhu.32 (SEQ ID NO: 122 of WO2005033321), AAVhu.34 (SEQ ID NO: 125 of WO2005033321), AAVhu.35 (SEQ ID NO: 164 of WO2005033321), AAVhu.37 (SEQ ID NO: 88 of WO2005033321), AAVhu.39 (SEQ ID NO: 102 of WO2005033321), AAVhu.4 (SEQ ID NO: 141 of WO2005033321), AAVhu.40 (SEQ ID NO: 87 of WO2005033321), AAVhu.41 (SEQ ID NO: 91 of WO2005033321), AAVhu.42 (SEQ ID NO: 85 of WO2005033321), AAVhu.43 (SEQ ID NO: 160 of WO2005033321), AAVhu.44 (SEQ ID NO: 144 of WO2005033321), AAVhu.45 (SEQ ID NO: 127 of WO2005033321), AAVhu.46 (SEQ ID NO: 159 of WO2005033321), AAVhu.47 (SEQ ID NO: 128 of WO2005033321), AAVhu.48 (SEQ ID NO: 157 of WO2005033321), AAVhu.49 (SEQ ID NO: 189 of WO2005033321), AAVhu.51 (SEQ ID NO: 190 of WO2005033321), AAVhu.52 (SEQ ID NO: 191 of WO2005033321), AAVhu.53 (SEQ ID NO: 186 of WO2005033321), AAVhu.54 (SEQ ID NO: 188 of WO2005033321), AAVhu.55 (SEQ ID NO: 187 of WO2005033321), AAVhu.56 (SEQ ID NO: 192 of WO2005033321), AAVhu.57 (SEQ ID NO: 193 of WO2005033321), AAVhu.58 (SEQ ID NO: 194 of WO2005033321), AAVhu.6 (SEQ ID NO: 84 of WO2005033321), AAVhu.60 (SEQ ID NO: 184 of WO2005033321), AAVhu.61 (SEQ ID NO: 185 of WO2005033321), AAVhu.63 (SEQ ID NO: 195 of WO2005033321), AAVhu.64 (SEQ ID NO: 196 of WO2005033321), AAVhu.66 (SEQ ID NO: 197 of WO2005033321), AAVhu.67 (SEQ ID NO: 198 of WO2005033321), AAVhu.7 (SEQ ID NO: 150 of WO2005033321), AAVhu.8 (WO2005033321 SEQ ID NO: 12), AAVhu.9 (SEQ ID NO:

155 of WO2005033321), AAVLG-10/rh.40 (SEQ ID No: 14 of WO2005033321), AAVLG-4/rh.38 (SEQ ID NO: 86 of WO2005033321), AAVLG-4/rh.38 (SEQ ID No: 7 of WO2005033321), AAVN721-8/rh.43 (SEQ ID NO: 163 of WO2005033321), AAVN721-8/rh.43 (SEQ ID No: 43 of WO2005033321), AAVpi.1 (WO2005033321 SEQ ID NO: 28), AAVpi.2 (WO2005033321 SEQ ID NO: 30), AAVpi.3 (WO2005033321 SEQ ID NO: 29), AAVrh.38 (SEQ ID NO: 86 of WO2005033321), AAVrh.40 (SEQ ID NO: 92 of WO2005033321), AAVrh.43 (SEQ ID NO: 163 of WO2005033321), AAVrh.44 (WO2005033321 SEQ ID NO: 34), AAVrh.45 (WO2005033321 SEQ ID NO: 41), AAVrh.47 (WO2005033321 SEQ ID NO: 38), AAVrh.48 (SEQ ID NO: 115 of WO2005033321), AAVrh.49 (SEQ ID NO: 103 of WO2005033321), AAVrh.50 (SEQ ID NO: 108 of WO2005033321), AAVrh.51 (SEQ ID NO: 104 of WO2005033321), AAVrh.52 (SEQ ID NO: 96 of WO2005033321), AAVrh.53 (SEQ ID NO: 97 of WO2005033321), AAVrh.55 (WO2005033321 SEQ ID NO: 37), AAVrh.56 (SEQ ID NO: 152 of WO2005033321), AAVrh.57 (SEQ ID NO: 105 of WO2005033321), AAVrh.58 (SEQ ID NO: 106 of WO2005033321), AAVrh.59 (WO2005033321 SEQ ID NO: 42), AAVrh.60 (WO2005033321 SEQ ID NO: 31), AAVrh.61 (SEQ ID NO: 107 of WO2005033321), AAVrh.62 (SEQ ID NO: 114 of WO2005033321), AAVrh.64 (SEQ ID NO: 99 of WO2005033321), AAVrh.65 (WO2005033321 SEQ ID NO: 35), AAVrh.68 (WO2005033321 SEQ ID NO: 16), AAVrh.69 (WO2005033321 SEQ ID NO: 39), AAVrh.70 (WO2005033321 SEQ ID NO: 20), AAVrh.72 (WO2005033321 SEQ ID NO: 9), or variants thereof including, but not limited to, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVcy.6, AAVrh.12, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.25/42 15, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.14. Non limiting examples of variants include SEQ ID NO: 13, 15, 17, 19, 24, 36, 40, 45, 47, 48, 51-54, 60-62, 64-77, 79, 80, 82, 89, 90, 93-95, 98, 100, 101, , 109-113, 118-120, 124, 126, 131, 139, 142, 151,154, 158, 161, 162, 165-183, 202, 204-212, 215, 219, 224-236, of WO2005033321, the contents of which are herein incorporated by reference in their entirety.

[00043] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015168666, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVrh8R (SEQ ID NO: 9 of WO2015168666), AAVrh8R A586R mutant (SEQ ID NO: 10 of WO2015168666), AAVrh8R R533A mutant (SEQ ID NO: 11 of WO2015168666), or variants thereof.

[00044] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US9233131, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVhE1.1 (SEQ ID NO:44 of US9233131), AAVhEr1.5 (SEQ ID NO:45 of US9233131), AAVhER1.14 (SEQ ID NO:46 of US9233131), AAVhEr1.8 (SEQ ID NO:47 of US9233131), AAVhEr1.16 (SEQ ID NO:48 of US9233131), AAVhEr1.18 (SEQ ID NO:49 of US9233131), AAVhEr1.35 (SEQ ID NO:50 of US9233131), AAVhEr1.7 (SEQ ID NO:51 of US9233131), AAVhEr1.36 (SEQ ID NO:52 of US9233131), AAVhEr2.29 (SEQ ID NO:53 of US9233131), AAVhEr2.4 (SEQ ID NO:54 of US9233131), AAVhEr2.16 (SEQ ID NO:55 of US9233131), AAVhEr2.30 (SEQ ID NO:56 of US9233131), AAVhEr2.31 (SEQ ID NO:58 of US9233131), AAVhEr2.36 (SEQ ID NO:57 of US9233131), AAVhER1.23 (SEQ ID NO:53 of US9233131), AAVhEr3.1 (SEQ ID NO:59 of US9233131), AAV2.5T (SEQ ID NO:42 of US9233131), or variants thereof.

[00045] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150376607, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-PAEC (SEQ ID NO:1 of US20150376607), AAV-LK01 (SEQ ID NO:2 of US20150376607), AAV-LK02 (SEQ ID NO:3 of US20150376607), AAV-LK03 (SEQ ID NO:4 of US20150376607), AAV-LK04 (SEQ ID NO:5 of US20150376607), AAV-LK05 (SEQ ID NO:6 of US20150376607), AAV-LK06 (SEQ ID NO:7 of US20150376607), AAV-LK07 (SEQ ID NO:8 of US20150376607), AAV-LK08 (SEQ ID NO:9 of US20150376607), AAV-LK09 (SEQ ID NO:10 of US20150376607), AAV-LK10 (SEQ ID NO:11 of US20150376607), AAV-LK11 (SEQ ID NO:12 of US20150376607), AAV-LK12 (SEQ ID NO:13 of US20150376607), AAV-LK13 (SEQ ID NO:14 of US20150376607), AAV-LK14 (SEQ ID NO:15 of US20150376607), AAV-LK15 (SEQ ID NO:16 of US20150376607), AAV-LK16 (SEQ ID NO:17 of US20150376607), AAV-LK17 (SEQ ID NO:18 of US20150376607), AAV-LK18 (SEQ ID NO:19 of US20150376607), AAV-LK19 (SEQ ID NO:20 of US20150376607), AAV-PAEC2 (SEQ ID NO:21 of US20150376607), AAV-PAEC4 (SEQ ID NO:22 of US20150376607), AAV-PAEC6 (SEQ ID NO:23 of US20150376607), AAV-PAEC7 (SEQ ID NO:24 of US20150376607), AAV-PAEC8 (SEQ ID NO:25 of US20150376607), AAV-PAEC11 (SEQ ID NO:26 of US20150376607), AAV-PAEC12 (SEQ ID NO:27, of US20150376607), or variants thereof.

[00046] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US9163261, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-2-pre-miRNA-101 (SEQ ID NO: 1 US9163261), or variants thereof.

[00047] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150376240, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-8h (SEQ ID NO: 6 of US20150376240), AAV-8b (SEQ ID NO: 5 of US20150376240), AAV-h (SEQ ID NO: 2 of US20150376240), AAV-b (SEQ ID NO: 1 of US20150376240), or variants thereof.

[00048] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20160017295, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV SM 10-2 (SEQ ID NO: 22 of US20160017295), AAV Shuffle 100-1 (SEQ ID NO: 23 of US20160017295), AAV Shuffle 100-3 (SEQ ID NO: 24 of US20160017295), AAV Shuffle 100-7 (SEQ ID NO: 25 of US20160017295), AAV Shuffle 10-2 (SEQ ID NO: 34 of US20160017295), AAV Shuffle 10-6 (SEQ ID NO: 35 of US20160017295), AAV Shuffle 10-8 (SEQ ID NO: 36 of US20160017295), AAV Shuffle 100-2 (SEQ ID NO: 37 of US20160017295), AAV SM 10-1 (SEQ ID NO: 38 of US20160017295), AAV SM 10-8 (SEQ ID NO: 39 of US20160017295), AAV SM 100-3 (SEQ ID NO: 40 of US20160017295), AAV SM 100-10 (SEQ ID NO: 41 of US20160017295), or variants thereof.

[00049] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150238550, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BNP61 AAV (SEQ ID NO: 1 of US20150238550), BNP62 AAV (SEQ ID NO: 3 of US20150238550), BNP63 AAV (SEQ ID NO: 4 of US20150238550), or variants thereof.

[00050] In some embodiments, the AAV serotype may be or may have a sequence as described in United States Patent Publication No. US20150315612, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVrh.50 (SEQ ID NO: 108 of US20150315612), AAVrh.43 (SEQ ID NO: 163 of US20150315612), AAVrh.62 (SEQ ID NO: 114 of US20150315612), AAVrh.48 (SEQ ID NO: 115 of US20150315612), AAVhu.19 (SEQ ID NO: 133 of US20150315612), AAVhu.11 (SEQ ID NO: 153 of US20150315612), AAVhu.53 (SEQ ID NO: 186 of US20150315612), AAV4-8/rh.64 (SEQ ID No: 15 of US20150315612), AAVLG-

9/hu.39 (SEQ ID No: 24 of US20150315612), AAV54.5/hu.23 (SEQ ID No: 60 of US20150315612), AAV54.2/hu.22 (SEQ ID No: 67 of US20150315612), AAV54.7/hu.24 (SEQ ID No: 66 of US20150315612), AAV54.1/hu.21 (SEQ ID No: 65 of US20150315612), AAV54.4R/hu.27 (SEQ ID No: 64 of US20150315612), AAV46.2/hu.28 (SEQ ID No: 68 of US20150315612), AAV46.6/hu.29 (SEQ ID No: 69 of US20150315612), AAV128.1/hu.43 (SEQ ID No: 80 of US20150315612), or variants thereof.

[00051] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015121501, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, true type AAV (ttAAV) (SEQ ID NO: 2 of WO2015121501), “UPenn AAV10” (SEQ ID NO: 8 of WO2015121501), “Japanese AAV10” (SEQ ID NO: 9 of WO2015121501), or variants thereof.

[00052] According to the present invention, AAV capsid serotype selection or use may be from a variety of species. In one embodiment, the AAV may be an avian AAV (AAAV). The AAAV serotype may be, or have, a sequence as described in United States Patent No. US 9238800, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAAV (SEQ ID NO: 1, 2, 4, 6, 8, 10, 12, and 14 of US 9,238,800), or variants thereof.

[00053] In one embodiment, the AAV may be a bovine AAV (BAAV). The BAAV serotype may be, or have, a sequence as described in United States Patent No. US 9,193,769, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 1 and 6 of US 9193769), or variants thereof. The BAAV serotype may be or have a sequence as described in United States Patent No. US7427396, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 5 and 6 of US7427396), or variants thereof.

[00054] In one embodiment, the AAV may be a caprine AAV. The caprine AAV serotype may be, or have, a sequence as described in United States Patent No. US7427396, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, caprine AAV (SEQ ID NO: 3 of US7427396), or variants thereof.

[00055] In other embodiments the AAV may be engineered as a hybrid AAV from two or more parental serotypes. In one embodiment, the AAV may be AAV2G9 which comprises sequences from AAV2 and AAV9. The AAV2G9 AAV serotype may be, or have, a sequence as described in

United States Patent Publication No. US20160017005, the contents of which are herein incorporated by reference in its entirety.

[00056] In one embodiment, the AAV may be a serotype generated by the AAV9 capsid library with mutations in amino acids 390-627 (VP1 numbering) as described by Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011), the contents of which are herein incorporated by reference in their entirety. The serotype and corresponding nucleotide and amino acid substitutions may be, but is not limited to, AAV9.1 (G1594C; D532H), AAV6.2 (T1418A and T1436X; V473D and I479K), AAV9.3 (T1238A; F413Y), AAV9.4 (T1250C and A1617T; F417S), AAV9.5 (A1235G, A1314T, A1642G, C1760T; Q412R, T548A, A587V), AAV9.6 (T1231A; F411I), AAV9.9 (G1203A, G1785T; W595C), AAV9.10 (A1500G, T1676C; M559T), AAV9.11 (A1425T, A1702C, A1769T; T568P, Q590L), AAV9.13 (A1369C, A1720T; N457H, T574S), AAV9.14 (T1340A, T1362C, T1560C, G1713A; L447H), AAV9.16 (A1775T; Q592L), AAV9.24 (T1507C, T1521G; W503R), AAV9.26 (A1337G, A1769C; Y446C, Q590P), AAV9.33 (A1667C; D556A), AAV9.34 (A1534G, C1794T; N512D), AAV9.35 (A1289T, T1450A, C1494T, A1515T, C1794A, G1816A; Q430L, Y484N, N98K, V606I), AAV9.40 (A1694T, E565V), AAV9.41 (A1348T, T1362C; T450S), AAV9.44 (A1684C, A1701T, A1737G; N562H, K567N), AAV9.45 (A1492T, C1804T; N498Y, L602F), AAV9.46 (G1441C, T1525C, T1549G; G481R, W509R, L517V), 9.47 (G1241A, G1358A, A1669G, C1745T; S414N, G453D, K557E, T582I), AAV9.48 (C1445T, A1736T; P482L, Q579L), AAV9.50 (A1638T, C1683T, T1805A; Q546H, L602H), AAV9.53 (G1301A, A1405C, C1664T, G1811T; R134Q, S469R, A555V, G604V), AAV9.54 (C1531A, T1609A; L511I, L537M), AAV9.55 (T1605A; F535L), AAV9.58 (C1475T, C1579A; T492I, H527N), AAV.59 (T1336C; Y446H), AAV9.61 (A1493T; N498I), AAV9.64 (C1531A, A1617T; L511I), AAV9.65 (C1335T, T1530C, C1568A; A523D), AAV9.68 (C1510A; P504T), AAV9.80 (G1441A,;G481R), AAV9.83 (C1402A, A1500T; P468T, E500D), AAV9.87 (T1464C, T1468C; S490P), AAV9.90 (A1196T; Y399F), AAV9.91 (T1316G, A1583T, C1782G, T1806C; L439R, K528I), AAV9.93 (A1273G, A1421G, A1638C, C1712T, G1732A, A1744T, A1832T; S425G, Q474R, Q546H, P571L, G578R, T582S, D611V), AAV9.94 (A1675T; M559L) and AAV9.95 (T1605A; F535L).

[00057] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016049230, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAVF1/HSC1 (SEQ ID NO: 2 and 20 of

WO2016049230), AAVF2/HSC2 (SEQ ID NO: 3 and 21 of WO2016049230), AAVF3/HSC3 (SEQ ID NO: 5 and 22 of WO2016049230), AAVF4/HSC4 (SEQ ID NO: 6 and 23 of WO2016049230), AAVF5/HSC5 (SEQ ID NO: 11 and 25 of WO2016049230), AAVF6/HSC6 (SEQ ID NO: 7 and 24 of WO2016049230), AAVF7/HSC7 (SEQ ID NO: 8 and 27 of WO2016049230), AAVF8/HSC8 (SEQ ID NO: 9 and 28 of WO2016049230), AAVF9/HSC9 (SEQ ID NO: 10 and 29 of WO2016049230), AAVF11/HSC11 (SEQ ID NO: 4 and 26 of WO2016049230), AAVF12/HSC12 (SEQ ID NO: 12 and 30 of WO2016049230), AAVF13/HSC13 (SEQ ID NO: 14 and 31 of WO2016049230), AAVF14/HSC14 (SEQ ID NO: 15 and 32 of WO2016049230), AAVF15/HSC15 (SEQ ID NO: 16 and 33 of WO2016049230), AAVF16/HSC16 (SEQ ID NO: 17 and 34 of WO2016049230), AAVF17/HSC17 (SEQ ID NO: 13 and 35 of WO2016049230), or variants or derivatives thereof.

[00058] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 8734809, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV CBr-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CBr-E2 (SEQ ID NO: 14 and 88 of US8734809), AAV CBr-E3 (SEQ ID NO: 15 and 89 of US8734809), AAV CBr-E4 (SEQ ID NO: 16 and 90 of US8734809), AAV CBr-E5 (SEQ ID NO: 17 and 91 of US8734809), AAV CBr-e5 (SEQ ID NO: 18 and 92 of US8734809), AAV CBr-E6 (SEQ ID NO: 19 and 93 of US8734809), AAV CBr-E7 (SEQ ID NO: 20 and 94 of US8734809), AAV CBr-E8 (SEQ ID NO: 21 and 95 of US8734809), AAV CLv-D1 (SEQ ID NO: 22 and 96 of US8734809), AAV CLv-D2 (SEQ ID NO: 23 and 97 of US8734809), AAV CLv-D3 (SEQ ID NO: 24 and 98 of US8734809), AAV CLv-D4 (SEQ ID NO: 25 and 99 of US8734809), AAV CLv-D5 (SEQ ID NO: 26 and 100 of US8734809), AAV CLv-D6 (SEQ ID NO: 27 and 101 of US8734809), AAV CLv-D7 (SEQ ID NO: 28 and 102 of US8734809), AAV CLv-D8 (SEQ ID NO: 29 and 103 of US8734809), AAV CLv-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CLv-R1 (SEQ ID NO: 30 and 104 of US8734809), AAV CLv-R2 (SEQ ID NO: 31 and 105 of US8734809), AAV CLv-R3 (SEQ ID NO: 32 and 106 of US8734809), AAV CLv-R4 (SEQ ID NO: 33 and 107 of US8734809), AAV CLv-R5 (SEQ ID NO: 34 and 108 of US8734809), AAV CLv-R6 (SEQ ID NO: 35 and 109 of US8734809), AAV CLv-R7 (SEQ ID NO: 36 and 110 of US8734809), AAV CLv-R8 (SEQ ID NO: X and X of US8734809), AAV CLv-R9 (SEQ ID NO: X and X of US8734809), AAV CLg-F1 (SEQ ID NO: 39 and 113 of US8734809), AAV CLg-F2 (SEQ ID NO: 40 and 114 of US8734809), AAV CLg-F3 (SEQ ID NO: 41 and 115 of US8734809), AAV CLg-F4 (SEQ ID NO:

42 and 116 of US8734809), AAV CLg-F5 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F6 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F7 (SEQ ID NO: 44 and 118 of US8734809), AAV CLg-F8 (SEQ ID NO: 43 and 117 of US8734809), AAV CSp-1 (SEQ ID NO: 45 and 119 of US8734809), AAV CSp-10 (SEQ ID NO: 46 and 120 of US8734809), AAV CSp-11 (SEQ ID NO: 47 and 121 of US8734809), AAV CSp-2 (SEQ ID NO: 48 and 122 of US8734809), AAV CSp-3 (SEQ ID NO: 49 and 123 of US8734809), AAV CSp-4 (SEQ ID NO: 50 and 124 of US8734809), AAV CSp-6 (SEQ ID NO: 51 and 125 of US8734809), AAV CSp-7 (SEQ ID NO: 52 and 126 of US8734809), AAV CSp-8 (SEQ ID NO: 53 and 127 of US8734809), AAV CSp-9 (SEQ ID NO: 54 and 128 of US8734809), AAV CHt-2 (SEQ ID NO: 55 and 129 of US8734809), AAV CHt-3 (SEQ ID NO: 56 and 130 of US8734809), AAV CKd-1 (SEQ ID NO: 57 and 131 of US8734809), AAV CKd-10 (SEQ ID NO: 58 and 132 of US8734809), AAV CKd-2 (SEQ ID NO: 59 and 133 of US8734809), AAV CKd-3 (SEQ ID NO: 60 and 134 of US8734809), AAV CKd-4 (SEQ ID NO: 61 and 135 of US8734809), AAV CKd-6 (SEQ ID NO: 62 and 136 of US8734809), AAV CKd-7 (SEQ ID NO: 63 and 137 of US8734809), AAV CKd-8 (SEQ ID NO: 64 and 138 of US8734809), AAV CLv-1 (SEQ ID NO: 35 and 139 of US8734809), AAV CLv-12 (SEQ ID NO: 66 and 140 of US8734809), AAV CLv-13 (SEQ ID NO: 67 and 141 of US8734809), AAV CLv-2 (SEQ ID NO: 68 and 142 of US8734809), AAV CLv-3 (SEQ ID NO: 69 and 143 of US8734809), AAV CLv-4 (SEQ ID NO: 70 and 144 of US8734809), AAV CLv-6 (SEQ ID NO: 71 and 145 of US8734809), AAV CLv-8 (SEQ ID NO: 72 and 146 of US8734809), AAV CKd-B1 (SEQ ID NO: 73 and 147 of US8734809), AAV CKd-B2 (SEQ ID NO: 74 and 148 of US8734809), AAV CKd-B3 (SEQ ID NO: 75 and 149 of US8734809), AAV CKd-B4 (SEQ ID NO: 76 and 150 of US8734809), AAV CKd-B5 (SEQ ID NO: 77 and 151 of US8734809), AAV CKd-B6 (SEQ ID NO: 78 and 152 of US8734809), AAV CKd-B7 (SEQ ID NO: 79 and 153 of US8734809), AAV CKd-B8 (SEQ ID NO: 80 and 154 of US8734809), AAV CKd-H1 (SEQ ID NO: 81 and 155 of US8734809), AAV CKd-H2 (SEQ ID NO: 82 and 156 of US8734809), AAV CKd-H3 (SEQ ID NO: 83 and 157 of US8734809), AAV CKd-H4 (SEQ ID NO: 84 and 158 of US8734809), AAV CKd-H5 (SEQ ID NO: 85 and 159 of US8734809), AAV CKd-H6 (SEQ ID NO: 77 and 151 of US8734809), AAV CHt-1 (SEQ ID NO: 86 and 160 of US8734809), AAV CLv1-1 (SEQ ID NO: 171 of US8734809), AAV CLv1-2 (SEQ ID NO: 172 of US8734809), AAV CLv1-3 (SEQ ID NO: 173 of US8734809), AAV CLv1-4 (SEQ ID NO: 174 of US8734809), AAV Clv1-7 (SEQ ID NO: 175 of US8734809), AAV Clv1-8 (SEQ ID NO: 176 of US8734809), AAV Clv1-9 (SEQ ID NO: 177 of US8734809),

AAV Clv1-10 (SEQ ID NO: 178 of US8734809), AAV.VR-355 (SEQ ID NO: 181 of US8734809), AAV.hu.48R3 (SEQ ID NO: 183 of US8734809), or variants or derivatives thereof.

[00059] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016065001, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV CHt-P2 (SEQ ID NO: 1 and 51 of WO2016065001), AAV CHt-P5 (SEQ ID NO: 2 and 52 of WO2016065001), AAV CHt-P9 (SEQ ID NO: 3 and 53 of WO2016065001), AAV CBr-7.1 (SEQ ID NO: 4 and 54 of WO2016065001), AAV CBr-7.2 (SEQ ID NO: 5 and 55 of WO2016065001), AAV CBr-7.3 (SEQ ID NO: 6 and 56 of WO2016065001), AAV CBr-7.4 (SEQ ID NO: 7 and 57 of WO2016065001), AAV CBr-7.5 (SEQ ID NO: 8 and 58 of WO2016065001), AAV CBr-7.7 (SEQ ID NO: 9 and 59 of WO2016065001), AAV CBr-7.8 (SEQ ID NO: 10 and 60 of WO2016065001), AAV CBr-7.10 (SEQ ID NO: 11 and 61 of WO2016065001), AAV CKd-N3 (SEQ ID NO: 12 and 62 of WO2016065001), AAV CKd-N4 (SEQ ID NO: 13 and 63 of WO2016065001), AAV CKd-N9 (SEQ ID NO: 14 and 64 of WO2016065001), AAV CLv-L4 (SEQ ID NO: 15 and 65 of WO2016065001), AAV CLv-L5 (SEQ ID NO: 16 and 66 of WO2016065001), AAV CLv-L6 (SEQ ID NO: 17 and 67 of WO2016065001), AAV CLv-K1 (SEQ ID NO: 18 and 68 of WO2016065001), AAV CLv-K3 (SEQ ID NO: 19 and 69 of WO2016065001), AAV CLv-K6 (SEQ ID NO: 20 and 70 of WO2016065001), AAV CLv-M1 (SEQ ID NO: 21 and 71 of WO2016065001), AAV CLv-M11 (SEQ ID NO: 22 and 72 of WO2016065001), AAV CLv-M2 (SEQ ID NO: 23 and 73 of WO2016065001), AAV CLv-M5 (SEQ ID NO: 24 and 74 of WO2016065001), AAV CLv-M6 (SEQ ID NO: 25 and 75 of WO2016065001), AAV CLv-M7 (SEQ ID NO: 26 and 76 of WO2016065001), AAV CLv-M8 (SEQ ID NO: 27 and 77 of WO2016065001), AAV CLv-M9 (SEQ ID NO: 28 and 78 of WO2016065001), AAV CHt-P1 (SEQ ID NO: 29 and 79 of WO2016065001), AAV CHt-P6 (SEQ ID NO: 30 and 80 of WO2016065001), AAV CHt-P8 (SEQ ID NO: 31 and 81 of WO2016065001), AAV CHt-6.1 (SEQ ID NO: 32 and 82 of WO2016065001), AAV CHt-6.10 (SEQ ID NO: 33 and 83 of WO2016065001), AAV CHt-6.5 (SEQ ID NO: 34 and 84 of WO2016065001), AAV CHt-6.6 (SEQ ID NO: 35 and 85 of WO2016065001), AAV CHt-6.7 (SEQ ID NO: 36 and 86 of WO2016065001), AAV CHt-6.8 (SEQ ID NO: 37 and 87 of WO2016065001), AAV CSp-8.10 (SEQ ID NO: 38 and 88 of WO2016065001), AAV CSp-8.2 (SEQ ID NO: 39 and 89 of WO2016065001), AAV CSp-8.4 (SEQ ID NO: 40 and 90 of WO2016065001), AAV CSp-8.5 (SEQ ID NO: 41 and 91 of WO2016065001), AAV CSp-8.6 (SEQ ID NO: 42 and 92 of WO2016065001),

AAV CSp-8.7 (SEQ ID NO: 43 and 93 of WO2016065001), AAV CSp-8.8 (SEQ ID NO: 44 and 94 of WO2016065001), AAV CSp-8.9 (SEQ ID NO: 45 and 95 of WO2016065001), AAV CBr-B7.3 (SEQ ID NO: 46 and 96 of WO2016065001), AAV CBr-B7.4 (SEQ ID NO: 47 and 97 of WO2016065001), AAV3B (SEQ ID NO: 48 and 98 of WO2016065001), AAV4 (SEQ ID NO: 49 and 99 of WO2016065001), AAV5 (SEQ ID NO: 50 and 100 of WO2016065001), or variants or derivatives thereof.

[00060] In some embodiments, the AAV serotype may be, or have, a modification as described in United States Publication No. US 20160361439, the contents of which are herein incorporated by reference in their entirety, such as but not limited to, Y252F, Y272F, Y444F, Y500F, Y700F, Y704F, Y730F, Y275F, Y281F, Y508F, Y576F, Y612G, Y673F, and Y720F of the wild-type AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, and hybrids thereof.

[00061] In some embodiments, the AAV serotype may be, or have, a mutation as described in United States Patent No. US 9546112, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, at least two, but not all the F129L, D418E, K531E, L584F, V598A and H642N mutations in the sequence of AAV6 (SEQ ID NO:4 of US 9546112), AAV1 (SEQ ID NO:6 of US 9546112), AAV2, AAV3, AAV4, AAV5, AAV7, AAV9, AAV10 or AAV11 or derivatives thereof. In yet another embodiment, the AAV serotype may be, or have, an AAV6 sequence comprising the K531E mutation (SEQ ID NO:5 of US 9546112).

[00062] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV1 sequence, as described in in United States Publication No. US 20130224836, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, at least one of the surface-exposed tyrosine residues, preferably, at positions 252, 273, 445, 701, 705 and 731 of AAV1 (SEQ ID NO: 2 of US 20130224836) substituted with another amino acid, preferably with a phenylalanine residue. In one embodiment, the AAV serotype may be, or have, a mutation in the AAV9 sequence, such as, but not limited to, at least one of the surface-exposed tyrosine residues, preferably, at positions 252, 272, 444, 500, 700, 704 and 730 of AAV2 (SEQ ID NO: 4 of US 20130224836) substituted with another amino acid, preferably with a phenylalanine residue. In one embodiment, the tyrosine residue at position 446 of AAV9 (SEQ ID NO: 6 US 20130224836) is substituted with a phenylalanine residue.

[00063] In some embodiments, the serotype may be AAV2 or a variant thereof, as described in International Publication No. WO2016130589, herein incorporated by reference in its entirety. The amino acid sequence of AAV2 may comprise N587A, E548A, or N708A mutations. In one embodiment, the amino acid sequence of any AAV may comprise a V708K mutation.

[00064] In one embodiment, the AAV may be a serotype selected from any of those found in Table 1.

[00065] In one embodiment, the AAV may comprise a sequence, fragment or variant thereof, of the sequences in Table 1.

[00066] In one embodiment, the AAV may be encoded by a sequence, fragment or variant as described in Table 1.

Table 1. AAV Serotypes

Serotype	SEQ ID NO	Reference Information
AAVPHP.B or G2B-26	1	WO2015038958 SEQ ID NO: 8 and 13
AAVPHP.B	2	WO2015038958 SEQ ID NO: 9
AAVG2B-13	3	WO2015038958 SEQ ID NO: 12
AAVTH1.1-32	4	WO2015038958 SEQ ID NO: 14
AAVTH1.1-35	5	WO2015038958 SEQ ID NO: 15
AAV1	6	US20150159173 SEQ ID NO: 11, US20150315612 SEQ ID NO: 202
AAV1	7	US20160017295 SEQ ID NO: 1, US20030138772 SEQ ID NO: 64, US20150159173 SEQ ID NO: 27, US20150315612 SEQ ID NO: 219, US7198951 SEQ ID NO: 5
AAV1	8	US20030138772 SEQ ID NO: 6
AAV1.3	9	US20030138772 SEQ ID NO: 14
AAV10	10	US20030138772 SEQ ID NO: 117
AAV10	11	WO2015121501 SEQ ID NO: 9
AAV10	12	WO2015121501 SEQ ID NO: 8
AAV11	13	US20030138772 SEQ ID NO: 118
AAV12	14	US20030138772 SEQ ID NO: 119
AAV2	15	US20150159173 SEQ ID NO: 7, US20150315612 SEQ ID NO: 211
AAV2	16	US20030138772 SEQ ID NO: 70, US20150159173 SEQ ID NO: 23, US20150315612 SEQ ID NO: 221, US20160017295 SEQ ID NO: 2, US6156303 SEQ ID NO: 4, US7198951 SEQ ID NO: 4, WO2015121501 SEQ ID NO: 1
AAV2	17	US6156303 SEQ ID NO: 8
AAV2	18	US20030138772 SEQ ID NO: 7
AAV2	19	US6156303 SEQ ID NO: 3
AAV2.5T	20	US9233131 SEQ ID NO: 42
AAV223.10	21	US20030138772 SEQ ID NO: 75

AAV223.2	22	US20030138772 SEQ ID NO: 49
AAV223.2	23	US20030138772 SEQ ID NO: 76
AAV223.4	24	US20030138772 SEQ ID NO: 50
AAV223.4	25	US20030138772 SEQ ID NO: 73
AAV223.5	26	US20030138772 SEQ ID NO: 51
AAV223.5	27	US20030138772 SEQ ID NO: 74
AAV223.6	28	US20030138772 SEQ ID NO: 52
AAV223.6	29	US20030138772 SEQ ID NO: 78
AAV223.7	30	US20030138772 SEQ ID NO: 53
AAV223.7	31	US20030138772 SEQ ID NO: 77
AAV29.3	32	US20030138772 SEQ ID NO: 82
AAV29.4	33	US20030138772 SEQ ID NO: 12
AAV29.5	34	US20030138772 SEQ ID NO: 83
AAV29.5 (AAVbb.2)	35	US20030138772 SEQ ID NO: 13
AAV3	36	US20150159173 SEQ ID NO: 12
AAV3	37	US20030138772 SEQ ID NO: 71, US20150159173 SEQ ID NO: 28, US20160017295 SEQ ID NO: 3, US7198951 SEQ ID NO: 6
AAV3	38	US20030138772 SEQ ID NO: 8
AAV3.3b	39	US20030138772 SEQ ID NO: 72
AAV3-3	40	US20150315612 SEQ ID NO: 200
AAV3-3	41	US20150315612 SEQ ID NO: 217
AAV3a	42	US6156303 SEQ ID NO: 5
AAV3a	43	US6156303 SEQ ID NO: 9
AAV3b	44	US6156303 SEQ ID NO: 6
AAV3b	45	US6156303 SEQ ID NO: 10
AAV3b	46	US6156303 SEQ ID NO: 1
AAV4	47	US20140348794 SEQ ID NO: 17
AAV4	48	US20140348794 SEQ ID NO: 5
AAV4	49	US20140348794 SEQ ID NO: 3
AAV4	50	US20140348794 SEQ ID NO: 14
AAV4	51	US20140348794 SEQ ID NO: 15
AAV4	52	US20140348794 SEQ ID NO: 19
AAV4	53	US20140348794 SEQ ID NO: 12
AAV4	54	US20140348794 SEQ ID NO: 13
AAV4	55	US20140348794 SEQ ID NO: 7
AAV4	56	US20140348794 SEQ ID NO: 8
AAV4	57	US20140348794 SEQ ID NO: 9
AAV4	58	US20140348794 SEQ ID NO: 2
AAV4	59	US20140348794 SEQ ID NO: 10
AAV4	60	US20140348794 SEQ ID NO: 11
AAV4	61	US20140348794 SEQ ID NO: 18

AAV4	62	US20030138772 SEQ ID NO: 63, US20160017295 SEQ ID NO: 4, US20140348794 SEQ ID NO: 4
AAV4	63	US20140348794 SEQ ID NO: 16
AAV4	64	US20140348794 SEQ ID NO: 20
AAV4	65	US20140348794 SEQ ID NO: 6
AAV4	66	US20140348794 SEQ ID NO: 1
AAV42.2	67	US20030138772 SEQ ID NO: 9
AAV42.2	68	US20030138772 SEQ ID NO: 102
AAV42.3b	69	US20030138772 SEQ ID NO: 36
AAV42.3B	70	US20030138772 SEQ ID NO: 107
AAV42.4	71	US20030138772 SEQ ID NO: 33
AAV42.4	72	US20030138772 SEQ ID NO: 88
AAV42.8	73	US20030138772 SEQ ID NO: 27
AAV42.8	74	US20030138772 SEQ ID NO: 85
AAV43.1	75	US20030138772 SEQ ID NO: 39
AAV43.1	76	US20030138772 SEQ ID NO: 92
AAV43.12	77	US20030138772 SEQ ID NO: 41
AAV43.12	78	US20030138772 SEQ ID NO: 93
AAV43.20	79	US20030138772 SEQ ID NO: 42
AAV43.20	80	US20030138772 SEQ ID NO: 99
AAV43.21	81	US20030138772 SEQ ID NO: 43
AAV43.21	82	US20030138772 SEQ ID NO: 96
AAV43.23	83	US20030138772 SEQ ID NO: 44
AAV43.23	84	US20030138772 SEQ ID NO: 98
AAV43.25	85	US20030138772 SEQ ID NO: 45
AAV43.25	86	US20030138772 SEQ ID NO: 97
AAV43.5	87	US20030138772 SEQ ID NO: 40
AAV43.5	88	US20030138772 SEQ ID NO: 94
AAV4-4	89	US20150315612 SEQ ID NO: 201
AAV4-4	90	US20150315612 SEQ ID NO: 218
AAV44.1	91	US20030138772 SEQ ID NO: 46
AAV44.1	92	US20030138772 SEQ ID NO: 79
AAV44.5	93	US20030138772 SEQ ID NO: 47
AAV44.5	94	US20030138772 SEQ ID NO: 80
AAV4407	95	US20150315612 SEQ ID NO: 90
AAV5	96	US7427396 SEQ ID NO: 1
AAV5	97	US20030138772 SEQ ID NO: 114
AAV5	98	US20160017295 SEQ ID NO: 5, US7427396 SEQ ID NO: 2, US20150315612 SEQ ID NO: 216
AAV5	99	US20150315612 SEQ ID NO: 199
AAV6	100	US20150159173 SEQ ID NO: 13

AAV6	101	US20030138772 SEQ ID NO: 65, US20150159173 SEQ ID NO: 29, US20160017295 SEQ ID NO: 6, US6156303 SEQ ID NO: 7
AAV6	102	US6156303 SEQ ID NO: 11
AAV6	103	US6156303 SEQ ID NO: 2
AAV6	104	US20150315612 SEQ ID NO: 203
AAV6	105	US20150315612 SEQ ID NO: 220
AAV6.1	106	US20150159173
AAV6.12	107	US20150159173
AAV6.2	108	US20150159173
AAV7	109	US20150159173 SEQ ID NO: 14
AAV7	110	US20150315612 SEQ ID NO: 183
AAV7	111	US20030138772 SEQ ID NO: 2, US20150159173 SEQ ID NO: 30, US20150315612 SEQ ID NO: 181, US20160017295 SEQ ID NO: 7
AAV7	112	US20030138772 SEQ ID NO: 3
AAV7	113	US20030138772 SEQ ID NO: 1, US20150315612 SEQ ID NO: 180
AAV7	114	US20150315612 SEQ ID NO: 213
AAV7	115	US20150315612 SEQ ID NO: 222
AAV8	116	US20150159173 SEQ ID NO: 15
AAV8	117	US20150376240 SEQ ID NO: 7
AAV8	118	US20030138772 SEQ ID NO: 4, US20150315612 SEQ ID NO: 182
AAV8	119	US20030138772 SEQ ID NO: 95, US20140359799 SEQ ID NO: 1, US20150159173 SEQ ID NO: 31, US20160017295 SEQ ID NO: 8, US7198951 SEQ ID NO: 7, US20150315612 SEQ ID NO: 223
AAV8	120	US20150376240 SEQ ID NO: 8
AAV8	121	US20150315612 SEQ ID NO: 214
AAV-8b	122	US20150376240 SEQ ID NO: 5
AAV-8b	123	US20150376240 SEQ ID NO: 3
AAV-8h	124	US20150376240 SEQ ID NO: 6
AAV-8h	125	US20150376240 SEQ ID NO: 4
AAV9	126	US20030138772 SEQ ID NO: 5
AAV9	127	US7198951 SEQ ID NO: 1
AAV9	128	US20160017295 SEQ ID NO: 9
AAV9	129	US20030138772 SEQ ID NO: 100, US7198951 SEQ ID NO: 2
AAV9	130	US7198951 SEQ ID NO: 3
AAV9 (AAVhu.14)	131	US7906111 SEQ ID NO: 3; WO2015038958 SEQ ID NO: 11
AAV9 (AAVhu.14)	132	US7906111 SEQ ID NO: 123; WO2015038958 SEQ ID NO: 2
AAVA3.1	133	US20030138772 SEQ ID NO: 120
AAVA3.3	134	US20030138772 SEQ ID NO: 57

AAVA3.3	135	US20030138772 SEQ ID NO: 66
AAVA3.4	136	US20030138772 SEQ ID NO: 54
AAVA3.4	137	US20030138772 SEQ ID NO: 68
AAVA3.5	138	US20030138772 SEQ ID NO: 55
AAVA3.5	139	US20030138772 SEQ ID NO: 69
AAVA3.7	140	US20030138772 SEQ ID NO: 56
AAVA3.7	141	US20030138772 SEQ ID NO: 67
AAV29.3 (AAVbb.1)	142	US20030138772 SEQ ID NO: 11
AAVC2	143	US20030138772 SEQ ID NO: 61
AAVCh.5	144	US20150159173 SEQ ID NO: 46, US20150315612 SEQ ID NO: 234
AAVcy.2 (AAV13.3)	145	US20030138772 SEQ ID NO: 15
AAV24.1	146	US20030138772 SEQ ID NO: 101
AAVcy.3 (AAV24.1)	147	US20030138772 SEQ ID NO: 16
AAV27.3	148	US20030138772 SEQ ID NO: 104
AAVcy.4 (AAV27.3)	149	US20030138772 SEQ ID NO: 17
AAVcy.5	150	US20150315612 SEQ ID NO: 227
AAV7.2	151	US20030138772 SEQ ID NO: 103
AAVcy.5 (AAV7.2)	152	US20030138772 SEQ ID NO: 18
AAV16.3	153	US20030138772 SEQ ID NO: 105
AAVcy.6 (AAV16.3)	154	US20030138772 SEQ ID NO: 10
AAVcy.5	155	US20150159173 SEQ ID NO: 8
AAVcy.5	156	US20150159173 SEQ ID NO: 24
AAVCy.5R1	157	US20150159173
AAVCy.5R2	158	US20150159173
AAVCy.5R3	159	US20150159173
AAVCy.5R4	160	US20150159173
AAVDJ	161	US20140359799 SEQ ID NO: 3, US7588772 SEQ ID NO: 2
AAVDJ	162	US20140359799 SEQ ID NO: 2, US7588772 SEQ ID NO: 1
AAVDJ-8	163	US7588772; Grimm et al 2008
AAVDJ-8	164	US7588772; Grimm et al 2008
AAVF5	165	US20030138772 SEQ ID NO: 110
AAVH2	166	US20030138772 SEQ ID NO: 26
AAVH6	167	US20030138772 SEQ ID NO: 25
AAVhE1.1	168	US9233131 SEQ ID NO: 44
AAVhEr1.14	169	US9233131 SEQ ID NO: 46
AAVhEr1.16	170	US9233131 SEQ ID NO: 48
AAVhEr1.18	171	US9233131 SEQ ID NO: 49
AAVhEr1.23 (AAVhEr2.29)	172	US9233131 SEQ ID NO: 53
AAVhEr1.35	173	US9233131 SEQ ID NO: 50
AAVhEr1.36	174	US9233131 SEQ ID NO: 52

AAVhEr1.5	175	US9233131 SEQ ID NO: 45
AAVhEr1.7	176	US9233131 SEQ ID NO: 51
AAVhEr1.8	177	US9233131 SEQ ID NO: 47
AAVhEr2.16	178	US9233131 SEQ ID NO: 55
AAVhEr2.30	179	US9233131 SEQ ID NO: 56
AAVhEr2.31	180	US9233131 SEQ ID NO: 58
AAVhEr2.36	181	US9233131 SEQ ID NO: 57
AAVhEr2.4	182	US9233131 SEQ ID NO: 54
AAVhEr3.1	183	US9233131 SEQ ID NO: 59
AAVhu.1	184	US20150315612 SEQ ID NO: 46
AAVhu.1	185	US20150315612 SEQ ID NO: 144
AAVhu.10 (AAV16.8)	186	US20150315612 SEQ ID NO: 56
AAVhu.10 (AAV16.8)	187	US20150315612 SEQ ID NO: 156
AAVhu.11 (AAV16.12)	188	US20150315612 SEQ ID NO: 57
AAVhu.11 (AAV16.12)	189	US20150315612 SEQ ID NO: 153
AAVhu.12	190	US20150315612 SEQ ID NO: 59
AAVhu.12	191	US20150315612 SEQ ID NO: 154
AAVhu.13	192	US20150159173 SEQ ID NO: 16, US20150315612 SEQ ID NO: 71
AAVhu.13	193	US20150159173 SEQ ID NO: 32, US20150315612 SEQ ID NO: 129
AAVhu.136.1	194	US20150315612 SEQ ID NO: 165
AAVhu.140.1	195	US20150315612 SEQ ID NO: 166
AAVhu.140.2	196	US20150315612 SEQ ID NO: 167
AAVhu.145.6	197	US20150315612 SEQ ID No: 178
AAVhu.15	198	US20150315612 SEQ ID NO: 147
AAVhu.15 (AAV33.4)	199	US20150315612 SEQ ID NO: 50
AAVhu.156.1	200	US20150315612 SEQ ID No: 179
AAVhu.16	201	US20150315612 SEQ ID NO: 148
AAVhu.16 (AAV33.8)	202	US20150315612 SEQ ID NO: 51
AAVhu.17	203	US20150315612 SEQ ID NO: 83
AAVhu.17 (AAV33.12)	204	US20150315612 SEQ ID NO: 4
AAVhu.172.1	205	US20150315612 SEQ ID NO: 171
AAVhu.172.2	206	US20150315612 SEQ ID NO: 172
AAVhu.173.4	207	US20150315612 SEQ ID NO: 173
AAVhu.173.8	208	US20150315612 SEQ ID NO: 175
AAVhu.18	209	US20150315612 SEQ ID NO: 52
AAVhu.18	210	US20150315612 SEQ ID NO: 149
AAVhu.19	211	US20150315612 SEQ ID NO: 62
AAVhu.19	212	US20150315612 SEQ ID NO: 133
AAVhu.2	213	US20150315612 SEQ ID NO: 48
AAVhu.2	214	US20150315612 SEQ ID NO: 143

AAVhu.20	215	US20150315612 SEQ ID NO: 63
AAVhu.20	216	US20150315612 SEQ ID NO: 134
AAVhu.21	217	US20150315612 SEQ ID NO: 65
AAVhu.21	218	US20150315612 SEQ ID NO: 135
AAVhu.22	219	US20150315612 SEQ ID NO: 67
AAVhu.22	220	US20150315612 SEQ ID NO: 138
AAVhu.23	221	US20150315612 SEQ ID NO: 60
AAVhu.23.2	222	US20150315612 SEQ ID NO: 137
AAVhu.24	223	US20150315612 SEQ ID NO: 66
AAVhu.24	224	US20150315612 SEQ ID NO: 136
AAVhu.25	225	US20150315612 SEQ ID NO: 49
AAVhu.25	226	US20150315612 SEQ ID NO: 146
AAVhu.26	227	US20150159173 SEQ ID NO: 17, US20150315612 SEQ ID NO: 61
AAVhu.26	228	US20150159173 SEQ ID NO: 33, US20150315612 SEQ ID NO: 139
AAVhu.27	229	US20150315612 SEQ ID NO: 64
AAVhu.27	230	US20150315612 SEQ ID NO: 140
AAVhu.28	231	US20150315612 SEQ ID NO: 68
AAVhu.28	232	US20150315612 SEQ ID NO: 130
AAVhu.29	233	US20150315612 SEQ ID NO: 69
AAVhu.29	234	US20150159173 SEQ ID NO: 42, US20150315612 SEQ ID NO: 132
AAVhu.29	235	US20150315612 SEQ ID NO: 225
AAVhu.29R	236	US20150159173
AAVhu.3	237	US20150315612 SEQ ID NO: 44
AAVhu.3	238	US20150315612 SEQ ID NO: 145
AAVhu.30	239	US20150315612 SEQ ID NO: 70
AAVhu.30	240	US20150315612 SEQ ID NO: 131
AAVhu.31	241	US20150315612 SEQ ID NO: 1
AAVhu.31	242	US20150315612 SEQ ID NO: 121
AAVhu.32	243	US20150315612 SEQ ID NO: 2
AAVhu.32	244	US20150315612 SEQ ID NO: 122
AAVhu.33	245	US20150315612 SEQ ID NO: 75
AAVhu.33	246	US20150315612 SEQ ID NO: 124
AAVhu.34	247	US20150315612 SEQ ID NO: 72
AAVhu.34	248	US20150315612 SEQ ID NO: 125
AAVhu.35	249	US20150315612 SEQ ID NO: 73
AAVhu.35	250	US20150315612 SEQ ID NO: 164
AAVhu.36	251	US20150315612 SEQ ID NO: 74
AAVhu.36	252	US20150315612 SEQ ID NO: 126
AAVhu.37	253	US20150159173 SEQ ID NO: 34, US20150315612 SEQ ID NO: 88

AAVhu.37 (AAV106.1)	254	US20150315612 SEQ ID NO: 10, US20150159173 SEQ ID NO: 18
AAVhu.38	255	US20150315612 SEQ ID NO: 161
AAVhu.39	256	US20150315612 SEQ ID NO: 102
AAVhu.39 (AAV1G-9)	257	US20150315612 SEQ ID NO: 24
AAVhu.4	258	US20150315612 SEQ ID NO: 47
AAVhu.4	259	US20150315612 SEQ ID NO: 141
AAVhu.40	260	US20150315612 SEQ ID NO: 87
AAVhu.40 (AAV114.3)	261	US20150315612 SEQ ID No: 11
AAVhu.41	262	US20150315612 SEQ ID NO: 91
AAVhu.41 (AAV127.2)	263	US20150315612 SEQ ID NO: 6
AAVhu.42	264	US20150315612 SEQ ID NO: 85
AAVhu.42 (AAV127.5)	265	US20150315612 SEQ ID NO: 8
AAVhu.43	266	US20150315612 SEQ ID NO: 160
AAVhu.43	267	US20150315612 SEQ ID NO: 236
AAVhu.43 (AAV128.1)	268	US20150315612 SEQ ID NO: 80
AAVhu.44	269	US20150159173 SEQ ID NO: 45, US20150315612 SEQ ID NO: 158
AAVhu.44 (AAV128.3)	270	US20150315612 SEQ ID NO: 81
AAVhu.44R1	271	US20150159173
AAVhu.44R2	272	US20150159173
AAVhu.44R3	273	US20150159173
AAVhu.45	274	US20150315612 SEQ ID NO: 76
AAVhu.45	275	US20150315612 SEQ ID NO: 127
AAVhu.46	276	US20150315612 SEQ ID NO: 82
AAVhu.46	277	US20150315612 SEQ ID NO: 159
AAVhu.46	278	US20150315612 SEQ ID NO: 224
AAVhu.47	279	US20150315612 SEQ ID NO: 77
AAVhu.47	280	US20150315612 SEQ ID NO: 128
AAVhu.48	281	US20150159173 SEQ ID NO: 38
AAVhu.48	282	US20150315612 SEQ ID NO: 157
AAVhu.48 (AAV130.4)	283	US20150315612 SEQ ID NO: 78
AAVhu.48R1	284	US20150159173
AAVhu.48R2	285	US20150159173
AAVhu.48R3	286	US20150159173
AAVhu.49	287	US20150315612 SEQ ID NO: 209
AAVhu.49	288	US20150315612 SEQ ID NO: 189
AAVhu.5	289	US20150315612 SEQ ID NO: 45
AAVhu.5	290	US20150315612 SEQ ID NO: 142
AAVhu.51	291	US20150315612 SEQ ID NO: 208
AAVhu.51	292	US20150315612 SEQ ID NO: 190
AAVhu.52	293	US20150315612 SEQ ID NO: 210

AAVhu.52	294	US20150315612 SEQ ID NO: 191
AAVhu.53	295	US20150159173 SEQ ID NO: 19
AAVhu.53	296	US20150159173 SEQ ID NO: 35
AAVhu.53 (AAV145.1)	297	US20150315612 SEQ ID NO: 176
AAVhu.54	298	US20150315612 SEQ ID NO: 188
AAVhu.54 (AAV145.5)	299	US20150315612 SEQ ID NO: 177
AAVhu.55	300	US20150315612 SEQ ID NO: 187
AAVhu.56	301	US20150315612 SEQ ID NO: 205
AAVhu.56 (AAV145.6)	302	US20150315612 SEQ ID NO: 168
AAVhu.56 (AAV145.6)	303	US20150315612 SEQ ID NO: 192
AAVhu.57	304	US20150315612 SEQ ID NO: 206
AAVhu.57	305	US20150315612 SEQ ID NO: 169
AAVhu.57	306	US20150315612 SEQ ID NO: 193
AAVhu.58	307	US20150315612 SEQ ID NO: 207
AAVhu.58	308	US20150315612 SEQ ID NO: 194
AAVhu.6 (AAV3.1)	309	US20150315612 SEQ ID NO: 5
AAVhu.6 (AAV3.1)	310	US20150315612 SEQ ID NO: 84
AAVhu.60	311	US20150315612 SEQ ID NO: 184
AAVhu.60 (AAV161.10)	312	US20150315612 SEQ ID NO: 170
AAVhu.61	313	US20150315612 SEQ ID NO: 185
AAVhu.61 (AAV161.6)	314	US20150315612 SEQ ID NO: 174
AAVhu.63	315	US20150315612 SEQ ID NO: 204
AAVhu.63	316	US20150315612 SEQ ID NO: 195
AAVhu.64	317	US20150315612 SEQ ID NO: 212
AAVhu.64	318	US20150315612 SEQ ID NO: 196
AAVhu.66	319	US20150315612 SEQ ID NO: 197
AAVhu.67	320	US20150315612 SEQ ID NO: 215
AAVhu.67	321	US20150315612 SEQ ID NO: 198
AAVhu.7	322	US20150315612 SEQ ID NO: 226
AAVhu.7	323	US20150315612 SEQ ID NO: 150
AAVhu.7 (AAV7.3)	324	US20150315612 SEQ ID NO: 55
AAVhu.71	325	US20150315612 SEQ ID NO: 79
AAVhu.8	326	US20150315612 SEQ ID NO: 53
AAVhu.8	327	US20150315612 SEQ ID NO: 12
AAVhu.8	328	US20150315612 SEQ ID NO: 151
AAVhu.9 (AAV3.1)	329	US20150315612 SEQ ID NO: 58
AAVhu.9 (AAV3.1)	330	US20150315612 SEQ ID NO: 155
AAV-LK01	331	US20150376607 SEQ ID NO: 2
AAV-LK01	332	US20150376607 SEQ ID NO: 29
AAV-LK02	333	US20150376607 SEQ ID NO: 3
AAV-LK02	334	US20150376607 SEQ ID NO: 30

AAV-LK03	335	US20150376607 SEQ ID NO: 4
AAV-LK03	336	WO2015121501 SEQ ID NO: 12, US20150376607 SEQ ID NO: 31
AAV-LK04	337	US20150376607 SEQ ID NO: 5
AAV-LK04	338	US20150376607 SEQ ID NO: 32
AAV-LK05	339	US20150376607 SEQ ID NO: 6
AAV-LK05	340	US20150376607 SEQ ID NO: 33
AAV-LK06	341	US20150376607 SEQ ID NO: 7
AAV-LK06	342	US20150376607 SEQ ID NO: 34
AAV-LK07	343	US20150376607 SEQ ID NO: 8
AAV-LK07	344	US20150376607 SEQ ID NO: 35
AAV-LK08	345	US20150376607 SEQ ID NO: 9
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AAV-LK09	347	US20150376607 SEQ ID NO: 10
AAV-LK09	348	US20150376607 SEQ ID NO: 37
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AAV-LK11	351	US20150376607 SEQ ID NO: 12
AAV-LK11	352	US20150376607 SEQ ID NO: 39
AAV-LK12	353	US20150376607 SEQ ID NO: 13
AAV-LK12	354	US20150376607 SEQ ID NO: 40
AAV-LK13	355	US20150376607 SEQ ID NO: 14
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AAV-LK14	357	US20150376607 SEQ ID NO: 15
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AAV-LK15	359	US20150376607 SEQ ID NO: 16
AAV-LK15	360	US20150376607 SEQ ID NO: 43
AAV-LK16	361	US20150376607 SEQ ID NO: 17
AAV-LK16	362	US20150376607 SEQ ID NO: 44
AAV-LK17	363	US20150376607 SEQ ID NO: 18
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AAV-PAEC	370	US20150376607 SEQ ID NO: 48
AAV-PAEC11	371	US20150376607 SEQ ID NO: 26
AAV-PAEC11	372	US20150376607 SEQ ID NO: 54
AAV-PAEC12	373	US20150376607 SEQ ID NO: 27
AAV-PAEC12	374	US20150376607 SEQ ID NO: 51
AAV-PAEC13	375	US20150376607 SEQ ID NO: 28

AAV-PAEC13	376	US20150376607 SEQ ID NO: 49
AAV-PAEC2	377	US20150376607 SEQ ID NO: 21
AAV-PAEC2	378	US20150376607 SEQ ID NO: 56
AAV-PAEC4	379	US20150376607 SEQ ID NO: 22
AAV-PAEC4	380	US20150376607 SEQ ID NO: 55
AAV-PAEC6	381	US20150376607 SEQ ID NO: 23
AAV-PAEC6	382	US20150376607 SEQ ID NO: 52
AAV-PAEC7	383	US20150376607 SEQ ID NO: 24
AAV-PAEC7	384	US20150376607 SEQ ID NO: 53
AAV-PAEC8	385	US20150376607 SEQ ID NO: 25
AAV-PAEC8	386	US20150376607 SEQ ID NO: 50
AAVpi.1	387	US20150315612 SEQ ID NO: 28
AAVpi.1	388	US20150315612 SEQ ID NO: 93
AAVpi.2	389	US20150315612 SEQ ID NO: 30
AAVpi.2	390	US20150315612 SEQ ID NO: 95
AAVpi.3	391	US20150315612 SEQ ID NO: 29
AAVpi.3	392	US20150315612 SEQ ID NO: 94
AAVrh.10	393	US20150159173 SEQ ID NO: 9
AAVrh.10	394	US20150159173 SEQ ID NO: 25
AAV44.2	395	US20030138772 SEQ ID NO: 59
AAVrh.10 (AAV44.2)	396	US20030138772 SEQ ID NO: 81
AAV42.1B	397	US20030138772 SEQ ID NO: 90
AAVrh.12 (AAV42.1b)	398	US20030138772 SEQ ID NO: 30
AAVrh.13	399	US20150159173 SEQ ID NO: 10
AAVrh.13	400	US20150159173 SEQ ID NO: 26
AAVrh.13	401	US20150315612 SEQ ID NO: 228
AAVrh.13R	402	US20150159173
AAV42.3A	403	US20030138772 SEQ ID NO: 87
AAVrh.14 (AAV42.3a)	404	US20030138772 SEQ ID NO: 32
AAV42.5A	405	US20030138772 SEQ ID NO: 89
AAVrh.17 (AAV42.5a)	406	US20030138772 SEQ ID NO: 34
AAV42.5B	407	US20030138772 SEQ ID NO: 91
AAVrh.18 (AAV42.5b)	408	US20030138772 SEQ ID NO: 29
AAV42.6B	409	US20030138772 SEQ ID NO: 112
AAVrh.19 (AAV42.6b)	410	US20030138772 SEQ ID NO: 38
AAVrh.2	411	US20150159173 SEQ ID NO: 39
AAVrh.2	412	US20150315612 SEQ ID NO: 231
AAVrh.20	413	US20150159173 SEQ ID NO: 1
AAV42.10	414	US20030138772 SEQ ID NO: 106
AAVrh.21 (AAV42.10)	415	US20030138772 SEQ ID NO: 35
AAV42.11	416	US20030138772 SEQ ID NO: 108

AAVrh.22 (AAV42.11)	417	US20030138772 SEQ ID NO: 37
AAV42.12	418	US20030138772 SEQ ID NO: 113
AAVrh.23 (AAV42.12)	419	US20030138772 SEQ ID NO: 58
AAV42.13	420	US20030138772 SEQ ID NO: 86
AAVrh.24 (AAV42.13)	421	US20030138772 SEQ ID NO: 31
AAV42.15	422	US20030138772 SEQ ID NO: 84
AAVrh.25 (AAV42.15)	423	US20030138772 SEQ ID NO: 28
AAVrh.2R	424	US20150159173
AAVrh.31 (AAV223.1)	425	US20030138772 SEQ ID NO: 48
AAVC1	426	US20030138772 SEQ ID NO: 60
AAVrh.32 (AAVC1)	427	US20030138772 SEQ ID NO: 19
AAVrh.32/33	428	US20150159173 SEQ ID NO: 2
AAVrh.33 (AAVC3)	429	US20030138772 SEQ ID NO: 20
AAVC5	430	US20030138772 SEQ ID NO: 62
AAVrh.34 (AAVC5)	431	US20030138772 SEQ ID NO: 21
AAVF1	432	US20030138772 SEQ ID NO: 109
AAVrh.35 (AAVF1)	433	US20030138772 SEQ ID NO: 22
AAVF3	434	US20030138772 SEQ ID NO: 111
AAVrh.36 (AAVF3)	435	US20030138772 SEQ ID NO: 23
AAVrh.37	436	US20030138772 SEQ ID NO: 24
AAVrh.37	437	US20150159173 SEQ ID NO: 40
AAVrh.37	438	US20150315612 SEQ ID NO: 229
AAVrh.37R2	439	US20150159173
AAVrh.38 (AAVLG-4)	440	US20150315612 SEQ ID NO: 7
AAVrh.38 (AAVLG-4)	441	US20150315612 SEQ ID NO: 86
AAVrh.39	442	US20150159173 SEQ ID NO: 20, US20150315612 SEQ ID NO: 13
AAVrh.39	443	US20150159173 SEQ ID NO: 3, US20150159173 SEQ ID NO: 36, US20150315612 SEQ ID NO: 89
AAVrh.40	444	US20150315612 SEQ ID NO: 92
AAVrh.40 (AAVLG-10)	445	US20150315612 SEQ ID NO: 14
AAVrh.43 (AAVN721-8)	446	US20150315612 SEQ ID NO: 43, US20150159173 SEQ ID NO: 21
AAVrh.43 (AAVN721-8)	447	US20150315612 SEQ ID NO: 163, US20150159173 SEQ ID NO: 37
AAVrh.44	448	US20150315612 SEQ ID NO: 34
AAVrh.44	449	US20150315612 SEQ ID NO: 111
AAVrh.45	450	US20150315612 SEQ ID NO: 41
AAVrh.45	451	US20150315612 SEQ ID NO: 109
AAVrh.46	452	US20150159173 SEQ ID NO: 22, US20150315612 SEQ ID NO: 19
AAVrh.46	453	US20150159173 SEQ ID NO: 4, US20150315612 SEQ ID NO: 101
AAVrh.47	454	US20150315612 SEQ ID NO: 38

AAVrh.47	455	US20150315612 SEQ ID NO: 118
AAVrh.48	456	US20150159173 SEQ ID NO: 44, US20150315612 SEQ ID NO: 115
AAVrh.48.1	457	US20150159173
AAVrh.48.1.2	458	US20150159173
AAVrh.48.2	459	US20150159173
AAVrh.48 (AAV1-7)	460	US20150315612 SEQ ID NO: 32
AAVrh.49 (AAV1-8)	461	US20150315612 SEQ ID NO: 25
AAVrh.49 (AAV1-8)	462	US20150315612 SEQ ID NO: 103
AAVrh.50 (AAV2-4)	463	US20150315612 SEQ ID NO: 23
AAVrh.50 (AAV2-4)	464	US20150315612 SEQ ID NO: 108
AAVrh.51 (AAV2-5)	465	US20150315612 SEQ ID No: 22
AAVrh.51 (AAV2-5)	466	US20150315612 SEQ ID NO: 104
AAVrh.52 (AAV3-9)	467	US20150315612 SEQ ID NO: 18
AAVrh.52 (AAV3-9)	468	US20150315612 SEQ ID NO: 96
AAVrh.53	469	US20150315612 SEQ ID NO: 97
AAVrh.53 (AAV3-11)	470	US20150315612 SEQ ID NO: 17
AAVrh.53 (AAV3-11)	471	US20150315612 SEQ ID NO: 186
AAVrh.54	472	US20150315612 SEQ ID NO: 40
AAVrh.54	473	US20150159173 SEQ ID NO: 49, US20150315612 SEQ ID NO: 116
AAVrh.55	474	US20150315612 SEQ ID NO: 37
AAVrh.55 (AAV4-19)	475	US20150315612 SEQ ID NO: 117
AAVrh.56	476	US20150315612 SEQ ID NO: 54
AAVrh.56	477	US20150315612 SEQ ID NO: 152
AAVrh.57	478	US20150315612 SEQ ID NO: 26
AAVrh.57	479	US20150315612 SEQ ID NO: 105
AAVrh.58	480	US20150315612 SEQ ID NO: 27
AAVrh.58	481	US20150159173 SEQ ID NO: 48, US20150315612 SEQ ID NO: 106
AAVrh.58	482	US20150315612 SEQ ID NO: 232
AAVrh.59	483	US20150315612 SEQ ID NO: 42
AAVrh.59	484	US20150315612 SEQ ID NO: 110
AAVrh.60	485	US20150315612 SEQ ID NO: 31
AAVrh.60	486	US20150315612 SEQ ID NO: 120
AAVrh.61	487	US20150315612 SEQ ID NO: 107
AAVrh.61 (AAV2-3)	488	US20150315612 SEQ ID NO: 21
AAVrh.62 (AAV2-15)	489	US20150315612 SEQ ID No: 33
AAVrh.62 (AAV2-15)	490	US20150315612 SEQ ID NO: 114
AAVrh.64	491	US20150315612 SEQ ID No: 15
AAVrh.64	492	US20150159173 SEQ ID NO: 43, US20150315612 SEQ ID NO: 99
AAVrh.64	493	US20150315612 SEQ ID NO: 233

AAVRh.64R1	494	US20150159173
AAVRh.64R2	495	US20150159173
AAVrh.65	496	US20150315612 SEQ ID NO: 35
AAVrh.65	497	US20150315612 SEQ ID NO: 112
AAVrh.67	498	US20150315612 SEQ ID NO: 36
AAVrh.67	499	US20150315612 SEQ ID NO: 230
AAVrh.67	500	US20150159173 SEQ ID NO: 47, US20150315612 SEQ ID NO: 113
AAVrh.68	501	US20150315612 SEQ ID NO: 16
AAVrh.68	502	US20150315612 SEQ ID NO: 100
AAVrh.69	503	US20150315612 SEQ ID NO: 39
AAVrh.69	504	US20150315612 SEQ ID NO: 119
AAVrh.70	505	US20150315612 SEQ ID NO: 20
AAVrh.70	506	US20150315612 SEQ ID NO: 98
AAVrh.71	507	US20150315612 SEQ ID NO: 162
AAVrh.72	508	US20150315612 SEQ ID NO: 9
AAVrh.73	509	US20150159173 SEQ ID NO: 5
AAVrh.74	510	US20150159173 SEQ ID NO: 6
AAVrh.8	511	US20150159173 SEQ ID NO: 41
AAVrh.8	512	US20150315612 SEQ ID NO: 235
AAVrh.8R	513	US20150159173, WO2015168666 SEQ ID NO: 9
AAVrh.8R A586R mutant	514	WO2015168666 SEQ ID NO: 10
AAVrh.8R R533A mutant	515	WO2015168666 SEQ ID NO: 11
BAAV (bovine AAV)	516	US9193769 SEQ ID NO: 8
BAAV (bovine AAV)	517	US9193769 SEQ ID NO: 10
BAAV (bovine AAV)	518	US9193769 SEQ ID NO: 4
BAAV (bovine AAV)	519	US9193769 SEQ ID NO: 2
BAAV (bovine AAV)	520	US9193769 SEQ ID NO: 6
BAAV (bovine AAV)	521	US9193769 SEQ ID NO: 1
BAAV (bovine AAV)	522	US9193769 SEQ ID NO: 5
BAAV (bovine AAV)	523	US9193769 SEQ ID NO: 3
BAAV (bovine AAV)	524	US9193769 SEQ ID NO: 11
BAAV (bovine AAV)	525	US7427396 SEQ ID NO: 5
BAAV (bovine AAV)	526	US7427396 SEQ ID NO: 6
BAAV (bovine AAV)	527	US9193769 SEQ ID NO: 7
BAAV (bovine AAV)	528	US9193769 SEQ ID NO: 9
BNP61 AAV	529	US20150238550 SEQ ID NO: 1
BNP61 AAV	530	US20150238550 SEQ ID NO: 2
BNP62 AAV	531	US20150238550 SEQ ID NO: 3
BNP63 AAV	532	US20150238550 SEQ ID NO: 4
caprine AAV	533	US7427396 SEQ ID NO: 3
caprine AAV	534	US7427396 SEQ ID NO: 4

true type AAV (ttAAV)	535	WO2015121501 SEQ ID NO: 2
AAAV (Avian AAV)	536	US9238800 SEQ ID NO: 12
AAAV (Avian AAV)	537	US9238800 SEQ ID NO: 2
AAAV (Avian AAV)	538	US9238800 SEQ ID NO: 6
AAAV (Avian AAV)	539	US9238800 SEQ ID NO: 4
AAAV (Avian AAV)	540	US9238800 SEQ ID NO: 8
AAAV (Avian AAV)	541	US9238800 SEQ ID NO: 14
AAAV (Avian AAV)	542	US9238800 SEQ ID NO: 10
AAAV (Avian AAV)	543	US9238800 SEQ ID NO: 15
AAAV (Avian AAV)	544	US9238800 SEQ ID NO: 5
AAAV (Avian AAV)	545	US9238800 SEQ ID NO: 9
AAAV (Avian AAV)	546	US9238800 SEQ ID NO: 3
AAAV (Avian AAV)	547	US9238800 SEQ ID NO: 7
AAAV (Avian AAV)	548	US9238800 SEQ ID NO: 11
AAAV (Avian AAV)	549	US9238800 SEQ ID NO: 13
AAAV (Avian AAV)	550	US9238800 SEQ ID NO: 1
AAV Shuffle 100-1	551	US20160017295 SEQ ID NO: 23
AAV Shuffle 100-1	552	US20160017295 SEQ ID NO: 11
AAV Shuffle 100-2	553	US20160017295 SEQ ID NO: 37
AAV Shuffle 100-2	554	US20160017295 SEQ ID NO: 29
AAV Shuffle 100-3	555	US20160017295 SEQ ID NO: 24
AAV Shuffle 100-3	556	US20160017295 SEQ ID NO: 12
AAV Shuffle 100-7	557	US20160017295 SEQ ID NO: 25
AAV Shuffle 100-7	558	US20160017295 SEQ ID NO: 13
AAV Shuffle 10-2	559	US20160017295 SEQ ID NO: 34
AAV Shuffle 10-2	560	US20160017295 SEQ ID NO: 26
AAV Shuffle 10-6	561	US20160017295 SEQ ID NO: 35
AAV Shuffle 10-6	562	US20160017295 SEQ ID NO: 27
AAV Shuffle 10-8	563	US20160017295 SEQ ID NO: 36
AAV Shuffle 10-8	564	US20160017295 SEQ ID NO: 28
AAV SM 100-10	565	US20160017295 SEQ ID NO: 41
AAV SM 100-10	566	US20160017295 SEQ ID NO: 33
AAV SM 100-3	567	US20160017295 SEQ ID NO: 40
AAV SM 100-3	568	US20160017295 SEQ ID NO: 32
AAV SM 10-1	569	US20160017295 SEQ ID NO: 38
AAV SM 10-1	570	US20160017295 SEQ ID NO: 30
AAV SM 10-2	571	US20160017295 SEQ ID NO: 10
AAV SM 10-2	572	US20160017295 SEQ ID NO: 22
AAV SM 10-8	573	US20160017295 SEQ ID NO: 39
AAV SM 10-8	574	US20160017295 SEQ ID NO: 31
AAVF1/HSC1	575	WO2016049230 SEQ ID NO: 20
AAVF2/HSC2	576	WO2016049230 SEQ ID NO: 21
AAVF3/HSC3	577	WO2016049230 SEQ ID NO: 22

AAVF4/HSC4	578	WO2016049230 SEQ ID NO: 23
AAVF5/HSC5	579	WO2016049230 SEQ ID NO: 25
AAVF6/HSC6	580	WO2016049230 SEQ ID NO: 24
AAVF7/HSC7	581	WO2016049230 SEQ ID NO: 27
AAVF8/HSC8	582	WO2016049230 SEQ ID NO: 28
AAVF9/HSC9	583	WO2016049230 SEQ ID NO: 29
AAVF11/HSC11	584	WO2016049230 SEQ ID NO: 26
AAVF12/HSC12	585	WO2016049230 SEQ ID NO: 30
AAVF13/HSC13	586	WO2016049230 SEQ ID NO: 31
AAVF14/HSC14	587	WO2016049230 SEQ ID NO: 32
AAVF15/HSC15	588	WO2016049230 SEQ ID NO: 33
AAVF16/HSC16	589	WO2016049230 SEQ ID NO: 34
AAVF17/HSC17	590	WO2016049230 SEQ ID NO: 35
AAVF1/HSC1	591	WO2016049230 SEQ ID NO: 2
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AAV CBr-E4	610	US8734809 SEQ ID NO: 16
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AAV CBr-e5	612	US8734809 SEQ ID NO: 18
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AAV CBr-E7	614	US8734809 SEQ ID NO: 20
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AAV CLv-D1	616	US8734809 SEQ ID NO: 22
AAV CLv-D2	617	US8734809 SEQ ID NO: 23
AAV CLv-D3	618	US8734809 SEQ ID NO: 24

AAV CLv-D4	619	US8734809 SEQ ID NO: 25
AAV CLv-D5	620	US8734809 SEQ ID NO: 26
AAV CLv-D6	621	US8734809 SEQ ID NO: 27
AAV CLv-D7	622	US8734809 SEQ ID NO: 28
AAV CLv-D8	623	US8734809 SEQ ID NO: 29
AAV CLv-E1	624	US8734809 SEQ ID NO: 13
AAV CLv-R1	625	US8734809 SEQ ID NO: 30
AAV CLv-R2	626	US8734809 SEQ ID NO: 31
AAV CLv-R3	627	US8734809 SEQ ID NO: 32
AAV CLv-R4	628	US8734809 SEQ ID NO: 33
AAV CLv-R5	629	US8734809 SEQ ID NO: 34
AAV CLv-R6	630	US8734809 SEQ ID NO: 35
AAV CLv-R7	631	US8734809 SEQ ID NO: 36
AAV CLv-R8	632	US8734809 SEQ ID NO: 37
AAV CLv-R9	633	US8734809 SEQ ID NO: 38
AAV CLg-F1	634	US8734809 SEQ ID NO: 39
AAV CLg-F2	635	US8734809 SEQ ID NO: 40
AAV CLg-F3	636	US8734809 SEQ ID NO: 41
AAV CLg-F4	637	US8734809 SEQ ID NO: 42
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AAV CSp-6	648	US8734809 SEQ ID NO: 51
AAV CSp-7	649	US8734809 SEQ ID NO: 52
AAV CSp-8	650	US8734809 SEQ ID NO: 53
AAV CSp-9	651	US8734809 SEQ ID NO: 54
AAV CHt-2	652	US8734809 SEQ ID NO: 55
AAV CHt-3	653	US8734809 SEQ ID NO: 56
AAV CKd-1	654	US8734809 SEQ ID NO: 57
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AAV CKd-2	656	US8734809 SEQ ID NO: 59
AAV CKd-3	657	US8734809 SEQ ID NO: 60
AAV CKd-4	658	US8734809 SEQ ID NO: 61
AAV CKd-6	659	US8734809 SEQ ID NO: 62

AAV CKd-7	660	US8734809 SEQ ID NO: 63
AAV CKd-8	661	US8734809 SEQ ID NO: 64
AAV CLv-1	662	US8734809 SEQ ID NO: 65
AAV CLv-12	663	US8734809 SEQ ID NO: 66
AAV CLv-13	664	US8734809 SEQ ID NO: 67
AAV CLv-2	665	US8734809 SEQ ID NO: 68
AAV CLv-3	666	US8734809 SEQ ID NO: 69
AAV CLv-4	667	US8734809 SEQ ID NO: 70
AAV CLv-6	668	US8734809 SEQ ID NO: 71
AAV CLv-8	669	US8734809 SEQ ID NO: 72
AAV CKd-B1	670	US8734809 SEQ ID NO: 73
AAV CKd-B2	671	US8734809 SEQ ID NO: 74
AAV CKd-B3	672	US8734809 SEQ ID NO: 75
AAV CKd-B4	673	US8734809 SEQ ID NO: 76
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AAV CKd-B6	675	US8734809 SEQ ID NO: 78
AAV CKd-B7	676	US8734809 SEQ ID NO: 79
AAV CKd-B8	677	US8734809 SEQ ID NO: 80
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AAV CKd-H5	682	US8734809 SEQ ID NO: 85
AAV CKd-H6	683	US8734809 SEQ ID NO: 77
AAV CHt-1	684	US8734809 SEQ ID NO: 86
AAV CLv1-1	685	US8734809 SEQ ID NO: 171
AAV CLv1-2	686	US8734809 SEQ ID NO: 172
AAV CLv1-3	687	US8734809 SEQ ID NO: 173
AAV CLv1-4	688	US8734809 SEQ ID NO: 174
AAV Clv1-7	689	US8734809 SEQ ID NO: 175
AAV Clv1-8	690	US8734809 SEQ ID NO: 176
AAV Clv1-9	691	US8734809 SEQ ID NO: 177
AAV Clv1-10	692	US8734809 SEQ ID NO: 178
AAV.VR-355	693	US8734809 SEQ ID NO: 181
AAV.hu.48R3	694	US8734809 SEQ ID NO: 183
AAV CBr-E1	695	US8734809 SEQ ID NO: 87
AAV CBr-E2	696	US8734809 SEQ ID NO: 88
AAV CBr-E3	697	US8734809 SEQ ID NO: 89
AAV CBr-E4	698	US8734809 SEQ ID NO: 90
AAV CBr-E5	699	US8734809 SEQ ID NO: 91
AAV CBr-e5	700	US8734809 SEQ ID NO: 92

AAV CBr-E6	701	US8734809 SEQ ID NO: 93
AAV CBr-E7	702	US8734809 SEQ ID NO: 94
AAV CBr-E8	703	US8734809 SEQ ID NO: 95
AAV CLv-D1	704	US8734809 SEQ ID NO: 96
AAV CLv-D2	705	US8734809 SEQ ID NO: 97
AAV CLv-D3	706	US8734809 SEQ ID NO: 98
AAV CLv-D4	707	US8734809 SEQ ID NO: 99
AAV CLv-D5	708	US8734809 SEQ ID NO: 100
AAV CLv-D6	709	US8734809 SEQ ID NO: 101
AAV CLv-D7	710	US8734809 SEQ ID NO: 102
AAV CLv-D8	711	US8734809 SEQ ID NO: 103
AAV CLv-E1	712	US8734809 SEQ ID NO: 87
AAV CLv-R1	713	US8734809 SEQ ID NO: 104
AAV CLv-R2	714	US8734809 SEQ ID NO: 105
AAV CLv-R3	715	US8734809 SEQ ID NO: 106
AAV CLv-R4	716	US8734809 SEQ ID NO: 107
AAV CLv-R5	717	US8734809 SEQ ID NO: 108
AAV CLv-R6	718	US8734809 SEQ ID NO: 109
AAV CLv-R7	719	US8734809 SEQ ID NO: 110
AAV CLv-R8	720	US8734809 SEQ ID NO: 111
AAV CLv-R9	721	US8734809 SEQ ID NO: 112
AAV CLg-F1	722	US8734809 SEQ ID NO: 113
AAV CLg-F2	723	US8734809 SEQ ID NO: 114
AAV CLg-F3	724	US8734809 SEQ ID NO: 115
AAV CLg-F4	725	US8734809 SEQ ID NO: 116
AAV CLg-F5	726	US8734809 SEQ ID NO: 117
AAV CLg-F6	727	US8734809 SEQ ID NO: 117
AAV CLg-F7	728	US8734809 SEQ ID NO: 118
AAV CLg-F8	729	US8734809 SEQ ID NO: 117
AAV CSp-1	730	US8734809 SEQ ID NO: 119
AAV CSp-10	731	US8734809 SEQ ID NO: 120
AAV CSp-11	732	US8734809 SEQ ID NO: 121
AAV CSp-2	733	US8734809 SEQ ID NO: 122
AAV CSp-3	734	US8734809 SEQ ID NO: 123
AAV CSp-4	735	US8734809 SEQ ID NO: 124
AAV CSp-6	736	US8734809 SEQ ID NO: 125
AAV CSp-7	737	US8734809 SEQ ID NO: 126
AAV CSp-8	738	US8734809 SEQ ID NO: 127
AAV CSp-9	739	US8734809 SEQ ID NO: 128
AAV CHt-2	740	US8734809 SEQ ID NO: 129
AAV CHt-3	741	US8734809 SEQ ID NO: 130

AAV CKd-1	742	US8734809 SEQ ID NO: 131
AAV CKd-10	743	US8734809 SEQ ID NO: 132
AAV CKd-2	744	US8734809 SEQ ID NO: 133
AAV CKd-3	745	US8734809 SEQ ID NO: 134
AAV CKd-4	746	US8734809 SEQ ID NO: 135
AAV CKd-6	747	US8734809 SEQ ID NO: 136
AAV CKd-7	748	US8734809 SEQ ID NO: 137
AAV CKd-8	749	US8734809 SEQ ID NO: 138
AAV CLv-1	750	US8734809 SEQ ID NO: 139
AAV CLv-12	751	US8734809 SEQ ID NO: 140
AAV CLv-13	752	US8734809 SEQ ID NO: 141
AAV CLv-2	753	US8734809 SEQ ID NO: 142
AAV CLv-3	754	US8734809 SEQ ID NO: 143
AAV CLv-4	755	US8734809 SEQ ID NO: 144
AAV CLv-6	756	US8734809 SEQ ID NO: 145
AAV CLv-8	757	US8734809 SEQ ID NO: 146
AAV CKd-B1	758	US8734809 SEQ ID NO: 147
AAV CKd-B2	759	US8734809 SEQ ID NO: 148
AAV CKd-B3	760	US8734809 SEQ ID NO: 149
AAV CKd-B4	761	US8734809 SEQ ID NO: 150
AAV CKd-B5	762	US8734809 SEQ ID NO: 151
AAV CKd-B6	763	US8734809 SEQ ID NO: 152
AAV CKd-B7	764	US8734809 SEQ ID NO: 153
AAV CKd-B8	765	US8734809 SEQ ID NO: 154
AAV CKd-H1	766	US8734809 SEQ ID NO: 155
AAV CKd-H2	767	US8734809 SEQ ID NO: 156
AAV CKd-H3	768	US8734809 SEQ ID NO: 157
AAV CKd-H4	769	US8734809 SEQ ID NO: 158
AAV CKd-H5	770	US8734809 SEQ ID NO: 159
AAV CKd-H6	771	US8734809 SEQ ID NO: 151
AAV CHt-1	772	US8734809 SEQ ID NO: 160
AAV CHt-P2	773	WO2016065001 SEQ ID NO: 1
AAV CHt-P5	774	WO2016065001 SEQ ID NO: 2
AAV CHt-P9	775	WO2016065001 SEQ ID NO: 3
AAV CBr-7.1	776	WO2016065001 SEQ ID NO: 4
AAV CBr-7.2	777	WO2016065001 SEQ ID NO: 5
AAV CBr-7.3	778	WO2016065001 SEQ ID NO: 6
AAV CBr-7.4	779	WO2016065001 SEQ ID NO: 7
AAV CBr-7.5	780	WO2016065001 SEQ ID NO: 8
AAV CBr-7.7	781	WO2016065001 SEQ ID NO: 9
AAV CBr-7.8	782	WO2016065001 SEQ ID NO: 10

AAV CBr-7.10	783	WO2016065001 SEQ ID NO: 11
AAV CKd-N3	784	WO2016065001 SEQ ID NO: 12
AAV CKd-N4	785	WO2016065001 SEQ ID NO: 13
AAV CKd-N9	786	WO2016065001 SEQ ID NO: 14
AAV CLv-L4	787	WO2016065001 SEQ ID NO: 15
AAV CLv-L5	788	WO2016065001 SEQ ID NO: 16
AAV CLv-L6	789	WO2016065001 SEQ ID NO: 17
AAV CLv-K1	790	WO2016065001 SEQ ID NO: 18
AAV CLv-K3	791	WO2016065001 SEQ ID NO: 19
AAV CLv-K6	792	WO2016065001 SEQ ID NO: 20
AAV CLv-M1	793	WO2016065001 SEQ ID NO: 21
AAV CLv-M11	794	WO2016065001 SEQ ID NO: 22
AAV CLv-M2	795	WO2016065001 SEQ ID NO: 23
AAV CLv-M5	796	WO2016065001 SEQ ID NO: 24
AAV CLv-M6	797	WO2016065001 SEQ ID NO: 25
AAV CLv-M7	798	WO2016065001 SEQ ID NO: 26
AAV CLv-M8	799	WO2016065001 SEQ ID NO: 27
AAV CLv-M9	800	WO2016065001 SEQ ID NO: 28
AAV CHt-P1	801	WO2016065001 SEQ ID NO: 29
AAV CHt-P6	802	WO2016065001 SEQ ID NO: 30
AAV CHt-P8	803	WO2016065001 SEQ ID NO: 31
AAV CHt-6.1	804	WO2016065001 SEQ ID NO: 32
AAV CHt-6.10	805	WO2016065001 SEQ ID NO: 33
AAV CHt-6.5	806	WO2016065001 SEQ ID NO: 34
AAV CHt-6.6	807	WO2016065001 SEQ ID NO: 35
AAV CHt-6.7	808	WO2016065001 SEQ ID NO: 36
AAV CHt-6.8	809	WO2016065001 SEQ ID NO: 37
AAV CSp-8.10	810	WO2016065001 SEQ ID NO: 38
AAV CSp-8.2	811	WO2016065001 SEQ ID NO: 39
AAV CSp-8.4	812	WO2016065001 SEQ ID NO: 40
AAV CSp-8.5	813	WO2016065001 SEQ ID NO: 41
AAV CSp-8.6	814	WO2016065001 SEQ ID NO: 42
AAV CSp-8.7	815	WO2016065001 SEQ ID NO: 43
AAV CSp-8.8	816	WO2016065001 SEQ ID NO: 44
AAV CSp-8.9	817	WO2016065001 SEQ ID NO: 45
AAV CBr-B7.3	818	WO2016065001 SEQ ID NO: 46
AAV CBr-B7.4	819	WO2016065001 SEQ ID NO: 47
AAV3B	820	WO2016065001 SEQ ID NO: 48
AAV4	821	WO2016065001 SEQ ID NO: 49
AAV5	822	WO2016065001 SEQ ID NO: 50
AAV CHt-P2	823	WO2016065001 SEQ ID NO: 51

AAV CHt-P5	824	WO2016065001 SEQ ID NO: 52
AAV CHt-P9	825	WO2016065001 SEQ ID NO: 53
AAV CBr-7.1	826	WO2016065001 SEQ ID NO: 54
AAV CBr-7.2	827	WO2016065001 SEQ ID NO: 55
AAV CBr-7.3	828	WO2016065001 SEQ ID NO: 56
AAV CBr-7.4	829	WO2016065001 SEQ ID NO: 57
AAV CBr-7.5	830	WO2016065001 SEQ ID NO: 58
AAV CBr-7.7	831	WO2016065001 SEQ ID NO: 59
AAV CBr-7.8	832	WO2016065001 SEQ ID NO: 60
AAV CBr-7.10	833	WO2016065001 SEQ ID NO: 61
AAV CKd-N3	834	WO2016065001 SEQ ID NO: 62
AAV CKd-N4	835	WO2016065001 SEQ ID NO: 63
AAV CKd-N9	836	WO2016065001 SEQ ID NO: 64
AAV CLv-L4	837	WO2016065001 SEQ ID NO: 65
AAV CLv-L5	838	WO2016065001 SEQ ID NO: 66
AAV CLv-L6	839	WO2016065001 SEQ ID NO: 67
AAV CLv-K1	840	WO2016065001 SEQ ID NO: 68
AAV CLv-K3	841	WO2016065001 SEQ ID NO: 69
AAV CLv-K6	842	WO2016065001 SEQ ID NO: 70
AAV CLv-M1	843	WO2016065001 SEQ ID NO: 71
AAV CLv-M11	844	WO2016065001 SEQ ID NO: 72
AAV CLv-M2	845	WO2016065001 SEQ ID NO: 73
AAV CLv-M5	846	WO2016065001 SEQ ID NO: 74
AAV CLv-M6	847	WO2016065001 SEQ ID NO: 75
AAV CLv-M7	848	WO2016065001 SEQ ID NO: 76
AAV CLv-M8	849	WO2016065001 SEQ ID NO: 77
AAV CLv-M9	850	WO2016065001 SEQ ID NO: 78
AAV CHt-P1	851	WO2016065001 SEQ ID NO: 79
AAV CHt-P6	852	WO2016065001 SEQ ID NO: 80
AAV CHt-P8	853	WO2016065001 SEQ ID NO: 81
AAV CHt-6.1	854	WO2016065001 SEQ ID NO: 82
AAV CHt-6.10	855	WO2016065001 SEQ ID NO: 83
AAV CHt-6.5	856	WO2016065001 SEQ ID NO: 84
AAV CHt-6.6	857	WO2016065001 SEQ ID NO: 85
AAV CHt-6.7	858	WO2016065001 SEQ ID NO: 86
AAV CHt-6.8	859	WO2016065001 SEQ ID NO: 87
AAV CSp-8.10	860	WO2016065001 SEQ ID NO: 88
AAV CSp-8.2	861	WO2016065001 SEQ ID NO: 89
AAV CSp-8.4	862	WO2016065001 SEQ ID NO: 90
AAV CSp-8.5	863	WO2016065001 SEQ ID NO: 91
AAV CSp-8.6	864	WO2016065001 SEQ ID NO: 92

AAV CSp-8.7	865	WO2016065001 SEQ ID NO: 93
AAV CSp-8.8	866	WO2016065001 SEQ ID NO: 94
AAV CSp-8.9	867	WO2016065001 SEQ ID NO: 95
AAV CBr-B7.3	868	WO2016065001 SEQ ID NO: 96
AAV CBr-B7.4	869	WO2016065001 SEQ ID NO: 97
AAV3B	870	WO2016065001 SEQ ID NO: 98
AAV4	871	WO2016065001 SEQ ID NO: 99
AAV5	872	WO2016065001 SEQ ID NO: 100
PHP.N/PHP.B-DGT	873	WO2017100671 SEQ ID NO: 46
PHP.S/G2A12	874	WO2017100671 SEQ ID NO: 47
AAV9/hu.14 K449R	875	WO2017100671 SEQ ID NO: 45
GPV	992	US9624274B2 SEQ ID NO: 192
B19	993	US9624274B2 SEQ ID NO: 193
MVM	994	US9624274B2 SEQ ID NO: 194
FPV	995	US9624274B2 SEQ ID NO: 195
CPV	996	US9624274B2 SEQ ID NO: 196
AAV6	997	US9546112B2 SEQ ID NO: 5
AAV6	998	US9457103B2 SEQ ID NO: 1
AAV2	999	US9457103B2 SEQ ID NO: 2
ShH10	1000	US9457103B2 SEQ ID NO: 3
ShH13	1001	US9457103B2 SEQ ID NO: 4
ShH10	1002	US9457103B2 SEQ ID NO: 5
ShH10	1003	US9457103B2 SEQ ID NO: 6
ShH10	1004	US9457103B2 SEQ ID NO: 7
ShH10	1005	US9457103B2 SEQ ID NO: 8
ShH10	1006	US9457103B2 SEQ ID NO: 9
rh74	1007	US9434928B2 SEQ ID NO: 1, US2015023924A1 SEQ ID NO: 2
rh74	1008	US9434928B2 SEQ ID NO: 2, US2015023924A1 SEQ ID NO: 1
AAV8	1009	US9434928B2 SEQ ID NO: 4
rh74	1010	US9434928B2 SEQ ID NO: 5
rh74 (RHM4-1)	1011	US2015023924A1 SEQ ID NO: 5, US20160375110A1 SEQ ID NO: 4
rh74 (RHM15-1)	1012	US2015023924A1 SEQ ID NO: 6, US20160375110A1 SEQ ID NO: 5
rh74 (RHM15-2)	1013	US2015023924A1 SEQ ID NO: 7, US20160375110A1 SEQ ID NO: 6
rh74 (RHM15-3/RHM15-5)	1014	US2015023924A1 SEQ ID NO: 8, US20160375110A1 SEQ ID NO: 7
rh74 (RHM15-4)	1015	US2015023924A1 SEQ ID NO: 9, US20160375110A1 SEQ ID NO: 8
rh74 (RHM15-6)	1016	US2015023924A1 SEQ ID NO: 10, US20160375110A1 SEQ ID NO: 9
rh74 (RHM4-1)	1017	US2015023924A1 SEQ ID NO: 11

rh74 (RHM15-1)	1018	US2015023924A1 SEQ ID NO: 12
rh74 (RHM15-2)	1019	US2015023924A1 SEQ ID NO: 13
rh74 (RHM15-3/RHM15-5)	1020	US2015023924A1 SEQ ID NO: 14
rh74 (RHM15-4)	1021	US2015023924A1 SEQ ID NO: 15
rh74 (RHM15-6)	1022	US2015023924A1 SEQ ID NO: 16
AAV2 (comprising lung specific polypeptide)	1023	US20160175389A1 SEQ ID NO: 9
AAV2 (comprising lung specific polypeptide)	1024	US20160175389A1 SEQ ID NO: 10
Anc80	1025	US20170051257A1 SEQ ID NO: 1
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Anc81	1027	US20170051257A1 SEQ ID NO: 3
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Anc94	1035	US20170051257A1 SEQ ID NO: 11
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Anc113	1037	US20170051257A1 SEQ ID NO: 13
Anc113	1038	US20170051257A1 SEQ ID NO: 14
Anc126	1039	US20170051257A1 SEQ ID NO: 15
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Anc127	1042	US20170051257A1 SEQ ID NO: 18
Anc80L27	1043	US20170051257A1 SEQ ID NO: 19
Anc80L59	1044	US20170051257A1 SEQ ID NO: 20
Anc80L60	1045	US20170051257A1 SEQ ID NO: 21
Anc80L62	1046	US20170051257A1 SEQ ID NO: 22
Anc80L65	1047	US20170051257A1 SEQ ID NO: 23
Anc80L33	1048	US20170051257A1 SEQ ID NO: 24
Anc80L36	1049	US20170051257A1 SEQ ID NO: 25
Anc80L44	1050	US20170051257A1 SEQ ID NO: 26
Anc80L1	1051	US20170051257A1 SEQ ID NO: 35
Anc80L1	1052	US20170051257A1 SEQ ID NO: 36
AAV-X1	1053	US8283151B2 SEQ ID NO: 11
AAV-X1b	1054	US8283151B2 SEQ ID NO: 12
AAV-X5	1055	US8283151B2 SEQ ID NO: 13
AAV-X19	1056	US8283151B2 SEQ ID NO: 14
AAV-X21	1057	US8283151B2 SEQ ID NO: 15

AAV-X22	1058	US8283151B2 SEQ ID NO: 16
AAV-X23	1059	US8283151B2 SEQ ID NO: 17
AAV-X24	1060	US8283151B2 SEQ ID NO: 18
AAV-X25	1061	US8283151B2 SEQ ID NO: 19
AAV-X26	1062	US8283151B2 SEQ ID NO: 20
AAV-X1	1063	US8283151B2 SEQ ID NO: 21
AAV-X1b	1064	US8283151B2 SEQ ID NO: 22
AAV-X5	1065	US8283151B2 SEQ ID NO: 23
AAV-X19	1066	US8283151B2 SEQ ID NO: 24
AAV-X21	1067	US8283151B2 SEQ ID NO: 25
AAV-X22	1068	US8283151B2 SEQ ID NO: 26
AAV-X23	1069	US8283151B2 SEQ ID NO: 27
AAV-X24	1070	US8283151B2 SEQ ID NO: 28
AAV-X25	1071	US8283151B2 SEQ ID NO: 29
AAV-X26	1072	US8283151B2 SEQ ID NO: 30
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AAVrh8VP2FC5	1074	WO2016054554A1 SEQ ID NO: 9
AAVrh8VP2FC44	1075	WO2016054554A1 SEQ ID NO: 10
AAVrh8VP2ApoB100	1076	WO2016054554A1 SEQ ID NO: 11
AAVrh8VP2RVG	1077	WO2016054554A1 SEQ ID NO: 12
AAVrh8VP2Angiopep-2 VP2	1078	WO2016054554A1 SEQ ID NO: 13
AAV9.47VP1.3	1079	WO2016054554A1 SEQ ID NO: 14
AAV9.47VP2ICAMg3	1080	WO2016054554A1 SEQ ID NO: 15
AAV9.47VP2RVG	1081	WO2016054554A1 SEQ ID NO: 16
AAV9.47VP2Angiopep-2	1082	WO2016054554A1 SEQ ID NO: 17
AAV9.47VP2A-string	1083	WO2016054554A1 SEQ ID NO: 18
AAVrh8VP2FC5 VP2	1084	WO2016054554A1 SEQ ID NO: 19
AAVrh8VP2FC44 VP2	1085	WO2016054554A1 SEQ ID NO: 20
AAVrh8VP2ApoB100 VP2	1086	WO2016054554A1 SEQ ID NO: 21
AAVrh8VP2RVG VP2	1087	WO2016054554A1 SEQ ID NO: 22
AAVrh8VP2Angiopep-2 VP2	1088	WO2016054554A1 SEQ ID NO: 23
AAV9.47VP2ICAMg3 VP2	1089	WO2016054554A1 SEQ ID NO: 24
AAV9.47VP2RVG VP2	1090	WO2016054554A1 SEQ ID NO: 25
AAV9.47VP2Angiopep-2 VP2	1091	WO2016054554A1 SEQ ID NO: 26
AAV9.47VP2A-string VP2	1092	WO2016054554A1 SEQ ID NO: 27
rAAV-B1	1093	WO2016054557A1 SEQ ID NO: 1
rAAV-B2	1094	WO2016054557A1 SEQ ID NO: 2
rAAV-B3	1095	WO2016054557A1 SEQ ID NO: 3
rAAV-B4	1096	WO2016054557A1 SEQ ID NO: 4
rAAV-B1	1097	WO2016054557A1 SEQ ID NO: 5

rAAV-B2	1098	WO2016054557A1 SEQ ID NO: 6
rAAV-B3	1099	WO2016054557A1 SEQ ID NO: 7
rAAV-B4	1100	WO2016054557A1 SEQ ID NO: 8
rAAV-L1	1101	WO2016054557A1 SEQ ID NO: 9
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rAAV-L4	1104	WO2016054557A1 SEQ ID NO: 12
rAAV-L1	1105	WO2016054557A1 SEQ ID NO: 13
rAAV-L2	1106	WO2016054557A1 SEQ ID NO: 14
rAAV-L3	1107	WO2016054557A1 SEQ ID NO: 15
rAAV-L4	1108	WO2016054557A1 SEQ ID NO: 16
AAV9	1109	WO2016073739A1 SEQ ID NO: 3
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rAAV	1179	WO2016081811A1 SEQ ID NO: 70
rAAV	1180	WO2016081811A1 SEQ ID NO: 71
rAAV	1181	WO2016081811A1 SEQ ID NO: 72

rAAV	1182	WO2016081811A1 SEQ ID NO: 73
rAAV	1183	WO2016081811A1 SEQ ID NO: 74
rAAV	1184	WO2016081811A1 SEQ ID NO: 75
rAAV	1185	WO2016081811A1 SEQ ID NO: 76
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rAAV	1198	WO2016081811A1 SEQ ID NO: 89
rAAV	1199	WO2016081811A1 SEQ ID NO: 90
rAAV	1200	WO2016081811A1 SEQ ID NO: 91
rAAV	1201	WO2016081811A1 SEQ ID NO: 92
rAAV	1202	WO2016081811A1 SEQ ID NO: 93
rAAV	1203	WO2016081811A1 SEQ ID NO: 94
rAAV	1204	WO2016081811A1 SEQ ID NO: 95
rAAV	1205	WO2016081811A1 SEQ ID NO: 96
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rAAV	1220	WO2016081811A1 SEQ ID NO: 111
rAAV	1221	WO2016081811A1 SEQ ID NO: 112
rAAV	1222	WO2016081811A1 SEQ ID NO: 113

rAAV	1223	WO2016081811A1 SEQ ID NO: 114
rAAV	1224	WO2016081811A1 SEQ ID NO: 115
rAAV	1225	WO2016081811A1 SEQ ID NO: 116
rAAV	1226	WO2016081811A1 SEQ ID NO: 117
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rAAV	1236	WO2016081811A1 SEQ ID NO: 127
rAAV	1237	WO2016081811A1 SEQ ID NO: 128
AAV8 E532K	1238	WO2016081811A1 SEQ ID NO: 133
AAV8 E532K	1239	WO2016081811A1 SEQ ID NO: 134
rAAV4	1240	WO2016115382A1 SEQ ID NO: 2
rAAV4	1241	WO2016115382A1 SEQ ID NO: 3
rAAV4	1242	WO2016115382A1 SEQ ID NO: 4
rAAV4	1243	WO2016115382A1 SEQ ID NO: 5
rAAV4	1244	WO2016115382A1 SEQ ID NO: 6
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rAAV4	1258	WO2016115382A1 SEQ ID NO: 20
rAAV4	1259	WO2016115382A1 SEQ ID NO: 21
AAV11	1260	WO2016115382A1 SEQ ID NO: 22
AAV12	1261	WO2016115382A1 SEQ ID NO: 23
rh32	1262	WO2016115382A1 SEQ ID NO: 25
rh33	1263	WO2016115382A1 SEQ ID NO: 26

rh34	1264	WO2016115382A1 SEQ ID NO: 27
rAAV4	1265	WO2016115382A1 SEQ ID NO: 28
rAAV4	1266	WO2016115382A1 SEQ ID NO: 29
rAAV4	1267	WO2016115382A1 SEQ ID NO: 30
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rAAV4	1269	WO2016115382A1 SEQ ID NO: 32
rAAV4	1270	WO2016115382A1 SEQ ID NO: 33
AAV2/8	1271	WO2016131981A1 SEQ ID NO: 47
AAV2/8	1272	WO2016131981A1 SEQ ID NO: 48
ancestral AAV	1273	WO2016154344A1 SEQ ID NO: 7
ancestral AAV variant C4	1274	WO2016154344A1 SEQ ID NO: 13
ancestral AAV variant C7	1275	WO2016154344A1 SEQ ID NO: 14
ancestral AAV variant G4	1276	WO2016154344A1 SEQ ID NO: 15
consensus amino acid sequence of ancestral AAV variants, C4, C7 and G4	1277	WO2016154344A1 SEQ ID NO: 16
consensus amino acid sequence of ancestral AAV variants, C4 and C7	1278	WO2016154344A1 SEQ ID NO: 17
AAV8 (with a AAV2 phospholipase domain)	1279	WO2016150403A1 SEQ ID NO: 13
AAV VR-942n	1280	US20160289275A1 SEQ ID NO: 10
AAV5-A (M569V)	1281	US20160289275A1 SEQ ID NO: 13
AAV5-A (M569V)	1282	US20160289275A1 SEQ ID NO: 14
AAV5-A (Y585V)	1283	US20160289275A1 SEQ ID NO: 16
AAV5-A (Y585V)	1284	US20160289275A1 SEQ ID NO: 17
AAV5-A (L587T)	1285	US20160289275A1 SEQ ID NO: 19
AAV5-A (L587T)	1286	US20160289275A1 SEQ ID NO: 20
AAV5-A (Y585V/L587T)	1287	US20160289275A1 SEQ ID NO: 22
AAV5-A (Y585V/L587T)	1288	US20160289275A1 SEQ ID NO: 23
AAV5-B (D652A)	1289	US20160289275A1 SEQ ID NO: 25
AAV5-B (D652A)	1290	US20160289275A1 SEQ ID NO: 26
AAV5-B (T362M)	1291	US20160289275A1 SEQ ID NO: 28
AAV5-B (T362M)	1292	US20160289275A1 SEQ ID NO: 29
AAV5-B (Q359D)	1293	US20160289275A1 SEQ ID NO: 31
AAV5-B (Q359D)	1294	US20160289275A1 SEQ ID NO: 32
AAV5-B (E350Q)	1295	US20160289275A1 SEQ ID NO: 34
AAV5-B (E350Q)	1296	US20160289275A1 SEQ ID NO: 35
AAV5-B (P533S)	1297	US20160289275A1 SEQ ID NO: 37
AAV5-B (P533S)	1298	US20160289275A1 SEQ ID NO: 38
AAV5-B (P533G)	1299	US20160289275A1 SEQ ID NO: 40
AAV5-B (P533G)	1300	US20160289275A1 SEQ ID NO: 41
AAV5-mutation in loop VII	1301	US20160289275A1 SEQ ID NO: 43

AAV5-mutation in loop VII	1302	US20160289275A1 SEQ ID NO: 44
AAV8	1303	US20160289275A1 SEQ ID NO: 47
Mut A (LK03/AAV8)	1304	WO2016181123A1 SEQ ID NO: 1
Mut B (LK03/AAV5)	1305	WO2016181123A1 SEQ ID NO: 2
Mut C (AAV8/AAV3B)	1306	WO2016181123A1 SEQ ID NO: 3
Mut D (AAV5/AAV3B)	1307	WO2016181123A1 SEQ ID NO: 4
Mut E (AAV8/AAV3B)	1308	WO2016181123A1 SEQ ID NO: 5
Mut F (AAV3B/AAV8)	1309	WO2016181123A1 SEQ ID NO: 6
AAV44.9	1310	WO2016183297A1 SEQ ID NO: 4
AAV44.9	1311	WO2016183297A1 SEQ ID NO: 5
AAVrh8	1312	WO2016183297A1 SEQ ID NO: 6
AAV44.9 (S470N)	1313	WO2016183297A1 SEQ ID NO: 9
rh74 VP1	1314	US20160375110A1 SEQ ID NO: 1
AAV-LK03 (L125I)	1315	WO2017015102A1 SEQ ID NO: 5
AAV3B (S663V+T492V)	1316	WO2017015102A1 SEQ ID NO: 6
Anc80	1317	WO2017019994A2 SEQ ID NO: 1
Anc80	1318	WO2017019994A2 SEQ ID NO: 2
Anc81	1319	WO2017019994A2 SEQ ID NO: 3
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Anc126	1332	WO2017019994A2 SEQ ID NO: 16
Anc127	1333	WO2017019994A2 SEQ ID NO: 17
Anc127	1334	WO2017019994A2 SEQ ID NO: 18
Anc80L27	1335	WO2017019994A2 SEQ ID NO: 19
Anc80L59	1336	WO2017019994A2 SEQ ID NO: 20
Anc80L60	1337	WO2017019994A2 SEQ ID NO: 21
Anc80L62	1338	WO2017019994A2 SEQ ID NO: 22
Anc80L65	1339	WO2017019994A2 SEQ ID NO: 23
Anc80L33	1340	WO2017019994A2 SEQ ID NO: 24
Anc80L36	1341	WO2017019994A2 SEQ ID NO: 25
Anc80L44	1342	WO2017019994A2 SEQ ID NO: 26

Anc80L1	1343	WO2017019994A2 SEQ ID NO: 35
Anc80L1	1344	WO2017019994A2 SEQ ID NO: 36
AAVrh10	1345	WO2017019994A2 SEQ ID NO: 41
Anc110	1346	WO2017019994A2 SEQ ID NO: 42
Anc110	1347	WO2017019994A2 SEQ ID NO: 43
AAVrh32.33	1348	WO2017019994A2 SEQ ID NO: 45
AAVrh74	1349	WO2017049031A1 SEQ ID NO: 1
AAV2	1350	WO2017053629A2 SEQ ID NO: 49
AAV2	1351	WO2017053629A2 SEQ ID NO: 50
AAV2	1352	WO2017053629A2 SEQ ID NO: 82
Parvo-like virus	1353	WO2017070476A2 SEQ ID NO: 1
Parvo-like virus	1354	WO2017070476A2 SEQ ID NO: 2
Parvo-like virus	1355	WO2017070476A2 SEQ ID NO: 3
Parvo-like virus	1356	WO2017070476A2 SEQ ID NO: 4
Parvo-like virus	1357	WO2017070476A2 SEQ ID NO: 5
Parvo-like virus	1358	WO2017070476A2 SEQ ID NO: 6
AAVrh.10	1359	WO2017070516A1 SEQ ID NO: 7
AAVrh.10	1360	WO2017070516A1 SEQ ID NO: 14
AAV2tYF	1361	WO2017070491A1 SEQ ID NO: 1
AAV-SPK	1362	WO2017075619A1 SEQ ID NO:28
AAV2.5	1363	US20170128528A1 SEQ ID NO: 13
AAV1.1	1364	US20170128528A1 SEQ ID NO: 15
AAV6.1	1365	US20170128528A1 SEQ ID NO: 17
AAV6.3.1	1366	US20170128528A1 SEQ ID NO: 18
AAV2i8	1367	US20170128528A1 SEQ ID NO: 28
AAV2i8	1368	US20170128528A1 SEQ ID NO: 29
ttAAV	1369	US20170128528A1 SEQ ID NO: 30
ttAAV-S312N	1370	US20170128528A1 SEQ ID NO: 32
ttAAV-S312N	1371	US20170128528A1 SEQ ID NO: 33
AAV6 (Y705, Y731, and T492)	1372	WO2016134337A1 SEQ ID NO: 24
AAV2	1373	WO2016134375A1 SEQ ID NO: 9
AAV2	1374	WO2016134375A1 SEQ ID NO: 10

[00067] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2015038958, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 2 and 11 of WO2015038958 or SEQ ID NO: 132 and 131 respectively herein), PHP.B (SEQ ID NO: 8 and 9 of WO2015038958 or SEQ ID NO: 1 and 2 herein), G2B-13 (SEQ ID NO: 12 of WO2015038958 or SEQ ID NO: 3 herein), G2B-26 (SEQ ID NO: 13 of WO2015038958 or SEQ ID NO: 1 herein), TH1.1-32 (SEQ ID NO: 14 of WO2015038958 or SEQ ID NO: 4 herein), TH1.1-35 (SEQ ID NO:

15 of WO2015038958 or SEQ ID NO: 5 herein) or variants thereof. Further, any of the targeting peptides or amino acid inserts described in WO2015038958, may be inserted into any parent AAV serotype, such as, but not limited to, AAV9 (SEQ ID NO: 131 for the DNA sequence and SEQ ID NO: 132 for the amino acid sequence). In one embodiment, the amino acid insert is inserted between amino acids 586-592 of the parent AAV (e.g., AAV9). In another embodiment, the amino acid insert is inserted between amino acids 588-589 of the parent AAV sequence. The amino acid insert may be, but is not limited to, any of the following amino acid sequences, TLAVPFK (SEQ ID NO: 1 of WO2015038958; herein SEQ ID NO: 876), KFPVALT (SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 877), LAVPFK (SEQ ID NO: 31 of WO2015038958; herein SEQ ID NO: 878), AVPFK (SEQ ID NO: 32 of WO2015038958; herein SEQ ID NO: 879), VPFK (SEQ ID NO: 33 of WO2015038958; herein SEQ ID NO: 880), TLAVPF (SEQ ID NO: 34 of WO2015038958; herein SEQ ID NO: 881), TLAVP (SEQ ID NO: 35 of WO2015038958; herein SEQ ID NO: 882), TLAV (SEQ ID NO: 36 of WO2015038958; herein SEQ ID NO: 883), SVSKPFL (SEQ ID NO: 28 of WO2015038958; herein SEQ ID NO: 884), FTLTTPK (SEQ ID NO: 29 of WO2015038958; herein SEQ ID NO: 885), MNATKNV (SEQ ID NO: 30 of WO2015038958; herein SEQ ID NO: 886), QSSQTPR (SEQ ID NO: 54 of WO2015038958; herein SEQ ID NO: 887), ILGTGTS (SEQ ID NO: 55 of WO2015038958; herein SEQ ID NO: 888), TRTNPEA (SEQ ID NO: 56 of WO2015038958; herein SEQ ID NO: 889), NGGTSSS (SEQ ID NO: 58 of WO2015038958; herein SEQ ID NO: 890), or YTLSQGW (SEQ ID NO: 60 of WO2015038958; herein SEQ ID NO: 891). Non-limiting examples of nucleotide sequences that may encode the amino acid inserts include the following, AAGTTTCCTGTGGCGTTGACT (for SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 892), ACTTTGGCGGTGCCTTTTAAG (SEQ ID NO: 24 and 49 of WO2015038958; herein SEQ ID NO: 893), AGTGTGAGTAAGCCTTTTTTG (SEQ ID NO: 25 of WO2015038958; herein SEQ ID NO: 894), TTTACGTTGACGACGCCTAAG (SEQ ID NO: 26 of WO2015038958; herein SEQ ID NO: 895), ATGAATGCTACGAAGAATGTG (SEQ ID NO: 27 of WO2015038958; herein SEQ ID NO: 896), CAGTCGTCGCAGACGCCTAGG (SEQ ID NO: 48 of WO2015038958; herein SEQ ID NO: 897), ATTCTGGGGACTGGTACTTCG (SEQ ID NO: 50 and 52 of WO2015038958; herein SEQ ID NO: 898), ACGCGGACTAATCCTGAGGCT (SEQ ID NO: 51 of WO2015038958; herein SEQ ID NO: 899), AATGGGGGGACTAGTAGTTCT (SEQ ID NO: 53 of WO2015038958; herein SEQ ID

NO: 900), or TATACTTTGTCGCAGGGTTGG (SEQ ID NO: 59 of WO2015038958; herein SEQ ID NO: 901).

[00068] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2017100671, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 45 of WO2017100671, herein SEQ ID NO: 875), PHP.N (SEQ ID NO: 46 of WO2017100671, herein SEQ ID NO: 873), PHP.S (SEQ ID NO: 47 of WO2017100671, herein SEQ ID NO: 874), or variants thereof. Further, any of the targeting peptides or amino acid inserts described in WO2017100671 may be inserted into any parent AAV serotype, such as, but not limited to, AAV9 (SEQ ID NO: 127 or SEQ ID NO: 875). In one embodiment, the amino acid insert is inserted between amino acids 586-592 of the parent AAV (e.g., AAV9). In another embodiment, the amino acid insert is inserted between amino acids 588-589 of the parent AAV sequence. The amino acid insert may be, but is not limited to, any of the following amino acid sequences, AQT LAVPFKAQ (SEQ ID NO: 1 of WO2017100671; herein SEQ ID NO: 902), AQS VSKPFLAQ (SEQ ID NO: 2 of WO2017100671; herein SEQ ID NO: 903), AQFTLTTPKAQ (SEQ ID NO: 3 in the sequence listing of WO2017100671; herein SEQ ID NO: 904), DGT LAVPFKAQ (SEQ ID NO: 4 in the sequence listing of WO2017100671; herein SEQ ID NO: 905), EST LAVPFKAQ (SEQ ID NO: 5 of WO2017100671; herein SEQ ID NO: 906), GGT LAVPFKAQ (SEQ ID NO: 6 of WO2017100671; herein SEQ ID NO: 907), AQT LATPFKAQ (SEQ ID NO: 7 and 33 of WO2017100671; herein SEQ ID NO: 908), ATT LATPFKAQ (SEQ ID NO: 8 of WO2017100671; herein SEQ ID NO: 909), DGT LATPFKAQ (SEQ ID NO: 9 of WO2017100671; herein SEQ ID NO: 910), GGT LATPFKAQ (SEQ ID NO: 10 of WO2017100671; herein SEQ ID NO: 911), SGS LAVPFKAQ (SEQ ID NO: 11 of WO2017100671; herein SEQ ID NO: 912), AQT LAQPFKAQ (SEQ ID NO: 12 of WO2017100671; herein SEQ ID NO: 913), AQT LQQPFKAQ (SEQ ID NO: 13 of WO2017100671; herein SEQ ID NO: 914), AQT LSNPFKAQ (SEQ ID NO: 14 of WO2017100671; herein SEQ ID NO: 915), AQT LAVPFSNP (SEQ ID NO: 15 of WO2017100671; herein SEQ ID NO: 916), QGT LAVPFKAQ (SEQ ID NO: 16 of WO2017100671; herein SEQ ID NO: 917), NQT LAVPFKAQ (SEQ ID NO: 17 of WO2017100671; herein SEQ ID NO: 918), EGS LAVPFKAQ (SEQ ID NO: 18 of WO2017100671; herein SEQ ID NO: 919), SGN LAVPFKAQ (SEQ ID NO: 19 of WO2017100671; herein SEQ ID NO: 920), EGT LAVPFKAQ (SEQ ID NO: 20 of WO2017100671; herein SEQ ID NO: 921), DST LAVPFKAQ (SEQ ID NO: 21 in Table 1 of WO2017100671; herein SEQ ID NO: 922),

AVTLAVPFKAQ (SEQ ID NO: 22 of WO2017100671; herein SEQ ID NO: 923),
 AQTLPSTPFKAQ (SEQ ID NO: 23 of WO2017100671; herein SEQ ID NO: 924), AQTLPQPFKAQ
 (SEQ ID NO: 24 and 32 of WO2017100671; herein SEQ ID NO: 925), AQTLSQPFKAQ (SEQ ID
 NO: 25 of WO2017100671; herein SEQ ID NO: 926), AQTLLPFKAQ (SEQ ID NO: 26 of
 WO2017100671; herein SEQ ID NO: 927), AQTLTMPFKAQ (SEQ ID NO: 27, and 34 of
 WO2017100671 and SEQ ID NO: 35 in the sequence listing of WO2017100671; herein SEQ ID
 NO: 928), AQTLTTPFKAQ (SEQ ID NO: 28 of WO2017100671; herein SEQ ID NO: 929),
 AQYTLSQGWQAQ (SEQ ID NO: 29 of WO2017100671; herein SEQ ID NO: 930),
 AQMNATKNVAQ (SEQ ID NO: 30 of WO2017100671; herein SEQ ID NO: 931),
 AQVSGGHHSQAQ (SEQ ID NO: 31 of WO2017100671; herein SEQ ID NO: 932),
 AQTLTAPFKAQ (SEQ ID NO: 35 in Table 1 of WO2017100671; herein SEQ ID NO: 933),
 AQTLSKPFKAQ (SEQ ID NO: 36 of WO2017100671; herein SEQ ID NO: 934), QAVRTSL (SEQ
 ID NO: 37 of WO2017100671; herein SEQ ID NO: 935), YTLSQGW (SEQ ID NO: 38 of
 WO2017100671; herein SEQ ID NO: 891), LAKERLS (SEQ ID NO: 39 of WO2017100671; herein
 SEQ ID NO: 936), TLAVPFK (SEQ ID NO: 40 in the sequence listing of WO2017100671; herein
 SEQ ID NO: 876), SVSKPFL (SEQ ID NO: 41 of WO2017100671; herein SEQ ID NO: 884),
 FTLTTPK (SEQ ID NO: 42 of WO2017100671; herein SEQ ID NO: 885), MNSTKNV (SEQ ID
 NO: 43 of WO2017100671; herein SEQ ID NO: 937), VSGGHHS (SEQ ID NO: 44 of
 WO2017100671; herein SEQ ID NO: 938), SAQTLAVPFKAQAQ (SEQ ID NO: 48 of
 WO2017100671; herein SEQ ID NO: 939), SXXXLAVPFKAQAQ (SEQ ID NO: 49 of
 WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 940),
 SAQXXXVPFKAQAQ (SEQ ID NO: 50 of WO2017100671 wherein X may be any amino acid;
 herein SEQ ID NO: 941), SAQTLXXXFKAQAQ (SEQ ID NO: 51 of WO2017100671 wherein X
 may be any amino acid; herein SEQ ID NO: 942), SAQTLAVXXXAQAQ (SEQ ID NO: 52 of
 WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 943),
 SAQTLAVPFXXXAQ (SEQ ID NO: 53 of WO2017100671 wherein X may be any amino acid;
 herein SEQ ID NO: 944), TNHQSAQ (SEQ ID NO: 65 of WO2017100671; herein SEQ ID NO:
 945), AQAQTGW (SEQ ID NO: 66 of WO2017100671; herein SEQ ID NO: 946), DGTLATPFK
 (SEQ ID NO: 67 of WO2017100671; herein SEQ ID NO: 947), DGTLATPFKXX (SEQ ID NO: 68
 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 948), LAVPFKAQ
 (SEQ ID NO: 80 of WO2017100671; herein SEQ ID NO: 949), VPFKAQ (SEQ ID NO: 81 of

WO2017100671; herein SEQ ID NO: 950), FKAQ (SEQ ID NO: 82 of WO2017100671; herein SEQ ID NO: 951), AQTLAV (SEQ ID NO: 83 of WO2017100671; herein SEQ ID NO: 952), AQTLAVPF (SEQ ID NO: 84 of WO2017100671; herein SEQ ID NO: 953), QAVR (SEQ ID NO: 85 of WO2017100671; herein SEQ ID NO: 954), AVRT (SEQ ID NO: 86 of WO2017100671; herein SEQ ID NO: 955), VRTS (SEQ ID NO: 87 of WO2017100671; herein SEQ ID NO: 956), RTSL (SEQ ID NO: 88 of WO2017100671; herein SEQ ID NO: 957), QAVRT (SEQ ID NO: 89 of WO2017100671; herein SEQ ID NO: 958), AVRVS (SEQ ID NO: 90 of WO2017100671; herein SEQ ID NO: 959), VRTSL (SEQ ID NO: 91 of WO2017100671; herein SEQ ID NO: 960), QAVRVS (SEQ ID NO: 92 of WO2017100671; herein SEQ ID NO: 961), or AVRTSL (SEQ ID NO: 93 of WO2017100671; herein SEQ ID NO: 962).

[00069] Non-limiting examples of nucleotide sequences that may encode the amino acid inserts include the following, GATGGGACTTTGGCGGTGCCTTTTAAGGCACAG (SEQ ID NO: 54 of WO2017100671; herein SEQ ID NO: 963), GATGGGACGTTGGCGGTGCCTTTTAAGGCACAG (SEQ ID NO: 55 of WO2017100671; herein SEQ ID NO: 964), CAGGCGGTTAGGACGTCTTTG (SEQ ID NO: 56 of WO2017100671; herein SEQ ID NO: 965), CAGGTCTTCACGGACTCAGACTATCAG (SEQ ID NO: 57 and 78 of WO2017100671; herein SEQ ID NO: 966), CAAGTAAAACCTCTACAAATGTGGTAAAATCG (SEQ ID NO: 58 of WO2017100671; herein SEQ ID NO: 967), ACTCATCGACCAATACTTGTACTATCTCTCTAGAAC (SEQ ID NO: 59 of WO2017100671; herein SEQ ID NO: 968), GGAAGTATTCCTTGGTTTTGAACCCA (SEQ ID NO: 60 of WO2017100671; herein SEQ ID NO: 969), GGTCGCGGTTCTTGTGTGGAT (SEQ ID NO: 61 of WO2017100671; herein SEQ ID NO: 970), CGACCTTGAAGCGCATGAACTCCT (SEQ ID NO: 62 of WO2017100671; herein SEQ ID NO: 971), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNMNNMNNMNNMNNMNTTGGGCACTCTGGTGGTTTGTC (SEQ ID NO: 63 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 972), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCMNNMNNMNNAAAAGGCACCGCCAAAGTTTG (SEQ ID NO: 69 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 973), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNCACCGCCAAAGTTTGGGCACT (SEQ ID NO: 70 of WO2017100671 wherein N may be A, C, T, or G; herein

SEQ ID NO: 974),

GTATTCCTTGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTTAAAMNNMNNMNNCAA
AGTTTGGGCACTCTGGTGG (SEQ ID NO: 71 of WO2017100671 wherein N may be A, C, T, or
G; herein SEQ ID NO: 975),

GTATTCCTTGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTTAAAAGGCACMNNMNN
MNNTTGGGCACTCTGGTGGTTTGTG (SEQ ID NO: 72 of WO2017100671 wherein N may be
A, C, T, or G; herein SEQ ID NO: 976), ACTTTGGCGGTGCCTTTTAAG (SEQ ID NO: 74 of
WO2017100671; herein SEQ ID NO: 893), AGTGTGAGTAAGCCTTTTTTG (SEQ ID NO: 75 of
WO2017100671; herein SEQ ID NO: 894), TTTACGTTGACGACGCCTAAG (SEQ ID NO: 76 of
WO2017100671; herein SEQ ID NO: 895), TATACTTTGTCGCAGGGTTGG (SEQ ID NO: 77 of
WO2017100671; herein SEQ ID NO: 901), or CTTGCGAAGGAGCGGCTTTCG (SEQ ID NO: 79
of WO2017100671; herein SEQ ID NO: 977).

[00070] In one embodiment, the AAV serotype may be, or may have a sequence as described in United States Patent No. US 9624274, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV1 (SEQ ID NO: 181 of US9624274), AAV6 (SEQ ID NO: 182 of US9624274), AAV2 (SEQ ID NO: 183 of US9624274), AAV3b (SEQ ID NO: 184 of US9624274), AAV7 (SEQ ID NO: 185 of US9624274), AAV8 (SEQ ID NO: 186 of US9624274), AAV10 (SEQ ID NO: 187 of US9624274), AAV4 (SEQ ID NO: 188 of US9624274), AAV11 (SEQ ID NO: 189 of US9624274), bAAV (SEQ ID NO: 190 of US9624274), AAV5 (SEQ ID NO: 191 of US9624274), GPV (SEQ ID NO: 192 of US9624274; herein SEQ ID NO: 992), B19 (SEQ ID NO: 193 of US9624274; herein SEQ ID NO: 993), MVM (SEQ ID NO: 194 of US9624274; herein SEQ ID NO: 994), FPV (SEQ ID NO: 195 of US9624274; herein SEQ ID NO: 995), CPV (SEQ ID NO: 196 of US9624274; herein SEQ ID NO: 996) or variants thereof. Further, any of the structural protein inserts described in US 9624274, may be inserted into, but not limited to, I-453 and I-587 of any parent AAV serotype, such as, but not limited to, AAV2 (SEQ ID NO: 183 of US9624274). The amino acid insert may be, but is not limited to, any of the following amino acid sequences, VNLTSRASG (SEQ ID NO: 50 of US9624274; herein SEQ ID NO: 1375), EFCINHRGYWVCGD (SEQ ID NO: 55 of US9624274; herein SEQ ID NO: 1376), EDGQVMDVDLS (SEQ ID NO: 85 of US9624274; herein SEQ ID NO: 1377), EKQRNGTLT (SEQ ID NO: 86 of US9624274; herein SEQ ID NO: 1378), TYQCRVTHPHLPRALMR (SEQ ID NO: 87 of US9624274; herein SEQ ID NO: 1379), RHSTTQPRKTKGSG (SEQ ID NO: 88 of

US9624274; herein SEQ ID NO: 1380), DSNPRGVSAYLSR (SEQ ID NO: 89 of US9624274; herein SEQ ID NO: 1381), TITCLWDLAPSK (SEQ ID NO: 90 of US9624274; herein SEQ ID NO: 1382), KTKGSGFFVF (SEQ ID NO: 91 of US9624274; herein SEQ ID NO: 1383), THPHLPRALMRS (SEQ ID NO: 92 of US9624274; herein SEQ ID NO: 1384), GETYQCRVTHPHLPRALMRSTTK (SEQ ID NO: 93 of US9624274; herein SEQ ID NO: 1385), LPRALMRS (SEQ ID NO: 94 of US9624274; herein SEQ ID NO: 1386), INHRGYWV (SEQ ID NO: 95 of US9624274; herein SEQ ID NO: 1387), CDAGSVRTNAPD (SEQ ID NO: 60 of US9624274; herein SEQ ID NO: 1388), AKAVSNLTESRSESLQS (SEQ ID NO: 96 of US9624274; herein SEQ ID NO: 1389), SLTGDEFKKVLET (SEQ ID NO: 97 of US9624274; herein SEQ ID NO: 1390), REAVAYRFEED (SEQ ID NO: 98 of US9624274; herein SEQ ID NO: 1391), INPEIITLDG (SEQ ID NO: 99 of US9624274; herein SEQ ID NO: 1392), DISVTGAPVITATYL (SEQ ID NO: 100 of US9624274; herein SEQ ID NO: 1393), DISVTGAPVITA (SEQ ID NO: 101 of US9624274; herein SEQ ID NO: 1394), PKTVSNLTESSESQVS (SEQ ID NO: 102 of US9624274; herein SEQ ID NO: 1395), SLMGDEFKAVLET (SEQ ID NO: 103 of US9624274; herein SEQ ID NO: 1396), QHSVAYTFEED (SEQ ID NO: 104 of US9624274; herein SEQ ID NO: 1397), INPEIITRDG (SEQ ID NO: 105 of US9624274; herein SEQ ID NO: 1398), DISLTGDPVITASYL (SEQ ID NO: 106 of US9624274; herein SEQ ID NO: 1399), DISLTGDPVITA (SEQ ID NO: 107 of US9624274; herein SEQ ID NO: 1400), DQSIDFEIDSA (SEQ ID NO: 108 of US9624274; herein SEQ ID NO: 1401), KNVSEDLPLPTFSPTLLGDS (SEQ ID NO: 109 of US9624274; herein SEQ ID NO: 1402), KNVSEDLPLPT (SEQ ID NO: 110 of US9624274; herein SEQ ID NO: 1403), CDSGRVRTDAPD (SEQ ID NO: 111 of US9624274; herein SEQ ID NO: 1404), FPEHLLVDFLQSL (SEQ ID NO: 112 of US9624274; herein SEQ ID NO: 1405), DAEFRHDSG (SEQ ID NO: 65 of US9624274; herein SEQ ID NO: 1406), HYAAAQWDFGNTMCQL (SEQ ID NO: 113 of US9624274; herein SEQ ID NO: 1407), YAAQWDFGNTMCQ (SEQ ID NO: 114 of US9624274; herein SEQ ID NO: 1408), RSQKEGLHYT (SEQ ID NO: 115 of US9624274; herein SEQ ID NO: 1409), SSRTPSDKPVAHWANPQAE (SEQ ID NO: 116 of US9624274; herein SEQ ID NO: 1410), SRTPSDKPVAHWANP (SEQ ID NO: 117 of US9624274; herein SEQ ID NO: 1411), SSRTPSDKP (SEQ ID NO: 118 of US9624274; herein SEQ ID NO: 1412), NADGNVDYHMNSVP (SEQ ID NO: 119 of US9624274; herein SEQ ID NO: 1413), DGNVDYHMNSV (SEQ ID NO: 120 of US9624274; herein SEQ ID NO: 1414),

RSFKEFLQSSLRALRQ (SEQ ID NO: 121 of US9624274; herein SEQ ID NO: 1415);

FKEFLQSSLRA (SEQ ID NO: 122 of US9624274; herein SEQ ID NO: 1416), or

QMWAPQWGPD (SEQ ID NO: 123 of US9624274; herein SEQ ID NO: 1417).

[00071] In one embodiment, the AAV serotype may be, or may have a sequence as described in United States Patent No. US 9475845, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV capsid proteins comprising modification of one or more amino acids at amino acid positions 585 to 590 of the native AAV2 capsid protein. Further the modification may result in, but not limited to, the amino acid sequence RGNRQA (SEQ ID NO: 3 of US9475845; herein SEQ ID NO: 1418), SSSTDP (SEQ ID NO: 4 of US9475845; herein SEQ ID NO: 1419), SSNTAP (SEQ ID NO: 5 of US9475845; herein SEQ ID NO: 1420), SNSNLP (SEQ ID NO: 6 of US9475845; herein SEQ ID NO: 1421), SSTTAP (SEQ ID NO: 7 of US9475845; herein SEQ ID NO: 1422), AANTAA (SEQ ID NO: 8 of US9475845; herein SEQ ID NO: 1423), QQNTAP (SEQ ID NO: 9 of US9475845; herein SEQ ID NO: 1424), SAQAQA (SEQ ID NO: 10 of US9475845; herein SEQ ID NO: 1425), QANTGP (SEQ ID NO: 11 of US9475845; herein SEQ ID NO: 1426), NATTAP (SEQ ID NO: 12 of US9475845; herein SEQ ID NO: 1427), SSTAGP (SEQ ID NO: 13 and 20 of US9475845; herein SEQ ID NO: 1428), QQNTAA (SEQ ID NO: 14 of US9475845; herein SEQ ID NO: 1429), PSTAGP (SEQ ID NO: 15 of US9475845; herein SEQ ID NO: 1430), NQNTAP (SEQ ID NO: 16 of US9475845; herein SEQ ID NO: 1431), QAANAP (SEQ ID NO: 17 of US9475845; herein SEQ ID NO: 1432), SIVGLP (SEQ ID NO: 18 of US9475845; herein SEQ ID NO: 1433), AASTAA (SEQ ID NO: 19, and 27 of US9475845; herein SEQ ID NO: 1434), SQNTTA (SEQ ID NO: 21 of US9475845; herein SEQ ID NO: 1435), QQDTAP (SEQ ID NO: 22 of US9475845; herein SEQ ID NO: 1436), QTNTGP (SEQ ID NO: 23 of US9475845; herein SEQ ID NO: 1437), QTNGAP (SEQ ID NO: 24 of US9475845; herein SEQ ID NO: 1438), QQNAAP (SEQ ID NO: 25 of US9475845; herein SEQ ID NO: 1439), or AANTQA (SEQ ID NO: 26 of US9475845; herein SEQ ID NO: 1440). In one embodiment, the amino acid modification is a substitution at amino acid positions 262 through 265 in the native AAV2 capsid protein or the corresponding position in the capsid protein of another AAV with a targeting sequence. The targeting sequence may be, but is not limited to, any of the amino acid sequences, NGRAHA (SEQ ID NO: 38 of US9475845; herein SEQ ID NO: 1441), QPEHSST (SEQ ID NO: 39 and 50 of US9475845; herein SEQ ID NO: 1442), VNTANST (SEQ ID NO: 40 of US9475845; herein SEQ ID NO: 1443), HGPMQKS (SEQ ID NO: 41 of US9475845; herein SEQ ID NO: 1444), PHKPPLA

(SEQ ID NO: 42 of US9475845; herein SEQ ID NO: 1445), IKNNEMW (SEQ ID NO: 43 of US9475845; herein SEQ ID NO: 1446), RNLDTPM (SEQ ID NO: 44 of US9475845; herein SEQ ID NO: 1447), VDSHRQS (SEQ ID NO: 45 of US9475845; herein SEQ ID NO: 1448), YDSKTKT (SEQ ID NO: 46 of US9475845; herein SEQ ID NO: 1449), SQLPHQK (SEQ ID NO: 47 of US9475845; herein SEQ ID NO: 1450), STMQQNT (SEQ ID NO: 48 of US9475845; herein SEQ ID NO: 1451), TERYMTQ (SEQ ID NO: 49 of US9475845; herein SEQ ID NO: 1452), DASLSTS (SEQ ID NO: 51 of US9475845; herein SEQ ID NO: 1453), DLPNKKT (SEQ ID NO: 52 of US9475845; herein SEQ ID NO: 1454), DLTAARL (SEQ ID NO: 53 of US9475845; herein SEQ ID NO: 1455), EPHQFNY (SEQ ID NO: 54 of US9475845; herein SEQ ID NO: 1456), EPQSNHT (SEQ ID NO: 55 of US9475845; herein SEQ ID NO: 1457), MSSWPSQ (SEQ ID NO: 56 of US9475845; herein SEQ ID NO: 1458), NPKHNAT (SEQ ID NO: 57 of US9475845; herein SEQ ID NO: 1459), PDGMRTT (SEQ ID NO: 58 of US9475845; herein SEQ ID NO: 1460), PNNNKTT (SEQ ID NO: 59 of US9475845; herein SEQ ID NO: 1461), QSTTHDS (SEQ ID NO: 60 of US9475845; herein SEQ ID NO: 1462), TGSKQKQ (SEQ ID NO: 61 of US9475845; herein SEQ ID NO: 1463), SLKHQAL (SEQ ID NO: 62 of US9475845; herein SEQ ID NO: 1464), SPIDGEQ (SEQ ID NO: 63 of US9475845; herein SEQ ID NO: 1465), WIFPWIQL (SEQ ID NO: 64 and 112 of US9475845; herein SEQ ID NO: 1466), CDCRGDCFC (SEQ ID NO: 65 of US9475845; herein SEQ ID NO: 1467), CNGRC (SEQ ID NO: 66 of US9475845; herein SEQ ID NO: 1468), CPRECES (SEQ ID NO: 67 of US9475845; herein SEQ ID NO: 1469), CTTHWGFTLC (SEQ ID NO: 68 and 123 of US9475845; herein SEQ ID NO: 1470), CGRRAGGSC (SEQ ID NO: 69 of US9475845; herein SEQ ID NO: 1471), CKGGRKDC (SEQ ID NO: 70 of US9475845; herein SEQ ID NO: 1472), CVPELGHEC (SEQ ID NO: 71 and 115 of US9475845; herein SEQ ID NO: 1473), CRRETAWAK (SEQ ID NO: 72 of US9475845; herein SEQ ID NO: 1474), VSWFSHRYSFPAVS (SEQ ID NO: 73 of US9475845; herein SEQ ID NO: 1475), GYRDGYAGPILYN (SEQ ID NO: 74 of US9475845; herein SEQ ID NO: 1476), XXXYXXX (SEQ ID NO: 75 of US9475845; herein SEQ ID NO: 1477), YXNW (SEQ ID NO: 76 of US9475845; herein SEQ ID NO: 1478), RPLPLP (SEQ ID NO: 77 of US9475845; herein SEQ ID NO: 1479), APPLPPR (SEQ ID NO: 78 of US9475845; herein SEQ ID NO: 1480), DVFYPYPYASGS (SEQ ID NO: 79 of US9475845; herein SEQ ID NO: 1481), MYWYPY (SEQ ID NO: 80 of US9475845; herein SEQ ID NO: 1482), DITWDQLWDLMK (SEQ ID NO: 81 of US9475845; herein SEQ ID NO: 1483), CWDDXWLC (SEQ ID NO: 82 of US9475845; herein

SEQ ID NO: 1484), EWCEYLGGYLR CYA (SEQ ID NO: 83 of US9475845; herein SEQ ID NO: 1485), YXCXXGPXTWXCXP (SEQ ID NO: 84 of US9475845; herein SEQ ID NO: 1486), IEGPTLRQWLAARA (SEQ ID NO: 85 of US9475845; herein SEQ ID NO: 1487), LWXXX (SEQ ID NO: 86 of US9475845; herein SEQ ID NO: 1488), XFXXYLW (SEQ ID NO: 87 of US9475845; herein SEQ ID NO: 1489), SSIISHFRWGLCD (SEQ ID NO: 88 of US9475845; herein SEQ ID NO: 1490), MSRPACPPNDKYE (SEQ ID NO: 89 of US9475845; herein SEQ ID NO: 1491), CLRSGRGC (SEQ ID NO: 90 of US9475845; herein SEQ ID NO: 1492), CHWMFSPWC (SEQ ID NO: 91 of US9475845; herein SEQ ID NO: 1493), WXXF (SEQ ID NO: 92 of US9475845; herein SEQ ID NO: 1494), CSSRLDAC (SEQ ID NO: 93 of US9475845; herein SEQ ID NO: 1495), CLPVASC (SEQ ID NO: 94 of US9475845; herein SEQ ID NO: 1496), CGFECVRQCPERC (SEQ ID NO: 95 of US9475845; herein SEQ ID NO: 1497), CVALCREACGEGC (SEQ ID NO: 96 of US9475845; herein SEQ ID NO: 1498), SWCEPGWCR (SEQ ID NO: 97 of US9475845; herein SEQ ID NO: 1499), YSGKWGW (SEQ ID NO: 98 of US9475845; herein SEQ ID NO: 1500), GLSGGRS (SEQ ID NO: 99 of US9475845; herein SEQ ID NO: 1501), LMLPRAD (SEQ ID NO: 100 of US9475845; herein SEQ ID NO: 1502), CSCFRDVCC (SEQ ID NO: 101 of US9475845; herein SEQ ID NO: 1503), CRDVVSVIC (SEQ ID NO: 102 of US9475845; herein SEQ ID NO: 1504), MARSGL (SEQ ID NO: 103 of US9475845; herein SEQ ID NO: 1505), MARAKE (SEQ ID NO: 104 of US9475845; herein SEQ ID NO: 1506), MSRTMS (SEQ ID NO: 105 of US9475845; herein SEQ ID NO: 1507), KCCYSL (SEQ ID NO: 106 of US9475845; herein SEQ ID NO: 1508), MYWGDSHWLQYWYE (SEQ ID NO: 107 of US9475845; herein SEQ ID NO: 1509), MQLPLAT (SEQ ID NO: 108 of US9475845; herein SEQ ID NO: 1510), EWLS (SEQ ID NO: 109 of US9475845; herein SEQ ID NO: 1511), SNEW (SEQ ID NO: 110 of US9475845; herein SEQ ID NO: 1512), TNYL (SEQ ID NO: 111 of US9475845; herein SEQ ID NO: 1513), WDLAWMFRLPVG (SEQ ID NO: 113 of US9475845; herein SEQ ID NO: 1514), CTVALPGGYVRVC (SEQ ID NO: 114 of US9475845; herein SEQ ID NO: 1515), CVAYCIEHHCWTC (SEQ ID NO: 116 of US9475845; herein SEQ ID NO: 1516), CVFAHNYDYLCV (SEQ ID NO: 117 of US9475845; herein SEQ ID NO: 1517), CVFTSNYAFC (SEQ ID NO: 118 of US9475845; herein SEQ ID NO: 1518), VHSPNKK (SEQ ID NO: 119 of US9475845; herein SEQ ID NO: 1519), CRGDGWC (SEQ ID NO: 120 of US9475845; herein SEQ ID NO: 1520), XRGCDX (SEQ ID NO: 121 of US9475845; herein SEQ ID NO: 1521), PXXX (SEQ ID NO: 122 of US9475845; herein SEQ ID NO: 1522), SGKGPQRITAL (SEQ ID NO: 124

of US9475845; herein SEQ ID NO: 1523), AAAAAAAAAAXXXXXX (SEQ ID NO: 125 of US9475845; herein SEQ ID NO: 1524), VYMSPF (SEQ ID NO: 126 of US9475845; herein SEQ ID NO: 1525), ATWLPPR (SEQ ID NO: 127 of US9475845; herein SEQ ID NO: 1526), HTMYHHYQHHL (SEQ ID NO: 128 of US9475845; herein SEQ ID NO: 1527), SEVGCRAGPLQWLCEKYFG (SEQ ID NO: 129 of US9475845; herein SEQ ID NO: 1528), CGLLPVGRPDNRNVWRWLC (SEQ ID NO: 130 of US9475845; herein SEQ ID NO: 1529), CKGQCDRFKGLPWEC (SEQ ID NO: 131 of US9475845; herein SEQ ID NO: 1530), SGRSA (SEQ ID NO: 132 of US9475845; herein SEQ ID NO: 1531), WGFP (SEQ ID NO: 133 of US9475845; herein SEQ ID NO: 1532), AEPMPHSLNFSQYLWYT (SEQ ID NO: 134 of US9475845; herein SEQ ID NO: 1533), WAYXSP (SEQ ID NO: 135 of US9475845; herein SEQ ID NO: 1534), IELLQAR (SEQ ID NO: 136 of US9475845; herein SEQ ID NO: 1535), AYTKCSRQWRTCMTH (SEQ ID NO: 137 of US9475845; herein SEQ ID NO: 1536), PQNSKIPGPTFLDPH (SEQ ID NO: 138 of US9475845; herein SEQ ID NO: 1537), SMEPALPDWWWKMFK (SEQ ID NO: 139 of US9475845; herein SEQ ID NO: 1538), ANTPCGPYTHDCPVKR (SEQ ID NO: 140 of US9475845; herein SEQ ID NO: 1539), TACHQHVRMVRP (SEQ ID NO: 141 of US9475845; herein SEQ ID NO: 1540), VPWMEPAYQRFL (SEQ ID NO: 142 of US9475845; herein SEQ ID NO: 1541), DPRATPGS (SEQ ID NO: 143 of US9475845; herein SEQ ID NO: 1542), FRPNRAQDYNTN (SEQ ID NO: 144 of US9475845; herein SEQ ID NO: 1543), CTKNSYLMC (SEQ ID NO: 145 of US9475845; herein SEQ ID NO: 1544), CXXTXXXGXGC (SEQ ID NO: 146 of US9475845; herein SEQ ID NO: 1545), CPIEDRPMC (SEQ ID NO: 147 of US9475845; herein SEQ ID NO: 1546), HEWSYLAPYPWF (SEQ ID NO: 148 of US9475845; herein SEQ ID NO: 1547), MCPKHPLGC (SEQ ID NO: 149 of US9475845; herein SEQ ID NO: 1548), RMWPSSTVNLSAGRR (SEQ ID NO: 150 of US9475845; herein SEQ ID NO: 1549), SAKTAVSQRVWLPSHRGGEP (SEQ ID NO: 151 of US9475845; herein SEQ ID NO: 1550), KSREHVNNNSACPSKRITAAL (SEQ ID NO: 152 of US9475845; herein SEQ ID NO: 1551), EGFR (SEQ ID NO: 153 of US9475845; herein SEQ ID NO: 1552), AGLGVR (SEQ ID NO: 154 of US9475845; herein SEQ ID NO: 1553), GTRQGHTMRLGVSDG (SEQ ID NO: 155 of US9475845; herein SEQ ID NO: 1554), IAGLATPGWSHWLAL (SEQ ID NO: 156 of US9475845; herein SEQ ID NO: 1555), SMSIARL (SEQ ID NO: 157 of US9475845; herein SEQ ID NO: 1556), HTFEPGV (SEQ ID NO: 158 of US9475845; herein SEQ ID NO: 1557), NTS�KRISNKRIRRK (SEQ ID NO: 159 of US9475845;

herein SEQ ID NO: 1558), LRIKRKRRKRKKTRK (SEQ ID NO: 160 of US9475845; herein SEQ ID NO: 1559), GGG, GFS, LWS, EGG, LLV, LSP, LBS, AGG, GRR, GGH and GTV.

[00072] In one embodiment, the AAV serotype may be, or may have a sequence as described in United States Publication No. US 20160369298, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, site-specific mutated capsid protein of AAV2 (SEQ ID NO: 97 of US 20160369298; herein SEQ ID NO: 1560) or variants thereof, wherein the specific site is at least one site selected from sites R447, G453, S578, N587, N587+1, S662 of VP1 or fragment thereof.

[00073] Further, any of the mutated sequences described in US 20160369298, may be or may have, but not limited to, any of the following sequences SDSGASN (SEQ ID NO: 1 and SEQ ID NO: 231 of US20160369298; herein SEQ ID NO: 1561), SPSGASN (SEQ ID NO: 2 of US20160369298; herein SEQ ID NO: 1562), SHSGASN (SEQ ID NO: 3 of US20160369298; herein SEQ ID NO: 1563), SRSGASN (SEQ ID NO: 4 of US20160369298; herein SEQ ID NO: 1564), SKSGASN (SEQ ID NO: 5 of US20160369298; herein SEQ ID NO: 1565), SNSGASN (SEQ ID NO: 6 of US20160369298; herein SEQ ID NO: 1566), SGSGASN (SEQ ID NO: 7 of US20160369298; herein SEQ ID NO: 1567), SASGASN (SEQ ID NO: 8, 175, and 221 of US20160369298; herein SEQ ID NO: 1568), SESGTSN (SEQ ID NO: 9 of US20160369298; herein SEQ ID NO: 1569), STTGGSN (SEQ ID NO: 10 of US20160369298; herein SEQ ID NO: 1570), SSAGSTN (SEQ ID NO: 11 of US20160369298; herein SEQ ID NO: 1571), NNDSQA (SEQ ID NO: 12 of US20160369298; herein SEQ ID NO: 1572), NNRNQA (SEQ ID NO: 13 of US20160369298; herein SEQ ID NO: 1573), NNNKQA (SEQ ID NO: 14 of US20160369298; herein SEQ ID NO: 1574), NAKRQA (SEQ ID NO: 15 of US20160369298; herein SEQ ID NO: 1575), NDEHQA (SEQ ID NO: 16 of US20160369298; herein SEQ ID NO: 1576), NTSQKA (SEQ ID NO: 17 of US20160369298; herein SEQ ID NO: 1577), YYLSRTNTPSGTDTQSRLVFSQAGA (SEQ ID NO: 18 of US20160369298; herein SEQ ID NO: 1578), YYLSRTNTDSGTETQSGLDFSQAGA (SEQ ID NO: 19 of US20160369298; herein SEQ ID NO: 1579), YYLSRTNTESGTPTQSALEFSQAGA (SEQ ID NO: 20 of US20160369298; herein SEQ ID NO: 1580), YYLSRTNTHSGTHTQSPLHFSQAGA (SEQ ID NO: 21 of US20160369298; herein SEQ ID NO: 1581), YYLSRTNTSSGTITISHLIFSQAGA (SEQ ID NO: 22 of US20160369298; herein SEQ ID NO: 1582), YYLSRTNTRSGIMTKSSLMFSQAGA (SEQ ID NO: 23 of US20160369298; herein SEQ ID NO: 1583), YYLSRTNTKSGRKTLNLSFSQAGA

(SEQ ID NO: 24 of US20160369298; herein SEQ ID NO: 1584),
 YYLSRTNDGSGPVTPSKLRFSQRGA (SEQ ID NO: 25 of US20160369298; herein SEQ ID NO: 1585), YYLSRTNAASGHATHSDLKFSQPGA (SEQ ID NO: 26 of US20160369298; herein SEQ ID NO: 1586), YYLSRTNGQAGSLTMSELGFSQVGA (SEQ ID NO: 27 of US20160369298; herein SEQ ID NO: 1587), YYLSRTNSTGGNQTTSQLLFSQLSA (SEQ ID NO: 28 of US20160369298; herein SEQ ID NO: 1588), YFLSRTNNNTGLNTNSTLNFSQGRA (SEQ ID NO: 29 of US20160369298; herein SEQ ID NO: 1589), SKTGADNNNSEYSWTG (SEQ ID NO: 30 of US20160369298; herein SEQ ID NO: 1590), SKTDADNNNSEYSWTG (SEQ ID NO: 31 of US20160369298; herein SEQ ID NO: 1591), SKTEADNNNSEYSWTG (SEQ ID NO: 32 of US20160369298; herein SEQ ID NO: 1592), SKTPADNNNSEYSWTG (SEQ ID NO: 33 of US20160369298; herein SEQ ID NO: 1593), SKTHADNNNSEYSWTG (SEQ ID NO: 34 of US20160369298; herein SEQ ID NO: 1594), SKTQADNNNSEYSWTG (SEQ ID NO: 35 of US20160369298; herein SEQ ID NO: 1595), SKTIADNNNSEYSWTG (SEQ ID NO: 36 of US20160369298; herein SEQ ID NO: 1596), SKTMADNNNSEYSWTG (SEQ ID NO: 37 of US20160369298; herein SEQ ID NO: 1597), SKTRADNNNSEYSWTG (SEQ ID NO: 38 of US20160369298; herein SEQ ID NO: 1598), SKTNADNNNSEYSWTG (SEQ ID NO: 39 of US20160369298; herein SEQ ID NO: 1599), SKTVGRNNNSEYSWTG (SEQ ID NO: 40 of US20160369298; herein SEQ ID NO: 1600), SKTADRNNNSEYSWTG (SEQ ID NO: 41 of US20160369298; herein SEQ ID NO: 1601), SKKLSQNNNSKYSWQG (SEQ ID NO: 42 of US20160369298; herein SEQ ID NO: 1602), SKPTTGNNNSDYSWPG (SEQ ID NO: 43 of US20160369298; herein SEQ ID NO: 1603), STQKNENNNNSNYSWPG (SEQ ID NO: 44 of US20160369298; herein SEQ ID NO: 1604), HKDDEGKF (SEQ ID NO: 45 of US20160369298; herein SEQ ID NO: 1605), HKDDNRKF (SEQ ID NO: 46 of US20160369298; herein SEQ ID NO: 1606), HKDDTNKF (SEQ ID NO: 47 of US20160369298; herein SEQ ID NO: 1607), HEDSDKNF (SEQ ID NO: 48 of US20160369298; herein SEQ ID NO: 1608), HRDGADSF (SEQ ID NO: 49 of US20160369298; herein SEQ ID NO: 1609), HGDNKSFR (SEQ ID NO: 50 of US20160369298; herein SEQ ID NO: 1610), KQGSEKTNVDFEEV (SEQ ID NO: 51 of US20160369298; herein SEQ ID NO: 1611), KQGSEKTNVDSEEV (SEQ ID NO: 52 of US20160369298; herein SEQ ID NO: 1612), KQGSEKTNVDVEEV (SEQ ID NO: 53 of US20160369298; herein SEQ ID NO: 1613), KQGSDKTNVDDAGV (SEQ ID NO: 54 of US20160369298; herein SEQ ID NO: 1614), KQGSSKTNVDPREV (SEQ ID NO: 55 of US20160369298; herein SEQ ID NO: 1615),

KQGSRKTNVDHKQV (SEQ ID NO: 56 of US20160369298; herein SEQ ID NO: 1616),
KQGSKGGNVDTNRV (SEQ ID NO: 57 of US20160369298; herein SEQ ID NO: 1617),
KQSGEANVDNGDV (SEQ ID NO: 58 of US20160369298; herein SEQ ID NO: 1618),
KQDAAADNIDYDHV (SEQ ID NO: 59 of US20160369298; herein SEQ ID NO: 1619),
KQSGTRSNAASSV (SEQ ID NO: 60 of US20160369298; herein SEQ ID NO: 1620),
KENTNTNDELTV (SEQ ID NO: 61 of US20160369298; herein SEQ ID NO: 1621),
QRGNNVAATADVNT (SEQ ID NO: 62 of US20160369298; herein SEQ ID NO: 1622),
QRGNNEAATADVNT (SEQ ID NO: 63 of US20160369298; herein SEQ ID NO: 1623),
QRGNNPAATADVNT (SEQ ID NO: 64 of US20160369298; herein SEQ ID NO: 1624),
QRGNNHAATADVNT (SEQ ID NO: 65 of US20160369298; herein SEQ ID NO: 1625),
QEENNIAATPGVNT (SEQ ID NO: 66 of US20160369298; herein SEQ ID NO: 1626),
QPPNNMAATHEVNT (SEQ ID NO: 67 of US20160369298; herein SEQ ID NO: 1627),
QHHNNSAATTIVNT (SEQ ID NO: 68 of US20160369298; herein SEQ ID NO: 1628),
QTTNNRAAFNMVET (SEQ ID NO: 69 of US20160369298; herein SEQ ID NO: 1629),
QKKNNNAASKKVAT (SEQ ID NO: 70 of US20160369298; herein SEQ ID NO: 1630),
QGGNNKAADDAVKT (SEQ ID NO: 71 of US20160369298; herein SEQ ID NO: 1631),
QAAKGGAADDAVKT (SEQ ID NO: 72 of US20160369298; herein SEQ ID NO: 1632),
QDDRAAAANESVDT (SEQ ID NO: 73 of US20160369298; herein SEQ ID NO: 1633),
QQQHDDAAYQRVHT (SEQ ID NO: 74 of US20160369298; herein SEQ ID NO: 1634),
QSSSLAAVSTVQT (SEQ ID NO: 75 of US20160369298; herein SEQ ID NO: 1635),
QNNQTAAIRNVTT (SEQ ID NO: 76 of US20160369298; herein SEQ ID NO: 1636),
NYNKKSDNVDF (SEQ ID NO: 77 of US20160369298; herein SEQ ID NO: 1637),
NYNKKSENVDF (SEQ ID NO: 78 of US20160369298; herein SEQ ID NO: 1638),
NYNKKSLNVDF (SEQ ID NO: 79 of US20160369298; herein SEQ ID NO: 1639),
NYNKKSPNVDF (SEQ ID NO: 80 of US20160369298; herein SEQ ID NO: 1640),
NYSKKSHCVDF (SEQ ID NO: 81 of US20160369298; herein SEQ ID NO: 1641),
NYRKTIYVDF (SEQ ID NO: 82 of US20160369298; herein SEQ ID NO: 1642),
NYKEKKDVHFT (SEQ ID NO: 83 of US20160369298; herein SEQ ID NO: 1643),
NYGHRAIVQFT (SEQ ID NO: 84 of US20160369298; herein SEQ ID NO: 1644),
NYANHQFVVCT (SEQ ID NO: 85 of US20160369298; herein SEQ ID NO: 1645),
NYDDDPDGVLLT (SEQ ID NO: 86 of US20160369298; herein SEQ ID NO: 1646),

NYDDPTGVLLT (SEQ ID NO: 87 of US20160369298; herein SEQ ID NO: 1647),
 NFEQQNSVEWT (SEQ ID NO: 88 of US20160369298; herein SEQ ID NO: 1648), SQSGASN
 (SEQ ID NO: 89 and SEQ ID NO: 241 of US20160369298; herein SEQ ID NO: 1649), NNGSQA
 (SEQ ID NO: 90 of US20160369298; herein SEQ ID NO: 1650),
 YYLSRTNTPSGTTTWSRLQFSQAGA (SEQ ID NO: 91 of US20160369298; herein SEQ ID NO:
 1651), SKTSADNNNSEYSWTG (SEQ ID NO: 92 of US20160369298; herein SEQ ID NO: 1652),
 HKDDEEKF (SEQ ID NO: 93, 209, 214, 219, 224, 234, 239, and 244 of US20160369298; herein
 SEQ ID NO: 1653), KQGSEKTNVDIEEV (SEQ ID NO: 94 of US20160369298; herein SEQ ID
 NO: 1654), QRGNNQAATADVNT (SEQ ID NO: 95 of US20160369298; herein SEQ ID NO:
 1655), NYNKKSVNVDF (SEQ ID NO: 96 of US20160369298; herein SEQ ID NO: 1656),
 SQSGASNYNTPSGTTTQSRLQFSTSADNNNSEYSWTGATKYH (SEQ ID NO: 106 of
 US20160369298; herein SEQ ID NO: 1657),
 SASGASNFNSEGGSLTQSSLGFSTDGENNNSDFSMTGATKYH (SEQ ID NO: 107 of
 US20160369298; herein SEQ ID NO: 1658),
 SQSGASNYNTPSGTTTQSRLQFSTDGENNNSDFSMTGATKYH (SEQ ID NO: 108 of
 US20160369298; herein SEQ ID NO: 1659),
 SASGASNYNTPSGTTTQSRLQFSTSADNNNSEFSWPGATTYH (SEQ ID NO: 109 of
 US20160369298; herein SEQ ID NO: 1660),
 SQSGASNFNSEGGSLTQSSLGFSTDGENNNSDFSMTGATKYH (SEQ ID NO: 110 of
 US20160369298; herein SEQ ID NO: 1661),
 SASGASNYNTPSGSLTQSSLGFSTDGENNNSDFSMTGATKYH (SEQ ID NO: 111 of
 US20160369298; herein SEQ ID NO: 1662),
 SQSGASNYNTPSGTTTQSRLQFSTSADNNNSDFSMTGATKYH (SEQ ID NO: 112 of
 US20160369298; herein SEQ ID NO: 1663),
 SGAGASNFNSEGGSLTQSSLGFSTDGENNNSDFSMTGATKYH (SEQ ID NO: 113 of
 US20160369298; herein SEQ ID NO: 1664), SGAGASN (SEQ ID NO: 176 of US20160369298;
 herein SEQ ID NO: 1665), NSEGGSLTQSSLGFS (SEQ ID NO: 177, 185, 193 and 202 of
 US20160369298; herein SEQ ID NO: 1666), TDGENNNSDFS (SEQ ID NO: 178 of
 US20160369298; herein SEQ ID NO: 1667), SEFSWPGATT (SEQ ID NO: 179 of
 US20160369298; herein SEQ ID NO: 1668), TSADNNNSDFSMT (SEQ ID NO: 180 of
 US20160369298; herein SEQ ID NO: 1669), SQSGASNY (SEQ ID NO: 181, 187, and 198 of

US20160369298; herein SEQ ID NO: 1670), NTPSGTTTQSRLQFS (SEQ ID NO: 182, 188, 191, and 199 of US20160369298; herein SEQ ID NO: 1671), TSADNNNSEYSWTGATKYH (SEQ ID NO: 183 of US20160369298; herein SEQ ID NO: 1672), SASGASNF (SEQ ID NO: 184 of US20160369298; herein SEQ ID NO: 1673), TDGENNNSDFSWTGATKYH (SEQ ID NO: 186, 189, 194, 197, and 203 of US20160369298; herein SEQ ID NO: 1674), SASGASNY (SEQ ID NO: 190 and SEQ ID NO: 195 of US20160369298; herein SEQ ID NO: 1675), TSADNNNSEFSWPGATTYH (SEQ ID NO: 192 of US20160369298; herein SEQ ID NO: 1676), NTPSGSLTQSSLGFS (SEQ ID NO: 196 of US20160369298; herein SEQ ID NO: 1677), TSADNNNSDFSWTGATKYH (SEQ ID NO: 200 of US20160369298; herein SEQ ID NO: 1678), SGAGASNF (SEQ ID NO: 201 of US20160369298; herein SEQ ID NO: 1679), CTCCAGVVSVMRSRVCVNSGCAGCTDHCVVSRNSGTCVMSACACAA (SEQ ID NO: 204 of US20160369298; herein SEQ ID NO: 1680), CTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATGTCAACACACAA (SEQ ID NO: 205 of US20160369298; herein SEQ ID NO: 1681), SAAGASN (SEQ ID NO: 206 of US20160369298; herein SEQ ID NO: 1682), YFLSRTNTESGSTTQSTLRFSQAG (SEQ ID NO: 207 of US20160369298; herein SEQ ID NO: 1683), SKTSADNNNSDFS (SEQ ID NO: 208, 228, and 253 of US20160369298; herein SEQ ID NO: 1684), KQGSEKTDVDIDKV (SEQ ID NO: 210 of US20160369298; herein SEQ ID NO: 1685), STAGASN (SEQ ID NO: 211 of US20160369298; herein SEQ ID NO: 1686), YFLSRTNTTSGIETQSTLRFSQAG (SEQ ID NO: 212 and SEQ ID NO: 247 of US20160369298; herein SEQ ID NO: 1687), SKTDGENNNSDFS (SEQ ID NO: 213 and SEQ ID NO: 248 of US20160369298; herein SEQ ID NO: 1688), KQGAAADDVEIDGV (SEQ ID NO: 215 and SEQ ID NO: 250 of US20160369298; herein SEQ ID NO: 1689), SEAGASN (SEQ ID NO: 216 of US20160369298; herein SEQ ID NO: 1690), YYLSRTNTPSGTTTQSRLQFSQAG (SEQ ID NO: 217, 232 and 242 of US20160369298; herein SEQ ID NO: 1691), SKTSADNNNSEYS (SEQ ID NO: 218, 233, 238, and 243 of US20160369298; herein SEQ ID NO: 1692), KQGSEKTNVDIEKV (SEQ ID NO: 220, 225 and 245 of US20160369298; herein SEQ ID NO: 1693), YFLSRTNDASGSDTKSTLLFSQAG (SEQ ID NO: 222 of US20160369298; herein SEQ ID NO: 1694), STTPSENNNSEYS (SEQ ID NO: 223 of US20160369298; herein SEQ ID NO: 1695), SAAGATN (SEQ ID NO: 226 and SEQ ID NO: 251 of US20160369298; herein SEQ ID NO: 1696), YFLSRTNGEAGSATLSELRFQAG (SEQ ID NO: 227 of US20160369298; herein SEQ ID NO: 1697), HGDDADRF (SEQ ID NO: 229 and SEQ ID NO: 254 of US20160369298;

herein SEQ ID NO: 1698), KQGAEKSDVEVDRV (SEQ ID NO: 230 and SEQ ID NO: 255 of US20160369298; herein SEQ ID NO: 1699), KQDSGGDNIDIDQV (SEQ ID NO: 235 of US20160369298; herein SEQ ID NO: 1700), SDAGASN (SEQ ID NO: 236 of US20160369298; herein SEQ ID NO: 1701), YFLSRTNTEGGHDTQSTLRFSQAG (SEQ ID NO: 237 of US20160369298; herein SEQ ID NO: 1702), KEDGGGSDVAIDEV (SEQ ID NO: 240 of US20160369298; herein SEQ ID NO: 1703), SNAGASN (SEQ ID NO: 246 of US20160369298; herein SEQ ID NO: 1704), and YFLSRTNGEAGSATLSELRFSPG (SEQ ID NO: 252 of US20160369298; herein SEQ ID NO: 1705). Non-limiting examples of nucleotide sequences that may encode the amino acid mutated sites include the following,

AGCVVMDCAGGARSCASCAAC (SEQ ID NO: 97 of US20160369298; herein SEQ ID NO: 1706), AACRACRRSMRSMAGGCA (SEQ ID NO: 98 of US20160369298; herein SEQ ID NO: 1707), CACRRGGACRRCRMSRRSARSTTT (SEQ ID NO: 99 of US20160369298; herein SEQ ID NO: 1708),
TATTTCTTGAGCAGAACAAACRVCVVSRCGGAMNCVHSACGMHSTCAVVSCCTTVDDTT
TTCTCAGSBCRGSGCG (SEQ ID NO: 100 of US20160369298; herein SEQ ID NO: 1709),
TCAAMAMMAVNSRVCSRSAACAACAACAGTRASTTCTCGTGGMAGGA (SEQ ID NO: 101 of US20160369298; herein SEQ ID NO: 1710),
AAGSAARRCRSCRVSRRVARVCRATRYCGMSNHCRVMVRSGTC (SEQ ID NO: 102 of US20160369298; herein SEQ ID NO: 1711),
CAGVVSVMRSRVCVNSGCAGCTDHCVVSRNSGTCVMSACA (SEQ ID NO: 103 of US20160369298; herein SEQ ID NO: 1712),
AACTWCRVSVASMVSVHSDDTGTGSWSTKSACT (SEQ ID NO: 104 of US20160369298; herein SEQ ID NO: 1713), TTGTTGAACATCACACGTGACGCACGTTC (SEQ ID NO: 256 of US20160369298; herein SEQ ID NO: 1714), TCCCCGTGGTTCTACTACATAATGTGGCCG (SEQ ID NO: 257 of US20160369298; herein SEQ ID NO: 1715),
TTCCACACTCCGTTTTGGATAATGTTGAAC (SEQ ID NO: 258 of US20160369298; herein SEQ ID NO: 1716), AGGGACATCCCCAGCTCCATGCTGTGGTCG (SEQ ID NO: 259 of US20160369298; herein SEQ ID NO: 1717), AGGGACAACCCCTCCGACTCGCCCTAATCC (SEQ ID NO: 260 of US20160369298; herein SEQ ID NO: 1718),
TCCTAGTAGAAGACACCCTCTCACTGCCCCG (SEQ ID NO: 261 of US20160369298; herein SEQ ID NO: 1719), AGTACCATGTACACCCACTCTCCAGTGCC (SEQ ID NO: 262 of

US20160369298; herein SEQ ID NO: 1720), ATATGGACGTTTCATGCTGATCACCATACCG (SEQ ID NO: 263 of US20160369298; herein SEQ ID NO: 1721), AGCAGGAGCTCCTTGGCCTCAGCGTGCGAG (SEQ ID NO: 264 of US20160369298; herein SEQ ID NO: 1722), ACAAGCAGCTTCACTATGACAACCACTGAC (SEQ ID NO: 265 of US20160369298; herein SEQ ID NO: 1723), CAGCCTAGGAACTGGCTTCCTGGACCCTGTTACCGCCAGCAGAGAGTCTCAAMAMMAV NSRVCSRSAACAACAACAGTRASTTCTCCTGGMMAGGAGCTACCAAGTACCACCTCAAT GGCAGAGACTCTCTGGTGAATCCCGGACCAGCTATGGCAAGCCACRRGGACRRCRMSR RSARSTTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGSAARRCRSCRVSRRVARVCR ATRYCGMSNHCRVMVRSBTCATGATTACAGACGAAGAGGAGATCTGGAC (SEQ ID NO: 266 of US20160369298; herein SEQ ID NO: 1724), TGGGACAATGGCGGTCGTCTCTCAGAGTTTKTKKT (SEQ ID NO: 267 of US20160369298; herein SEQ ID NO: 1725), AGAGGACCKKTCCTCGATGGTTCATGGTGGAGTTA (SEQ ID NO: 268 of US20160369298; herein SEQ ID NO: 1726), CCACTTAGGGCCTGGTCGATACCGTTCGGTG (SEQ ID NO: 269 of US20160369298; herein SEQ ID NO: 1727), and TCTCGCCCCAAGAGTAGAAACCCTTCSTYYG (SEQ ID NO: 270 of US20160369298; herein SEQ ID NO: 1728).

[00074] In some embodiments, the AAV serotype may comprise an ocular cell targeting peptide as described in International Patent Publication WO2016134375, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to SEQ ID NO: 9, and SEQ ID NO:10 of WO2016134375. Further, any of the ocular cell targeting peptides or amino acids described in WO2016134375, may be inserted into any parent AAV serotype, such as, but not limited to, AAV2 (SEQ ID NO:8 of WO2016134375; herein SEQ ID NO: 1729), or AAV9 (SEQ ID NO: 11 of WO2016134375; herein SEQ ID NO: 1730). In some embodiments, modifications, such as insertions are made in AAV2 proteins at P34-A35, T138-A139, A139-P140, G453- T454, N587-R588, and/or R588-Q589. In certain embodiments, insertions are made at D384, G385, 1560, T561, N562, E563, E564, E565, N704, and/or Y705 of AAV9. The ocular cell targeting peptide may be, but is not limited to, any of the following amino acid sequences, GSTPPPM (SEQ ID NO: 1 of WO2016134375; herein SEQ ID NO: 1731), or GETRAPL (SEQ ID NO: 4 of WO2016134375; herein SEQ ID NO: 1732).

[00075] In some embodiments, the AAV serotype may be modified as described in the United States Publication US 20170145405 the contents of which are herein incorporated by reference in their entirety. AAV serotypes may include, modified AAV2(e.g., modifications at Y444F, Y500F, Y730F and/or S662V), modified AAV3 (e.g., modifications at Y705F, Y731F and/or T492V), and modified AAV6 (e.g., modifications at S663V and/or T492V).

[00076] In some embodiments, the AAV serotype may be modified as described in the International Publication WO2017083722 the contents of which are herein incorporated by reference in their entirety. AAV serotypes may include, AAV1 (Y705+731F+T492V), AAV2 (Y444+500+730F+T491V), AAV3 (Y705+731F), AAV5, AAV 5(Y436+693+719F), AAV6 (VP3 variant Y705F/Y731F/T492V), AAV8 (Y733F), AAV9, AAV9 (VP3 variant Y731F), and AAV10 (Y733F).

[00077] In some embodiments, the AAV serotype may comprise, as described in International Patent Publication WO2017015102, the contents of which are herein incorporated by reference in their entirety, an engineered epitope comprising the amino acids SPAKFA (SEQ ID NO: 24 of WO2017015102; herein SEQ ID NO: 1733) or NKDKLN (SEQ ID NO:2 of WO2017015102; herein SEQ ID NO: 1734). The epitope may be inserted in the region of amino acids 665 to 670 based on the numbering of the VP1 capsid of AAV8 (SEQ ID NO:3 of WO2017015102) and/or residues 664 to 668 of AAV3B (SEQ ID NO:3).

[00078] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2017058892, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV variants with capsid proteins that may comprise a substitution at one or more (e.g., 2, 3, 4, 5, 6, or 7) of amino acid residues 262-268, 370-379, 451 -459, 472-473, 493-500, 528-534, 547-552, 588- 597, 709-710, 716-722 of AAV1, in any combination, or the equivalent amino acid residues in AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAVrh8, AAVrh10, AAVrh32.33, bovine AAV or avian AAV. The amino acid substitution may be, but is not limited to, any of the amino acid sequences described in WO2017058892. In one embodiment, the AAV may comprise an amino acid substitution at residues 256L, 258K, 259Q, 261S, 263A, 264S, 265T, 266G, 272H, 385S, 386Q, S472R, V473D, N500E 547S, 709A, 710N, 716D, 717N, 718N, 720L, A456T, Q457T, N458Q, K459S, T492S, K493A, S586R, S587G, S588N, T589R and/or 722T of AAV1 (SEQ ID NO: 1 of WO2017058892) in any combination, 244N, 246Q, 248R, 249E, 250I, 251K, 252S, 253G, 254S,

255V, 256D, 263Y, 377E, 378N, 453L, 456R, 532Q, 533P, 535N, 536P, 537G, 538T, 539T, 540A, 541T, 542Y, 543L, 546N, 653V, 654P, 656S, 697Q, 698F, 704D, 705S, 706T, 707G, 708E, 709Y and/or 710R of AAV5 (SEQ ID NO:5 of WO2017058892) in any combination, 248R, 316V, 317Q, 318D, 319S, 443N, 530N, 531S, 532Q 533P, 534A, 535N, 540A, 541 T, 542Y, 543L, 545G, 546N, 697Q, 704D, 706T, 708E, 709Y and/or 710R of AAV5 (SEQ ID NO: 5 of WO2017058892) in any combination, 264S, 266G, 269N, 272H, 457Q, 588S and/or 589I of AAV6 (SEQ ID NO:6 WO2017058892) in any combination, 457T, 459N, 496G, 499N, 500N, 589Q, 590N and/or 592A of AAV8 (SEQ ID NO: 8 WO2017058892) in any combination, 451I, 452N, 453G, 454S, 455G, 456Q, 457N and/or 458Q of AAV9 (SEQ ID NO: 9 WO2017058892) in any combination.

[00079] In some embodiments, the AAV may include a sequence of amino acids at positions 155, 156 and 157 of VP1 or at positions 17, 18, 19 and 20 of VP2, as described in International Publication No. WO 2017066764, the contents of which are herein incorporated by reference in their entirety. The sequences of amino acid may be, but not limited to, N-S-S, S-X-S, S-S-Y, N-X-S, N-S-Y, S-X-Y and N-X-Y, where N, X and Y are, but not limited to, independently non-serine, or non-threonine amino acids, wherein the AAV may be, but not limited to AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11 and AAV12. In some embodiments, the AAV may include a deletion of at least one amino acid at positions 156, 157 or 158 of VP1 or at positions 19, 20 or 21 of VP2, wherein the AAV may be, but not limited to AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11 and AAV12.

Viral Genome Component: Inverted Terminal Repeats (ITRs)

[00080] The AAV particles of the present invention comprise a viral genome with at least one ITR region and a payload region. In one embodiment, the viral genome has two ITRs. These two ITRs flank the payload region at the 5' and 3' ends. The ITRs function as origins of replication comprising recognition sites for replication. ITRs comprise sequence regions which can be complementary and symmetrically arranged. ITRs incorporated into viral genomes of the invention may be comprised of naturally occurring polynucleotide sequences or recombinantly derived polynucleotide sequences.

[00081] The ITRs may be derived from the same serotype as the capsid, selected from any of the serotypes listed in Table 1, or a derivative thereof. The ITR may be of a different serotype than the capsid. In one embodiment, the AAV particle has more than one ITR. In a non-limiting example, the AAV particle has a viral genome comprising two ITRs. In one embodiment, the ITRs are of the

same serotype as one another. In another embodiment, the ITRs are of different serotypes. Non-limiting examples include zero, one or both of the ITRs having the same serotype as the capsid. In one embodiment both ITRs of the viral genome of the AAV particle are AAV2 ITRs.

[00082] Independently, each ITR may be about 100 to about 150 nucleotides in length. An ITR may be about 100-105 nucleotides in length, 106-110 nucleotides in length, 111-115 nucleotides in length, 116-120 nucleotides in length, 121-125 nucleotides in length, 126-130 nucleotides in length, 131-135 nucleotides in length, 136-140 nucleotides in length, 141-145 nucleotides in length or 146-150 nucleotides in length. In one embodiment, the ITRs are 140-142 nucleotides in length. Non-limiting examples of ITR length are 102, 140, 141, 142, 145 nucleotides in length, and those having at least 95% identity thereto.

Viral Genome Component: Promoters

[00083] In one embodiment, the payload region of the viral genome comprises at least one element to enhance the transgene target specificity and expression (See e.g., Powell et al. Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in its entirety). Non-limiting examples of elements to enhance the transgene target specificity and expression include promoters, endogenous miRNAs, post-transcriptional regulatory elements (PREs), polyadenylation (PolyA) signal sequences and upstream enhancers (USEs), CMV enhancers and introns.

[00084] A person skilled in the art may recognize that expression of the polypeptides of the invention in a target cell may require a specific promoter, including but not limited to, a promoter that is species specific, inducible, tissue-specific, or cell cycle-specific (Parr et al., *Nat. Med.* 3:1145-9 (1997); the contents of which are herein incorporated by reference in their entirety).

[00085] In one embodiment, the promoter is deemed to be efficient when it drives expression of the polypeptide(s) encoded in the payload region of the viral genome of the AAV particle. As a non-limiting example, that polypeptide is AADC.

[00086] In one embodiment, the promoter is a promoter deemed to be efficient when it drives expression in the cell being targeted.

[00087] In one embodiment, the promoter is a promoter having a tropism for the cell being targeted.

[00088] In one embodiment, the promoter drives expression of the payload for a period of time in targeted tissues. Expression driven by a promoter may be for a period of 1 hour, 2, hours, 3 hours, 4

hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 3 weeks, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years. Expression may be for 1-5 hours, 1-12 hours, 1-2 days, 1-5 days, 1-2 weeks, 1-3 weeks, 1-4 weeks, 1-2 months, 1-4 months, 1-6 months, 2-6 months, 3-6 months, 3-9 months, 4-8 months, 6-12 months, 1-2 years, 1-5 years, 2-5 years, 3-6 years, 3-8 years, 4-8 years or 5-10 years. As a non-limiting example, the promoter is a weak promoter for sustained expression of a payload in nervous tissues.

[00089] In one embodiment, the promoter drives expression of the polypeptides of the invention for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, 11 years, 12 years, 13 years, 14 years, 15 years, 16 years, 17 years, 18 years, 19 years, 20 years, 21 years, 22 years, 23 years, 24 years, 25 years, 26 years, 27 years, 28 years, 29 years, 30 years, 31 years, 32 years, 33 years, 34 years, 35 years, 36 years, 37 years, 38 years, 39 years, 40 years, 41 years, 42 years, 43 years, 44 years, 45 years, 46 years, 47 years, 48 years, 49 years, 50 years, 55 years, 60 years, 65 years, or more than 65 years.

[00090] Promoters may be naturally occurring or non-naturally occurring. Non-limiting examples of promoters include viral promoters, plant promoters and mammalian promoters. In some embodiments, the promoters may be human promoters. In some embodiments, the promoter may be truncated.

[00091] Promoters which drive or promote expression in most tissues include, but are not limited to, human elongation factor 1 α -subunit (EF1 α), cytomegalovirus (CMV) immediate-early enhancer and/or promoter, chicken β -actin (CBA) and its derivative CAG, β glucuronidase (GUSB), or ubiquitin C (UBC). Tissue-specific expression elements can be used to restrict expression to certain cell types such as, but not limited to, muscle specific promoters, B cell promoters, monocyte promoters, leukocyte promoters, macrophage promoters, pancreatic acinar cell promoters,

endothelial cell promoters, lung tissue promoters, astrocyte promoters, or nervous system promoters which can be used to restrict expression to neurons, astrocytes, or oligodendrocytes.

[00092] Non-limiting examples of muscle-specific promoters include mammalian muscle creatine kinase (MCK) promoter, mammalian desmin (DES) promoter, mammalian troponin I (TNNI2) promoter, and mammalian skeletal alpha-actin (ASKA) promoter (see, e.g. U.S. Patent Publication US 20110212529, the contents of which are herein incorporated by reference in their entirety)

[00093] Non-limiting examples of tissue-specific expression elements for neurons include neuron-specific enolase (NSE), platelet-derived growth factor (PDGF), platelet-derived growth factor B-chain (PDGF- β), synapsin (Syn), methyl-CpG binding protein 2 (MeCP2), Ca^{2+} /calmodulin-dependent protein kinase II (CaMKII), metabotropic glutamate receptor 2 (mGluR2), neurofilament light (NFL) or heavy (NFH), β -globin minigene $\eta\beta 2$, preproenkephalin (PPE), enkephalin (Enk) and excitatory amino acid transporter 2 (EAAT2) promoters. Non-limiting examples of tissue-specific expression elements for astrocytes include glial fibrillary acidic protein (GFAP) and EAAT2 promoters. A non-limiting example of a tissue-specific expression element for oligodendrocytes includes the myelin basic protein (MBP) promoter.

[00094] In one embodiment, the promoter may be less than 1 kb. The promoter may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800 nucleotides. The promoter may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800.

[00095] In one embodiment, the promoter may be a combination of two or more components of the same or different starting or parental promoters such as, but not limited to, CMV and CBA. Each component may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800. Each component may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800. In one embodiment, the promoter is a

combination of a 382 nucleotide CMV-enhancer sequence and a 260 nucleotide CBA-promoter sequence.

[00096] In one embodiment, the viral genome comprises a ubiquitous promoter. Non-limiting examples of ubiquitous promoters include CMV, CBA (including derivatives CAG, CBh, etc.), EF-1 α , PGK, UBC, GUSB (hGBp), and UCOE (promoter of HNRPA2B1-CBX3).

[00097] Yu et al. (Molecular Pain 2011, 7:63; the contents of which are herein incorporated by reference in their entirety) evaluated the expression of eGFP under the CAG, EF1 α , PGK and UBC promoters in rat DRG cells and primary DRG cells using lentiviral vectors and found that UBC showed weaker expression than the other 3 promoters and only 10-12% glial expression was seen for all promoters. Soderblom et al. (E. Neuro 2015; the contents of which are herein incorporated by reference in its entirety) evaluated the expression of eGFP in AAV8 with CMV and UBC promoters and AAV2 with the CMV promoter after injection in the motor cortex. Intranasal administration of a plasmid containing a UBC or EF1 α promoter showed a sustained airway expression greater than the expression with the CMV promoter (See e.g., Gill et al., Gene Therapy 2001, Vol. 8, 1539-1546; the contents of which are herein incorporated by reference in their entirety). Husain et al. (Gene Therapy 2009; the contents of which are herein incorporated by reference in its entirety) evaluated an H β H construct with a hGUSB promoter, a HSV-1LAT promoter and an NSE promoter and found that the H β H construct showed weaker expression than NSE in mouse brain. Passini and Wolfe (J. Virol. 2001, 12382-12392, the contents of which are herein incorporated by reference in its entirety) evaluated the long term effects of the H β H vector following an intraventricular injection in neonatal mice and found that there was sustained expression for at least 1 year. Low expression in all brain regions was found by Xu et al. (Gene Therapy 2001, 8, 1323-1332; the contents of which are herein incorporated by reference in their entirety) when NFL and NFH promoters were used as compared to the CMV-lacZ, CMV-luc, EF, GFAP, hENK, nAChR, PPE, PPE + wpre, NSE (0.3 kb), NSE (1.8 kb) and NSE (1.8 kb + wpre). Xu et al. found that the promoter activity in descending order was NSE (1.8 kb), EF, NSE (0.3 kb), GFAP, CMV, hENK, PPE, NFL and NFH. NFL is a 650 nucleotide promoter and NFH is a 920 nucleotide promoter which are both absent in the liver but NFH is abundant in the sensory proprioceptive neurons, brain and spinal cord and NFH is present in the heart. SCN8A is a 470 nucleotide promoter which expresses throughout the DRG, spinal cord and brain with particularly high expression seen in the hippocampal neurons and cerebellar Purkinje cells, cortex, thalamus and hypothalamus (See e.g., Drews et al. *Identification of evolutionary*

conserved, functional noncoding elements in the promoter region of the sodium channel gene SCN8A, Mamm Genome (2007) 18:723-731; and Raymond et al. *Expression of Alternatively Spliced Sodium Channel α -subunit genes*, Journal of Biological Chemistry (2004) 279(44) 46234-46241; the contents of each of which are herein incorporated by reference in their entireties).

[00098] Any of promoters taught by the aforementioned Yu, Soderblom, Gill, Husain, Passini, Xu, Drews or Raymond may be used in the present inventions.

[00099] In one embodiment, the promoter is not cell specific.

[000100] In one embodiment, the promoter is an ubiquitin c (UBC) promoter. The UBC promoter may have a size of 300-350 nucleotides. As a non-limiting example, the UBC promoter is 332 nucleotides.

[000101] In one embodiment, the promoter is a β -glucuronidase (GUSB) promoter. The GUSB promoter may have a size of 350-400 nucleotides. As a non-limiting example, the GUSB promoter is 378 nucleotides.

[000102] In one embodiment, the promoter is a neurofilament light (NFL) promoter. The NFL promoter may have a size of 600-700 nucleotides. As a non-limiting example, the NFL promoter is 650 nucleotides.

[000103] In one embodiment, the promoter is a neurofilament heavy (NFH) promoter. The NFH promoter may have a size of 900-950 nucleotides. As a non-limiting example, the NFH promoter is 920 nucleotides.

[000104] In one embodiment, the promoter is a SCN8A promoter. The SCN8A promoter may have a size of 450-500 nucleotides. As a non-limiting example, the SCN8A promoter is 470 nucleotides.

[000105] In one embodiment, the promoter is a frataxin (FXN) promoter. The FXN promoter may also be referred to as the FRDA promoter.

[000106] In one embodiment, the promoter is a phosphoglycerate kinase 1 (PGK) promoter.

[000107] In one embodiment, the promoter is a chicken β -actin (CBA) promoter.

[000108] In one embodiment, the promoter is a cytomegalovirus (CMV) promoter.

[000109] In one embodiment, the promoter is a H1 promoter.

[000110] In one embodiment, the promoter is an engineered promoter.

[000111] In one embodiment, the promoter is a liver or a skeletal muscle promoter. Non-limiting examples of liver promoters include human α -1-antitrypsin (hAAT) and thyroxine binding globulin

(TBG). Non-limiting examples of skeletal muscle promoters include Desmin, MCK or synthetic C5-12.

[000112] In one embodiment, the promoter is a RNA pol III promoter. As a non-limiting example, the RNA pol III promoter is U6. As a non-limiting example, the RNA pol III promoter is H1.

[000113] In one embodiment, the viral genome comprises two promoters. As a non-limiting example, the promoters are an EF1 α promoter and a CMV promoter.

[000114] In one embodiment, the viral genome comprises an enhancer element, a promoter and/or a 5'UTR intron. The enhancer element, also referred to herein as an "enhancer," may be, but is not limited to, a CMV enhancer, the promoter may be, but is not limited to, a CMV, CBA, UBC, GUSB, NSE, Synapsin, MeCP2, and GFAP promoter and the 5'UTR/intron may be, but is not limited to, SV40, and CBA-MVM. As a non-limiting example, the enhancer, promoter and/or intron used in combination may be: (1) CMV enhancer, CMV promoter, SV40 5'UTR intron; (2) CMV enhancer, CBA promoter, SV 40 5'UTR intron; (3) CMV enhancer, CBA promoter, CBA-MVM 5'UTR intron; (4) UBC promoter; (5) GUSB promoter; (6) NSE promoter; (7) Synapsin promoter; (8) MeCP2 promoter and (9) GFAP promoter.

[000115] In one embodiment, the viral genome comprises an engineered promoter.

[000116] In another embodiment, the viral genome comprises a promoter from a naturally expressed protein.

[000117] In one embodiment, a region located approximately ~5 kb upstream of the first exon of the payload in order to allow for expression of the payload with the promoter. (See e.g., Puspasari et al. *Long Range Regulation of Human FXN Gene Expression*, PLOS ONE, 2011; the contents of which is herein incorporated by reference in its entirety; a 17 bp region located approximately 4.9 kb upstream of the first exon of the frataxin gene in order to allow for expression with the FRDA promoter).

[000118] In one embodiment, the vector genome may comprise a promoter such as, but not limited to, CMV or U6. As a non-limiting example, the promoter for the AAV particles comprising the payload of the present invention is a CMV promoter. As another non-limiting example, the promoter for the AAV particles comprising the payload of the present invention is a U6 promoter.

[000119] In one embodiment, the vector genome may comprise a CMV and a U6 promoter.

[000120] In one embodiment, the vector genome may comprise a CBA promoter.

Viral Genome Component: Untranslated Regions (UTRs)

[000121] By definition, wild type untranslated regions (UTRs) of a gene are transcribed but not translated. Generally, the 5' UTR starts at the transcription start site and ends at the start codon and the 3' UTR starts immediately following the stop codon and continues until the termination signal for transcription.

[000122] Features typically found in abundantly expressed genes of specific target organs may be engineered into UTRs to enhance the stability and protein production. As a non-limiting example, a 5' UTR from mRNA normally expressed in the liver (e.g., albumin, serum amyloid A, Apolipoprotein A/B/E, transferrin, alpha fetoprotein, erythropoietin, or Factor VIII) may be used in the viral genomes of the AAV particles of the invention to enhance expression in hepatic cell lines or liver.

[000123] While not wishing to be bound by theory, wild-type 5' untranslated regions (UTRs) include features which play roles in translation initiation. Kozak sequences, which are commonly known to be involved in the process by which the ribosome initiates translation of many genes, are usually included in 5' UTRs. Kozak sequences have the consensus CCR(A/G)CCAUGG, where R is a purine (adenine or guanine) three bases upstream of the start codon (ATG), which is followed by another 'G'.

[000124] In one embodiment, the 5'UTR in the viral genome includes a Kozak sequence.

[000125] In one embodiment, the 5'UTR in the viral genome does not include a Kozak sequence.

[000126] While not wishing to be bound by theory, wild-type 3' UTRs are known to have stretches of Adenosines and Uridines embedded therein. These AU rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU rich elements (AREs) can be separated into three classes (Chen et al, 1995, the contents of which are herein incorporated by reference in its entirety): Class I AREs, such as, but not limited to, c-Myc and MyoD, contain several dispersed copies of an AUUUA motif within U-rich regions. Class II AREs, such as, but not limited to, GM-CSF and TNF- α , possess two or more overlapping UUAUUUA(U/A)(U/A) nonamers. Class III AREs, such as, but not limited to, c-Jun and Myogenin, are less well defined. These U rich regions do not contain an AUUUA motif. Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR

binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3' UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message *in vivo*.

[000127] Introduction, removal or modification of 3' UTR AU rich elements (AREs) can be used to modulate the stability of polynucleotides. When engineering specific polynucleotides, e.g., payload regions of viral genomes, one or more copies of an ARE can be introduced to make polynucleotides less stable and thereby curtail translation and decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein.

[000128] In one embodiment, the 3' UTR of the viral genome may include an oligo(dT) sequence for templated addition of a poly-A tail.

[000129] In one embodiment, the viral genome may include at least one miRNA seed, binding site or full sequence. microRNAs (or miRNA or miR) are 19-25 nucleotide noncoding RNAs that bind to the sites of nucleic acid targets and down-regulate gene expression either by reducing nucleic acid molecule stability or by inhibiting translation. A microRNA sequence comprises a “seed” region, i.e., a sequence in the region of positions 2-8 of the mature microRNA, which sequence has perfect Watson-Crick complementarity to the miRNA target sequence of the nucleic acid.

[000130] In one embodiment, the viral genome may be engineered to include, alter or remove at least one miRNA binding site, sequence or seed region.

[000131] Any UTR from any gene known in the art may be incorporated into the viral genome of the AAV particle. These UTRs, or portions thereof, may be placed in the same orientation as in the gene from which they were selected or they may be altered in orientation or location. In one embodiment, the UTR used in the viral genome of the AAV particle may be inverted, shortened, lengthened, made with one or more other 5' UTRs or 3' UTRs known in the art. As used herein, the term “altered” as it relates to a UTR, means that the UTR has been changed in some way in relation to a reference sequence. For example, a 3' or 5' UTR may be altered relative to a wild type or native UTR by the change in orientation or location as taught above or may be altered by the inclusion of additional nucleotides, deletion of nucleotides, swapping or transposition of nucleotides.

[000132] In one embodiment, the viral genome of the AAV particle comprises at least one artificial UTRs which is not a variant of a wild type UTR.

[000133] In one embodiment, the viral genome of the AAV particle comprises UTRs which have been selected from a family of transcripts whose proteins share a common function, structure, feature or property.

Viral Genome Component: Polyadenylation Sequence

[000134] In one embodiment, the viral genome of the AAV particles of the present invention comprise at least one polyadenylation sequence. The viral genome of the AAV particle may comprise a polyadenylation sequence between the 3' end of the payload coding sequence and the 5' end of the 3' ITR.

[000135] In one embodiment, the polyadenylation sequence or “polyA sequence” may range from absent to about 500 nucleotides in length. The polyadenylation sequence may be, but is not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 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, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447,

448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, and 500 nucleotides in length.

[000136] In one embodiment, the polyadenylation sequence is 50-100 nucleotides in length.

[000137] In one embodiment, the polyadenylation sequence is 50-150 nucleotides in length.

[000138] In one embodiment, the polyadenylation sequence is 50-160 nucleotides in length.

[000139] In one embodiment, the polyadenylation sequence is 50-200 nucleotides in length.

[000140] In one embodiment, the polyadenylation sequence is 60-100 nucleotides in length.

[000141] In one embodiment, the polyadenylation sequence is 60-150 nucleotides in length.

[000142] In one embodiment, the polyadenylation sequence is 60-160 nucleotides in length.

[000143] In one embodiment, the polyadenylation sequence is 60-200 nucleotides in length.

[000144] In one embodiment, the polyadenylation sequence is 70-100 nucleotides in length.

[000145] In one embodiment, the polyadenylation sequence is 70-150 nucleotides in length.

[000146] In one embodiment, the polyadenylation sequence is 70-160 nucleotides in length.

[000147] In one embodiment, the polyadenylation sequence is 70-200 nucleotides in length.

[000148] In one embodiment, the polyadenylation sequence is 80-100 nucleotides in length.

[000149] In one embodiment, the polyadenylation sequence is 80-150 nucleotides in length.

[000150] In one embodiment, the polyadenylation sequence is 80-160 nucleotides in length.

[000151] In one embodiment, the polyadenylation sequence is 80-200 nucleotides in length.

[000152] In one embodiment, the polyadenylation sequence is 90-100 nucleotides in length.

[000153] In one embodiment, the polyadenylation sequence is 90-150 nucleotides in length.

[000154] In one embodiment, the polyadenylation sequence is 90-160 nucleotides in length.

[000155] In one embodiment, the polyadenylation sequence is 90-200 nucleotides in length.

Viral Genome Component: Introns

[000156] In one embodiment, the payload region comprises at least one element to enhance the expression such as one or more introns or portions thereof. Non-limiting examples of introns include, MVM (67-97 bps), F.IX truncated intron 1 (300 bps), β -globin SD/immunoglobulin heavy chain splice acceptor (250 bps), adenovirus splice donor/immunoglobulin splice acceptor (500 bps), SV40 late splice donor/splice acceptor (19S/16S) (180 bps) and hybrid adenovirus splice donor/IgG splice acceptor (230 bps).

[000157] In one embodiment, the intron or intron portion may be 100-500 nucleotides in length. The intron may have a length of 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490 or 500. The intron may have a length between 80-100, 80-120, 80-140, 80-160, 80-180, 80-200, 80-250, 80-300, 80-350, 80-400, 80-450, 80-500, 200-300, 200-400, 200-500, 300-400, 300-500, or 400-500.

[000158] In one embodiment, the vector genome comprises at least one element to enhance the transgene target specificity and expression (See e.g., Powell et al. *Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy*, 2015; the contents of which are herein incorporated by reference in its entirety) such as an intron. Non-limiting examples of introns include, MVM (67-97 bps), F.IX truncated intron 1 (300 bps), β -globin SD/immunoglobulin heavy chain splice acceptor (250 bps), adenovirus splice donor/immunoglobulin splice acceptor (500 bps), SV40 late splice donor/splice acceptor (19S/16S) (180 bps) and hybrid adenovirus splice donor/IgG splice acceptor (230 bps).

[000159] In one embodiment, the intron may be 100-500 nucleotides in length. The intron may have a length of 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490 or 500. The intron may have a length between 80-100, 80-120, 80-140, 80-160, 80-180, 80-200, 80-250, 80-300, 80-350, 80-400, 80-450, 80-500, 200-300, 200-400, 200-500, 300-400, 300-500, or 400-500.

Viral Genome Component: Filler Sequence

[000160] In one embodiment, the viral genome comprises one or more filler sequences.

[000161] In one embodiment, the viral genome comprises one or more filler sequences in order to have the length of the viral genome be the optimal size for packaging. As a non-limiting example, the viral genome comprises at least one filler sequence in order to have the length of the viral genome be about 2.3 kb. As a non-limiting example, the viral genome comprises at least one filler sequence in order to have the length of the viral genome be about 4.6 kb.

[000162] In one embodiment, the viral genome is a single stranded (ss) viral genome and comprises one or more filler sequences which have a length about between 0.1 kb - 3.8 kb, such as, but not limited to, 0.1 kb, 0.2 kb, 0.3 kb, 0.4 kb, 0.5 kb, 0.6 kb, 0.7 kb, 0.8 kb, 0.9 kb, 1 kb, 1.1 kb, 1.2 kb, 1.3 kb, 1.4 kb, 1.5 kb, 1.6 kb, 1.7 kb, 1.8 kb, 1.9 kb, 2 kb, 2.1 kb, 2.2 kb, 2.3 kb, 2.4 kb, 2.5

kb, 2.6 kb, 2.7 kb, 2.8 kb, 2.9 kb, 3 kb, 3.1 kb, 3.2 kb, 3.3 kb, 3.4 kb, 3.5 kb, 3.6 kb, 3.7 kb, or 3.8 kb. As a non-limiting example, the total length filler sequence in the vector genome is 3.1 kb. As a non-limiting example, the total length filler sequence in the vector genome is 2.7 kb. As a non-limiting example, the total length filler sequence in the vector genome is 0.8 kb. As a non-limiting example, the total length filler sequence in the vector genome is 0.4 kb. As a non-limiting example, the length of each filler sequence in the vector genome is 0.8 kb. As a non-limiting example, the length of each filler sequence in the vector genome is 0.4 kb.

[000163] In one embodiment, the viral genome is a self-complementary (sc) viral genome and comprises one or more filler sequences which have a length about between 0.1 kb – 1.5 kb, such as, but not limited to, 0.1 kb, 0.2 kb, 0.3 kb, 0.4 kb, 0.5 kb, 0.6 kb, 0.7 kb, 0.8 kb, 0.9 kb, 1 kb, 1.1 kb, 1.2 kb, 1.3 kb, 1.4 kb, or 1.5 kb. As a non-limiting example, the total length filler sequence in the vector genome is 0.8 kb. As a non-limiting example, the total length filler sequence in the vector genome is 0.4 kb. As a non-limiting example, the length of each filler sequence in the vector genome is 0.8 kb. As a non-limiting example, the length of each filler sequence in the vector genome is 0.4 kb.

[000164] In one embodiment, the viral genome comprises any portion of a filler sequence. The viral genome may comprise 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of a filler sequence.

[000165] In one embodiment, the viral genome is a single stranded (ss) viral genome and comprises one or more filler sequences in order to have the length of the viral genome be about 4.6 kb. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 3' to the 5' ITR sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 5' to a promoter sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 5' to the 3' ITR sequence. As a non-limiting example, the viral genome comprises at least one filler sequence, and the filler sequence is located between two intron sequences. As a non-limiting example, the viral genome comprises at least one filler sequence, and the filler sequence is located within an intron sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first

filler sequence is located 3' to the 5' ITR sequence and the second filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first filler sequence is located 5' to a promoter sequence and the second filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first filler sequence is located 3' to the 5' ITR sequence and the second filler sequence is located 5' to the 5' ITR sequence.

[000166] In one embodiment, the viral genome is a self-complementary (sc) viral genome and comprises one or more filler sequences in order to have the length of the viral genome be about 2.3 kb. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 3' to the 5' ITR sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 5' to a promoter sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises at least one filler sequence and the filler sequence is located 5' to the 3' ITR sequence. As a non-limiting example, the viral genome comprises at least one filler sequence, and the filler sequence is located between two intron sequences. As a non-limiting example, the viral genome comprises at least one filler sequence, and the filler sequence is located within an intron sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first filler sequence is located 3' to the 5' ITR sequence and the second filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first filler sequence is located 5' to a promoter sequence and the second filler sequence is located 3' to the polyadenylation signal sequence. As a non-limiting example, the viral genome comprises two filler sequences, and the first filler sequence is located 3' to the 5' ITR sequence and the second filler sequence is located 5' to the 5' ITR sequence.

[000167] In one embodiment, the viral genome may comprise one or more filler sequences between one of more regions of the viral genome. In one embodiment, the filler region may be located before a region such as, but not limited to, a payload region, an inverted terminal repeat (ITR), a promoter region, an intron region, an enhancer region, a polyadenylation signal sequence region, a multiple cloning site (MCS) region, and/or an exon region. In one embodiment, the filler region may be located after a region such as, but not limited to, a payload region, an inverted terminal repeat (ITR), a promoter region, an intron region, an enhancer region, a polyadenylation

signal sequence region, a multiple cloning site (MCS) region, and/or an exon region. In one embodiment, the filler region may be located before and after a region such as, but not limited to, a payload region, an inverted terminal repeat (ITR), a promoter region, an intron region, an enhancer region, a polyadenylation signal sequence region, a multiple cloning site (MCS) region, and/or an exon region.

[000168] In one embodiment, the viral genome may comprise one or more filler sequences which bifurcates at least one region of the viral genome. The bifurcated region of the viral genome may comprise 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the of the region to the 5' of the filler sequence region. As a non-limiting example, the filler sequence may bifurcate at least one region so that 10% of the region is located 5' to the filler sequence and 90% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 20% of the region is located 5' to the filler sequence and 80% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 30% of the region is located 5' to the filler sequence and 70% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 40% of the region is located 5' to the filler sequence and 60% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 50% of the region is located 5' to the filler sequence and 50% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 60% of the region is located 5' to the filler sequence and 40% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 70% of the region is located 5' to the filler sequence and 30% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 80% of the region is located 5' to the filler sequence and 20% of the region is located 3' to the filler sequence. As a non-limiting example, the filler sequence may bifurcate at least one region so that 90% of the region is located 5' to the filler sequence and 10% of the region is located 3' to the filler sequence.

[000169] In one embodiment, the viral genome comprises a filler sequence after the 5' ITR.

[000170] In one embodiment, the viral genome comprises a filler sequence after the promoter region. In one embodiment, the viral genome comprises a filler sequence after the payload region. In

one embodiment, the viral genome comprises a filler sequence after the intron region. In one embodiment, the viral genome comprises a filler sequence after the enhancer region. In one embodiment, the viral genome comprises a filler sequence after the polyadenylation signal sequence region. In one embodiment, the viral genome comprises a filler sequence after the MCS region. In one embodiment, the viral genome comprises a filler sequence after the exon region.

[000171] In one embodiment, the viral genome comprises a filler sequence before the promoter region. In one embodiment, the viral genome comprises a filler sequence before the payload region. In one embodiment, the viral genome comprises a filler sequence before the intron region. In one embodiment, the viral genome comprises a filler sequence before the enhancer region. In one embodiment, the viral genome comprises a filler sequence before the polyadenylation signal sequence region. In one embodiment, the viral genome comprises a filler sequence before the MCS region. In one embodiment, the viral genome comprises a filler sequence before the exon region.

[000172] In one embodiment, the viral genome comprises a filler sequence before the 3' ITR.

[000173] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the promoter region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the payload region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the intron region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the enhancer region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the polyadenylation signal sequence region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the MCS region.

[000174] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the 5' ITR and the exon region.

[000175] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the payload region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the intron region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the enhancer region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the polyadenylation signal sequence region. In one embodiment, a filler sequence may be located

between two regions, such as, but not limited to, the promoter region and the MCS region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the exon region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the promoter region and the 3' ITR.

[000176] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the intron region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the enhancer region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the polyadenylation signal sequence region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the MCS region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the exon region.

[000177] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the payload region and the 3' ITR.

[000178] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the intron region and the enhancer region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the intron region and the polyadenylation signal sequence region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the intron region and the MCS region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the intron region and the exon region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the intron region and the 3' ITR. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the enhancer region and the polyadenylation signal sequence region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the enhancer region and the MCS region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the enhancer region and the exon region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the enhancer region and the 3' ITR.

[000179] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the polyadenylation signal sequence region and the MCS region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the

polyadenylation signal sequence region and the exon region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the polyadenylation signal sequence region and the 3' ITR.

[000180] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the MCS region and the exon region. In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the MCS region and the 3' ITR.

[000181] In one embodiment, a filler sequence may be located between two regions, such as, but not limited to, the exon region and the 3' ITR.

[000182] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located

between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located

between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and promoter region, and the second filler sequence may be located between the exon region and 3' ITR.

[000183] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and

payload region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler

sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and payload region, and the second filler sequence may be located between the exon region and 3' ITR.

[000184] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may

be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the payload region and 3' ITR.

In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral

genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and intron region, and the second filler sequence may be located between the exon region and 3' ITR.

[000185] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the

first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may

be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and enhancer region, and the second filler sequence may be located between the exon region and 3' ITR.

[000186] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the

promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the

intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the

second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and polyadenylation signal sequence region, and the second filler sequence may be located between the exon region and 3' ITR.

[000187] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the promoter region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and

MCS region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence

region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000188] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and payload region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the promoter region and 3' ITR. In one

embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first

filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the 5' ITR and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000189] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the

first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral

genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and payload region, and the second filler sequence may be located between the exon region and 3' ITR.

[000190] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region,

and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler

sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and intron region, and the second filler sequence may be located between the exon region and 3' ITR.

[000191] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the

intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be

located between the promoter region and enhancer region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and enhancer region, and the second filler sequence may be located between the exon region and 3' ITR.

[000192] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler

sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between

the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and polyadenylation signal sequence region, and the second filler sequence may be located between the exon region and 3' ITR.

[000193] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler

sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000194] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler

sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may

be located between the promoter region and MCS region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000195] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and intron region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and polyadenylation signal sequence region.

In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the payload region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two

filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the promoter region and 3' ITR, and the second filler sequence may be located between the exon region and 3' ITR.

[000196] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler

sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and intron region, and the second filler sequence may be located between the exon region and 3' ITR.

[000197] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may

comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be

located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and enhancer region, and the second filler sequence may be located between the exon region and 3' ITR.

[000198] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region,

and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and polyadenylation signal sequence region, and the second filler sequence may be located between the exon region and 3' ITR.

[000199] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler

sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000200] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may

comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the MCS

region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000201] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the intron region and enhancer region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the intron region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the intron region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the intron region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the intron region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region

and 3' ITR region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the payload region and 3' ITR region, and the second filler sequence may be located between the exon region and 3' ITR.

[000202] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the polyadenylation signal sequence region

and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and enhancer region, and the second filler sequence may be located between the exon region and 3' ITR.

[000203] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the

MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and polyadenylation signal sequence region, and the second filler sequence may be located between the exon region and 3' ITR.

[000204] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron

region and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000205] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000206] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may

be located between the enhancer region and polyadenylation signal sequence region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the enhancer region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the enhancer region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the enhancer region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the intron region and 3' ITR, and the second filler sequence may be located between the exon region and 3' ITR.

[000207] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the

first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and polyadenylation signal sequence region, and the second filler sequence may be located between the exon region and 3' ITR.

[000208] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000209] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In

one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000210] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and MCS region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the polyadenylation signal sequence region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the enhancer region and 3' ITR, and the second filler sequence may be located between the exon region and 3' ITR.

[000211] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and MCS region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and MCS region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and MCS region, and the second filler sequence may be located between the exon region and 3' ITR.

[000212] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and exon region, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and exon region, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

[000213] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and 3' ITR, and the second filler sequence may be located between the MCS region and exon region. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and 3' ITR, and the second filler sequence may be located between the MCS region and 3' ITR. In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the polyadenylation signal sequence region and 3' ITR, and the second filler sequence may be located between the exon region and 3' ITR.

[000214] In one embodiment, a viral genome may comprise two filler sequences, the first filler sequence may be located between the MCS region and exon region, and the second filler sequence may be located between the exon region and 3' ITR.

AAV Production

[000215] The present invention provides methods for the generation of parvoviral particles, *e.g.* AAV particles, by viral genome replication in a viral replication cell.

[000216] In accordance with the invention, the viral genome comprising a payload region will be incorporated into the AAV particle produced in the viral replication cell. Methods of making AAV particles are well known in the art and are described in *e.g.*, United States Patent Nos. US6204059, US5756283, US6258595, US6261551, US6270996, US6281010, US6365394, US6475769, US6482634, US6485966, US6943019, US6953690, US7022519, US7238526, US7291498 and US7491508, US5064764, US6194191, US6566118, US8137948; or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597; *Methods In Molecular Biology*, ed. Richard, Humana Press, NJ (1995); O'Reilly et al., *Baculovirus Expression Vectors*, A Laboratory Manual, Oxford Univ. Press (1994); Samulski et al., *J. Vir.* 63:3822-8 (1989); Kajigaya et al., *Proc. Nat'l. Acad. Sci. USA* 88: 4646-50 (1991); Ruffing et al., *J. Vir.* 66:6922-30 (1992); Kimbauer et al., *Vir.*, 219:37-44 (1996); Zhao et al., *Vir.* 272:382-93 (2000); the contents of each of which are herein incorporated by reference in their entirety. In one embodiment, the AAV particles are made using the methods described in WO2015191508, the contents of which are herein incorporated by reference in their entirety.

[000217] Viral replication cells commonly used for production of recombinant AAV particles include but are not limited to 293 cells, COS cells, HeLa cells, KB cells, and other mammalian cell lines as described in U.S. Pat. Nos. US6156303, US5387484, US5741683, US5691176, and US5688676; U.S. patent publication No. 2002/0081721, and International Patent Publication Nos. WO 00/47757, WO 00/24916, and WO 96/17947, the contents of each of which are herein incorporated by reference in their entireties.

[000218] In some embodiments, the present invention provides a method for producing an AAV particle having enhanced (increased, improved) transduction efficiency comprising the steps of: 1) co-transfecting competent bacterial cells with a bacmid vector and either a viral construct vector and/or AAV payload construct vector, 2) isolating the resultant viral construct expression vector and AAV payload construct expression vector and separately transfecting viral replication cells, 3) isolating and purifying resultant payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, 4) co-infecting a viral replication

cell with both the AAV payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, and 5) harvesting and purifying the AAV particle comprising a viral genome.

[000219] In some embodiments, the present invention provides a method for producing an AAV particle comprising the steps of 1) simultaneously co-transfecting mammalian cells, such as, but not limited to HEK293 cells, with a payload region, a construct expressing rep and cap genes and a helper construct, 2) harvesting and purifying the AAV particle comprising a viral genome.

[000220] In some embodiments, the viral genome of the AAV particle of the invention optionally encodes a selectable marker. The selectable marker may comprise a cell-surface marker, such as any protein expressed on the surface of the cell including, but not limited to receptors, CD markers, lectins, integrins, or truncated versions thereof.

[000221] In some embodiments, selectable marker reporter genes as described in International application No. WO 96/23810; Heim et al., *Current Biology* 2:178-182 (1996); Heim et al., *Proc. Natl. Acad. Sci. USA* (1995); or Heim et al., *Science* 373:663-664 (1995); WO 96/30540, the contents of each of which are incorporated herein by reference in their entireties).

Genome Size

[000222] In one embodiment, the AAV particle which comprises a payload described herein may be single stranded or double stranded vector genome. The size of the vector genome may be small, medium, large or the maximum size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000223] In one embodiment, the vector genome which comprises a payload described herein may be a small single stranded vector genome. A small single stranded vector genome may be 2.7 to 3.5 kb in size such as about 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, and 3.5 kb in size. As a non-limiting example, the small single stranded vector genome may be 3.2 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000224] In one embodiment, the vector genome which comprises a payload described herein may be a small double stranded vector genome. A small double stranded vector genome may be 1.3 to 1.7 kb in size such as about 1.3, 1.4, 1.5, 1.6, and 1.7 kb in size. As a non-limiting example, the small double stranded vector genome may be 1.6 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000225] In one embodiment, the vector genome which comprises a payload described herein may be a medium single stranded vector genome. A medium single stranded vector genome may be 3.6 to 4.3 kb in size such as about 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2 and 4.3 kb in size. As a non-limiting example, the medium single stranded vector genome may be 4.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000226] In one embodiment, the vector genome which comprises a payload described herein may be a medium double stranded vector genome. A medium double stranded vector genome may be 1.8 to 2.1 kb in size such as about 1.8, 1.9, 2.0, and 2.1 kb in size. As a non-limiting example, the medium double stranded vector genome may be 2.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000227] In one embodiment, the vector genome which comprises a payload described herein may be a large single stranded vector genome. A large single stranded vector genome may be 4.4 to 6.0 kb in size such as about 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9 and 6.0 kb in size. As a non-limiting example, the large single stranded vector genome may be 4.7 kb in size. As another non-limiting example, the large single stranded vector genome may be 4.8 kb in size. As yet another non-limiting example, the large single stranded vector genome may be 6.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[000228] In one embodiment, the vector genome which comprises a payload described herein may be a large double stranded vector genome. A large double stranded vector genome may be 2.2 to 3.0 kb in size such as about 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 and 3.0 kb in size. As a non-limiting example, the large double stranded vector genome may be 2.4 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

Payloads of the Invention

[000229] The AAV particles of the present disclosure comprise at least one payload region. As used herein, “payload” or “payload region” refers to one or more polynucleotides or polynucleotide regions encoded by or within a viral genome or an expression product of such polynucleotide or polynucleotide region, e.g., a transgene, a polynucleotide encoding a polypeptide or multi-polypeptide or a modulatory nucleic acid or regulatory nucleic acid. Payloads of the present invention typically encode polypeptides or fragments or variants thereof.

[000230] The payload region may be constructed in such a way as to reflect a region similar to or mirroring the natural organization of an mRNA.

[000231] The payload region may comprise a combination of coding and non-coding nucleic acid sequences.

[000232] In some embodiments, the AAV payload region may encode a coding or non-coding RNA.

[000233] In one embodiment, the AAV particle comprises a viral genome with a payload region comprising nucleic acid sequences encoding more than one polypeptide of interest. In such an embodiment, a viral genome encoding more than one polypeptide may be replicated and packaged into a viral particle. A target cell transduced with a viral particle comprising more than one polypeptide may express each of the polypeptides in a single cell.

[000234] In one embodiment, the payload region may comprise the components as shown in FIG. 1. The payload region **110** is located within the viral genome **100**. At the 5' and/or the 3' end of the payload region **110** there may be at least one inverted terminal repeat (ITR) **120**. Within the payload region, there is a promoter region **130**, an intron region **140** and a coding region **150**.

[000235] Where the AAV particle payload region encodes a polypeptide, the polypeptide may be a peptide or protein. The viral genomes encoding polypeptides described herein may be useful in the fields of human disease, viruses, infections veterinary applications and a variety of *in vivo* and *in vitro* settings.

[000236] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of neurological diseases and/or disorders.

[000237] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Parkinson's Disease.

[000238] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of diseases of the central nervous system.

The nature of the polypeptides and variants

[000239] Amino acid sequences encoded by payload regions of the viral genomes of the invention may be translated as a whole polypeptide, a plurality of polypeptides or fragments of polypeptides, which independently may be encoded by one or more nucleic acids, fragments of nucleic acids or variants of any of the aforementioned. As used herein, "polypeptide" means a polymer of amino acid residues (natural or unnatural) linked together most often by peptide bonds. The term, as used herein, refers to proteins, polypeptides, and peptides of any size, structure, or function. In some instances, the polypeptide encoded is smaller than about 50 amino acids and the polypeptide is then

termed a peptide. If the polypeptide is a peptide, it will be at least about 2, 3, 4, or at least 5 amino acid residues long. Thus, polypeptides include gene products, naturally occurring polypeptides, synthetic polypeptides, homologs, orthologs, paralogs, fragments and other equivalents, variants, and analogs of the foregoing. A polypeptide may be a single molecule or may be a multi-molecular complex such as a dimer, trimer or tetramer. They may also comprise single chain or multichain polypeptides and may be associated or linked. The term polypeptide may also apply to amino acid polymers in which one or more amino acid residues are an artificial chemical analogue of a corresponding naturally occurring amino acid.

[000240] The term “polypeptide variant” refers to molecules which differ in their amino acid sequence from a native or reference sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence, as compared to a native or reference sequence. Ordinarily, variants will possess at least about 50% identity (homology) to a native or reference sequence, and preferably, they will be at least about 80%, more preferably at least about 90% identical (homologous) to a native or reference sequence.

[000241] In some embodiments “variant mimics” are provided. As used herein, the term “variant mimic” is one which contains one or more amino acids which would mimic an activated sequence. For example, glutamate may serve as a mimic for phospho-threonine and/or phospho-serine. Alternatively, variant mimics may result in deactivation or in an inactivated product containing the mimic, e.g., phenylalanine may act as an inactivating substitution for tyrosine; or alanine may act as an inactivating substitution for serine.

[000242] The term “amino acid sequence variant” refers to molecules with some differences in their amino acid sequences as compared to a native or starting sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence. “Native” or “starting” sequence should not be confused with a wild type sequence. As used herein, a native or starting sequence is a relative term referring to an original molecule against which a comparison may be made. “Native” or “starting” sequences or molecules may represent the wild-type (that sequence found in nature) but do not have to be the wild-type sequence.

[000243] Ordinarily, variants will possess at least about 70% homology to a native sequence, and preferably, they will be at least about 80%, more preferably at least about 90% homologous to a native sequence. “Homology” as it applies to amino acid sequences is defined as the percentage of residues in the candidate amino acid sequence that are identical with the residues in the amino acid

sequence of a second sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology. Methods and computer programs for the alignment are well known in the art. It is understood that homology depends on a calculation of percent identity but may differ in value due to gaps and penalties introduced in the calculation.

[000244] By "homologs" as it applies to amino acid sequences is meant the corresponding sequence of other species having substantial identity to a second sequence of a second species.

[000245] "Analog" is meant to include polypeptide variants which differ by one or more amino acid alterations, e.g., substitutions, additions or deletions of amino acid residues that still maintain the properties of the parent polypeptide.

[000246] Sequence tags or amino acids, such as one or more lysines, can be added to the peptide sequences of the invention (e.g., at the N-terminal or C-terminal ends). Sequence tags can be used for peptide purification or localization. Lysines can be used to increase peptide solubility or to allow for biotinylation. Alternatively, amino acid residues located at the carboxy and amino terminal regions of the amino acid sequence of a peptide or protein may optionally be deleted providing for truncated sequences. Certain amino acids (e.g., C-terminal or N-terminal residues) may alternatively be deleted depending on the use of the sequence, as for example, expression of the sequence as part of a larger sequence which is soluble, or linked to a solid support.

[000247] "Substitutional variants" when referring to proteins are those that have at least one amino acid residue in a native or starting sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule.

[000248] As used herein the term "conservative amino acid substitution" refers to the substitution of an amino acid that is normally present in the sequence with a different amino acid of similar size, charge, or polarity. Examples of conservative substitutions include the substitution of a non-polar (hydrophobic) residue such as isoleucine, valine and leucine for another non-polar residue. Likewise, examples of conservative substitutions include the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, and between glycine and serine. Additionally, the substitution of a basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue such as aspartic acid or glutamic acid for another acidic residue are additional examples of conservative substitutions. Examples of

non-conservative substitutions include the substitution of a non-polar (hydrophobic) amino acid residue such as isoleucine, valine, leucine, alanine, methionine for a polar (hydrophilic) residue such as cysteine, glutamine, glutamic acid or lysine and/or a polar residue for a non-polar residue.

[000249] "Insertional variants" when referring to proteins are those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in a native or starting sequence. "Immediately adjacent" to an amino acid means connected to either the alpha-carboxy or alpha-amino functional group of the amino acid.

[000250] "Deletional variants" when referring to proteins, are those with one or more amino acids in the native or starting amino acid sequence removed. Ordinarily, deletional variants will have one or more amino acids deleted in a particular region of the molecule.

[000251] As used herein, the term "derivative" is used synonymously with the term "variant" and refers to a molecule that has been modified or changed in any way relative to a reference molecule or starting molecule. In some embodiments, derivatives include native or starting proteins that have been modified with an organic proteinaceous or non-proteinaceous derivatizing agent, and post-translational modifications. Covalent modifications are traditionally introduced by reacting targeted amino acid residues of the protein with an organic derivatizing agent that is capable of reacting with selected side-chains or terminal residues, or by harnessing mechanisms of post-translational modifications that function in selected recombinant host cells. The resultant covalent derivatives are useful in programs directed at identifying residues important for biological activity, for immunoassays, or for the preparation of anti-protein antibodies for immunoaffinity purification of the recombinant glycoprotein. Such modifications are within the ordinary skill in the art and are performed without undue experimentation.

[000252] Certain post-translational modifications are the result of the action of recombinant host cells on the expressed polypeptide. Glutaminyl and asparaginyl residues are frequently post-translationally deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues may be present in the proteins used in accordance with the present invention.

[000253] Other post-translational modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)).

[000254] "Features" when referring to proteins are defined as distinct amino acid sequence-based components of a molecule. Features of the proteins of the present invention include surface manifestations, local conformational shape, folds, loops, half-loops, domains, half-domains, sites, termini or any combination thereof.

[000255] As used herein when referring to proteins the term "surface manifestation" refers to a polypeptide based component of a protein appearing on an outermost surface.

[000256] As used herein when referring to proteins the term "local conformational shape" means a polypeptide based structural manifestation of a protein which is located within a definable space of the protein.

[000257] As used herein when referring to proteins the term "fold" means the resultant conformation of an amino acid sequence upon energy minimization. A fold may occur at the secondary or tertiary level of the folding process. Examples of secondary level folds include beta sheets and alpha helices. Examples of tertiary folds include domains and regions formed due to aggregation or separation of energetic forces. Regions formed in this way include hydrophobic and hydrophilic pockets, and the like.

[000258] As used herein the term "turn" as it relates to protein conformation means a bend which alters the direction of the backbone of a peptide or polypeptide and may involve one, two, three or more amino acid residues.

[000259] As used herein when referring to proteins the term "loop" refers to a structural feature of a peptide or polypeptide which reverses the direction of the backbone of a peptide or polypeptide and comprises four or more amino acid residues. Oliva et al. have identified at least 5 classes of protein loops (J. Mol Biol 266 (4): 814-830; 1997).

[000260] As used herein when referring to proteins the term "half-loop" refers to a portion of an identified loop having at least half the number of amino acid residues as the loop from which it is derived. It is understood that loops may not always contain an even number of amino acid residues. Therefore, in those cases where a loop contains or is identified to comprise an odd number of amino acids, a half-loop of the odd-numbered loop will comprise the whole number portion or next whole number portion of the loop (number of amino acids of the loop/2+/-0.5 amino acids). For example, a loop identified as a 7 amino acid loop could produce half-loops of 3 amino acids or 4 amino acids ($7/2=3.5+/-0.5$ being 3 or 4).

[000261] As used herein when referring to proteins the term "domain" refers to a motif of a polypeptide having one or more identifiable structural or functional characteristics or properties (e.g., binding capacity, serving as a site for protein-protein interactions).

[000262] As used herein when referring to proteins the term "half-domain" means portion of an identified domain having at least half the number of amino acid residues as the domain from which it is derived. It is understood that domains may not always contain an even number of amino acid residues. Therefore, in those cases where a domain contains or is identified to comprise an odd number of amino acids, a half-domain of the odd-numbered domain will comprise the whole number portion or next whole number portion of the domain (number of amino acids of the domain/2+/-0.5 amino acids). For example, a domain identified as a 7 amino acid domain could produce half-domains of 3 amino acids or 4 amino acids ($7/2=3.5\pm0.5$ being 3 or 4). It is also understood that sub-domains may be identified within domains or half-domains, these subdomains possessing less than all of the structural or functional properties identified in the domains or half domains from which they were derived. It is also understood that the amino acids that comprise any of the domain types herein need not be contiguous along the backbone of the polypeptide (i.e., nonadjacent amino acids may fold structurally to produce a domain, half-domain or subdomain).

[000263] As used herein when referring to proteins the terms "site" as it pertains to amino acid based embodiments is used synonymous with "amino acid residue" and "amino acid side chain". A site represents a position within a peptide or polypeptide that may be modified, manipulated, altered, derivatized or varied within the polypeptide based molecules of the present invention.

[000264] As used herein the terms "termini or terminus" when referring to proteins refers to an extremity of a peptide or polypeptide. Such extremity is not limited only to the first or final site of the peptide or polypeptide but may include additional amino acids in the terminal regions. The polypeptide based molecules of the present invention may be characterized as having both an N-terminus (terminated by an amino acid with a free amino group (NH₂)) and a C-terminus (terminated by an amino acid with a free carboxyl group (COOH)). Proteins of the invention are in some cases made up of multiple polypeptide chains brought together by disulfide bonds or by non-covalent forces (multimers, oligomers). These sorts of proteins will have multiple N- and C-termini. Alternatively, the termini of the polypeptides may be modified such that they begin or end, as the case may be, with a non-polypeptide based moiety such as an organic conjugate.

[000265] Once any of the features have been identified or defined as a component of a molecule of the invention, any of several manipulations and/or modifications of these features may be performed by moving, swapping, inverting, deleting, randomizing or duplicating. Furthermore, it is understood that manipulation of features may result in the same outcome as a modification to the molecules of the invention. For example, a manipulation which involves deleting a domain would result in the alteration of the length of a molecule just as modification of a nucleic acid to encode less than a full length molecule would.

[000266] Modifications and manipulations can be accomplished by methods known in the art such as site directed mutagenesis. The resulting modified molecules may then be tested for activity using in vitro or in vivo assays such as those described herein or any other suitable screening assay known in the art.

Payload: AADC polynucleotide constructs

[000267] According to the present invention, aromatic L-amino acid decarboxylase (AADC; also known as dopa decarboxylase and DDC) polynucleotides are provided which function alone or in combination with additional nucleic acid sequence(s) to encode the AADC protein. As used herein an “AADC polynucleotide” is any nucleic acid polymer which encodes an AADC protein and when present in a vector, plasmid or translatable construct, expresses such AADC protein in a cell, tissue, organ or organism.

[000268] AADC polynucleotides include precursor molecules which are processed inside the cell. AADC polynucleotides or the processed forms thereof may be encoded in a plasmid, vector, genome or other nucleic acid expression vector for delivery to a cell.

[000269] In some embodiments AADC polynucleotides are designed as components of AAV viral genomes and packaged in AAV particles which are processed within the cell to produce the wild type AADC protein.

[000270] In some embodiments, the AADC polynucleotide may be the payload of the AAV particle.

[000271] As used herein, the wild type AADC protein may be any of the naturally occurring isoforms or variants from the *DDC gene*. Multiple alternatively spliced transcript variants encoding different isoforms of AADC have been identified. Specifically, the *DDC gene* produces seven transcript variants that encode six distinct isoforms. DDC transcript variants 1 and 2 both encode AADC isoform 1. In some embodiments, the AADC polynucleotides encode DDC transcript variant

2, thereby encoding a native AADC isoform 1 (NCBI Reference Sequence: NP_000781.1). This sequence is given here:

MNASEFRRRGKEMVDYVANYMEGIEGRQVYPDVEPGYLRPLIPAAAPQEPDTFEDIINDVE
KIIMPGVTHWHSPYFFAYFPTASSYPAMLADMLCGAIGCIGFSWAASPACTELETVMMDW
LGKMLELPKAFLNEKAGEGGGVIQGSASEATLVALLAARTKVIHRLQAASPELTQAAIMEK
LVAYSSDQAHSSVERAGLIGGVKLKAIPSDGNFAMRASALQEALERDKAAGLIPFFMVATL
GTTTCCSFDNLLEVGPICNKEDIWLHVDAAYAGSAFICPEFRHLLNGVEFADSFNFNPHKWL
LVNFDCSAMWVKKRTDLTGAFRLDPTYLKSHQDSGLITDYRHWQIPLGRRFRSLKMWV
FRMYGVKGLQAYIRKQHVQLSHEFESLVRQDPRFEICVEVILGLVCFRLKGSNKVNEALLQRI
NSAKKIHLVPCHLRDKFVLRFACISRTVESAHVQRAWHEHIKELAADVLRAERE (SEQ ID
NO: 978)

[000272] The AADC polynucleotides of the invention, may be engineered to contain modular elements and/or sequence motifs assembled to create AADC polynucleotide constructs.

[000273] According to the present invention, AADC polynucleotides are provided. Such polynucleotides comprise nucleic acid polymers which comprise a region of linked nucleosides encoding one or more isoforms or variants of the AADC protein.

[000274] In some embodiments, the AADC polynucleotide comprises a codon optimized transcript encoding an AADC protein.

[000275] In some embodiments, the AADC polynucleotide comprises a sequence region encoding one or more wild type isoforms or variants of an AADC protein. Such polynucleotides may also comprise a sequence region encoding any one or more of the following: a 5' ITR, a cytomegalovirus (CMV) Enhancer, a CMV Promoter, an iel exon 1, an iel intron1, an hbBglobin intron2, an hBglobin exon 3, a 5' UTR, a 3' UTR, an hGH poly(A) signal, and/or a 3' ITR. Such sequence regions are taught herein or may be any of those known in the art.

[000276] In some embodiments, the AADC polynucleotide comprises a SEQ ID NO: 979 or a fragment or variant thereof.

[000277] In one embodiment, the AADC polynucleotide comprises a sequence which has a percent identity to any of SEQ ID NO: 979 or a fragment or variant thereof. The AADC polynucleotide may have 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or 100% identity to any of SEQ ID NO: 979 or a fragment or variant thereof. The AADC polynucleotide may have 1-10%, 10-20%, 30-

40%, 50-60%, 50-70%, 50-80%, 50-90%, 50-99%, 50-100%, 60-70%, 60-80%, 60-90%, 60-99%, 60-100%, 70-80%, 70-90%, 70-99%, 70-100%, 80-85%, 80-90%, 80-95%, 80-99%, 80-100%, 90-95%, 90-99%, or 90-100% to any of SEQ ID NO: 979 or a fragment or variant thereof. As a non-limiting example, the AADC polynucleotide comprises a sequence which as 80% identity to any of SEQ ID NO: 979 or a fragment or variant thereof. As another non-limiting example, the AADC polynucleotide comprises a sequence which as 85% identity to any of SEQ ID NO: 979 or a fragment or variant thereof. As another non-limiting example, the AADC polynucleotide comprises a sequence which as 90% identity to any of SEQ ID NO: 979 or a fragment or variant thereof. As another non-limiting example, the AADC polynucleotide comprises a sequence which as 95% identity to any of SEQ ID NO: 979 or a fragment or variant thereof. As another non-limiting example, the AADC polynucleotide comprises a sequence which as 99% identity to any of SEQ ID NO: 979 or a fragment or variant thereof.

[000278] In some embodiments, the coding region of the AADC polynucleotide is 1440 nucleotides in length. Such an AADC polynucleotide may be codon optimized over all or a portion of the polynucleotide.

[000279] In some embodiments, the AADC polynucleotide comprises any of SEQ ID NO: 979 or a fragment or variant thereof but lacking the 5' and/or 3' ITRs. Such a polynucleotide may be incorporated into a plasmid or vector and utilized to express the encoded AADC protein.

[000280] In one embodiment, the AADC polynucleotides may be produced in insect cells (e.g., Sf9 cells).

[000281] In one embodiment, the AADC polynucleotides may be produced using triple transfection.

[000282] In one embodiment, the AADC polynucleotide may comprise a codon optimized open reading frame of an AADC mRNA, at least one 5' ITR and at least one 3' UTR where the one or more of the 5' ITRs may be located at the 5' end of the promoter region and one or more 3' ITRs may be located at the 3' end of the poly(A) signal. The AADC mRNA may comprise a promoter region, a 5' untranslated region (UTR), a 3' UTR and a poly(A) signal. The promoter region may include, but is not limited to, enhancer element, a promoter element, a first exon region, a first intron region, a second intron region and a second exon region. As a non-limiting example, the enhancer element and the promoter element are derived from CMV. As another non-limiting example, the first exon region is ie1 exon 1 or fragments thereof, the first intron region is ie1 intron 1 or fragments thereof,

the second intron region is hbBglobin intron 2 or fragments thereof and the second exon region is hbBglobin exon 3 or fragments thereof. As yet another non-limiting example, the poly(A) signal is derived from human growth hormone.

[000283] In one embodiment, at least one element may be used with the AADC polynucleotides described herein to enhance the transgene target specificity and expression (See e.g., Powell et al. *Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy*, 2015; the contents of which are herein incorporated by reference in its entirety). Non-limiting examples of elements to enhance the transgene target specificity and expression include promoters, endogenous miRNAs, post-transcriptional regulatory elements (PREs), polyadenylation (PolyA) signal sequences and upstream enhancers (USEs), CMV enhancers and introns.

[000284] In one embodiment, at least one element may be used with the AADC polynucleotides described herein to enhance the transgene target specificity and expression (See e.g., Powell et al. *Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy*, 2015; the contents of which are herein incorporated by reference in its entirety) such as promoters.

[000285] In one embodiment, the AADC polynucleotide is encoded in a plasmid or vector, which may be derived from an adeno-associated virus (AAV). The AAV may comprise a capsid serotype such as, but not limited to, PHP.B, PHP.A, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/rh.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55,

AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T, AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101, AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2, AAV Shuffle 100-1, AAV Shuffle 100-3, AAV Shuffle 100-7, AAV

Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8, AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV CLv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV CLv1-7, AAV CLv1-8, AAV CLv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, AAVF9/HSC9, PHP.B (AAV-PHP.B), PHP.A (AAV.PHP.A), G2B-26, G2B-13, TH1.1-32, TH1.1-35, AAVPHP.B2, AAVPHP.B3, AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT,

AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3, AAVG2B4, and/or AAVG2B5, and variants thereof.

II. FORMULATION AND DELIVERY

Pharmaceutical Compositions

[000286] According to the present invention the AAV particles may be prepared as pharmaceutical compositions. It will be understood that such compositions necessarily comprise one or more active ingredients and, most often, a pharmaceutically acceptable excipient.

[000287] Relative amounts of the active ingredient (e.g. AAV particle), a pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the present disclosure may vary, depending upon the identity, size, and/or condition of the subject being treated and further depending upon the route by which the composition is to be administered. For example, the composition may comprise between 0.1% and 99% (w/w) of the active ingredient. By way of example, the composition may comprise between 0.1% and 100%, e.g., between .5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

[000288] In some embodiments, the AAV particle pharmaceutical compositions described herein may comprise at least one payload. As a non-limiting example, the pharmaceutical compositions may contain an AAV particle with 1, 2, 3, 4 or 5 payloads.

[000289] Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to any other animal, e.g., to non-human animals, e.g. non-human mammals. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and/or perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical

compositions is contemplated include, but are not limited to, humans and/or other primates; mammals, including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, dogs, mice, rats, birds, including commercially relevant birds such as poultry, chickens, ducks, geese, and/or turkeys.

[000290] In some embodiments, compositions are administered to humans, human patients or subjects.

Formulations

[000291] Formulations of the present invention can include, without limitation, saline, liposomes, lipid nanoparticles, polymers, peptides, proteins, cells transfected with AAV particles (e.g., for transfer or transplantation into a subject) and combinations thereof.

[000292] Formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. As used herein the term “pharmaceutical composition” refers to compositions comprising at least one active ingredient and optionally one or more pharmaceutically acceptable excipients.

[000293] In general, such preparatory methods include the step of associating the active ingredient with an excipient and/or one or more other accessory ingredients. As used herein, the phrase “active ingredient” generally refers either to an AAV particle carrying a payload region encoding the polypeptides of the invention or to the end product encoded by a viral genome of by an AAV particle as described herein.

[000294] Formulations of the AAV particles and pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with an excipient and/or one or more other accessory ingredients, and then, if necessary and/or desirable, dividing, shaping and/or packaging the product into a desired single- or multi-dose unit.

[000295] A pharmaceutical composition in accordance with the present disclosure may be prepared, packaged, and/or sold in bulk, as a single unit dose, and/or as a plurality of single unit doses. As used herein, a “unit dose” refers to a discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject and/or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[000296] In one embodiment, the AAV particles of the invention may be formulated in PBS with 0.001% of pluronic acid (F-68) at a pH of about 7.0.

[000297] In some embodiments, the AAV formulations described herein may contain sufficient AAV particles for expression of at least one expressed functional payload. As a non-limiting example, the AAV particles may contain viral genomes encoding 1, 2, 3, 4 or 5 functional payloads.

[000298] According to the present invention AAV particles may be formulated for CNS delivery. Agents that cross the brain blood barrier may be used. For example, some cell penetrating peptides that can target molecules to the brain blood barrier endothelium may be used for formulation (e.g., Mathupala, *Expert Opin Ther Pat.*, 2009, 19, 137-140; the content of which is incorporated herein by reference in its entirety).

Excipients and Diluents

[000299] The AAV particles of the invention can be formulated using one or more excipients or diluents to (1) increase stability; (2) increase cell transfection or transduction; (3) permit the sustained or delayed release of the payload; (4) alter the biodistribution (e.g., target the viral particle to specific tissues or cell types); (5) increase the translation of encoded protein; (6) alter the release profile of encoded protein and/or (7) allow for regulatable expression of the payload of the invention.

[000300] In some embodiments, a pharmaceutically acceptable excipient may be at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% pure. In some embodiments, an excipient is approved for use for humans and for veterinary use. In some embodiments, an excipient may be approved by United States Food and Drug Administration. In some embodiments, an excipient may be of pharmaceutical grade. In some embodiments, an excipient may meet the standards of the United States Pharmacopoeia (USP), the European Pharmacopoeia (EP), the British Pharmacopoeia, and/or the International Pharmacopoeia.

[000301] Excipients, as used herein, include, but are not limited to, any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, and the like, as suited to the particular dosage form desired. Various excipients for formulating pharmaceutical compositions and techniques for preparing the composition are known in the art (see Remington: The Science and Practice of Pharmacy, 21st Edition, A. R. Gennaro, Lippincott, Williams & Wilkins, Baltimore, MD, 2006; incorporated herein by reference in its entirety). The use of a conventional excipient

medium may be contemplated within the scope of the present disclosure, except insofar as any conventional excipient medium may be incompatible with a substance or its derivatives, such as by producing any undesirable biological effect or otherwise interacting in a deleterious manner with any other component(s) of the pharmaceutical composition.

[000302] Exemplary diluents include, but are not limited to, calcium carbonate, sodium carbonate, calcium phosphate, dicalcium phosphate, calcium sulfate, calcium hydrogen phosphate, sodium phosphate lactose, sucrose, cellulose, microcrystalline cellulose, kaolin, mannitol, sorbitol, inositol, sodium chloride, dry starch, cornstarch, powdered sugar, *etc.*, and/or combinations thereof.

[000303] In one embodiment, the AAV particles may be formulated in a hydrogel prior to administration. Hydrogels have a degree of flexibility which is similar to natural tissue as a result of their significant water content.

[000304] In another embodiment, a hydrogel may be administered to a subject prior to the administration of an AAV particle formulation. As a non-limiting example, the site of administration of the hydrogel may be within 3 inches (e.g., within 2.9, 2.8, 2.7, 2.6, 2.5, 2.4, 2.3, 2.2., 2.1, 2.0, 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1, 1.0, 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1 or less than 0.1 inches) of the site of administration of the AAV particle formulation.

Inactive Ingredients

[000305] In some embodiments, AAV particle formulations may comprise at least one inactive ingredient. As used herein, the term “inactive ingredient” refers to one or more agents that do not contribute to the activity of the active ingredient of the pharmaceutical composition included in formulations. In some embodiments, all, none or some of the inactive ingredients which may be used in the formulations of the present invention may be approved by the US Food and Drug Administration (FDA).

[000306] In one embodiment, the AAV particle pharmaceutical compositions comprise at least one inactive ingredient such as, but not limited to, 1,2,6-Hexanetriol; 1,2-Dimyristoyl-Sn-Glycero-3-(Phospho-S-(1-Glycerol)); 1,2-Dimyristoyl-Sn-Glycero-3-Phosphocholine; 1,2-Dioleoyl-Sn-Glycero-3-Phosphocholine; 1,2-Dipalmitoyl-Sn-Glycero-3-(Phospho-Rac-(1-Glycerol)); 1,2-Distearoyl-Sn-Glycero-3-(Phospho-Rac-(1-Glycerol)); 1,2-Distearoyl-Sn-Glycero-3-Phosphocholine; 1-O-Tolylbiguanide; 2-Ethyl-1,6-Hexanediol; Acetic Acid; Acetic Acid, Glacial; Acetic Anhydride; Acetone; Acetone Sodium Bisulfite; Acetylated Lanolin Alcohols; Acetylated Monoglycerides; Acetylcysteine; Acetyltryptophan, DL-; Acrylates Copolymer; Acrylic Acid-

Isooctyl Acrylate Copolymer; Acrylic Adhesive 788; Activated Charcoal; Adcote 72A103; Adhesive Tape; Adipic Acid; Aerotex Resin 3730; Alanine; Albumin Aggregated; Albumin Colloidal; Albumin Human; Alcohol; Alcohol, Dehydrated; Alcohol, Denatured; Alcohol, Diluted; Alfadex; Alginic Acid; Alkyl Ammonium Sulfonic Acid Betaine; Alkyl Aryl Sodium Sulfonate; Allantoin; Allyl .Alpha.-Ionone; Almond Oil; Alpha-Terpineol; Alpha-Tocopherol; Alpha-Tocopherol Acetate, DI-; Alpha-Tocopherol, DI-; Aluminum Acetate; Aluminum Chlorhydroxy Allantoinate; Aluminum Hydroxide; Aluminum Hydroxide - Sucrose, Hydrated; Aluminum Hydroxide Gel; Aluminum Hydroxide Gel F 500; Aluminum Hydroxide Gel F 5000; Aluminum Monostearate; Aluminum Oxide; Aluminum Polyester; Aluminum Silicate; Aluminum Starch Octenylsuccinate; Aluminum Stearate; Aluminum Subacetate; Aluminum Sulfate Anhydrous; Amerchol C; Amerchol-Cab; Aminomethylpropanol; Ammonia; Ammonia Solution; Ammonia Solution, Strong; Ammonium Acetate; Ammonium Hydroxide; Ammonium Lauryl Sulfate; Ammonium Nonoxynol-4 Sulfate; Ammonium Salt Of C-12-C-15 Linear Primary Alcohol Ethoxylate; Ammonium Sulfate; Ammonyx; Amphoteric-2; Amphoteric-9; Anethole; Anhydrous Citric Acid; Anhydrous Dextrose; Anhydrous Lactose; Anhydrous Trisodium Citrate; Aniseed Oil; Anoxid Sbn; Antifoam; Antipyrine; Apaflurane; Apricot Kernel Oil Peg-6 Esters; Aquaphor; Arginine; Arlacel; Ascorbic Acid; Ascorbyl Palmitate; Aspartic Acid; Balsam Peru; Barium Sulfate; Beeswax; Beeswax, Synthetic; Beheneth-10; Bentonite; Benzalkonium Chloride; Benzenesulfonic Acid; Benzethonium Chloride; Benzododecinium Bromide; Benzoic Acid; Benzyl Alcohol; Benzyl Benzoate; Benzyl Chloride; Betadex; Bibapcitide; Bismuth Subgallate; Boric Acid; Brocrinat; Butane; Butyl Alcohol; Butyl Ester Of Vinyl Methyl Ether/Maleic Anhydride Copolymer (125000 Mw); Butyl Stearate; Butylated Hydroxyanisole; Butylated Hydroxytoluene; Butylene Glycol; Butylparaben; Butyric Acid; C20-40 Pareth-24; Caffeine; Calcium; Calcium Carbonate; Calcium Chloride; Calcium Gluceptate; Calcium Hydroxide; Calcium Lactate; Calcobutrol; Caldiamide Sodium; Caloxetate Trisodium; Calteridol Calcium; Canada Balsam; Caprylic/Capric Triglyceride; Caprylic/Capric/Stearic Triglyceride; Captan; Captisol; Caramel; Carbomer 1342; Carbomer 1382; Carbomer 934; Carbomer 934p; Carbomer 940; Carbomer 941; Carbomer 980; Carbomer 981; Carbomer Homopolymer Type B (Allyl Pentaerythritol Crosslinked); Carbomer Homopolymer Type C (Allyl Pentaerythritol Crosslinked); Carbon Dioxide; Carboxy Vinyl Copolymer; Carboxymethylcellulose; Carboxymethylcellulose Sodium; Carboxypolymethylene; Carrageenan; Carrageenan Salt; Castor Oil; Cedar Leaf Oil; Cellulose; Cellulose, Microcrystalline; Cerasynt-Se;

Ceresin; Cetareth-12; Cetareth-15; Cetareth-30; Cetearyl Alcohol/Cetareth-20; Cetearyl Ethylhexanoate; Ceteth-10; Ceteth-2; Ceteth-20; Ceteth-23; Cetostearyl Alcohol; Cetrimonium Chloride; Cetyl Alcohol; Cetyl Esters Wax; Cetyl Palmitate; Cetylpyridinium Chloride; Chlorobutanol; Chlorobutanol Hemihydrate; Chlorobutanol, Anhydrous; Chlorocresol; Chloroxylenol; Cholesterol; Choleth; Choleth-24; Citrate; Citric Acid; Citric Acid Monohydrate; Citric Acid, Hydrated; Cocamide Ether Sulfate; Cocamine Oxide; Coco Betaine; Coco Diethanolamide; Coco Monoethanolamide; Cocoa Butter; Coco-Glycerides; Coconut Oil; Coconut Oil, Hydrogenated; Coconut Oil/Palm Kernel Oil Glycerides, Hydrogenated; Cocoyl Caprylocaprate; Cola Nitida Seed Extract; Collagen; Coloring Suspension; Corn Oil; Cottonseed Oil; Cream Base; Creatine; Creatinine; Cresol; Croscarmellose Sodium; Crospovidone; Cupric Sulfate; Cupric Sulfate Anhydrous; Cyclomethicone; Cyclomethicone/Dimethicone Copolyol; Cysteine; Cysteine Hydrochloride; Cysteine Hydrochloride Anhydrous; Cysteine, DL-; D&C Red No. 28; D&C Red No. 33; D&C Red No. 36; D&C Red No. 39; D&C Yellow No. 10; Dalfampridine; Daubert 1-5 Pestr (Matte) 164z; Decyl Methyl Sulfoxide; Dehydag Wax Sx; Dehydroacetic Acid; Dehymuls E; Denatonium Benzoate; Deoxycholic Acid; Dextran; Dextran 40; Dextrin; Dextrose; Dextrose Monohydrate; Dextrose Solution; Diatrizoic Acid; Diazolidinyl Urea; Dichlorobenzyl Alcohol; Dichlorodifluoromethane; Dichlorotetrafluoroethane; Diethanolamine; Diethyl Pyrocarbonate; Diethyl Sebacate; Diethylene Glycol Monoethyl Ether; Diethylhexyl Phthalate; Dihydroxyaluminum Aminoacetate; Diisopropanolamine; Diisopropyl Adipate; Diisopropyl Dilinoleate; Dimethicone 350; Dimethicone Copolyol; Dimethicone Mdx4-4210; Dimethicone Medical Fluid 360; Dimethyl Isosorbide; Dimethyl Sulfoxide; Dimethylaminoethyl Methacrylate - Butyl Methacrylate - Methyl Methacrylate Copolymer; Dimethyldioctadecylammonium Bentonite; Dimethylsiloxane/Methylvinylsiloxane Copolymer; Dinoseb Ammonium Salt; Dipalmitoylphosphatidylglycerol, DL-; Dipropylene Glycol; Disodium Cocoamphodiacetate; Disodium Laureth Sulfosuccinate; Disodium Lauryl Sulfosuccinate; Disodium Sulfosalicylate; Disofenin; Divinylbenzene Styrene Copolymer; Dmdm Hydantoin; Docosanol; Docusate Sodium; Duro-Tak 280-2516; Duro-Tak 387-2516; Duro-Tak 80-1196; Duro-Tak 87-2070; Duro-Tak 87-2194; Duro-Tak 87-2287; Duro-Tak 87-2296; Duro-Tak 87-2888; Duro-Tak 87-2979; Edetate Calcium Disodium; Edetate Disodium; Edetate Disodium Anhydrous; Edetate Sodium; Edetic Acid; Egg Phospholipids; Entsufoin; Entsufoin Sodium; Epilactose; Eptetracycline Hydrochloride; Essence Bouquet 9200; Ethanolamine Hydrochloride; Ethyl Acetate; Ethyl Oleate;

Ethylcelluloses; Ethylene Glycol; Ethylene Vinyl Acetate Copolymer; Ethylenediamine;
 Ethylenediamine Dihydrochloride; Ethylene-Propylene Copolymer; Ethylene-Vinyl Acetate
 Copolymer (28% Vinyl Acetate); Ethylene-Vinyl Acetate Copolymer (9% Vinylacetate); Ethylhexyl
 Hydroxystearate; Ethylparaben; Eucalyptol; Exametazime; Fat, Edible; Fat, Hard; Fatty Acid Esters;
 Fatty Acid Pentaerythriol Ester; Fatty Acids; Fatty Alcohol Citrate; Fatty Alcohols; Fd&C Blue No.
 1; Fd&C Green No. 3; Fd&C Red No. 4; Fd&C Red No. 40; Fd&C Yellow No. 10 (Delisted);
 Fd&C Yellow No. 5; Fd&C Yellow No. 6; Ferric Chloride; Ferric Oxide; Flavor 89-186; Flavor 89-
 259; Flavor Df-119; Flavor Df-1530; Flavor Enhancer; Flavor Fig 827118; Flavor Raspberry Pfc-
 8407; Flavor Rhodia Pharmaceutical No. Rf 451; Fluorochlorohydrocarbons; Formaldehyde;
 Formaldehyde Solution; Fractionated Coconut Oil; Fragrance 3949-5; Fragrance 520a; Fragrance
 6.007; Fragrance 91-122; Fragrance 9128-Y; Fragrance 93498g; Fragrance Balsam Pine No. 5124;
 Fragrance Bouquet 10328; Fragrance Chemoderm 6401-B; Fragrance Chemoderm 6411; Fragrance
 Cream No. 73457; Fragrance Cs-28197; Fragrance Felton 066m; Fragrance Firmenich 47373;
 Fragrance Givaudan Ess 9090/1c; Fragrance H-6540; Fragrance Herbal 10396; Fragrance Nj-1085;
 Fragrance P O Fl-147; Fragrance Pa 52805; Fragrance Pera Derm D; Fragrance Rbd-9819;
 Fragrance Shaw Mudge U-7776; Fragrance Tf 044078; Fragrance Ungerer Honeysuckle K 2771;
 Fragrance Ungerer N5195; Fructose; Gadolinium Oxide; Galactose; Gamma Cyclodextrin; Gelatin;
 Gelatin, Crosslinked; Gelfoam Sponge; Gellan Gum (Low Acyl); Gelva 737; Gentisic Acid;
 Gentisic Acid Ethanolamide; Gluceptate Sodium; Gluceptate Sodium Dihydrate; Gluconolactone;
 Glucuronic Acid; Glutamic Acid, DL-; Glutathione; Glycerin; Glycerol Ester Of Hydrogenated
 Rosin; Glyceryl Citrate; Glyceryl Isostearate; Glyceryl Laurate; Glyceryl Monostearate; Glyceryl
 Oleate; Glyceryl Oleate/Propylene Glycol; Glyceryl Palmitate; Glyceryl Ricinoleate; Glyceryl
 Stearate; Glyceryl Stearate - Laureth-23; Glyceryl Stearate/Peg Stearate; Glyceryl Stearate/Peg-100
 Stearate; Glyceryl Stearate/Peg-40 Stearate; Glyceryl Stearate-Stearamidoethyl Diethylamine;
 Glyceryl Trioleate; Glycine; Glycine Hydrochloride; Glycol Distearate; Glycol Stearate; Guanidine
 Hydrochloride; Guar Gum; Hair Conditioner (18n195-1m); Heptane; Hetastarch; Hexylene Glycol;
 High Density Polyethylene; Histidine; Human Albumin Microspheres; Hyaluronate Sodium;
 Hydrocarbon; Hydrocarbon Gel, Plasticized; Hydrochloric Acid; Hydrochloric Acid, Diluted;
 Hydrocortisone; Hydrogel Polymer; Hydrogen Peroxide; Hydrogenated Castor Oil; Hydrogenated
 Palm Oil; Hydrogenated Palm/Palm Kernel Oil Peg-6 Esters; Hydrogenated Polybutene 635-690;
 Hydroxide Ion; Hydroxyethyl Cellulose; Hydroxyethylpiperazine Ethane Sulfonic Acid;

Hydroxymethyl Cellulose; Hydroxyoctacosanyl Hydroxystearate; Hydroxypropyl Cellulose; Hydroxypropyl Methylcellulose 2906; Hydroxypropyl-Beta-cyclodextrin; Hypromellose 2208 (15000 Mpa.S); Hypromellose 2910 (15000 Mpa.S); Hypromelloses; Imidurea; Iodine; Iodoxamic Acid; Iofetamine Hydrochloride; Irish Moss Extract; Isobutane; Isoceteth-20; Isoleucine; Isooctyl Acrylate; Isopropyl Alcohol; Isopropyl Isostearate; Isopropyl Myristate; Isopropyl Myristate - Myristyl Alcohol; Isopropyl Palmitate; Isopropyl Stearate; Isostearic Acid; Isostearyl Alcohol; Isotonic Sodium Chloride Solution; Jelene; Kaolin; Kathon Cg; Kathon Cg II; Lactate; Lactic Acid; Lactic Acid, DL-; Lactic Acid, L-; Lactobionic Acid; Lactose; Lactose Monohydrate; Lactose, Hydrous; Laneth; Lanolin; Lanolin Alcohol - Mineral Oil; Lanolin Alcohols; Lanolin Anhydrous; Lanolin Cholesterols; Lanolin Nonionic Derivatives; Lanolin, Ethoxylated; Lanolin, Hydrogenated; Lauralkonium Chloride; Lauramine Oxide; Laurdimonium Hydrolyzed Animal Collagen; Laureth Sulfate; Laureth-2; Laureth-23; Laureth-4; Lauric Diethanolamide; Lauric Myristic Diethanolamide; Lauroyl Sarcosine; Lauryl Lactate; Lauryl Sulfate; Lavandula Angustifolia Flowering Top; Lecithin; Lecithin Unbleached; Lecithin, Egg; Lecithin, Hydrogenated; Lecithin, Hydrogenated Soy; Lecithin, Soybean; Lemon Oil; Leucine; Levulinic Acid; Lidofenin; Light Mineral Oil; Light Mineral Oil (85 Ssu); Limonene, (+/-)-; Lipocol Sc-15; Lysine; Lysine Acetate; Lysine Monohydrate; Magnesium Aluminum Silicate; Magnesium Aluminum Silicate Hydrate; Magnesium Chloride; Magnesium Nitrate; Magnesium Stearate; Maleic Acid; Mannitol; Maprofix; Mebrofenin; Medical Adhesive Modified S-15; Medical Antiform A-F Emulsion; Medronate Disodium; Medronic Acid; Meglumine; Menthol; Metacresol; Metaphosphoric Acid; Methanesulfonic Acid; Methionine; Methyl Alcohol; Methyl Gluceth-10; Methyl Gluceth-20; Methyl Gluceth-20 Sesquistearate; Methyl Glucose Sesquistearate; Methyl Laurate; Methyl Pyrrolidone; Methyl Salicylate; Methyl Stearate; Methylboronic Acid; Methylcellulose (4000 Mpa.S); Methylcelluloses; Methylchloroisothiazolinone; Methylene Blue; Methylisothiazolinone; Methylparaben; Microcrystalline Wax; Mineral Oil; Mono And Diglyceride; Monostearyl Citrate; Monothioglycerol; Multisterol Extract; Myristyl Alcohol; Myristyl Lactate; Myristyl-.Gamma.-Picolinium Chloride; N-(Carbamoyl-Methoxy Peg-40)-1,2-Distearoyl-Cephalin Sodium; N,N-Dimethylacetamide; Niacinamide; Nioxime; Nitric Acid; Nitrogen; Nonoxynol Iodine; Nonoxynol-15; Nonoxynol-9; Norflurane; Oatmeal; Octadecene-1/Maleic Acid Copolymer; Octanoic Acid; Octisalate; Octoxynol-1; Octoxynol-40; Octoxynol-9; Octyldodecanol; Octylphenol Polymethylene; Oleic Acid; Oleth-10/Oleth-5; Oleth-2; Oleth-20; Oleyl Alcohol; Oleyl Oleate; Olive Oil;

Oxidronate Disodium; Oxyquinoline; Palm Kernel Oil; Palmitamine Oxide; Parabens; Paraffin; Paraffin, White Soft; Parfum Creme 45/3; Peanut Oil; Peanut Oil, Refined; Pectin; Peg 6-32 Stearate/Glycol Stearate; Peg Vegetable Oil; Peg-100 Stearate; Peg-12 Glyceryl Laurate; Peg-120 Glyceryl Stearate; Peg-120 Methyl Glucose Dioleate; Peg-15 Cocamine; Peg-150 Distearate; Peg-2 Stearate; Peg-20 Sorbitan Isostearate; Peg-22 Methyl Ether/Dodecyl Glycol Copolymer; Peg-25 Propylene Glycol Stearate; Peg-4 Dilaurate; Peg-4 Laurate; Peg-40 Castor Oil; Peg-40 Sorbitan Diisostearate; Peg-45/Dodecyl Glycol Copolymer; Peg-5 Oleate; Peg-50 Stearate; Peg-54 Hydrogenated Castor Oil; Peg-6 Isostearate; Peg-60 Castor Oil; Peg-60 Hydrogenated Castor Oil; Peg-7 Methyl Ether; Peg-75 Lanolin; Peg-8 Laurate; Peg-8 Stearate; Pegoxol 7 Stearate; Pentadecalactone; Pentaerythritol Cocoate; Pentasodium Pentetate; Pentetate Calcium Trisodium; Pentetic Acid; Peppermint Oil; Perflutren; Perfume 25677; Perfume Bouquet; Perfume E-1991; Perfume Gd 5604; Perfume Tana 90/42 Scba; Perfume W-1952-1; Petrolatum; Petrolatum, White; Petroleum Distillates; Phenol; Phenol, Liquefied; Phenonip; Phenoxyethanol; Phenylalanine; Phenylethyl Alcohol; Phenylmercuric Acetate; Phenylmercuric Nitrate; Phosphatidyl Glycerol, Egg; Phospholipid; Phospholipid, Egg; Phospholipon 90g; Phosphoric Acid; Pine Needle Oil (Pinus Sylvestris); Piperazine Hexahydrate; Plastibase-50w; Polacrilin; Polidronium Chloride; Poloxamer 124; Poloxamer 181; Poloxamer 182; Poloxamer 188; Poloxamer 237; Poloxamer 407; Poly(Bis(P-Carboxyphenoxy)Propane Anhydride); Sebacic Acid; Poly(Dimethylsiloxane/Methylvinylsiloxane/Methylhydrogensiloxane) Dimethylvinyl Or Dimethylhydroxy Or Trimethyl Endblocked; Poly(DL-Lactic-Co-Glycolic Acid), (50:50; Poly(DL-Lactic-Co-Glycolic Acid), Ethyl Ester Terminated, (50:50; Polyacrylic Acid (250000 Mw); Polybutene (1400 Mw); Polycarbophil; Polyester; Polyester Polyamine Copolymer; Polyester Rayon; Polyethylene Glycol 1000; Polyethylene Glycol 1450; Polyethylene Glycol 1500; Polyethylene Glycol 1540; Polyethylene Glycol 200; Polyethylene Glycol 300; Polyethylene Glycol 300-1600; Polyethylene Glycol 3350; Polyethylene Glycol 400; Polyethylene Glycol 4000; Polyethylene Glycol 540; Polyethylene Glycol 600; Polyethylene Glycol 6000; Polyethylene Glycol 8000; Polyethylene Glycol 900; Polyethylene High Density Containing Ferric Oxide Black (<1%); Polyethylene Low Density Containing Barium Sulfate (20-24%); Polyethylene T; Polyethylene Terephthalates; Polyglactin; Polyglyceryl-3 Oleate; Polyglyceryl-4 Oleate; Polyhydroxyethyl Methacrylate; Polyisobutylene; Polyisobutylene (1100000 Mw); Polyisobutylene (35000 Mw); Polyisobutylene 178-236; Polyisobutylene 241-294; Polyisobutylene 35-39; Polyisobutylene Low

Molecular Weight; Polyisobutylene Medium Molecular Weight; Polyisobutylene/Polybutene Adhesive; Polylactide; Polyols; Polyoxyethylene - Polyoxypropylene 1800; Polyoxyethylene Alcohols; Polyoxyethylene Fatty Acid Esters; Polyoxyethylene Propylene; Polyoxyl 20 Cetostearyl Ether; Polyoxyl 35 Castor Oil; Polyoxyl 40 Hydrogenated Castor Oil; Polyoxyl 40 Stearate; Polyoxyl 400 Stearate; Polyoxyl 6 And Polyoxyl 32 Palmitostearate; Polyoxyl Distearate; Polyoxyl Glyceryl Stearate; Polyoxyl Lanolin; Polyoxyl Palmitate; Polyoxyl Stearate; Polypropylene; Polypropylene Glycol; Polyquaternium-10; Polyquaternium-7 (70/30 Acrylamide/Dadmac; Polysiloxane; Polysorbate 20; Polysorbate 40; Polysorbate 60; Polysorbate 65; Polysorbate 80; Polyurethane; Polyvinyl Acetate; Polyvinyl Alcohol; Polyvinyl Chloride; Polyvinyl Chloride-Polyvinyl Acetate Copolymer; Polyvinylpyridine; Poppy Seed Oil; Potash; Potassium Acetate; Potassium Alum; Potassium Bicarbonate; Potassium Bisulfite; Potassium Chloride; Potassium Citrate; Potassium Hydroxide; Potassium Metabisulfite; Potassium Phosphate, Dibasic; Potassium Phosphate, Monobasic; Potassium Soap; Potassium Sorbate; Povidone Acrylate Copolymer; Povidone Hydrogel; Povidone K17; Povidone K25; Povidone K29/32; Povidone K30; Povidone K90; Povidone K90f; Povidone/Eicosene Copolymer; Povidones; Ppg-12/Smdi Copolymer; Ppg-15 Stearyl Ether; Ppg-20 Methyl Glucose Ether Distearate; Ppg-26 Oleate; Product Wat; Proline; Promulgen D; Promulgen G; Propane; Propellant A-46; Propyl Gallate; Propylene Carbonate; Propylene Glycol; Propylene Glycol Diacetate; Propylene Glycol Dicaprylate; Propylene Glycol Monolaurate; Propylene Glycol Monopalmitostearate; Propylene Glycol Palmitostearate; Propylene Glycol Ricinoleate; Propylene Glycol/Diazolidinyl Urea/Methylparaben/Propylparben; Propylparaben; Protamine Sulfate; Protein Hydrolysate; Pvm/Ma Copolymer; Quaternium-15; Quaternium-15 Cis-Form; Quaternium-52; Ra-2397; Ra-3011; Saccharin; Saccharin Sodium; Saccharin Sodium Anhydrous; Safflower Oil; Sd Alcohol 3a; Sd Alcohol 40; Sd Alcohol 40-2; Sd Alcohol 40b; Sepineo P 600; Serine; Sesame Oil; Shea Butter; Silastic Brand Medical Grade Tubing; Silastic Medical Adhesive, Silicone Type A; Silica, Dental; Silicon; Silicon Dioxide; Silicon Dioxide, Colloidal; Silicone; Silicone Adhesive 4102; Silicone Adhesive 4502; Silicone Adhesive Bio-Psa Q7-4201; Silicone Adhesive Bio-Psa Q7-4301; Silicone Emulsion; Silicone/Polyester Film Strip; Simethicone; Simethicone Emulsion; Sipon Ls 20np; Soda Ash; Sodium Acetate; Sodium Acetate Anhydrous; Sodium Alkyl Sulfate; Sodium Ascorbate; Sodium Benzoate; Sodium Bicarbonate; Sodium Bisulfate; Sodium Bisulfite; Sodium Borate; Sodium Borate Decahydrate; Sodium Carbonate; Sodium Carbonate Decahydrate; Sodium Carbonate Monohydrate; Sodium

Cetostearyl Sulfate; Sodium Chlorate; Sodium Chloride; Sodium Chloride Injection; Sodium Chloride Injection, Bacteriostatic; Sodium Cholesteryl Sulfate; Sodium Citrate; Sodium Cocoyl Sarcosinate; Sodium Desoxycholate; Sodium Dithionite; Sodium Dodecylbenzenesulfonate; Sodium Formaldehyde Sulfoxylate; Sodium Gluconate; Sodium Hydroxide; Sodium Hypochlorite; Sodium Iodide; Sodium Lactate; Sodium Lactate, L-; Sodium Laureth-2 Sulfate; Sodium Laureth-3 Sulfate; Sodium Laureth-5 Sulfate; Sodium Lauroyl Sarcosinate; Sodium Lauryl Sulfate; Sodium Lauryl Sulfoacetate; Sodium Metabisulfite; Sodium Nitrate; Sodium Phosphate; Sodium Phosphate Dihydrate; Sodium Phosphate, Dibasic; Sodium Phosphate, Dibasic, Anhydrous; Sodium Phosphate, Dibasic, Dihydrate; Sodium Phosphate, Dibasic, Dodecahydrate; Sodium Phosphate, Dibasic, Heptahydrate; Sodium Phosphate, Monobasic; Sodium Phosphate, Monobasic, Anhydrous; Sodium Phosphate, Monobasic, Dihydrate; Sodium Phosphate, Monobasic, Monohydrate; Sodium Polyacrylate (2500000 Mw); Sodium Pyrophosphate; Sodium Pyrrolidone Carboxylate; Sodium Starch Glycolate; Sodium Succinate Hexahydrate; Sodium Sulfate; Sodium Sulfate Anhydrous; Sodium Sulfate Decahydrate; Sodium Sulfite; Sodium Sulfosuccinated Undecyclenic Monoalkylolamide; Sodium Tartrate; Sodium Thioglycolate; Sodium Thiomalate; Sodium Thiosulfate; Sodium Thiosulfate Anhydrous; Sodium Trimetaphosphate; Sodium Xylenesulfonate; Somay 44; Sorbic Acid; Sorbitan; Sorbitan Isostearate; Sorbitan Monolaurate; Sorbitan Monooleate; Sorbitan Monopalmitate; Sorbitan Monostearate; Sorbitan Sesquioleate; Sorbitan Trioleate; Sorbitan Tristearate; Sorbitol; Sorbitol Solution; Soybean Flour; Soybean Oil; Spearmint Oil; Spermaceti; Squalane; Stabilized Oxychloro Complex; Stannous 2-Ethylhexanoate; Stannous Chloride; Stannous Chloride Anhydrous; Stannous Fluoride; Stannous Tartrate; Starch; Starch 1500, Pregelatinized; Starch, Corn; Stearalkonium Chloride; Stearalkonium Hectorite/Propylene Carbonate; Stearamidoethyl Diethylamine; Steareth-10; Steareth-100; Steareth-2; Steareth-20; Steareth-21; Steareth-40; Stearic Acid; Stearic Diethanolamide; Stearoxytrimethylsilane; Steartrimonium Hydrolyzed Animal Collagen; Stearyl Alcohol; Sterile Water For Inhalation; Styrene/Isoprene/Styrene Block Copolymer; Succimer; Succinic Acid; Sucralose; Sucrose; Sucrose Distearate; Sucrose Polyesters; Sulfacetamide Sodium; Sulfobutylether .Beta.-Cyclodextrin; Sulfur Dioxide; Sulfuric Acid; Sulfurous Acid; Surfactol Qs; Tagatose, D-; Talc; Tall Oil; Tallow Glycerides; Tartaric Acid; Tartaric Acid, DL-; Tenox; Tenox-2; Tert-Butyl Alcohol; Tert-Butyl Hydroperoxide; Tert-Butylhydroquinone; Tetrakis(2-Methoxyisobutylisocyanide)Copper(I) Tetrafluoroborate; Tetrapropyl Orthosilicate; Tetrofosmin; Theophylline; Thimerosal; Threonine;

Thymol; Tin; Titanium Dioxide; Tocopherol; Tocophersolan; Total parenteral nutrition, lipid emulsion; Triacetin; Tricaprylin; Trichloromonofluoromethane; Trideceth-10; Triethanolamine Lauryl Sulfate; Trifluoroacetic Acid; Triglycerides, Medium Chain; Trihydroxystearin; Trilane-4 Phosphate; Trilaureth-4 Phosphate; Trisodium Citrate Dihydrate; Trisodium Hedta; Triton 720; Triton X-200; Trolamine; Tromantadine; Tromethamine (TRIS); Tryptophan; Tyloxapol; Tyrosine; Undecylenic Acid; Union 76 Amsco-Res 6038; Urea; Valine; Vegetable Oil; Vegetable Oil Glyceride, Hydrogenated; Vegetable Oil, Hydrogenated; Versetamide; Viscarin; Viscose/Cotton; Vitamin E; Wax, Emulsifying; Wecobee Fs; White Ceresin Wax; White Wax; Xanthan Gum; Zinc; Zinc Acetate; Zinc Carbonate; Zinc Chloride; and Zinc Oxide.

[000307] Pharmaceutical composition formulations of AAV particles disclosed herein may include cations or anions. In one embodiment, the formulations include metal cations such as, but not limited to, Zn^{2+} , Ca^{2+} , Cu^{2+} , Mn^{2+} , Mg^{+} and combinations thereof. As a non-limiting example, formulations may include polymers and complexes with a metal cation (*See e.g.*, U.S. Pat. Nos. 6,265,389 and 6,555,525, each of which is herein incorporated by reference in its entirety).

[000308] Formulations of the invention may also include one or more pharmaceutically acceptable salts. As used herein, “pharmaceutically acceptable salts” refers to derivatives of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., by reacting the free base group with a suitable organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycerophosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium,

tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids.

[000309] The pharmaceutically acceptable salts of the present disclosure can be synthesized from the parent compound which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, Pa., 1985, p. 1418, Pharmaceutical Salts: Properties, Selection, and Use, P.H. Stahl and C.G. Wermuth (eds.), Wiley-VCH, 2008, and Berge et al., Journal of Pharmaceutical Science, 66, 1-19 (1977); the content of each of which is incorporated herein by reference in their entirety.

[000310] The term "pharmaceutically acceptable solvate," as used herein, means a compound of the invention wherein molecules of a suitable solvent are incorporated in the crystal lattice. A suitable solvent is physiologically tolerable at the dosage administered. Solvates may be prepared by crystallization, recrystallization, or precipitation from a solution that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), *N*-methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), *N,N'*-dimethylformamide (DMF), *N,N'*-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate."

III. ADMINISTRATION AND DOSING

Administration

[000311] In one embodiment, the AAV particle may be administered to a subject (e.g., to the CNS of a subject) in a therapeutically effective amount to reduce the symptoms of the disease of the central nervous system (e.g., Parkinson's Disease) of a subject (e.g., determined using a known evaluation method).

[000312] The AAV particles of the present invention may be administered by any delivery route which results in a therapeutically effective outcome. These include, but are not limited to, enteral (into the intestine), gastroenteral, epidural (into the dura mater), oral (by way of the mouth), transdermal, intracerebral (into the cerebrum), intracerebroventricular (into the cerebral ventricles), epicutaneous (application onto the skin), intradermal, (into the skin itself), subcutaneous (under the skin), nasal administration (through the nose), intravenous (into a vein), intravenous bolus, intravenous drip, intra-arterial (into an artery), intramuscular (into a muscle), intracardiac (into the heart), intraosseous infusion (into the bone marrow), intrathecal (into the spinal canal), intraparenchymal (into brain tissue), intraperitoneal, (infusion or injection into the peritoneum), intravesical infusion, intravitreal, (through the eye), intracavernous injection (into a pathologic cavity) intracavitary (into the base of the penis), intravaginal administration, intrauterine, extra-amniotic administration, transdermal (diffusion through the intact skin for systemic distribution), transmucosal (diffusion through a mucous membrane), transvaginal, insufflation (snorting), sublingual, sublabial, enema, eye drops (onto the conjunctiva), or in ear drops, auricular (in or by way of the ear), buccal (directed toward the cheek), conjunctival, cutaneous, dental (to a tooth or teeth), electro-osmosis, endocervical, endosinusial, endotracheal, extracorporeal, hemodialysis, infiltration, interstitial, intra-abdominal, intra-amniotic, intra-articular, intrabiliary, intrabronchial, intrabursal, intracartilaginous (within a cartilage), intracaudal (within the cauda equine), intracisternal (within the cisterna magna cerebellomedularis), intracorneal (within the cornea), dental intracoronal, intracoronary (within the coronary arteries), intracorporus cavernosum (within the dilatable spaces of the corporus cavernosa of the penis), intradiscal (within a disc), intraductal (within a duct of a gland), intraduodenal (within the duodenum), intradural (within or beneath the dura), intraepidermal (to the epidermis), intraesophageal (to the esophagus), intragastric (within the stomach), intragingival (within the gingivae), intraileal (within the distal portion of the small intestine), intralesional (within or introduced directly to a localized lesion), intraluminal (within a lumen of a tube), intralymphatic (within the lymph), intramedullary (within the marrow cavity of a bone), intrameningeal (within the meninges), intramyocardial (within the myocardium), intraocular (within the eye), intraovarian (within the ovary), intrapericardial (within the pericardium), intrapleural (within the pleura), intraprostatic (within the prostate gland), intrapulmonary (within the lungs or its bronchi), intrasinal (within the nasal or periorbital sinuses), intraspinal (within the vertebral column), intrasynovial (within the synovial cavity of a joint), intratendinous (within a

tendon), intratesticular (within the testicle), intrathecal (within the cerebrospinal fluid at any level of the cerebrospinal axis), intrathoracic (within the thorax), intratubular (within the tubules of an organ), intratumor (within a tumor), intratympanic (within the aural media), intravascular (within a vessel or vessels), intraventricular (within a ventricle), iontophoresis (by means of electric current where ions of soluble salts migrate into the tissues of the body), irrigation (to bathe or flush open wounds or body cavities), laryngeal (directly upon the larynx), nasogastric (through the nose and into the stomach), occlusive dressing technique (topical route administration which is then covered by a dressing which occludes the area), ophthalmic (to the external eye), oropharyngeal (directly to the mouth and pharynx), parenteral, percutaneous, periarticular, peridural, perineural, periodontal, rectal, respiratory (within the respiratory tract by inhaling orally or nasally for local or systemic effect), retrobulbar (behind the pons or behind the eyeball), soft tissue, subarachnoid, subconjunctival, submucosal, topical, transplacental (through or across the placenta), transtracheal (through the wall of the trachea), transtympanic (across or through the tympanic cavity), ureteral (to the ureter), urethral (to the urethra), vaginal, caudal block, diagnostic, nerve block, biliary perfusion, cardiac perfusion, photophoresis and spinal.

[000313] In some embodiments, compositions may be administered in a way which allows them to cross the blood-brain barrier, vascular barrier, or other epithelial barrier. The AAV particles of the present invention may be administered in any suitable form, either as a liquid solution or suspension, as a solid form suitable for liquid solution or suspension in a liquid solution. The AAV particles may be formulated with any appropriate and pharmaceutically acceptable excipient.

[000314] In one embodiment, the AAV particles of the present invention may be delivered to a subject via a single route administration.

[000315] In one embodiment, the AAV particles of the present invention may be delivered to a subject via a multi-site route of administration. A subject may be administered at 2, 3, 4, 5 or more than 5 sites.

[000316] In one embodiment, a subject may be administered the AAV particles of the present invention using a bolus infusion.

[000317] In one embodiment, a subject may be administered the AAV particles of the present invention using sustained delivery over a period of minutes, hours or days. The infusion rate may be changed depending on the subject, distribution, formulation or another delivery parameter.

[000318] In one embodiment, the AAV particles of the present invention may be delivered by intramuscular delivery route. (See, e.g., U. S. Pat. No. 6506379; the content of which is incorporated herein by reference in its entirety). Non-limiting examples of intramuscular administration include an intravenous injection or a subcutaneous injection.

[000319] In one embodiment, the AAV particles of the present invention may be delivered by oral administration. Non-limiting examples of oral administration include a digestive tract administration and a buccal administration.

[000320] In one embodiment, the AAV particles of the present invention may be delivered by intraocular delivery route. A non-limiting example of intraocular administration include an intravitreal injection.

[000321] In one embodiment, the AAV particles of the present invention may be delivered by intranasal delivery route. Non-limiting examples of intranasal delivery include administration of nasal drops or nasal sprays.

[000322] In some embodiments, the AAV particles that may be administered to a subject by peripheral injections. Non-limiting examples of peripheral injections include intraperitoneal, intramuscular, intravenous, conjunctival or joint injection. It was disclosed in the art that the peripheral administration of AAV particles can be transported to the central nervous system, for example, to the motor neurons (e.g., U. S. Patent Publication Nos. 20100240739; and 20100130594; the content of each of which is incorporated herein by reference in their entirety).

[000323] In one embodiment, the AAV particles may be delivered by injection into the CSF pathway. Non-limiting examples of delivery to the CSF pathway include intrathecal and intracerebroventricular administration.

[000324] In one embodiment, the AAV particles may be delivered by systemic delivery. As a non-limiting example, the systemic delivery may be by intravascular administration.

[000325] In one embodiment, the AAV particles of the present invention may be administered to a subject by intracranial delivery (See, e.g., U. S. Pat. No. 8,119,611; the content of which is incorporated herein by reference in its entirety).

[000326] In some embodiments, the AAV particles of the present invention may be administered by injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by injection.

[000327] In some embodiments, the AAV particles of the present invention may be administered by muscular injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by muscular administration.

[000328] In some embodiments, the AAV particles of the present invention may be administered by intramuscular administration. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intramuscular administration.

[000329] In one embodiment, the AAV particles of the present invention are administered to a subject and transduce muscle of a subject. As a non-limiting example, the AAV particles are administered by intramuscular administration.

[000330] In some embodiments, the AAV particles of the present invention may be administered via intraparenchymal injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intraparenchymal administration.

[000331] In some embodiments, the AAV particles of the present invention may be administered by intravenous administration. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intravenous administration.

[000332] In one embodiment, the AAV particles of the present invention may be administered via intravenous delivery.

[000333] In one embodiment, the AAV particles of the present invention may be administered via a single dose intravenous delivery. As a non-limiting example, the single dose intravenous delivery may be a one-time treatment. In the context of diseases of the central nervous system (e.g., Parkinson's Disease), the single dose intravenous delivery can produce durable relief for subjects with central nervous system (e.g., Parkinson's Disease) and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or

more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[000334] In one embodiment, the AAV particles of the present invention may be administered via intravenous delivery to the DRG nociceptive neurons.

[000335] In one embodiment, the AAV particles of the present invention may be administered via a single dose intravenous delivery to the DRG nociceptive neurons. As a non-limiting example, the single dose intravenous delivery may be a one-time treatment. In the context of diseases of the central nervous system (e.g., Parkinson's Disease), the single dose intravenous delivery can produce durable relief for subjects with diseases of the central nervous system (e.g., Parkinson's Disease) and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[000336] In some embodiments, the AAV particles of the present invention may be administered by intrathecal injection. As a non-limiting example, the AAV particles of the present invention may be administered by intrathecal injection.

[000337] In one embodiment, the AAV particle may be administered to the cisterna magna in a therapeutically effective amount to transduce spinal cord motor neurons and/or astrocytes. As a non-limiting example, the AAV particle may be administered intrathecally.

[000338] In one embodiment, the AAV particle may be administered using intrathecal infusion in a therapeutically effective amount to transduce spinal cord motor neurons and/or astrocytes.

[000339] In some embodiments, the AAV particles of the present invention may be administered via a single dose intrathecal injection. As a non-limiting example, the single dose intrathecal injection may be a one-time treatment. In the context of diseases of the central nervous system (e.g.,

Parkinson's Disease), the single dose intrathecal injection can produce durable relief for subjects with diseases of the central nervous system (e.g., Parkinson's Disease) and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[000340] In some embodiments, the AAV particles of the present invention may be administered via intrathecal injection to the DRG nociceptive neurons.

[000341] In some embodiments, the AAV particles of the present invention may be administered via a single dose intrathecal injection to the DRG nociceptive neurons. As a non-limiting example, the single dose intrathecal injection may be a one-time treatment. In the context of diseases of the central nervous system (e.g., Parkinson's Disease), the single dose intrathecal injection can produce durable relief for subjects with diseases of the central nervous system (e.g., Parkinson's Disease) and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[000342] In one embodiment, the AAV particle described herein is administered via intrathecal (IT) infusion at C1. The infusion may be for 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more than 15 hours.

[000343] In some embodiments, the AAV particles of the present invention may be administered by intraparenchymal injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intraparenchymal injection.

[000344] In one embodiment, the AAV particle may be administered to the cisterna magna in a therapeutically effective amount to transduce spinal cord motor neurons and/or astrocytes. As a non-limiting example, the AAV particle may be administered intraparenchymal injection.

[000345] In some embodiments, the AAV particles of the present invention may be administered by intraparenchymal injection and intrathecal injection. As a non-limiting example, the AAV particles of the present invention may be administered via intraparenchymal injection and intrathecal injection.

[000346] In some embodiments, the AAV particles of the present invention may be administered by subcutaneous injection. As a non-limiting example, the AAV particles In one embodiment, the AAV particles of the present invention may be administered to a subject by subcutaneous injection.

[000347] In some embodiments, the AAV particles of the present invention may be administered topically. As a non-limiting example, the AAV particles of the present invention may be administered to a subject topically.

[000348] In one embodiment, the AAV particles may be delivered by direct injection into the brain. As a non-limiting example, the brain delivery may be by intrastriatal administration.

[000349] In one embodiment, the AAV particles of the present invention may be administered via intrastriatal injection.

[000350] In one embodiment, the AAV particles of the present invention may be administered via intrastriatal injection and another route of administration described herein.

[000351] In one embodiment, the AAV particles may be delivered by more than one route of administration. As non-limiting examples of combination administrations, AAV particles may be delivered by intrathecal and intracerebroventricular, or by intravenous and intraparenchymal administration.

[000352] In one embodiment, the AAV particle may be administered to the CNS in a therapeutically effective amount to improve function and/or survival for a subject with diseases of

the central nervous system (e.g., Parkinson's Disease). As a non-limiting example, the vector may be administered by direct infusion into the striatum.

[000353] The AAV particle may be administered in a "therapeutically effective" amount, i.e., an amount that is sufficient to alleviate and/or prevent at least one symptom associated with the disease, or provide improvement in the condition of the subject.

[000354] In one embodiment, the catheter may be located at more than one site in the spine for multi-site delivery. The AAV particle may be delivered in a continuous and/or bolus infusion. Each site of delivery may be a different dosing regimen or the same dosing regimen may be used for each site of delivery. As a non-limiting example, the sites of delivery may be in the cervical and the lumbar region. As another non-limiting example, the sites of delivery may be in the cervical region. As another non-limiting example, the sites of delivery may be in the lumbar region.

[000355] In one embodiment, a subject may be analyzed for spinal anatomy and pathology prior to delivery of the AAV particle described herein. As a non-limiting example, a subject with scoliosis may have a different dosing regimen and/or catheter location compared to a subject without scoliosis.

[000356] In one embodiment, the orientation of the spine of the subject during delivery of the AAV particle may be vertical to the ground.

[000357] In another embodiment, the orientation of the spine of the subject during delivery of the AAV particle may be horizontal to the ground.

[000358] In one embodiment, the spine of the subject may be at an angle as compared to the ground during the delivery of the AAV particle. The angle of the spine of the subject as compared to the ground may be at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 or 180 degrees.

[000359] In one embodiment, the delivery method and duration is chosen to provide broad transduction in the spinal cord. As a non-limiting example, intrathecal delivery is used to provide broad transduction along the rostral-caudal length of the spinal cord. As another non-limiting example, multi-site infusions provide a more uniform transduction along the rostral-caudal length of the spinal cord. As yet another non-limiting example, prolonged infusions provide a more uniform transduction along the rostral-caudal length of the spinal cord.

[000360] In one embodiment, administration occurs by a posterior (e.g., back of the head) surgical delivery approach to the putamen. As a non-limiting example, the average putaminal coverage is 50% with posterior delivery and the surgical time is less than 10 hours.

[000361] In one embodiment, administration occurs by a transfrontal (e.g., top of the head) surgical delivery approach to the putamen. As a non-limiting example, the average putaminal coverage less than 50% with posterior delivery and the surgical time is more than 10 hours.

Parenteral and injectable administration

[000362] In some embodiments, pharmaceutical compositions, AAV particles of the present invention may be administered parenterally. Liquid dosage forms for oral and parenteral administration include, but are not limited to, pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups, and/or elixirs. In addition to active ingredients, liquid dosage forms may comprise inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, oral compositions can include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and/or perfuming agents. In certain embodiments for parenteral administration, compositions are mixed with solubilizing agents such as CREMOPHOR[®], alcohols, oils, modified oils, glycols, polysorbates, cyclodextrins, polymers, and/or combinations thereof. In other embodiments, surfactants are included such as hydroxypropylcellulose.

[000363] Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing agents, wetting agents, and/or suspending agents. Sterile injectable preparations may be sterile injectable solutions, suspensions, and/or emulsions in nontoxic parenterally acceptable diluents and/or solvents, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P., and isotonic sodium chloride solution. Sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono- or diglycerides. Fatty acids such as oleic acid can be used in the preparation of injectables.

[000364] Injectable formulations may be sterilized, for example, by filtration through a bacterial-retaining filter, and/or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

[000365] In order to prolong the effect of active ingredients, it is often desirable to slow the absorption of active ingredients from subcutaneous or intramuscular injections. This may be accomplished by the use of liquid suspensions of crystalline or amorphous material with poor water solubility. The rate of absorption of active ingredients depends upon the rate of dissolution which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle. Injectable depot forms are made by forming microencapsule matrices of the drug in biodegradable polymers such as polylactide-polyglycolide. Depending upon the ratio of drug to polymer and the nature of the particular polymer employed, the rate of drug release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissues.

Depot administration

[000366] As described herein, in some embodiments, pharmaceutical compositions, AAV particles of the present invention are formulated in depots for extended release. Generally, specific organs or tissues ("target tissues") are targeted for administration.

[000367] In some aspects of the invention, pharmaceutical compositions, AAV particles of the present invention are spatially retained within or proximal to target tissues. Provided are methods of providing pharmaceutical compositions, AAV particles, to target tissues of mammalian subjects by contacting target tissues (which comprise one or more target cells) with pharmaceutical compositions, AAV particles, under conditions such that they are substantially retained in target tissues, meaning that least 10, 20, 30, 40, 50, 60, 70, 80, 85, 90, 95, 96, 97, 98, 99, 99.9, 99.99 or greater than 99.99% of the composition is retained in the target tissues. Advantageously, retention is determined by measuring the amount of pharmaceutical compositions, AAV particles, that enter one or more target cells. For example, at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99% or greater than 99.99% of pharmaceutical compositions, AAV particles, administered to subjects are present intracellularly at a period of time following administration. For example, intramuscular injection to mammalian subjects may be

performed using aqueous compositions comprising pharmaceutical compositions, AAV particles of the present invention and one or more transfection reagents, and retention is determined by measuring the amount of pharmaceutical compositions, AAV particles, present in muscle cells.

[000368] Certain aspects of the invention are directed to methods of providing pharmaceutical compositions, AAV particles of the present invention to a target tissues of mammalian subjects, by contacting target tissues (comprising one or more target cells) with pharmaceutical compositions, AAV particles under conditions such that they are substantially retained in such target tissues. Pharmaceutical compositions, AAV particles comprise enough active ingredient such that the effect of interest is produced in at least one target cell. In some embodiments, pharmaceutical compositions, AAV particles generally comprise one or more cell penetration agents, although “naked” formulations (such as without cell penetration agents or other agents) are also contemplated, with or without pharmaceutically acceptable carriers.

Delivery to the Central Nervous System

[000369] In one embodiment, delivery of the pharmaceutical compositions comprising AAV particles to cells of the central nervous system (e.g., parenchyma) comprises infusion of up to 1 mL. In one embodiment, delivery of the pharmaceutical compositions comprising AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise infusion of 0.001, 0.002, 0.003, 0.004, 0.005, 0.010, 0.015, 0.020, 0.025, 0.030, 0.040, 0.050, 0.060, 0.070, 0.080, 0.090, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, or 0.9 mL.

[000370] In one embodiment, delivery of pharmaceutical composition comprising AAV particles to cells of the central nervous system (e.g., parenchyma) comprises infusion of between about 1 mL to about 120 mL. In one embodiment, delivery of pharmaceutical composition comprising AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise infusion of 0.1, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 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, or 120 mL. In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) comprises infusion of at least 3 mL. In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) consists of infusion of 3 mL. In one

embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) comprises infusion of at least 10 mL. In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) consists of infusion of 10 mL.

[000371] In one embodiment, the volume of the pharmaceutical composition comprising AAV particles delivered to the cells of the central nervous system (e.g., parenchyma) of a subject is 50 ul, 100 ul, 200 ul, 300 ul, 400 ul, 500 ul, 600 ul, 700 ul, 800 ul, 900 ul, 1000 ul, 1100 ul, 1200 ul, 1300 ul, 1400 ul, 1500 ul, 1600 ul, 1700 ul, 1800 ul, 1900 ul, 2000 ul or more than 2000 ul.

[000372] In one embodiment, the volume of the pharmaceutical composition comprising AAV particles delivered to a region in both hemispheres of a subject brain is 50 ul, 100 ul, 200 ul, 300 ul, 400 ul, 500 ul, 600 ul, 700 ul, 800 ul, 900 ul, 1000 ul, 1100 ul, 1200 ul, 1300 ul, 1400 ul, 1500 ul, 1600 ul, 1700 ul, 1800 ul, 1900 ul, 2000 ul or more than 2000 ul. As a non-limiting example, the volume delivered to a region in both hemispheres is 200 ul. As another non-limiting example, the volume delivered to a region in both hemispheres is 900 ul. As yet another non-limiting example, the volume delivered to a region in both hemispheres is 1800 ul.

[000373] In one embodiment, the volume of the pharmaceutical composition comprising AAV particles delivered to the putamen in both hemispheres of a subject brain is 50 ul, 100 ul, 200 ul, 300 ul, 400 ul, 450 ul, 500 ul, 600 ul, 700 ul, 800 ul, 900 ul, 1000 ul, 1100 ul, 1200 ul, 1300 ul, 1400 ul, 1500 ul, 1600 ul, 1700 ul, 1800 ul, 1900 ul, 2000 ul or more than 2000 ul. As a non-limiting example, the volume delivered to the putamen in both hemispheres is 100 ul. As another non-limiting example, the volume delivered to the putamen in both hemispheres is 200 ul. As a non-limiting example, the volume delivered to the putamen in both hemispheres is 300 ul. As another non-limiting example, the volume delivered to the putamen in both hemispheres is 450 ul. As another non-limiting example, the volume delivered to the putamen in both hemispheres is 900 ul. As yet another non-limiting example, the volume delivered to the putamen both hemispheres is 1800 ul.

[000374] In one embodiment, the volume of the pharmaceutical composition comprising AAV particles delivered to a subject is 900 ul to each putamen.

[000375] In one embodiment, the volume of the pharmaceutical composition comprising AAV particles delivered to a subject is 450 ul to each putamen.

[000376] In one embodiment, the total volume delivered to a subject may be split between one or more administration sites e.g., 1, 2, 3, 4, 5 or more than 5 sites. As a non-limiting example, the total

volume is split between administration to the left and right putamen. As another non-limiting example, the total volume is split between two sites of administration to each of the left and right putamen.

[000377] In one embodiment, the pharmaceutical composition comprising AAV particles is administered using a fenestrated needle. Non-limiting examples of fenestrated needles are described in US Patent Nos. 8,333,734, 7,135,010, 7,575,572, 7,699,852, 4,411,657, 6,890,319, 6,613,026, 6,726,659, 6,565,572, 6,520,949, 6,382,212, 5,848,996, 5,759,179, 5,674,267, 5,588,960, 5,484,401, 5,199,441, 5,012,818, 4,474,569, 3,766,907, 3,552,394, the contents of each of which are herein incorporated by reference in its entirety.

[000378] In one embodiment, a composition comprises at least one payload described herein and the payloads are components of a viral genome packaged in an AAV particle. The percent (%) ratio of AAV particles comprising the payload to the AAV particles without the payload (also referred to herein as empty capsids) in the composition may be 0:100, 1:99, 0: 90, 15:85, 25:75, 30:70, 50:50, 70:30, 85:15, 90:10, 99:1 or 100:0. As a non-limiting example, the percent ratio of AAV particles comprising the payload to empty capsids is 50:50. As another non-limiting example, the percent ratio of AAV particles comprising the payload to empty capsids is 70:30. As another non-limiting example, the percent ratio of AAV particles comprising the payload to empty capsids is 85:15. As another non-limiting example, the percent ratio of AAV particles comprising the payload to empty capsids is 100:0.

[000379] In one embodiment, the composition described herein comprises at least 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 51, 52, 53, 54, 55, 60, 65, 70, 75, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or greater than 99% AAV particles comprising the payload. As a non-limiting example, the composition comprises at least 50% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 52% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 58% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 70% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 83% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 85% AAV particles comprising the payload. As another non-limiting example, the composition comprises at least 99% AAV particles

comprising the payload. As another non-limiting example, the composition comprises 100% AAV particles comprising the payload.

[000380] In one embodiment, the composition described herein comprises 1-10%, 10-20%, 30-40%, 50-60%, 50-70%, 50-80%, 50-90%, 50-99%, 50-100%, 60-70%, 60-80%, 60-90%, 60-99%, 60-100%, 70-80%, 70-90%, 70-99%, 70-100%, 80-85%, 80-90%, 80-95%, 80-99%, 80-100%, 90-95%, 90-99%, or 90-100% AAV particles comprising the payload. As a non-limiting example, the composition described herein comprises 50-100% AAV particles comprising the payload. As another non-limiting example, the composition described herein comprises 50-60% AAV particles comprising the payload. As another non-limiting example, the composition described herein comprises 80-99% AAV particles comprising the payload. As another non-limiting example, the composition described herein comprises 80-90% AAV particles comprising the payload. As a non-limiting example, the composition described herein comprises 80-95% AAV particles comprising the payload. As a non-limiting example, the composition described herein comprises 80-85% AAV particles comprising the payload.

[000381] In one embodiment, the composition described herein comprises less than 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 51, 52, 53, 54, 55, 60, 65, 70, 75, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% empty particles. As a non-limiting example, the composition comprises less than 50% empty particles. As a non-limiting example, the composition comprises less than 45% empty particles. As a non-limiting example, the composition comprises less than 40% empty particles. As a non-limiting example, the composition comprises less than 35% empty particles. As a non-limiting example, the composition comprises less than 30% empty particles. As a non-limiting example, the composition comprises less than 25% empty particles. As a non-limiting example, the composition comprises less than 20% empty particles. As a non-limiting example, the composition comprises less than 15% empty particles. As a non-limiting example, the composition comprises less than 10% empty particles. As a non-limiting example, the composition comprises less than 5% empty particles. As a non-limiting example, the composition comprises less than 1% empty particles.

[000382] In the composition described herein comprises 1-10%, 10-20%, 30-40%, 50-60%, 50-70%, 50-80%, 50-90%, 50-99%, 50-100%, 60-70%, 60-80%, 60-90%, 60-99%, 60-100%, 70-80%, 70-90%, 70-99%, 70-100%, 80-85%, 80-90%, 80-95%, 80-99%, 80-100%, 90-95%, 90-99%, or 90-100% empty particles. As a non-limiting example, the composition described herein comprises 30-

40% empty particles. As another non-limiting example, the composition described herein comprises 30-50% empty particles. As another non-limiting example, the composition described herein comprises 30-60% empty particles. As another non-limiting example, the composition described herein comprises 30-70% empty particles. As a non-limiting example, the composition described herein comprises 30-80% empty particles. As a non-limiting example, the composition described herein comprises 30-90% empty particles.

[000383] In one embodiment, the ratio of distribution volume in the parenchyma of an area of a subject to the infusion volume of an area of a subject may be 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0 or more than 6.0. As a non-limiting example, the ratio of distribution volume in the parenchyma to infusion volume was 1.6 in the caudate nucleus. As a non-limiting example, the ratio of distribution volume in the parenchyma to infusion volume was 3.1 in the putamen. As a non-limiting example, the distribution of the AAV particles in the putamen may be 2-3 times the volume infused.

[000384] In one embodiment, the effectiveness of the dose, route of administration and/or volume of administration may be evaluated using various methods described herein such as, but not limited to, PET imaging, L-DOPA challenge test (e.g., see Forsayeth et al. 2006, Mol. Ther. 14(4): 571-577), UPDRS scores and patient diaries (e.g., Hauser diary). As a non-limiting example, a subject may have decreased dyskinesia or periods of decreased dyskinesia after administration of the Pharmaceutical composition comprising AAV particles. As another non-limiting example, a subject may have a decrease in Parkinson's Disease related symptoms including limited mobility and dyskinesia. As yet another non-limiting example, a subject may show improvement in off time and motor fluctuations. The improvement may be at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% or greater than 90%. The improvement may last for minutes (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55 or more than 55), hours (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or more than 24), days (e.g., 1, 2, 3, 4, 5, 6 or more than 7), weeks (1, 2, 3, 4, 5, 6, 7 or more than 7), months (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or more than 11) or years (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or more than 9).

[000385] In one embodiment, the selection of subjects for administration of the AAV particles described herein and/or the effectiveness of the dose, route of administration and/or volume of administration may be evaluated using imaging of the perivascular spaces (PVS) which are also known as Virchow-Robin spaces. PVS surround the arterioles and venules as they perforate brain parenchyma and are filled with cerebrospinal fluid (CSF)/interstitial fluid. PVS are common in the midbrain, BG, and centrum semiovale. While not wishing to be bound by theory, PVS may play a role in the normal clearance of metabolites and have been associated with worse cognition and several disease states including Parkinson's disease. PVS are usually normal in size but they can increase in size in a number of disease states. Potter et al. (Cerebrovasc Dis. 2015 Jan; 39(4): 224–231; the contents of which are herein incorporated by reference in its entirety) developed a grading method where they studied a full range of PVS and rated basal ganglia, centrum semiovale and midbrain PVS. They used the frequency and range of PVS used by Mac and Lulich et al. (J Neurol Neurosurg Psychiatry. 2004 Nov;75(11):1519-23; the contents of which are herein incorporated by reference in its entirety) and Potter et al. gave 5 ratings to basal ganglia and centrum semiovale PVS: 0 (none), 1 (1-10), 2 (11-20), 3 (21-40) and 4 (>40) and 2 ratings to midbrain PVS: 0 (non visible) or 1 (visible). The user guide for the rating system by Potter et al. can be found at: www.sbirc.ed.ac.uk/documents/epvs-rating-scale-user-guide.pdf.

[000386] In one embodiment, the selection of subjects for administration of the AAV particles described herein and/or the effectiveness of the dose, route of administration and/or volume of administration may be evaluated using positron emission tomography (PET) measurements of neuroimaging biomarkers such as, but not limited to [¹⁸F]FDOPA. Neuroimaging biomarkers such as [¹⁸F]FDOPA may be used to identify affected individuals and/or may be used to detect a nigrostriatal defect prior to the onset of clinical manifestations. Further, PET-based criteria may be used to categorize subjects based on their nigrostriatal neuronal integrity (e.g., abnormal, normal or uncertain nigrostriatal neuronal integrity) (Rachette et al. Am J Med Genet B Neuropsychiatr Genet. 2006 Apr 5; 141B(3): 245–249; the contents of which are herein incorporated by reference in its entirety).

[000387] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may have advanced PD and still respond to levodopa therapy but the subject also experiences medically refractory motor complications (e.g., severe motor fluctuations and/or dyskinesias that occur during levodopa and other dopaminergic therapies despite adjustments in and

optimization of medication). The subject may be healthy enough to undergo a neurosurgical procedure which may be determined by methods known in the art. As a non-limiting example, the subject may meet the selection criteria for deep brain stimulation (DBS). The subject may have idiopathic PD, younger than 69 years of age, have pronounced responses to levodopa, have medication-refractory symptoms (e.g., motor fluctuation and/or dyskinesia) and/or have little or no cognitive dysfunction.

[000388] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may also suffer from dementia or cognitive impairment.

[000389] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may have been previously treated with the same or similar therapeutic. In another embodiment, a subject may have been treated with a therapeutic which has been shown to reduce the symptoms of Parkinson's Disease.

[000390] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may have failed to derive adequate benefit from standard medical therapy. As a non-limiting example, the subject may not have responded to treatment. As another non-limiting example, a subject may have residual disability despite treatment.

[000391] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may undergo testing to evaluate the levels of neurotransmitter analytes to determine the effectiveness of the dose. As a non-limiting example, CSF neurotransmitters, plasma AADC activity and/or urine VLA may be analyzed.

[000392] In one embodiment, a subject who may be administered a dose of the AAV particles described herein may be videotaped or recorded in order to monitor the progress of the subject during the course of treatment.

Delivery to the Putamen

[000393] In one embodiment, the AAV particles may be administered to the right putamen and/or the left putamen. The administration may be at one or more sites in the putamen such as, but not limited to, 2 sites, 3 sites, 4 sites or more than 4 sites. As a non-limiting example, the AAV particles are delivered to 2 sites in the left putamen and 2 sites in the right putamen.

[000394] In one embodiment, the administration of the formulation of the AAV particles to a subject provides coverage of the putamen of a subject (e.g., the left and/or right putamen). In one aspect, the administration of the AAV particles may provide at least 8%, 9%, 10%, 13%, 14%, 15%,

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%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more than 95% to the left and/or right putamen of a subject. As a non-limiting example, the coverage is at least 20%. As a non-limiting example, the coverage is at least 40%. In another aspect, the administration of the AAV particles may provide at least 8%, 9%, 10%, 13%, 14%, 15%, 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%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more than 95% coverage of the surface area of the left and/or right putamen of a subject. As a non-limiting example, the total coverage is at least 20%. As a non-limiting example, the total coverage is at least 40%. In yet another aspect, the administration of the AAV particles may provide 10-40%, 20-40%, 20-30%, 20-35%, 20-50%, 30-40%, 35-40%, 30-60%, 40-70%, 50-80% or 60-90% coverage to the left and/or right putamen of a subject or to the total surface area of the left and/or right putamen of a subject.

[000395] In one embodiment, the administration of the formulation of the AAV particles to a subject provides coverage of the posterior putamen of a subject (e.g., the left and/or right posterior putamen). In one aspect, the administration of the AAV particles may provide at least 10%, 15%, 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%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more than 95% to the left and/or right posterior putamen of a subject. As a non-limiting example, the coverage is at least 20%. As a non-limiting example, the coverage is at least 40%. In another aspect, the administration of the AAV particles may provide at least 10%, 15%, 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%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more than 95% coverage of the surface area of the left and/or right posterior putamen of a subject. As a non-limiting example, the total coverage is at least 20%. As a non-limiting example, the total coverage is at least 40%. In yet another aspect, the administration of the AAV particles may provide 10-40%, 20-50%, 30-60%, 40-70%, 50-80% or 60-90% coverage to the left and/or right posterior putamen of a subject or to the total surface area of the left and/or right putamen of a subject.

[000396] In one embodiment, the AAV particles described herein may be administered using acute bilateral placement of catheters into each putamen. The placement may use magnetic resonance image (MRI)-guided stereotactic neurosurgical techniques known in the art or described herein. Additionally, a contrast agent such as, but not limited to a gadolinium based contrast agent (e.g., PROHANCE®) may be used in the formulation to monitor and confirm the distribution of the formulation.

[000397] In one embodiment, a subject may be administered the AAV particles in a bilateral stereotactic CED-assisted step infusion into the putamen (e.g., the post commissural putamen).

[000398] In one embodiment, a subject may be administered the AAV particles of the present invention at a dose of 4.5×10^{12} vector genomes at a volume of 900 ul per putamen.

[000399] In one embodiment, a subject may be administered the AAV particles of the present invention at a dose of 1.5×10^{12} vector genomes at a volume of 900 ul per putamen.

[000400] In one embodiment, a subject may be administered the AAV particles of the present invention at a dose of 7.5×10^{11} vector genomes at a volume of 450 ul per putamen.

[000401] In one embodiment, a subject may be administered the AAV particles with a bilateral surgical infusion into at least one putamen using a posterior (i.e., back of the head) surgical delivery approach. The number of posterior bilateral surgical infusions may be one or more such as, but not limited to, 1 infusion, 2 infusions, 3 infusions, 4 infusions or more than 4 infusions. As a non-limiting example, the AAV particles are delivered in the left putamen with one posterior bilateral surgical infusion. As a non-limiting example, the AAV particles are delivered in the right putamen with one posterior bilateral surgical infusion. As a non-limiting example, the AAV particles are delivered in the left putamen with two posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right putamen with two posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right and left putamen with two posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the left putamen with three posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right putamen with three posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right and left putamen with three posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the left putamen with four posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right putamen with four posterior bilateral surgical

infusions. As a non-limiting example, the AAV particles are delivered in the right and left putamen with four posterior bilateral surgical infusions.

[000402] In one embodiment, a subject may be administered the AAV particles with a bilateral surgical infusion into at least one putamen using a transfrontal (i.e., top of the head) surgical delivery approach. The number of bilateral surgical infusions may be two or more such as, but not limited to, 2 infusions, 3 infusions, 4 infusions or more than 4 infusions. As a non-limiting example, the AAV particles are delivered in the left putamen with 2 posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the right putamen with 2 posterior bilateral surgical infusions. As a non-limiting example, the AAV particles are delivered in the left and right putamen with 2 posterior bilateral surgical infusions.

Delivery to the SNpc and VTA or STN

[000403] In one embodiment, a subject may be administered the AAV particles of the present invention safely delivered to substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA) via bilateral infusions, or alternatively, intrastriatally (into the caudate nucleus and putamen), or into the subthalamic nucleus (STN).

Delivery, Dose and Regimen

[000404] The present invention provides methods of administering AAV particles in accordance with the invention to a subject in need thereof. The pharmaceutical, diagnostic, or prophylactic AAV particles and compositions of the present invention may be administered to a subject using any amount and any route of administration effective for preventing, treating, managing, or diagnosing diseases, disorders and/or conditions. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration, its mode of activity, and the like. The subject may be a human, a mammal, or an animal. Compositions in accordance with the invention are typically formulated in unit dosage form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of the compositions of the present invention may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate diagnostic dose level for any particular individual will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific payload employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of

administration, route of administration, and rate of excretion of the specific AAV particle employed; the duration of the treatment; drugs used in combination or coincidental with the specific AAV particle employed; and like factors well known in the medical arts.

[000405] In one embodiment, delivery of the AAV particles of the present invention results in minimal serious adverse events (SAEs) as a result of the delivery of the AAV particles.

[000406] In one embodiment, the AAV particle may be delivered a multi-dose regimen. The multi-dose regimen may be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more than 10 doses.

[000407] In one embodiment, the AAV particle may be delivered to a subject via a multi-site route of administration. A subject may be administered the AAV particle at 2, 3, 4, 5 or more than 5 sites.

Dosage Levels

[000408] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present invention may be administered at dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic, diagnostic, or prophylactic, effect. It will be understood that the above dosing concentrations may be converted to vg or viral genomes per kg or into total viral genomes administered by one of skill in the art.

[000409] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present disclosure may be administered at about 10 to about 600 μ l/site, 50 to about 500 μ l/site, 100 to about 400 μ l/site, 120 to about 300 μ l/site, 140 to about 200 μ l/site, about 160 μ l/site. As non-limiting examples, AAV particles may be administered at 50 μ l/site and/or 150 μ l/site.

[000410] In one embodiment, delivery of the compositions in accordance with the present invention to cells comprises a rate of delivery defined by $[VG/\text{hour} = \text{mL}/\text{hour} * VG/\text{mL}]$ wherein VG is viral genomes, VG/mL is composition concentration, and mL/hour is rate of prolonged delivery.

[000411] In one embodiment, delivery of compositions in accordance with the present invention to cells may comprise a total concentration per subject between about 1×10^6 VG and about 1×10^{16} VG. In some embodiments, delivery may comprise a composition concentration of about 1×10^6 ,

2×10^6 , 3×10^6 , 4×10^6 , 5×10^6 , 6×10^6 , 7×10^6 , 8×10^6 , 9×10^6 , 1×10^7 , 2×10^7 , 3×10^7 , 4×10^7 , 5×10^7 , 6×10^7 , 7×10^7 , 8×10^7 , 9×10^7 , 1×10^8 , 2×10^8 , 3×10^8 , 4×10^8 , 5×10^8 , 6×10^8 , 7×10^8 , 8×10^8 , 9×10^8 , 1×10^9 , 2×10^9 , 3×10^9 , 4×10^9 , 5×10^9 , 6×10^9 , 7×10^9 , 8×10^9 , 9×10^9 , 1×10^{10} , 2×10^{10} , 3×10^{10} , 4×10^{10} , 5×10^{10} , 6×10^{10} , 7×10^{10} , 8×10^{10} , 9×10^{10} , 1×10^{11} , 2×10^{11} , 2.1×10^{11} , 2.2×10^{11} , 2.3×10^{11} , 2.4×10^{11} , 2.5×10^{11} , 2.6×10^{11} , 2.7×10^{11} , 2.8×10^{11} , 2.9×10^{11} , 3×10^{11} , 4×10^{11} , 5×10^{11} , 6×10^{11} , 7×10^{11} , 7.1×10^{11} , 7.2×10^{11} , 7.3×10^{11} , 7.4×10^{11} , 7.5×10^{11} , 7.6×10^{11} , 7.7×10^{11} , 7.8×10^{11} , 7.9×10^{11} , 8×10^{11} , 9×10^{11} , 1×10^{12} , 1.1×10^{12} , 1.2×10^{12} , 1.3×10^{12} , 1.4×10^{12} , 1.5×10^{12} , 1.6×10^{12} , 1.7×10^{12} , 1.8×10^{12} , 1.9×10^{12} , 2×10^{12} , 3×10^{12} , 4×10^{12} , 4.1×10^{12} , 4.2×10^{12} , 4.3×10^{12} , 4.4×10^{12} , 4.5×10^{12} , 4.6×10^{12} , 4.7×10^{12} , 4.8×10^{12} , 4.9×10^{12} , 5×10^{12} , 6×10^{12} , 7×10^{12} , 8×10^{12} , 8.1×10^{12} , 8.2×10^{12} , 8.3×10^{12} , 8.4×10^{12} , 8.5×10^{12} , 8.6×10^{12} , 8.7×10^{12} , 8.8×10^{12} , 8.9×10^{12} , 9×10^{12} , 1×10^{13} , 2×10^{13} , 3×10^{13} , 4×10^{13} , 5×10^{13} , 6×10^{13} , 6.7×10^{13} , 7×10^{13} , 8×10^{13} , 9×10^{13} , 1×10^{14} , 2×10^{14} , 3×10^{14} , 4×10^{14} , 5×10^{14} , 6×10^{14} , 7×10^{14} , 8×10^{14} , 9×10^{14} , 1×10^{15} , 2×10^{15} , 3×10^{15} , 4×10^{15} , 5×10^{15} , 6×10^{15} , 7×10^{15} , 8×10^{15} , 9×10^{15} , or 1×10^{16} VG/subject. In one embodiment, the concentration of the AAV particle in the composition is 1×10^{13} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 3×10^{12} VG/ subject. As a non-limiting example, the composition administered to the subject has a concentration of about 3×10^{11} VG/subject. As a non-limiting example, the composition administered to the subject has a concentration of about 9×10^{11} VG/subject. In one embodiment, the concentration of the AAV particle in the composition is 2.3×10^{11} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 7.2×10^{11} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 7.5×10^{11} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 1.4×10^{12} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 4.8×10^{12} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 8.8×10^{12} VG/ subject. In one embodiment, the concentration of the AAV particle in the composition is 2.3×10^{12} VG/ subject.

[000412] In one embodiment, delivery of compositions in accordance with the present invention to cells may comprise a total concentration per subject between about 1×10^6 VG/kg and about 1×10^{16} VG/kg. In some embodiments, delivery may comprise a composition concentration of about 1×10^6 , 2×10^6 , 3×10^6 , 4×10^6 , 5×10^6 , 6×10^6 , 7×10^6 , 8×10^6 , 9×10^6 , 1×10^7 , 2×10^7 , 3×10^7 , 4×10^7 , 5×10^7 , 6×10^7 , 7×10^7 , 8×10^7 , 9×10^7 , 1×10^8 , 2×10^8 , 3×10^8 , 4×10^8 , 5×10^8 , 6×10^8 , 7×10^8 , 8×10^8 , 9×10^8 , 1×10^9 , 2×10^9 , 3×10^9 , 4×10^9 , 5×10^9 , 6×10^9 , 7×10^9 , 8×10^9 , 9×10^9 , 1×10^{10} , 2×10^{10} , 3×10^{10} , 4×10^{10} , 5×10^{10} , 6×10^{10} , 7×10^{10} , 8×10^{10} , 9×10^{10} , 1×10^{11} , 2×10^{11} , 2.1×10^{11} , 2.2×10^{11} , 2.3×10^{11} , 2.4×10^{11} , 2.5×10^{11} , 2.6×10^{11} ,

2.7x10¹¹, 2.8x10¹¹, 2.9x10¹¹, 3x10¹¹, 4x10¹¹, 5x10¹¹, 6x10¹¹, 7x10¹¹, 7.1x10¹¹, 7.2x10¹¹, 7.3x10¹¹, 7.4x10¹¹, 7.5x10¹¹, 7.6x10¹¹, 7.7x10¹¹, 7.8x10¹¹, 7.9x10¹¹, 8x10¹¹, 9x10¹¹, 1x10¹², 1.1 x10¹², 1.2x10¹², 1.3x10¹², 1.4x10¹², 1.5x10¹², 1.6x10¹², 1.7x10¹², 1.8x10¹², 1.9x10¹², 2x10¹², 3x10¹², 4x10¹², 4.1x10¹², 4.2x10¹², 4.3x10¹², 4.4x10¹², 4.5x10¹², 4.6x10¹², 4.7x10¹², 4.8x10¹², 4.9x10¹², 5x10¹², 6x10¹², 7x10¹², 8x10¹², 8.1x10¹², 8.2x10¹², 8.3x10¹², 8.4x10¹², 8.5x10¹², 8.6x10¹², 8.7x10¹², 8.8 x10¹², 8.9x10¹², 9x10¹², 1x10¹³, 2x10¹³, 3x10¹³, 4x10¹³, 5x10¹³, 6x10¹³, 6.7x10¹³, 7x10¹³, 8x10¹³, 9x10¹³, 1x10¹⁴, 2x10¹⁴, 3x10¹⁴, 4x10¹⁴, 5x10¹⁴, 6x10¹⁴, 7x10¹⁴, 8x10¹⁴, 9x10¹⁴, 1x10¹⁵, 2x10¹⁵, 3x10¹⁵, 4x10¹⁵, 5x10¹⁵, 6x10¹⁵, 7x10¹⁵, 8x10¹⁵, 9x10¹⁵, or 1x10¹⁶ VG/kg.

[000413] In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise a total dose between about 1x10⁶ VG and about 1x10¹⁶ VG. In some embodiments, delivery may comprise a total dose of about 1x10⁶, 2x10⁶, 3x10⁶, 4x10⁶, 5x10⁶, 6x10⁶, 7x10⁶, 8x10⁶, 9x10⁶, 1x10⁷, 2x10⁷, 3x10⁷, 4x10⁷, 5x10⁷, 6x10⁷, 7x10⁷, 8x10⁷, 9x10⁷, 1x10⁸, 2x10⁸, 3x10⁸, 4x10⁸, 5x10⁸, 6x10⁸, 7x10⁸, 8x10⁸, 9x10⁸, 1x10⁹, 2x10⁹, 3x10⁹, 4x10⁹, 5x10⁹, 6x10⁹, 7x10⁹, 8x10⁹, 9x10⁹, 1x10¹⁰, 1.9x10¹⁰, 2x10¹⁰, 3x10¹⁰, 3.73x10¹⁰, 4x10¹⁰, 5x10¹⁰, 6x10¹⁰, 7x10¹⁰, 8x10¹⁰, 9x10¹⁰, 1x10¹¹, 2x10¹¹, 2.5x10¹¹, 3x10¹¹, 4x10¹¹, 5x10¹¹, 6x10¹¹, 7x10¹¹, 8x10¹¹, 9x10¹¹, 1x10¹², 2x10¹², 3x10¹², 4x10¹², 5x10¹², 6x10¹², 7x10¹², 8x10¹², 9x10¹², 1x10¹³, 2x10¹³, 3x10¹³, 4x10¹³, 5x10¹³, 6x10¹³, 7x10¹³, 8x10¹³, 9x10¹³, 1x10¹⁴, 2x10¹⁴, 3x10¹⁴, 4x10¹⁴, 5x10¹⁴, 6x10¹⁴, 7x10¹⁴, 8x10¹⁴, 9x10¹⁴, 1x10¹⁵, 2x10¹⁵, 3x10¹⁵, 4x10¹⁵, 5x10¹⁵, 6x10¹⁵, 7x10¹⁵, 8x10¹⁵, 9x10¹⁵, or 1x10¹⁶ VG. As a non-limiting example, the total dose is 1x10¹³ VG. As another non-limiting example, the total dose is 2.1x10¹² VG.

[000414] In one embodiment, about 10⁵ to 10⁶ viral genome (unit) may be administered per dose.

[000415] In one embodiment, delivery of the compositions in accordance with the present invention to cells may comprise a total concentration between about 1x10⁶ VG/mL and about 1x10¹⁶ VG/mL. In some embodiments, delivery may comprise a composition concentration of about 1x10⁶, 2x10⁶, 3x10⁶, 4x10⁶, 5x10⁶, 6x10⁶, 7x10⁶, 8x10⁶, 9x10⁶, 1x10⁷, 2x10⁷, 3x10⁷, 4x10⁷, 5x10⁷, 6x10⁷, 7x10⁷, 8x10⁷, 9x10⁷, 1x10⁸, 2x10⁸, 3x10⁸, 4x10⁸, 5x10⁸, 6x10⁸, 7x10⁸, 8x10⁸, 9x10⁸, 1x10⁹, 2x10⁹, 3x10⁹, 4x10⁹, 5x10⁹, 6x10⁹, 7x10⁹, 8x10⁹, 9x10⁹, 1x10¹⁰, 2x10¹⁰, 3x10¹⁰, 4x10¹⁰, 5x10¹⁰, 6x10¹⁰, 7x10¹⁰, 8x10¹⁰, 9x10¹⁰, 1x10¹¹, 2x10¹¹, 3x10¹¹, 4x10¹¹, 5x10¹¹, 6x10¹¹, 7x10¹¹, 8x10¹¹, 9x10¹¹, 1x10¹², 1.1x10¹², 1.2x10¹², 1.3x10¹², 1.4x10¹², 1.5x10¹², 1.6x10¹², 1.7x10¹², 1.8x10¹², 1.9x10¹², 2x10¹², 2.1x10¹², 2.2x10¹², 2.3x10¹², 2.4x10¹², 2.5x10¹², 2.6x10¹², 2.7x10¹², 2.8x10¹², 2.9x10¹², 3x10¹², 3.1x10¹², 3.2x10¹², 3.3x10¹², 3.4x10¹², 3.5x10¹², 3.6x10¹², 3.7x10¹², 3.8x10¹², 3.9x10¹²,

4×10^{12} , 4.1×10^{12} , 4.2×10^{12} , 4.3×10^{12} , 4.4×10^{12} , 4.5×10^{12} , 4.6×10^{12} , 4.7×10^{12} , 4.8×10^{12} , 4.9×10^{12} , 5×10^{12} , 6×10^{12} , 7×10^{12} , 8×10^{12} , 9×10^{12} , 1×10^{13} , 2×10^{13} , 3×10^{13} , 4×10^{13} , 5×10^{13} , 6×10^{13} , 6.7×10^{13} , 7×10^{13} , 8×10^{13} , 9×10^{13} , 1×10^{14} , 2×10^{14} , 3×10^{14} , 4×10^{14} , 5×10^{14} , 6×10^{14} , 7×10^{14} , 8×10^{14} , 9×10^{14} , 1×10^{15} , 2×10^{15} , 3×10^{15} , 4×10^{15} , 5×10^{15} , 6×10^{15} , 7×10^{15} , 8×10^{15} , 9×10^{15} , or 1×10^{16} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 1×10^{13} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 3×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 1.1×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 3.7×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 8×10^{11} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 2.6×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 4.9×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 0.8×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is 0.83×10^{12} VG/mL. In one embodiment, the concentration of the AAV particle in the composition is the maximum final dose which can be contained in a vial.

[000416] In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise a composition concentration between about 1×10^6 VG/mL and about 1×10^{16} VG/mL. In some embodiments, delivery may comprise a composition concentration of about 1×10^6 , 2×10^6 , 3×10^6 , 4×10^6 , 5×10^6 , 6×10^6 , 7×10^6 , 8×10^6 , 9×10^6 , 1×10^7 , 2×10^7 , 3×10^7 , 4×10^7 , 5×10^7 , 6×10^7 , 7×10^7 , 8×10^7 , 9×10^7 , 1×10^8 , 2×10^8 , 3×10^8 , 4×10^8 , 5×10^8 , 6×10^8 , 7×10^8 , 8×10^8 , 9×10^8 , 1×10^9 , 2×10^9 , 3×10^9 , 4×10^9 , 5×10^9 , 6×10^9 , 7×10^9 , 8×10^9 , 9×10^9 , 1×10^{10} , 2×10^{10} , 3×10^{10} , 4×10^{10} , 5×10^{10} , 6×10^{10} , 7×10^{10} , 8×10^{10} , 9×10^{10} , 1×10^{11} , 2×10^{11} , 3×10^{11} , 4×10^{11} , 5×10^{11} , 6×10^{11} , 7×10^{11} , 8×10^{11} , 9×10^{11} , 1×10^{12} , 2×10^{12} , 3×10^{12} , 4×10^{12} , 5×10^{12} , 6×10^{12} , 7×10^{12} , 8×10^{12} , 9×10^{12} , 1×10^{13} , 2×10^{13} , 3×10^{13} , 4×10^{13} , 5×10^{13} , 6×10^{13} , 7×10^{13} , 8×10^{13} , 9×10^{13} , 1×10^{14} , 2×10^{14} , 3×10^{14} , 4×10^{14} , 5×10^{14} , 6×10^{14} , 7×10^{14} , 8×10^{14} , 9×10^{14} , 1×10^{15} , 2×10^{15} , 3×10^{15} , 4×10^{15} , 5×10^{15} , 6×10^{15} , 7×10^{15} , 8×10^{15} , 9×10^{15} , or 1×10^{16} VG/mL. In one embodiment, the delivery comprises a composition concentration of 1×10^{13} VG/mL. In one embodiment, the delivery comprises a composition concentration of 2.1×10^{12} VG/mL.

Regimen

[000417] The desired dosage of the AAV particles of the present invention may be delivered only once, three times a day, two times a day, once a day, every other day, every third day, every week,

every two weeks, every three weeks, or every four weeks. In certain embodiments, the desired dosage may be delivered using multiple administrations (*e.g.*, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described herein may be used. As used herein, a “split dose” is the division of “single unit dose” or total daily dose into two or more doses, *e.g.*, two or more administrations of the “single unit dose”. As used herein, a “single unit dose” is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, *i.e.*, single administration event.

[000418] The desired dosage of the AAV particles of the present invention may be administered as a “pulse dose” or as a “continuous flow”. As used herein, a “pulse dose” is a series of single unit doses of any therapeutic administered with a set frequency over a period of time. As used herein, a “continuous flow” is a dose of therapeutic administered continuously for a period of time in a single route/single point of contact, *i.e.*, continuous administration event. A total daily dose, an amount given or prescribed in 24 hour period, may be administered by any of these methods, or as a combination of these methods, or by any other methods suitable for a pharmaceutical administration.

[000419] In one embodiment, delivery of the AAV particles of the present invention to a subject provides regulating activity of AADC in a subject. The regulating activity may be an increase in the production of AADC in a subject. The regulating activity can be for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years.

[000420] In some embodiments, the AAV particle of the present invention may be administered to a subject using a single dose, one-time treatment. The dose of the one-time treatment may be administered by any methods known in the art and/or described herein. As used herein, a “one-time treatment” refers to a composition which is only administered one time. If needed, a booster dose may be administered to the subject to ensure the appropriate efficacy is reached. A booster may be administered 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 2 years, 3

years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, or more than 10 years after the one-time treatment.

Delivery Methods

[000421] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for treatment of disease described in US Patent No. 8,999,948, or International Publication No. WO2014178863, the contents of which are herein incorporated by reference in their entirety.

[000422] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering gene therapy in Alzheimer's Disease or other neurodegenerative conditions as described in US Application No. 20150126590, the contents of which are herein incorporated by reference in their entirety.

[000423] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivery of a CNS gene therapy as described in US Patent Nos. 6,436,708, and 8,946,152, and International Publication No. WO2015168666, the contents of which are herein incorporated by reference in their entirety.

[000424] In one embodiment, the AAV particle comprising an AADC polynucleotide may be administered or delivered using the methods for the delivery of AAV virions described in European Patent Application No. EP1857552, the contents of which are herein incorporated by reference in its entirety.

[000425] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering proteins using AAV particles described in European Patent Application No. EP2678433, the contents of which are herein incorporated by reference in their entirety.

[000426] In one embodiment, the AAV particle comprising an AADC polynucleotide may be administered or delivered using the methods for delivering DNA molecules using AAV particles described in US Patent No. US 5,858,351, the contents of which are herein incorporated by reference in its entirety.

[000427] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering DNA to the bloodstream described in US Patent No. US 6,211,163, the contents of which are herein incorporated by reference in their entirety.

[000428] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload to the central nervous system described in US Patent No. US 7,588,757, the contents of which are herein incorporated by reference in their entirety.

[000429] In one embodiment, the AAV particle may be administered or delivered using the methods for delivering AAV virions described in US Patent No. US 6,325,998, the contents of which are herein incorporated by reference in its entirety.

[000430] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload described in US Patent No. US 8,283,151, the contents of which are herein incorporated by reference in their entirety.

[000431] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload using a glutamic acid decarboxylase (GAD) delivery vector described in International Patent Publication No. WO2001089583, the contents of which are herein incorporated by reference in their entirety.

[000432] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload to neural cells described in International Patent Publication No. WO2012057363, the contents of which are herein incorporated by reference in their entirety.

Delivery to Cells

[000433] The present disclosure provides a method of delivering to a cell or tissue any of the above-described AAV particles, comprising contacting the cell or tissue with said AAV particle or contacting the cell or tissue with a formulation comprising said AAV particle, or contacting the cell or tissue with any of the described compositions, including pharmaceutical compositions. The method of delivering the AAV particle to a cell or tissue can be accomplished *in vitro*, *ex vivo*, or *in vivo*.

Delivery to Subjects

[000434] The present disclosure additionally provides a method of delivering to a subject, including a mammalian subject, any of the above-described AAV particles comprising administering to the subject said AAV particle, or administering to the subject a formulation

comprising said AAV particle, or administering to the subject any of the described compositions, including pharmaceutical compositions.

Combinations

[000435] The AAV particles may be used in combination with one or more other therapeutic, prophylactic, research or diagnostic agents. By “in combination with,” it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present invention. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent. In some embodiments, the present disclosure encompasses the delivery of pharmaceutical, prophylactic, research, or diagnostic compositions in combination with agents that may improve their bioavailability, reduce and/or modify their metabolism, inhibit their excretion, and/or modify their distribution within the body.

[000436] In one embodiment, the AAV particles described herein may be administered to a subject who is also undergoing levodopa therapy. As a non-limiting example, the subject may have a positive response to levodopa therapy and at least one symptom of PD is reduced. As another non-limiting example, the subject may have a response to levodopa therapy where the symptoms of PD experienced by the subject are stable. As yet another non-limiting example, the subject may have a negative response to levodopa therapy where the symptoms of PD experienced by the subject are increasing.

[000437] In one embodiment, the dose of levodopa administered to the subject prior to the AAV articles is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more than 25 mg/kg. As a non-limiting example, the dose is 3 mg/kg. As another non-limiting example, the dose is 10 mg/kg. As yet another non-limiting example, the dose is 20 mg/kg. The subject's response (e.g., behavioral response) to levodopa may be assessed prior to administration of the AAV particles. Additionally, the subject may be administered levodopa again after the administration of the AADC polynucleotides (e.g., 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year or more than 1 year after the administration of AAV particles). The behavioral response can be re-assessed and compared to the initial response to determine the effects of the AAV particles. The subject may

have 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or 100% behavioral improvement.

[000438] In one embodiment, Levodopa may be administered multiple times after the administration of the AAV particles. Levodopa may be administered on a repeating schedule (e.g., every 5 days, weekly, every 10 days, every 15 days, every 30 days, monthly, bimonthly, every 3 months, every 4 months, every 5 months, every 6 months, every 7 months, every 8 months, every 9 months, every 10 months, every 11 months or yearly) or as symptoms arise. As a non-limiting example, 3 years post administration of AADC polynucleotides a subject may have 1-10%, 5-15%, 10-20%, 15-30%, 20-40%, 25-50%, 30-50%, 40-50%, 40-60%, 50-70%, 50-80%, 60-70%, 60-75%, 60-80%, 60-90%, 70-80%, 70-90%, 75-90%, 80-90%, 90-100% of the striatal neurons within the infused region of the putamen to be AADC-immunoreactive. As a non-limiting example, 6 years post administration of AAV particles a subject may have 1-10%, 5-15%, 10-20%, 15-30%, 20-40%, 25-50%, 30-50%, 40-50%, 40-60%, 50-70%, 50-80%, 60-70%, 60-75%, 60-80%, 60-90%, 70-80%, 70-90%, 75-90%, 80-90%, 90-100% of the striatal neurons within the infused region of the putamen to be AADC-immunoreactive. As a non-limiting example, 9 years post administration of AADC polynucleotides a subject may have 1-10%, 5-15%, 10-20%, 15-30%, 20-40%, 25-50%, 30-50%, 40-50%, 40-60%, 50-70%, 50-80%, 60-70%, 60-75%, 60-80%, 60-90%, 70-80%, 70-90%, 75-90%, 80-90%, 90-100% of the striatal neurons within the infused region of the putamen to be AADC-immunoreactive.

[000439] In one embodiment, a subject who may be administered the AAV particles described herein have a documented response to levodopa therapy but have medically refractory fluctuations and are considered good surgical candidates. The determination if a subject is a good surgical candidate may be made by the physician treating the subject for PD or the physician administering the AAV particles who takes into consideration the overall risk to benefit ratio for the patient for the surgical intervention required for delivery of the AAV particles.

Measurement of Expression

[000440] Expression of payloads from viral genomes may be determined using various methods known in the art such as, but not limited to immunochemistry (e.g., IHC), *in situ* hybridization (ISH), enzyme-linked immunosorbent assay (ELISA), affinity ELISA, ELISPOT, flow cytometry, immunocytology, surface plasmon resonance analysis, kinetic exclusion assay, liquid chromatography-mass spectrometry (LCMS), high-performance liquid chromatography (HPLC),

BCA assay, immunoelectrophoresis, Western blot, SDS-PAGE, protein immunoprecipitation, and/or PCR.

[000441] The pharmaceutical compositions of AAV particles described herein may be characterized by one or more of bioavailability, therapeutic window and/or volume of distribution.

Bioavailability

[000442] The AAV particles, when formulated into a composition with a delivery agent as described herein, can exhibit an increase in bioavailability as compared to a composition lacking a delivery agent as described herein. As used herein, the term “bioavailability” refers to the systemic availability of a given amount of AAV particle or expressed payload administered to a mammal. Bioavailability can be assessed by measuring the area under the curve (AUC) or the maximum serum or plasma concentration ($C_{\max}$) of the composition following. AUC is a determination of the area under the curve plotting the serum or plasma concentration of a compound (e.g., AAV particles or expressed payloads) along the ordinate (Y-axis) against time along the abscissa (X-axis). Generally, the AUC for a particular compound can be calculated using methods known to those of ordinary skill in the art and as described in G. S. Banker, Modern Pharmaceutics, Drugs and the Pharmaceutical Sciences, v. 72, Marcel Dekker, New York, Inc., 1996, the contents of which are herein incorporated by reference in its entirety.

[000443] The $C_{\max}$ value is the maximum concentration of the AAV particle or expressed payload achieved in the serum or plasma of a mammal following administration of the AAV particle to the mammal. The $C_{\max}$ value of can be measured using methods known to those of ordinary skill in the art. The phrases “increasing bioavailability” or “improving the pharmacokinetics,” as used herein mean that the systemic availability of a first AAV particle or expressed payload, measured as AUC, $C_{\max}$, or $C_{\min}$ in a mammal is greater, when co-administered with a delivery agent as described herein, than when such co-administration does not take place. In some embodiments, the bioavailability can increase by at least about 2%, 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 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%.

Therapeutic Window

[000444] As used herein “therapeutic window” refers to the range of plasma concentrations, or the range of levels of therapeutically active substance at the site of action, with a high probability of eliciting a therapeutic effect. In some embodiments, the therapeutic window of the AAV particle as described herein can increase by at least about 2%, 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 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%.

Volume of Distribution

[000445] As used herein, the term “volume of distribution” refers to the fluid volume that would be required to contain the total amount of the drug in the body at the same concentration as in the blood or plasma: V_{dist} equals the amount of drug in the body/concentration of drug in blood or plasma. For example, for a 10 mg dose and a plasma concentration of 10 mg/L, the volume of distribution would be 1 liter. The volume of distribution reflects the extent to which the drug is present in the extravascular tissue. A large volume of distribution reflects the tendency of a compound to bind to the tissue components compared with plasma protein binding. In a clinical setting, V_{dist} can be used to determine a loading dose to achieve a steady state concentration. In some embodiments, the volume of distribution of the AAV particles as described herein can decrease at least about 2%, 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 55%, at least about 60%, at least about 65%, at least about 70%.

Biological Effect

[000446] In one embodiment, the biological effect of the AAV particles delivered to the animals may be categorized by analyzing the payload expression in the animals. The payload expression may be determined from analyzing a biological sample collected from a mammal administered the AAV particles of the present invention. For example, a protein expression of 50-200 pg/ml for the protein encoded by the AAV particles delivered to the mammal may be seen as a therapeutically effective amount of protein in the mammal.

IV. METHODS AND USES OF THE COMPOSITIONS OF THE INVENTION

CNS Diseases

[000447] The polynucleotides of the present invention may be used in the treatment, prophylaxis or amelioration of any disease or disorder characterized by aberrant or undesired target expression. In one embodiment, the invention relates to AAV particles for use in the treatment of Parkinson's disease.

[000448] In some embodiments, the AAV particles may be used in the treatment, prophylaxis or amelioration of any disease or disorder characterized by aberrant or undesired target expression wherein the payload, i.e. AADC, is swapped for an alternate payload.

[000449] The present disclosure provides a method for treating a disease, disorder and/or condition in a mammalian subject, including a human subject, comprising administering to the subject AAV particles described herein.

[000450] In one embodiment, the disease, disorder and/or condition is a neurological disease, disorder and/or condition. The CNS diseases may be diseases that affect any component of the brain (including the cerebral hemispheres, diencephalon, brain stem, and cerebellum) or the spinal cord.

[000451] In some embodiments, viral particles of the present invention, through delivery of a functional payload that is a therapeutic product that can modulate the level or function of a gene product in the CNS, may be used to treat a neurodegenerative diseases and/or diseases or disorders that are characteristic with neurodegeneration, neuromuscular diseases, lysosomal diseases, trauma, bone marrow injuries, pain (including neuropathic pain), cancers of the nervous system, demyelinating diseases, autoimmune diseases of the nervous system, neurotoxic syndromes, sleeping disorders, genetic brain disorders and developmental CNS disorders. A functional payload may alleviate or reduce symptoms that result from abnormal level and/or function of a gene product (e.g., an absence or defect in a protein) in a subject in need thereof or that otherwise confers a benefit to a CNS disorder in a subject in need thereof.

[000452] As non-limiting examples, therapeutic products delivered by AAV particles of the present invention may include, but are not limited to, growth and trophic factors, cytokines, hormones, neurotransmitters, enzymes, anti-apoptotic factors, angiogenic factors, and any protein known to be mutated in pathological disorders such as the "survival of motor neuron " protein (SMN); antisense RNA or RNAi targeting messenger RNAs coding for proteins having a therapeutic interest in any of CNS diseases discussed herein; or microRNAs that function in gene silencing and post-transcriptionally regulation of gene expression in the CNS (e.g., brain specific

Mir-128a, See Adlakha and Saini, Molecular cancer, 2014, 13:33) . For example, an RNAi targeting the superoxide dismutase enzyme may be packaged by viral particles of the present invention, for the treatment of ALS.

[000453] The growth and trophic factors may include, but are not limited to brain-derived growth factor (BDNF), epidermal growth factor (EGF), basic Fibroblast growth factor (bFGF), Ciliary neurotrophic factor (CNTF), corticotropin-releasing factor (CRF), Glial cell line derived growth factor (GDNF), Insulin-like growth factor-1 (IGF-1), nerve growth factor (NGF), neurotrophin-3 (NT-3), neurotrophin-4 (NT-4), and vascular endothelial growth factor (VEGF). Cytokines may include interleukin-10 (IL-10), interleukin-6, Interleukin-8, chemokine CXCL12 (SDF-1), TGF-beta, and Growth and differentiation factor (GDF-1/10).

[000454] In some embodiments, the neurological disorders may be neurodegenerative disorders including, but not limited to, Alzheimer's Diseases (AD); Amyotrophic lateral sclerosis (ALS); Creutzfeldt-Jakob Disease (CJD); Huntingtin's disease (HD); Friedreich's ataxia (FA); Parkinson Disease (PD); Multiple System Atrophy (MSA); Spinal Muscular Atrophy (SMA), Multiple Sclerosis (MS); Primary progressive aphasia; Progressive supranuclear palsy (PSP); Dementia; Brain Cancer, Degenerative Nerve Diseases, Encephalitis, Epilepsy, Genetic Brain Disorders that cause neurodegeneration, Retinitis pigmentosa (RP), Head and Brain Malformations, Hydrocephalus, Stroke, Prion disease, Infantile neuronal ceroid lipofuscinosis (INCL) (a neurodegenerative disease of children caused by a deficiency in the lysosomal enzyme palmitoyl protein thioesterase-1 (PPT1)), and others.

[000455] In some embodiments, viral particles of the present invention may be used to treat diseases that are associated with impairments of the growth and development of the CNS, i.e., neurodevelopmental disorders. In some aspects, such neurodevelopmental disorders may be caused by genetic mutations, including but not limited to, Fragile X syndrome (caused by mutations in FMR1 gene), Down syndrome (caused by trisomy of chromosome 21), Rett syndrome, Williams syndrome, Angelman syndrome, Smith-Magenis syndrome, ATR-X syndrome, Barth syndrome, Immune dysfunction and/or infectious diseases during infancy such as Sydenham's chorea, Schizophrenia Congenital toxoplasmosis, Congenital rubella syndrome, Metabolic disorders such as diabetes mellitus and phenylketonuria; nutritional defects and/or brain trauma, Autism and autism spectrum.

[000456] In some embodiments, viral particles of the present invention, may be used to treat a tumor in the CNS, including but not limited to, acoustic neuroma, Astrocytoma (Grades I, II, III and IV), Chordoma, CNS Lymphoma, Craniopharyngioma, Gliomas (e.g., brain stem glioma, ependymoma, optical nerve glioma, subependymoma), Medulloblastoma, Meningioma, Metastatic brain tumors, Oligodendroglioma, Pituitary Tumors, Primitive neuroectodermal (PNET), and Schwannoma.

[000457] In some embodiments, the neurological disorders may be functional neurological disorders with motor and/or sensory symptoms which have neurological origin in the CNS. As non-limiting examples, functional neurological disorders may be chronic pain, seizures, speech problems, involuntary movements, and sleep disturbances.

[000458] In some embodiments, the neurological disorders may be white matter disorders (a group of diseases that affects nerve fibers in the CNS) including but not limited to, Pelizaeus-Merzbacher disease, Hypomyelination with atrophy of basal ganglia and cerebellum, Aicardi-Goutières syndrome, Megalencephalic leukoencephalopathy with subcortical cysts, Congenital muscular dystrophies, Myotonic dystrophy, Wilson disease, Lowe syndrome, Sjögren-Larsson syndrome, PIBD or Tay syndrome, Cockayne's disease, erebrotendinous xanthomatosis, Zellweger syndrome, Neonatal adrenoleukodystrophy, Infantile Refsum disease, Zellweger-like syndrome, Pseudo-Zellweger syndrome, Pseudo-neonatal adrenoleukodystrophy, Bifunctional protein deficiency, X-linked adrenoleukodystrophy and adrenomyeloneuropathy and Refsum disease.

[000459] In some embodiments, the neurological disorders may be lysosomal storage disorders (LSDs) caused by the inability of cells in the CNS to break down metabolic end products, including but not limited to Niemann-Pick disease (a LSD resulting from inherited deficiency in acid sphingomyelinase (ASM); Metachromatic leukodystrophy (MLD) (a LSD characterized by accumulation of sulfatides in glial cells and neurons, the result of an inherited deficiency of arylsulfatase A (ARSA)); Globoid-cell leukodystrophy (GLD) (a LSD caused by mutations in galactosylceramidase); Fabry disease (a LSD caused by mutations in the alpha-galactosidase A (GLA) gene); Gaucher disease (caused by mutations in the beta-glucocerebrosidase (GBA) gene); GM1/GM2 gangliosidosis; Mucopolysaccharidoses disorder; Pompe disease; and Neuronal ceroid lipofuscinosis.

[000460] In another embodiment, the neurological disease, disorder and/or condition is Friedreich's Ataxia. In one embodiment, the AAV particle used to treat Friedreich's Ataxia

comprises a nucleic acid sequence such as, but not limited to, SEQ ID NO: 979 or a fragment or variant thereof, wherein the payload is replaced by Frataxin or any other payload known in the art for treating Friedreich's Ataxia.

[000461] In another embodiment, the neurological disease, disorder and/or condition is Amyotrophic lateral sclerosis (ALS). In one embodiment the AAV particle used to treat ALS comprises a nucleic acid sequence such as, but not limited to, SEQ ID NO: 979 or a fragment or variant thereof, wherein the payload is replaced by replaced by an shRNA, miRNA, siRNA, RNAi for SOD1 or any other payload known in the art for treating ALS.

[000462] In another embodiment, the neurological disease, disorder and/or condition is Huntington's disease. In one embodiment the AAV particle used to treat Huntington's disease comprises a nucleic acid sequence such as, but not limited to, SEQ ID NO: 979 or a fragment or variant thereof, wherein the payload is replaced by replaced by an shRNA, miRNA, siRNA, RNAi for Htt or any other payload known in the art for treating Huntington's disease.

[000463] In another embodiment, the neurological disease, disorder or condition is spinal muscular atrophy (SMA). In another embodiment, the neurological disease, disorder and/or condition is Friedreich's Ataxia. In one embodiment the AAV particle used to treat SMN comprises a nucleic acid sequence such as, but not limited to, SEQ ID NO: 979 or a fragment or variant thereof, wherein the payload is replaced by Frataxin or any other payload known in the art for treating SMA.

Parkinson's Disease

[000464] In one embodiment, the neurological disease, disorder and/or condition is Parkinson's disease. In one embodiment the AAV particle used to treat Parkinson's disease comprises a payload such as, but not limited to, SEQ ID NO: 979 or a fragment or variant thereof.

[000465] In one embodiment, the subject is a human patient who has a minimum motor score of about 30 to a maximum score of about 100, about 10 to a maximum score of about 100, about 20 to a maximum score of about 100 in the Unified Parkinson's Disease Rating Scale.

[000466] In one embodiment, the subject has been diagnosed with Parkinson's disease within the past 5 years prior to treatment with the compositions described herein. As a non-limiting example, the subject may have been diagnosed with Parkinson's disease within a week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 14 months,

15 months, 16 months, 17 months, 18 months, 1 year, 2 years, 3 years, 4 years or less than 5 years prior to treatment with the compositions described herein.

[000467] In one embodiment, the subject has been diagnosed with Parkinson's disease between 5 and 10 years prior to treatment with the compositions described herein. As a non-limiting example, the subject may have been diagnosed with Parkinson's disease 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 years prior to treatment with the compositions described herein.

[000468] In one embodiment, the subject has been diagnosed with Parkinson's disease more than 10 years prior to treatment with the compositions described herein. As a non-limiting example, the subject may have been diagnosed with Parkinson's disease 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24 or more than 24 years prior to treatment with the compositions described herein.

[000469] In one embodiment, a subject is 50-65 years of age. As a non-limiting example, the subject is 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, or 65 years of age. As a non-limiting example, the subject is 50 years of age. As a non-limiting example, the subject is 51 years of age. As a non-limiting example, the subject is 52 years of age. As a non-limiting example, the subject is 53 years of age. As a non-limiting example, the subject is 54 years of age. As a non-limiting example, the subject is 55 years of age. As a non-limiting example, the subject is 56 years of age. As a non-limiting example, the subject is 57 years of age. As a non-limiting example, the subject is 58 years of age. As a non-limiting example, the subject is 59 years of age. As a non-limiting example, the subject is 60 years of age. As a non-limiting example, the subject is 61 years of age. As a non-limiting example, the subject is 62 years of age. As a non-limiting example, the subject is 63 years of age. As a non-limiting example, the subject is 64 years of age. As a non-limiting example, the subject is 65 years of age.

[000470] In one embodiment, a subject is 30 to 50 years of age. As a non-limiting example, the subject is 30 years of age. As a non-limiting example, the subject is 31 years of age. As a non-limiting example, the subject is 32 years of age. As a non-limiting example, the subject is 33 years of age. As a non-limiting example, the subject is 34 years of age. As a non-limiting example, the subject is 35 years of age. As a non-limiting example, the subject is 36 years of age. As a non-limiting example, the subject is 37 years of age. As a non-limiting example, the subject is 38 years of age. As a non-limiting example, the subject is 39 years of age. As a non-limiting example, the subject is 40 years of age. As a non-limiting example, the subject is 41 years of age. As a non-

limiting example, the subject is 42 years of age. As a non-limiting example, the subject is 43 years of age. As a non-limiting example, the subject is 44 years of age. As a non-limiting example, the subject is 45 years of age. As a non-limiting example, the subject is 46 years of age. As a non-limiting example, the subject is 47 years of age. As a non-limiting example, the subject is 48 years of age. As a non-limiting example, the subject is 49 years of age. As a non-limiting example, the subject is 50 years of age.

[000471] In one embodiment, a subject is 65 to 85 years of age. As a non-limiting example, the subject is 65 years of age. As a non-limiting example, the subject is 66 years of age. As a non-limiting example, the subject is 67 years of age. As a non-limiting example, the subject is 68 years of age. As a non-limiting example, the subject is 69 years of age. As a non-limiting example, the subject is 70 years of age. As a non-limiting example, the subject is 71 years of age. As a non-limiting example, the subject is 72 years of age. As a non-limiting example, the subject is 73 years of age. As a non-limiting example, the subject is 74 years of age. As a non-limiting example, the subject is 75 years of age. As a non-limiting example, the subject is 76 years of age. As a non-limiting example, the subject is 77 years of age. As a non-limiting example, the subject is 78 years of age. As a non-limiting example, the subject is 79 years of age. As a non-limiting example, the subject is 80 years of age. As a non-limiting example, the subject is 81 years of age. As a non-limiting example, the subject is 82 years of age. As a non-limiting example, the subject is 83 years of age. As a non-limiting example, the subject is 84 years of age. As a non-limiting example, the subject is 85 years of age.

[000472] In one embodiment, a subject has seen a change in motor symptoms such as tremors and movements prior to administration of the composition described herein. Non-limiting examples of tremors include, unilateral or bilateral mild tremors, bilateral or midline moderate tremors or intractable tremors. Non-limiting examples of movements include mild bradykinesia, moderate bradykinesia, severe bradykinesia and morning akinesia.

[000473] In one embodiment, a subject may have changes in balance such as, but not limited to, impaired balance, impaired righting reflexes, significant balance disorder or falling.

[000474] In one embodiment, a subject may have a reduced quality of life. As a non-limiting example, the subject may have a moderate impact on their quality of life such as experiencing some limitations to activities of daily living. As another non-limiting example, the subject may have a quality of life which has been diminished by illness.

[000475] In one embodiment, a subject has seen a change in non-motor symptoms prior to administration of the composition described herein. As a non-limiting example, the subject may have mild to moderate cognitive impairment prior to administration to the composition described herein. As another non-limiting example, the subject may have significant cognitive impairment such as dementia which may also include behavioral disturbances such as hallucinations.

[000476] In one embodiment, a subject may have a satisfactory response with limited fluctuations on one or more dopaminergic medications prior to administration of the compositions described herein.

[000477] In one embodiment, a subject may have motor fluctuations causing mild to moderate disability on one or more dopaminergic medications prior to administration of the compositions described herein.

[000478] In one embodiment, a subject may have medically refractory motor fluctuations consisting of “wearing off” and/or levodopa-induced dyskinesias causing significant disability prior to administration of the compositions described herein.

[000479] In one embodiment, a subject may have mild symptoms associated with Parkinson’s disease such as, but not limited to, no cognitive impairment, diagnosed within the past 5 years, satisfactory response with limited fluctuations on one or more dopaminergic medications, unilateral or bilateral mild tremors, little to no impact on the quality of life, and/or no balance impairment.

[000480] In one embodiment, a subject may have moderate symptoms associated with Parkinson’s disease such as, but not limited to, mild to moderate cognitive impairment, first signs of impaired balance and righting reflexes, motor fluctuations causing mild-moderate disability on one or more dopaminergic medications, diagnosed within the past 5 to 10 years, bilateral or midline moderate tremors, moderate bradykinesia and/or subject experiencing some limitations to activities of daily living.

[000481] In one embodiment, a subject may have advanced symptoms associated with Parkinson’s disease such as, but not limited to, being diagnosed with Parkinson’s more than 10 years, medium refractory motor fluctuations wearing off and/or levodopa-induced dyskinesia causing significant disability, intractable tremors, significant balance disorder and/or falling, significant cognitive impairment (such as dementia with or without behavioral disturbances), severe bradykinesia, quality of life markedly diminished by illness and/or morning akinesia.

[000482] In one embodiment, a subject has been referred to a movement disorder specialist (MDS) but has not undergone deep brain stimulation.

[000483] In one embodiment, a subject is using DUOPATM in combination with the compositions described herein. As a non-limiting example, the subject may have success with using DUOPATM alone. As a non-limiting example, the subject may not have any success or limited success using DUOPATM alone.

[000484] In one embodiment, a subject is one who was a candidate for surgical intervention including, but not limited to, deep-brain stimulation. As a non-limiting example, deep-brain stimulation was suggested due to disabling motor complications despite treatment with optimal anti-Parkinsonian medication.

[000485] In one embodiment, a subject has an average on-time of 7.5-14 hours based on the subject diary. As a non-limiting example, the average on-time is 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, or 14 hours. In one embodiment, a subject has an average on-time of 10.5 hours based on the subject diary.

[000486] In one embodiment, a subject experiences about 1.5 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.5 hours more of diary on-time 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome.

[000487] In one embodiment, a subject experiences about 2.2 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 2.2 hours more of diary on-time 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000488] In one embodiment, a subject experiences about 4 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 4 hours more of diary on-time 6

months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000489] In one embodiment, a subject experiences about 1.6 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 12 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.6 hours more of diary on-time 12 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000490] In one embodiment, a subject experiences about 3.3 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 12 months after administration of the present invention. As a non-limiting example, a subject experiences about 3.3 hours more of diary on-time 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000491] In one embodiment, a subject experiences about 4 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 12 months after administration of the present invention. As a non-limiting example, a subject experiences about 4 hours more of diary on-time 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000492] In one embodiment, a subject experiences about 2.3 hours more of diary on-time (without troublesome dyskinesia), as compared to baseline, 24 months after administration of the present invention. As a non-limiting example, a subject experiences about 2.3 hours more of diary on-time 24 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000493] In one embodiment, a subject has an average off-time of 2-7 hours based on the subject diary. As a non-limiting example, the average off-time is 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, or 7. In one embodiment, a subject has an average off-time of 4.6 hours based on the subject diary.

[000494] In one embodiment, a subject experiences about 1.3 hours less of diary off-time, as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.3 hours less of diary off-time 6 months after administration

of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome.

[000495] In one embodiment, a subject experiences about 1.1 hours less of diary off-time, as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.1 hours less of diary off-time 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000496] In one embodiment, a subject experiences about 0.8 hours less of diary off-time, as compared to baseline, 6 months after administration of the present invention. As a non-limiting example, a subject experiences about 0.8 hours less of diary off-time 6 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000497] In one embodiment, a subject experiences about 2.3 hours less of diary off-time, as compared to baseline, 12 months after administration of the present invention. As a non-limiting example, a subject experiences about 2.3 hours less of diary off-time 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000498] In one embodiment, a subject experiences about 1.4 hours less of diary off-time, as compared to baseline, 12 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.4 hours less of diary off-time 12 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000499] In one embodiment, a subject experiences about 1.8 hours less of diary off-time, as compared to baseline, 24 months after administration of the present invention. As a non-limiting example, a subject experiences about 1.8 hours less of diary off-time 24 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000500] In one embodiment, a subject experiences 10% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 10% less diary off-time 12 months after administration of the present invention.

[000501] In one embodiment, a subject experiences 20% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 20% less diary off-time 12 months after administration of the present invention.

[000502] In one embodiment, a subject experiences 30% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 30% less diary off-time 12 months after administration of the present invention.

[000503] In one embodiment, a subject experiences 40% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 40% less diary off-time 12 months after administration of the present invention.

[000504] In one embodiment, a subject experiences 50% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 50% less diary off-time 12 months after administration of the present invention.

[000505] In one embodiment, a subject experiences 60% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 60% less diary off-time 12 months after administration of the present invention.

[000506] In one embodiment, a subject experiences 70% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 70% less diary off-time 12 months after administration of the present invention.

[000507] In one embodiment, a subject experiences 80% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 80% less diary off-time 12 months after administration of the present invention.

[000508] In one embodiment, a subject experiences 90% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 90% less diary off-time 12 months after administration of the present invention.

[000509] In one embodiment, a subject experiences 95% less diary off-time 6 months after administration of the present invention. In one embodiment, a subject experiences 95% less diary off-time 12 months after administration of the present invention.

[000510] In one embodiment, a subject's UPDRS-3 (or UPDRS-III) medication score is evaluated prior to administration of the present invention. As a non-limiting example, the subject's UPDRS-3 (or UPDRS-III) medication score prior to administration of the present invention is between 1-40, 1-10, 1-15, 1-20, 1-25, 1-30, 1-35, 1-40, 5-10, 5-15, 5-20, 5-25, 5-30, 5-35, 5-40, 10-15, 10-20, 10-25,

10-30, 10-35, 10-40, 15-20, 15-25, 15-30, 15-35, 15-40, 20-25, 20-30, 20-35, 20-40, 25-30, 25-35, 25-40, 30-35, 30-40, or 35-40. As a non-limiting example, the subject's UPDRS-3 (or UPDRS-III) medication score prior to administration of the present invention is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40. As a non-limiting example, the subject's UPDRS-3 (or UPDRS-III) medication score prior to administration of the present invention is 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15. As a non-limiting example, the subjects UPDRS-3 medication score prior to administration of the present invention is 13.5.

[000511] In one embodiment, a subject's UPDRS-3 (or UPDRS-III) medication score is reduced after administration of the present invention.

[000512] A subject's UPDRS-3 (or UPDRS-III) medication score may be reduced by a percentage such as, but not limited to, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more than 95%. As a non-limiting example, a subject's UPDRS-3 score is reduced 10% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 20% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 30% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 40% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 50% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 60% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 70% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 80% after administration of the present invention. As a non-limiting example, a subject's UPDRS-3 score is reduced 90% after administration of the present invention.

[000513] A subject's UPDRS-3 (or UPDRS-III) medication score may change by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10,

10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points. As a non-limiting example, a subject's UPDRS-3 score is changed by 0.4 points. As a non-limiting example, a subject's UPDRS-3 score is changed by 1.6 points. As a non-limiting example, a subject's UPDRS-3 score is changed by 1.8 points. As a non-limiting example, a subject's UPDRS-3 score is changed by 8.6 points. As a non-limiting example, a subject's UPDRS-3 score is changed by 9.6 points.

[000514] A subject's UPDRS-3 (or UPDRS-III) medication score may increase by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points. As a non-limiting example, a subject's UPDRS-3 score is increased by 0.4 points. As a non-limiting example, a subject's UPDRS-3 score is increased by 1.6 points. As a non-limiting example, a subject's UPDRS-3 score is increased by 1.8 points. As a non-limiting example, a subject's UPDRS-3 score is increased by 8.6 points. As a non-limiting example, a subject's UPDRS-3 score is increased by 9.6 points.

[000515] A subject's UPDRS-3 (or UPDRS-III) medication score may decrease by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points. As a non-limiting example, a subject's UPDRS-3 score is decreased by 0.4 points. As a non-limiting example, a subject's UPDRS-3 score is decreased by 1.6 points. As a non-limiting example, a subject's UPDRS-3 score is decreased by 1.8 points. As a non-limiting example, a subject's UPDRS-3 score

is decrease by 8.6 points. As a non-limiting example, a subject's UPDRS-3 score is decreased by 9.6 points.

[000516] In one embodiment, a subject's UPDRS-3 (or UPDRS-III) medication score is reduced by 8.6 at 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome.

[000517] In one embodiment, a subject's UPDRS-3 (or UPDRS-III) medication score is reduced by 9.6 at 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000518] In one embodiment, a subject's UPDRS-3 (or UPDRS-III) medication score is reduced by 9.6 at 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000519] In one embodiment, a subject's average amount of Parkinson's disease medication was about 1500 mg per day prior to administration of the present invention. As a non-limiting example, the Parkinson's disease medication is levodopa.

[000520] In one embodiment, a subject's UPDRS-II score is evaluated prior to administration of the present invention. The UPDRS-II score of a subject prior to administration of the present invention is between 20 and 50, such as, but not limited to, 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, and 50.

[000521] A subject's UPDRS-2 (or UPDRS-II) score may change by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points.

[000522] A subject's UPDRS-2 (or UPDRS-II) score may increase by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1,

10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points.

[000523] A subject's UPDRS-2 (or UPDRS-II) score may decrease by 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, or 15 points. As a non-limiting example, a 3.6 point reduction is seen 12 months after administration with the present invention. As a non-limiting example, a 3.6 point reduction is seen 6 months after administration with the present invention.

[000524] In one embodiment, a subject's UPDRS-II score is decreased by 2 to 4 points after administration of the present invention as compared to the UPDRS-II score prior to administration.

[000525] In one embodiment, a subject's UPDRS-II score is decreased by 2 to 3 points 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome, as compared to the UPDRS-II medication score prior to administration.

[000526] In one embodiment, a subject's UPDRS-II score is decreased by 2 to 3 points 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome, as compared to the UPDRS-II medication score prior to administration.

[000527] In one embodiment, a subject's UPDRS-II score is decreased by 3 to 4 points 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome, as compared to the UPDRS-II medication score prior to administration.

[000528] In one embodiment, the present invention is used to improve a subject's motor function.

[000529] In one embodiment, the present invention is used to control a subject's motor function and improve their quality of life.

[000530] In one embodiment, the present invention is used to reduce the dosage of Parkinson's medication a subject needs to take to improve a subject's motor function.

[000531] In one embodiment, a single administration of the present invention into the putamen of a subject provides improved motor function as compared to motor function prior to treatment.

[000532] In one embodiment, a single administration of the present invention in to the putamen of a subject provides improved motor function and a reduction in the amount of levodopa the subject requires to manage symptoms.

[000533] In one embodiment, a single administration of the present invention in to the putamen of a subject provides improved motor function and a reduction in the amount of dopaminergic medication the subject requires to manage symptoms.

[000534] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 10-50% after administration of the present invention. As a non-limiting example, the reduction is seen 6 months after administration of the present invention. As a non-limiting example, the reduction is seen 12 months after administration of the present invention.

[000535] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 10-20% after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 10%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 11%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 12%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 13%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 14%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 15%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 16%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 17%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 18%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 19%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 20%.

[000536] In one embodiment, a 14% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000537] In one embodiment, a 10% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000538] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 20-30% after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 20%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 21%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 22%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 23%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 24%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 25%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 26%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 27%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 28%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 29%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 30%.

[000539] In one embodiment, a 27% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000540] In one embodiment, a 28% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000541] In one embodiment, a 29% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000542] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 30-40% after administration of the present invention. As a non-limiting

example, the reduction of Parkinson's medication (e.g., Levodopa) is 30%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 31%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 32%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 33%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 34%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 35%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 36%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 37%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 38%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 39%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 40%.

[000543] In one embodiment, a 34% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000544] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 40-50% after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 40%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 41%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 42%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 43%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 44%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 45%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 46%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 47%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 48%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 49%. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 50%.

[000545] In one embodiment, a 34% reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after

administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome.

[000546] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 108-641 mg after administration of the present invention. As a non-limiting example, the reduction is seen 6 months after administration of the present invention. As a non-limiting example, the reduction is seen 12 months after administration of the present invention.

[000547] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 108-339 mg after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 108 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 134 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 159 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 154 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 208 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 231 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 254 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 276 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 298 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 319 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 339 mg.

[000548] In one embodiment, a 208 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000549] In one embodiment, a 108 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000550] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 339-505 mg after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 339 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 358 mg. As a non-

limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 377 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 396 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 413 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 430 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 446 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 462 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 477 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 491 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 505 mg.

[000551] In one embodiment, a 462 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000552] In one embodiment, a 477 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000553] In one embodiment, a 491 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 12 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000554] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 505-606 mg after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 505 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 518 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 530 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 542 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 553 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 563 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 573 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 582 mg. As a non-

limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 591 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 599 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 606 mg.

[000555] In one embodiment, a 553 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000556] In one embodiment, the amount the daily dose of Parkinson's medication (e.g., Levodopa) is reduced by 606-641 mg after administration of the present invention. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 606 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 612 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 618 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 623 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 628 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 632 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 635 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 637 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 639 mg. As a non-limiting example, the reduction of Parkinson's medication (e.g., Levodopa) is 641 mg.

[000557] In one embodiment, a 553 mg reduction in the amount of the daily dose of Parkinson's medication (e.g., Levodopa) required by a subject to manage symptoms occurs 6 months after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 4.5×10^{12} vector genome.

[000558] In one embodiment, the putaminal AADC enzyme activity is increased in a subject after administration with the present invention. As a non-limiting example, the increase is seen for at least 6 months relative to the baseline.

[000559] In one embodiment, the putaminal AADC enzyme activity is increased by 10-20% in a subject after administration of the present invention. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 10%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 11%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 12%. As a non-limiting example, the increase in

putaminal AADC enzyme activity is about 13%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 14%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 15%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 16%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 17%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 18%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 19%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 20%.

[000560] In one embodiment, the putaminal AADC enzyme activity is increased by about 13% in a subject after administration of the present invention at a dose volume of up to 450 uL per putamen and a total dose of 7.5×10^{11} vector genome.

[000561] In one embodiment, the putaminal AADC enzyme activity is increased by 50-60% in a subject after administration of the present invention. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 50%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 51%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 52%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 53%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 54%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 55%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 56%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 57%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 58%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 59%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 60%.

[000562] In one embodiment, the putaminal AADC enzyme activity is increased by about 56% in a subject after administration of the present invention at a dose volume of up to 900 uL per putamen and a total dose of 1.5×10^{12} vector genome.

[000563] In one embodiment, the putaminal AADC enzyme activity is increased by 70-85% in a subject after administration of the present invention. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 70%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 71%. As a non-limiting example, the increase in

putaminal AADC enzyme activity is about 72%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 73%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 74%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 75%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 76%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 77%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 78%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 79%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 80%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 81%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 82%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 83%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 84%. As a non-limiting example, the increase in putaminal AADC enzyme activity is about 85%.

[000564] In one embodiment, the putaminal AADC enzyme activity is increased by about 79% in a subject after administration of the present invention at a dose volume of up to 900 μ L per putamen and a total dose of 4.5×10^{12} vector genome.

[000565] In one embodiment, the dopamine level of a subject increased after administration of the present invention. As a non-limiting example, the amount of dopamine increased by 10-20%, 15-25%, 20-30%, 25-35%, 30-40%, 35-45%, 40-50%, 45-55%, 50-60%, 55-65%, 60-70%, 65-75%, 70-80%, 75-85%, 80-90%, 85-95%, 90-100%, or 95-100%.

Circadian Rhythm and Sleep-Wake Cycles

[000566] Circadian rhythms are physical, mental and behavioral changes that tend to follow a 24 hour cycle. Circadian rhythms can influence sleep-wake cycles, hormone release, body temperature and other bodily functions. Changes in the circadian rhythm can cause conditions and/or disorder such as, but not limited to sleep disorders (e.g., insomnia), depression, bipolar disorder, seasonal affective disorder, obesity and diabetes.

[000567] In one embodiment, the AAV particles described herein may be used to treat insomnia.

[000568] The sleep-wake cycle comprises periods of sleep and periods of wake. Generally, in a 24 hour period the total hours of sleep are less than the total hours of wakefulness. As a non-limiting example, the sleep-wake cycle comprises 7-9 hours of sleep and 15-17 hours of wakefulness. As a

non-limiting example, the sleep-wake cycle comprises 8 hours of sleep and 16 hours of wakefulness. As a non-limiting example, the sleep-wake cycle comprises 8-10 hours of sleep and 14-16 hours of wakefulness.

[000569] In one embodiment, the sleep-wake cycle of a subject is improved by administering to the subject the AAV particles described herein.

[000570] In one embodiment, the sleep-wake cycle of a subject is regulated by administering to the subject the AAV particles described herein. As a non-limiting example, the regulation may be the correction of more periods of sleep occurring at night and less periods of sleep occurring

[000571] In one embodiment, the sleep-wake cycle of a subject administered the AAV particles described herein improves as compared to the sleep-wake cycle of the subject prior to administration of the AAV particles. As a non-limiting example, the subject has an increased period of sleep and a decreased period of wakefulness. As another non-limiting example, the subject has a decreased period of sleep and an increased period of wakefulness.

[000572] In one embodiment, the sleep-wake cycle of a subject administered the AAV particles described herein is regulated as compared to the sleep-wake cycle of the subject prior to administration of the AAV particles. As a non-limiting example, the length of the periods of sleep and the periods of wakefulness may be about the same (e.g., +/- 1 hour) for at least 2 days. As another non-limiting example, the length of the periods of sleep and the periods of wakefulness if a 24 hours period may be within 10 minutes, 15 minutes, 20 minutes, 25 minutes, 30 minutes, 35 minutes, 40 minutes, 45 minutes, 50 minutes, 55 minutes, 1 hour, 1.5 hours, or 2 hours of the previous 24 hour period.

[000573] In one embodiment, the amount of rapid eye movement (REM) sleep a subject experiences in a 24 hour period is altered after the subject is administered the AAV particles described herein. REM sleep is generally considered an active period of sleep marked by intense brain activity where brain waves are fast and desynchronized. An adult, on average, spends about 20-25% of their total daily sleep period in REM sleep. As a non-limiting example, the amount of REM sleep is decreased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of REM sleep is decreased by 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%. As a non-limiting example, the amount of REM sleep is increased by 1%, 2%, 3%, 4%, 5%, 6%,

7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of REM sleep is increased by 1-5%, 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%.

[000574] In one embodiment, the amount of non-REM (NREM) sleep a subject experiences in a 24 hour period is altered after the subject is administered the AAV particles described herein. NREM sleep is generally characterized by a reduction in physiological activity since as the brain waves, measured by EEG, get slower and have greater amplitude. NREM has four stages: Stage 1 is the time of drowsiness or transition from being awake to falling asleep where the brain waves and muscle activity begin to slow; Stage 2 is a period of light sleep during which eye movements stop and brain waves become slower with occasional bursts of rapid waves (sometimes called sleep spindles); Stage 3 and Stage 4 (collectively referred to as slow wave sleep) are characterized by the presence of slow brain waves (delta waves) interspersed with smaller faster waves where there are no eye movements. An adult, on average, spends about 75-80% of their total daily sleep period in NREM sleep with about half of their total daily sleep time in NREM stage 2 sleep.

[000575] In one embodiment, the amount of NREM sleep a subject experiences is altered after the subject is administered the AAV particles described herein. As a non-limiting example, the amount of NREM sleep is decreased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM sleep is decreased by 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%. As a non-limiting example, the amount of NREM sleep is increased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM sleep is increased by 1-5%, 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%.

[000576] In one embodiment, the amount of NREM Stage 1 sleep a subject experiences is altered after the subject is administered the AAV particles described herein. As a non-limiting example, the amount of NREM Stage 1 sleep is decreased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 1 sleep is decreased by 1-10%, 5-10%, 5-

15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%. As a non-limiting example, the amount of NREM Stage 1 sleep is increased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 1 sleep is increased by 1-5%, 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%.

[000577] In one embodiment, the amount of NREM Stage 2 sleep a subject experiences is altered after the subject is administered the AAV particles described herein. As a non-limiting example, the amount of NREM Stage 2 sleep is decreased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 2 sleep is decreased by 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%. As a non-limiting example, the amount of NREM Stage 2 sleep is increased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 2 sleep is increased by 1-5%, 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%.

[000578] In one embodiment, the amount of NREM Stage 3 and 4 sleep a subject experiences is altered after the subject is administered the AAV particles described herein. As a non-limiting example, the amount of NREM Stage 3 and 4 sleep is decreased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 3 and 4 sleep is decreased by 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%. As a non-limiting example, the amount of NREM Stage 3 and 4 sleep is increased by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65% or more than 65%. As a non-limiting example, the amount of NREM Stage 3 and 4 sleep is increased by 1-5%, 1-10%, 5-10%, 5-15%, 10-15%, 15-20%, 15-25%, 20-25%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 40-50% or 40-60%.

[000579] In one embodiment, periods of NREM and REM cycles are more consistent in a subject after the subject is administered the AAV particles described herein. Generally NREM and REM cycles alternate every 90 to 110 minutes four to six times per night.

V. KITS AND DEVICES

Kits

[000580] In one embodiment, the invention provides a variety of kits for conveniently and/or effectively carrying out methods of the present invention. Typically kits will comprise sufficient amounts and/or numbers of components to allow a user to perform multiple treatments of a subject(s) and/or to perform multiple experiments.

[000581] Any of the AAV particles of the present invention may be comprised in a kit. In some embodiments, kits may further include reagents and/or instructions for creating and/or synthesizing compounds and/or compositions of the present invention. In some embodiments, kits may also include one or more buffers. In some embodiments, kits of the invention may include components for making protein or nucleic acid arrays or libraries and thus, may include, for example, solid supports.

[000582] In some embodiments, kit components may be packaged either in aqueous media or in lyophilized form. The container means of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which a component may be placed, and preferably, suitably aliquoted. Where there is more than one kit component, (labeling reagent and label may be packaged together), kits may also generally contain second, third or other additional containers into which additional components may be separately placed. In some embodiments, kits may also comprise second container means for containing sterile, pharmaceutically acceptable buffers and/or other diluents. In some embodiments, various combinations of components may be comprised in one or more vial. Kits of the present invention may also typically include means for containing compounds and/or compositions of the present invention, e.g., proteins, nucleic acids, and any other reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which desired vials are retained.

[000583] In some embodiments, kit components are provided in one and/or more liquid solutions. In some embodiments, liquid solutions are aqueous solutions, with sterile aqueous solutions being particularly preferred. In some embodiments, kit components may be provided as dried powder(s). When reagents and/or components are provided as dry powders, such powders may be reconstituted

by the addition of suitable volumes of solvent. In some embodiments, it is envisioned that solvents may also be provided in another container means. In some embodiments, labeling dyes are provided as dried powders. In some embodiments, it is contemplated that 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900, 1000 micrograms or at least or at most those amounts of dried dye are provided in kits of the invention. In such embodiments, dye may then be resuspended in any suitable solvent, such as DMSO.

[000584] In some embodiments, kits may include instructions for employing kit components as well the use of any other reagent not included in the kit. Instructions may include variations that may be implemented.

Devices

[000585] In some embodiments, AAV particles of the present invention may be combined with, coated onto or embedded in a device. Devices may include, but are not limited to stents, pumps, and/or other implantable therapeutic device. Additionally AAV particles may be delivered to a subject while the subject is using a compression device such as, but not limited to, a compression device to reduce the chances of deep vein thrombosis (DVT) in a subject.

[000586] The present invention provides for devices which may incorporate AAV particles. These devices contain in a stable formulation the AAV particles which may be immediately delivered to a subject in need thereof, such as a human patient.

[000587] Devices for administration may be employed to deliver the AAV particles of the present invention according to single, multi- or split-dosing regimens taught herein.

[000588] Method and devices known in the art for multi-administration to cells, organs and tissues are contemplated for use in conjunction with the methods and compositions disclosed herein as embodiments of the present invention. These include, for example, those methods and devices having multiple needles, hybrid devices employing for example lumens or catheters as well as devices utilizing heat, electric current or radiation driven mechanisms.

[000589] In some embodiments, AAV particles of the present invention may be delivered using a device such as, but not limited to, a stent, a tube, a catheter, a pipe, a straw, needle and/or a duct. Methods of using these devices are described herein and are known in the art.

[000590] In one embodiment, the AAV particles of the present invention may be administered to a subject using delivery systems which integrate image guided therapy and integrate imaging such as, but not limited to, laser, MRgFUS, endoscopic and robotic surgery devices.

[000591] In one embodiment, the AAV particles of the present invention may be administered to a subject using the CLEARPOINT® neuro intervention system by MRI Interventions, Inc. The CLEARPOINT® neuro intervention system may be used alone or in combination with any of the other administration methods and devices described herein. The CLEARPOINT® neuro intervention system helps to provide stereotactic guidance in the placement and operation of instruments or devices during the planning and operation of neurological procedures.

[000592] In one embodiment, the AAV particles of the present invention may be administered to a subject using the NEUROMATE® stereotactic robot system by Renishaw PLC. The NEUROMATE® system may be used alone or in combination with any of the other administration methods and devices described herein. As a non-limiting example, the NEUROMATE® system may be used with head holders, CT image localizers, frame attachments, remote controls and software.

[000593] In one embodiment, the AAV particles of the present invention may be administered to a subject using the Elekta MICRODRIVE™ device by Elekta AB. The MICRODRIVE™ device may be used alone or in combination with any of the other administration methods and devices described herein. As a non-limiting example, the MICRODRIVE™ device may be used to position electrodes (e.g., for micro electrode recording (MER), macro stimulation and deep brain stimulation (DBS) electrode implantation), implantation of catheters, tubes or DBS electrodes using cross-hair and A-P holders to verify position, biopsies, injections and aspirations, brain lesioning, endoscope guidance and GAMMA KNIFE® radiosurgery.

[000594] In one embodiment, the AAV particles of the present invention may be administered to a subject using the AXIIS® stereotactic miniframe by MONTERIS® Medical, Inc. The AXIIS® stereotactic miniframe may be used alone or in combination with any of the other administration methods and devices described herein. The AXIIS® stereotactic miniframe is a trajectory alignment device which may be used for laser coagulation, biopsies, catheter placement, electrode implant, endoscopy, and clot evacuation. The miniframe allows for 360 degree interface and provides access to multiple intracranial targets with a simple adjustment. Further, the miniframe is compatible with MRI.

[000595] In one embodiment, the AAV particles of the present invention may be administered to a subject using the INTEGRA™ CRW® system by Integra LifeSciences Corporation. The INTEGRA™ CRW® system may be used alone or in combination with any of the other administration methods and devices described herein. The CRW® system may be used for various

applications such as, but not limited to, stereotactic surgery, microsurgery, catheterization and biopsy. The CRW® system is designed to provide accuracy to those who use the system (e.g., thumb lock screws, Vernier scaling, double bolt fixation, and a solid frame).

[000596] In one embodiment, the AAV particles of the present invention may be administered to a subject using the EPOCH® solution system by Stereotaxis, Inc. which may include the NIOBE® ES magnetic navigation system, the VDRIVE® robotic navigation system and/or the ODYSSEY® information solution (all by Stereotaxis, Inc.). The EPOCH® solution system may be used alone or in combination with any of the other administration methods and devices described herein. As a non-limiting example, the NIOBE® ES magnetic navigation system may be used to accurately contact a subject. As another non-limiting example the NIOBE® ES magnetic system may be used with the VDRIVE® robotic navigation system to provide precise movement and stability.

[000597] In one embodiment, the AAV particles of the present invention may be administered to a subject using a NeuroStation workstation which uses frameless stereotactic methods to provide image-guidance for applications such as, but not limited to, surgical planning, biopsies, craniotomies, endoscopy, intra-operative ultrasound and radiation therapy.

[000598] In one embodiment, the AAV particles of the present invention may be administered to a subject using a robotic stereotaxis system such as, but not limited to the device described in US Patent No. 5,078,140, the contents of which are herein incorporated by reference in its entirety. The robotic arm of the device may be used to precisely orient the surgical tools or other implements used to conduct a procedure.

[000599] In one embodiment, the AAV particles of the present invention may be administered to a subject using an automatic delivery system such as, but not limited to the device described in US Patent No. 5,865,744, the contents of which are herein incorporated by reference in its entirety. Based on the images gathered by the delivery system, the computer adjusts the administration of the needle to be the appropriate depth for the particular subject.

[000600] In one embodiment, the AAV particles of the present invention may be administered to a subject who is simultaneously using during administration, and/or uses for a period of time before and/or after administration a compression device such as, but not limited to, a compression device which reduces the chances of deep vein thrombosis (DVT) in a subject. The compression device may be used for at least 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, or more than 8 hours before a subject is administered the

AAV particles. The compression device may be used for at least 5 minutes, 15 minutes, 30 minutes, 45 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks or a month after the AAV particles are administered. As a non-limiting example, the compression device is used simultaneously during the procedure of the delivery of the AAV particles. As another non-limiting example, the compression device is used before the administration of the AAV particles. As another non-limiting example, the compression device is used after administration of the AAV particles. As another non-limiting example, the compression device is used before, during and after administration of the AAV particles.

[000601] Non-limiting examples, of compression devices include ActiveCare +S.F.T. intermittent compression device, ActiveCare +S.F.T. pneumatic compression device, DVTlite's Venowave, KCI system compression pump, Aircast VenaFlow system, SCD Express Compression System or Bio Compression Systems, Inc. pneumatic compression therapy equipment (e.g., the pump may be selected from Model SC-2004, Model SC-2004-FC, Model SC-3004, Model SC-3004-FC, Model SC-2008, Model SC-2008-DL, Model SC-3008-T, the BioCryo system, Model IC-BAP-DL or multi-flo DVT combo IC_1545-DL and the garment used with the pump may be a 4 chamber, 8 chamber, BioCryo, Multi-Flo or BioArterial garment).

[000602] In one embodiment, the AAV particles may delivered to a subject using a device to deliver the AAV particles and a head fixation assembly. The head fixation assembly may be, but is not limited to, any of the head fixation assemblies sold by MRI interventions. As a non-limiting example, the head fixation assembly may be any of the assemblies described in US Patent Nos. 8,099,150, 8,548,569 and 9,031,636 and International Patent Publication Nos. WO201108495 and WO2014014585, the contents of each of which are incorporated by reference in their entireties. A head fixation assembly may be used in combination with an MRI compatible drill such as, but not limited to, the MRI compatible drills described in International Patent Publication No. WO2013181008 and US Patent Publication No. US20130325012, the contents of which are herein incorporated by reference in its entirety.

[000603] In one embodiment, the AAV particles may be delivered using a method, system and/or computer program for positioning apparatus to a target point on a subject to deliver the AAV particles. As a non-limiting example, the method, system and/or computer program may be the

methods, systems and/or computer programs described in US Patent No. 8, 340,743, the contents of which are herein incorporated by reference in its entirety. The method may include: determining a target point in the body and a reference point, wherein the target point and the reference point define a planned trajectory line (PTL) extending through each; determining a visualization plane, wherein the PTL intersects the visualization plane at a sighting point; mounting the guide device relative to the body to move with respect to the PTL, wherein the guide device does not intersect the visualization plane; determining a point of intersection (GPP) between the guide axis and the visualization plane; and aligning the GPP with the sighting point in the visualization plane.

[000604] In one embodiment, the AAV particles may be delivered to a subject using a convention-enhanced delivery device. Non-limiting examples of targeted delivery of drugs using convection are described in US Patent Publication Nos. US20100217228, US20130035574 and US20130035660 and International Patent Publication No. WO2013019830 and WO2008144585, the contents of each of which are herein incorporated by reference in their entireties.

[000605] In one embodiment, a subject may be imaged prior to, during and/or after delivery of the AAV particles. The imaging method may be a method known in the art and/or described herein, such as but not limited to, magnetic resonance imaging (MRI). As a non-limiting example, imaging may be used to assess therapeutic effect. As another non-limiting example, imaging may be used for assisted delivery of AAV particles.

[000606] In one embodiment, the AAV particles may be delivered using an MRI-guided device. Non-limiting examples of MRI-guided devices are described in US Patent Nos. 9,055,884, 9,042,958, 8,886,288, 8,768,433, 8,396,532, 8,369,930, 8,374,677 and 8,175,677 and US Patent Application No. US20140024927 the contents of each of which are herein incorporated by reference in their entireties. As a non-limiting example, the MRI-guided device may be able to provide data in real time such as those described in US Patent Nos. 8,886,288 and 8,768,433, the contents of each of which is herein incorporated by reference in its entirety. As another non-limiting example, the MRI-guided device or system may be used with a targeting cannula such as the systems described in US Patent Nos. 8,175,677 and 8,374,677, the contents of each of which are herein incorporated by reference in their entireties. As yet another non-limiting example, the MRI-guided device includes a trajectory guide frame for guiding an interventional device as described, for example, in US Patent No. 9,055,884 and US Patent Application No. US20140024927, the contents of each of which are herein incorporated by reference in their entireties.

[000607] In one embodiment the AAV particles may be delivered using an MRI-compatible tip assembly. Non-limiting examples of MRI-compatible tip assemblies are described in US Patent Publication No. US20140275980, the contents of which is herein incorporated by reference in its entirety.

[000608] In one embodiment, the AAV particles may be delivered using a cannula which is MRI-compatible. Non-limiting examples of MRI-compatible cannulas include those taught in International Patent Publication No. WO2011130107, the contents of which are herein incorporated by reference in its entirety.

[000609] In one embodiment, the AAV particles may be delivered using a catheter which is MRI-compatible. Non-limiting examples of MRI-compatible catheters include those taught in International Patent Publication No. WO2012116265, US Patent Publication No. 8,825,133 and US Patent Publication No. US20140024909, the contents of each of which are herein incorporated by reference in their entireties.

[000610] In one embodiment, the AAV particles may be delivered using a device with an elongated tubular body and a diaphragm as described in US Patent Publication Nos. US20140276582 and US20140276614, the contents of each of which are herein incorporated by reference in their entireties.

[000611] In one embodiment, the AAV particles may be delivered using an MRI compatible localization and/or guidance system such as, but not limited to, those described in US Patent Publication Nos. US20150223905 and US20150230871, the contents of each of which are herein incorporated by reference in their entireties. As a non-limiting example, the MRI compatible localization and/or guidance systems may comprise a mount adapted for fixation to a patient, a targeting cannula with a lumen configured to attach to the mount so as to be able to controllably translate in at least three dimensions, and an elongate probe configured to snugly advance via slide and retract in the targeting cannula lumen, the elongate probe comprising at least one of a stimulation or recording electrode.

[000612] In one embodiment, the AAV particles may be delivered to a subject using a trajectory frame as described in US Patent Publication Nos. US20150031982 and US20140066750 and International Patent Publication Nos. WO2015057807 and WO2014039481, the contents of each of which are herein incorporated by reference in their entireties.

[000613] In one embodiment, the AAV particles may be delivered to a subject using a gene gun.

DEFINITIONS

[000614] At various places in the present specification, substituents of compounds of the present disclosure are disclosed in groups or in ranges. It is specifically intended that the present disclosure include each and every individual subcombination of the members of such groups and ranges.

[000615] *About*: As used herein, the term “about” means +/- 10% of the recited value.

[000616] *Activity*: As used herein, the term “activity” refers to the condition in which things are happening or being done. Compositions described herein may have activity and this activity may involve one or more biological events.

[000617] *Adeno-associated virus*: The term “adeno-associated virus” or “AAV” as used herein refers to members of the dependovirus genus comprising any particle, sequence, gene, protein, or component derived therefrom. The term “AAV particle” as used herein comprises a capsid and a polynucleotide. The AAV particle may be derived from any serotype, described herein or known in the art, including combinations of serotypes (i.e., “pseudotyped” AAV) or from various genomes (e.g., single stranded or self-complementary). In addition, the AAV particle may be replication defective and/or targeted.

[000618] *Administered in combination*: As used herein, the term “administered in combination” or “combined administration” means that two or more agents (e.g., AAV) are administered to a subject at the same time or within an interval such that there may be an overlap of an effect of each agent on the patient and/or the subject is at some point in time simultaneously exposed to both. In some embodiments, they are administered within about 60, 30, 15, 10, 5, or 1 minutes of one another or within about 24 hours, 12 hours, 6 hours, 3 hours of at least one dose of one or more other agents. In some embodiments, administration occurs in overlapping dosage regimens. As used herein, the term “dosage regimen” refers to a plurality of doses spaced apart in time. Such doses may occur at regular intervals or may include one or more hiatus in administration. In some embodiments, the administrations of the agents are spaced sufficiently closely together such that a combinatorial (e.g., a synergistic) effect is achieved.

[000619] *Amelioration*: As used herein, the term “amelioration” or “ameliorating” refers to a lessening of severity of at least one indicator of a condition or disease. For example, in the context of neurodegeneration disorder, amelioration includes the reduction of neuron loss.

[000620] *Animal*: As used herein, the term “animal” refers to any member of the animal kingdom. In some embodiments, “animal” refers to humans at any stage of development. In some

embodiments, “animal” refers to non-human animals at any stage of development. In certain embodiments, the non-human animal is a mammal (*e.g.*, a rodent, a mouse, a rat, a rabbit, a monkey, a dog, a cat, a sheep, cattle, a primate, or a pig). In some embodiments, animals include, but are not limited to, mammals, birds, reptiles, amphibians, fish, and worms. In some embodiments, the animal is a transgenic animal, genetically-engineered animal, or a clone.

[000621] *Antisense strand*: As used herein, the term “the antisense strand” or “the first strand” or “the guide strand” of a siRNA molecule refers to a strand that is substantially complementary to a section of about 10-50 nucleotides, *e.g.*, about 15-30, 16-25, 18-23 or 19-22 nucleotides of the mRNA of the gene targeted for silencing. The antisense strand or first strand has sequence sufficiently complementary to the desired target mRNA sequence to direct target-specific silencing, *e.g.*, complementarity sufficient to trigger the destruction of the desired target mRNA by the RNAi machinery or process.

[000622] *Approximately*: As used herein, the term “approximately” or “about,” as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term “approximately” or “about” refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[000623] *Associated with*: As used herein, the terms “associated with,” “conjugated,” “linked,” “attached,” and “tethered,” when used with respect to two or more moieties, means that the moieties are physically associated or connected with one another, either directly or via one or more additional moieties that serves as a linking agent, to form a structure that is sufficiently stable so that the moieties remain physically associated under the conditions in which the structure is used, *e.g.*, physiological conditions. An “association” need not be strictly through direct covalent chemical bonding. It may also suggest ionic or hydrogen bonding or a hybridization based connectivity sufficiently stable such that the “associated” entities remain physically associated.

[000624] *Bifunctional*: As used herein, the term “bifunctional” refers to any substance, molecule or moiety which is capable of or maintains at least two functions. The functions may affect the same outcome or a different outcome. The structure that produces the function may be the same or different.

[000625] *Biologically active*: As used herein, the phrase “biologically active” refers to a characteristic of any substance (e.g., AAV) that has activity in a biological system and/or organism. For instance, a substance that, when administered to an organism, has a biological effect on that organism, is considered to be biologically active. In particular embodiments, a polynucleotide of the present invention may be considered biologically active if even a portion of the polynucleotides is biologically active or mimics an activity considered biologically relevant.

[000626] *Biological system*: As used herein, the term “biological system” refers to a group of organs, tissues, cells, intracellular components, proteins, nucleic acids, molecules (including, but not limited to biomolecules) that function together to perform a certain biological task within cellular membranes, cellular compartments, cells, tissues, organs, organ systems, multicellular organisms, or any biological entity. In some embodiments, biological systems are cell signaling pathways comprising intracellular and/or extracellular cell signaling biomolecules. In some embodiments, biological systems comprise growth factor signaling events within the extracellular/cellular matrix and/or cellular niches.

[000627] *Biomolecule*: As used herein, the term “biomolecule” is any natural molecule which is amino acid-based, nucleic acid-based, carbohydrate-based or lipid-based, and the like.

[000628] *Complementary and substantially complementary*: As used herein, the term “complementary” refers to the ability of polynucleotides to form base pairs with one another. Base pairs are typically formed by hydrogen bonds between nucleotide units in antiparallel polynucleotide strands. Complementary polynucleotide strands can form base pairs in the Watson-Crick manner (e.g., A to T, A to U, C to G), or in any other manner that allows for the formation of duplexes. As persons skilled in the art are aware, when using RNA as opposed to DNA, uracil rather than thymine is the base that is considered to be complementary to adenosine. However, when a U is denoted in the context of the present invention, the ability to substitute a T is implied, unless otherwise stated. Perfect complementarity or 100% complementarity refers to the situation in which each nucleotide unit of one polynucleotide strand can form a hydrogen bond with a nucleotide unit of a second polynucleotide strand. Less than perfect complementarity refers to the situation in which some, but not all, nucleotide units of two strands can form hydrogen bonds with each other. For example, for two 20-mers, if only two base pairs on each strand can form hydrogen bonds with each other, the polynucleotide strands exhibit 10% complementarity. In the same example, if 18 base pairs on each strand can form hydrogen bonds with each other, the polynucleotide strands exhibit

90% complementarity. As used herein, the term “substantially complementary” means that the siRNA has a sequence (e.g., in the antisense strand) which is sufficient to bind the desired target mRNA, and to trigger the RNA silencing of the target mRNA.

[000629] *Compound*: As used herein, the term “compound,” refers to a distinct chemical entity. In some embodiments, a particular compound may exist in one or more isomeric or isotopic forms (including, but not limited to stereoisomers, geometric isomers and isotopes). In some embodiments, a compound is provided or utilized in only a single such form. In some embodiments, a compound is provided or utilized as a mixture of two or more such forms (including, but not limited to a racemic mixture of stereoisomers). Those of skill in the art appreciate that some compounds exist in different such forms, show different properties and/or activities (including, but not limited to biological activities). In such cases it is within the ordinary skill of those in the art to select or avoid particular forms of the compound for use in accordance with the present invention. For example, compounds that contain asymmetrically substituted carbon atoms can be isolated in optically active or racemic forms. Methods on how to prepare optically active forms from optically active starting materials are known in the art, such as by resolution of racemic mixtures or by stereoselective synthesis. Many geometric isomers of olefins, C=N double bonds, and the like can also be present in the compounds described herein, and all such stable isomers are contemplated in the present disclosure. Cis and trans geometric isomers of the compounds of the present disclosure are described and may be isolated as a mixture of isomers or as separated isomeric forms.

[000630] Compounds of the present disclosure also include tautomeric forms. Tautomeric forms result from the swapping of a single bond with an adjacent double bond and the concomitant migration of a proton. Tautomeric forms include prototropic tautomers which are isomeric protonation states having the same empirical formula and total charge.

[000631] Compounds of the present disclosure also include all of the isotopes of the atoms occurring in the intermediate or final compounds. “Isotopes” refers to atoms having the same atomic number but different mass numbers resulting from a different number of neutrons in the nuclei. For example, isotopes of hydrogen include tritium and deuterium.

[000632] The compounds and salts of the present disclosure can be prepared in combination with solvent or water molecules to form solvates and hydrates by routine methods.

[000633] *Conserved*: As used herein, the term “conserved” refers to nucleotides or amino acid residues of a polynucleotide sequence or polypeptide sequence, respectively, that are those that

occur unaltered in the same position of two or more sequences being compared. Nucleotides or amino acids that are relatively conserved are those that are conserved amongst more related sequences than nucleotides or amino acids appearing elsewhere in the sequences.

[000634] In some embodiments, two or more sequences are said to be “completely conserved” if they are 100% identical to one another. In some embodiments, two or more sequences are said to be “highly conserved” if they are at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be “highly conserved” if they are about 70% identical, about 80% identical, about 90% identical, about 95%, about 98%, or about 99% identical to one another. In some embodiments, two or more sequences are said to be “conserved” if they are at least 30% identical, at least 40% identical, at least 50% identical, at least 60% identical, at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be “conserved” if they are about 30% identical, about 40% identical, about 50% identical, about 60% identical, about 70% identical, about 80% identical, about 90% identical, about 95% identical, about 98% identical, or about 99% identical to one another. Conservation of sequence may apply to the entire length of an oligonucleotide, a polynucleotide or polypeptide or may apply to a portion, region or feature thereof.

[000635] In one embodiment, conserved sequences are not contiguous. Those skilled in the art are able to appreciate how to achieve alignment when gaps in contiguous alignment are present between sequences, and to align corresponding residues notwithstanding insertions or deletions present.

[000636] In one embodiment, conserved sequences are not contiguous. Those skilled in the art are able to appreciate how to achieve alignment when gaps in contiguous alignment are present between sequences, and to align corresponding residues notwithstanding insertions or deletions present.

[000637] *Delivery*: As used herein, “delivery” refers to the act or manner of delivering a compound such as a parvovirus, e.g. an AAV and/or AAV compound, substance, entity, moiety, cargo or payload to a target. Such target may be a cell, tissue, organ, organism, or system (whether biological or production).

[000638] *Delivery Agent*: As used herein, “delivery agent” refers to any agent or substance which facilitates, at least in part, the *in vivo* and/or *in vitro* delivery of a polynucleotide and/or one or more substances (including, but not limited to a compounds and/or compositions of the present invention, e.g., viral particles or expression vectors) to targeted cells.

[000639] *Destabilized*: As used herein, the term “destable,” “destabilize,” or “destabilizing region” means a region or molecule that is less stable than a starting, reference, wild-type or native form of the same region or molecule.

[000640] *Detectable label*: As used herein, “detectable label” refers to one or more markers, signals, or moieties which are attached, incorporated or associated with another entity that is readily detected by methods known in the art including radiography, fluorescence, chemiluminescence, enzymatic activity, absorbance immunological detection, and the like. Detectable labels may include radioisotopes, fluorophores, chromophores, enzymes, dyes, metal ions, ligands such as biotin, avidin, streptavidin and haptens, quantum dots, and the like. Detectable labels may be located at any position in the entity with which they are attached, incorporated or associated. For example, when attached, incorporated in or associated with a peptide or protein, they may be within the amino acids, the peptides, or proteins, or located at the N- or C- termini.

[000641] *Dosing regimen*: As used herein, a “dosing regimen” is a schedule of administration or physician determined regimen of treatment, prophylaxis, or palliative care.

[000642] *Effective Amount*: As used herein, the term “effective amount” of an agent is that amount sufficient to effect beneficial or desired results, for example, upon single or multiple dose administration to a subject cell, in curing, alleviating, relieving or improving one or more symptoms of a disorder, clinical results, and, as such, an “effective amount” depends upon the context in which it is being applied. For example, in the context of administering an agent that treats Parkinson’s Disease, an effective amount of an agent is, for example, an amount sufficient to achieve treatment, as defined herein, of Parkinson’s Disease, as compared to the response obtained without administration of the agent.

[000643] *Encapsulate*: As used herein, the term “encapsulate” means to enclose, surround or encase.

[000644] *Engineered*: As used herein, embodiments are “engineered” when they are designed to have a feature or property, whether structural or chemical, that varies from a starting point, wild-type or native molecule. Thus, engineered agents or entities are those whose design and/or production include an act of the hand of man.

[000645] *Epitope*: As used herein, an “epitope” refers to a surface or region on a molecule that is capable of interacting with a biomolecule. For example a protein may contain one or more amino acids, e.g., an epitope, which interacts with an antibody, e.g., a biomolecule. In some embodiments,

when referring to a protein or protein module, an epitope may comprise a linear stretch of amino acids or a three dimensional structure formed by folded amino acid chains.

[000646] *Expression:* As used herein, “expression” of a nucleic acid sequence refers to one or more of the following events: (1) production of an RNA template from a DNA sequence (*e.g.*, by transcription); (2) processing of an RNA transcript (*e.g.*, by splicing, editing, 5' cap formation, and/or 3' end processing); (3) translation of an RNA into a polypeptide or protein; (4) folding of a polypeptide or protein; and (5) post-translational modification of a polypeptide or protein.

[000647] *Feature:* As used herein, a “feature” refers to a characteristic, a property, or a distinctive element.

[000648] *Formulation:* As used herein, a “formulation” includes at least one polynucleotide and/or compound and/or composition of the present disclosure (*e.g.*, a vector, AAV particle, etc.) and a delivery agent.

[000649] *Fragment:* A “fragment,” as used herein, refers to a contiguous portion of a whole. For example, fragments of proteins may comprise polypeptides obtained by digesting full-length protein isolated from cultured cells. In some embodiments, a fragment of a protein includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250 or more amino acids. In some embodiments, fragments of an antibody include portions of an antibody subjected to enzymatic digestion or synthesized as such.

[000650] *Functional:* As used herein, a “functional” biological molecule is a biological molecule and/or entity with a structure and in a form in which it exhibits a property and/or activity by which it is characterized.

[000651] *Gene expression:* The term “gene expression” refers to the process by which a nucleic acid sequence undergoes successful transcription and in most instances translation to produce a protein or peptide. For clarity, when reference is made to measurement of “gene expression”, this should be understood to mean that measurements may be of the nucleic acid product of transcription, *e.g.*, RNA or mRNA or of the amino acid product of translation, *e.g.*, polypeptides or peptides. Methods of measuring the amount or levels of RNA, mRNA, polypeptides and peptides are well known in the art.

[000652] *Homology:* As used herein, the term “homology” refers to the overall relatedness between polymeric molecules, *e.g.* between nucleic acid molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric

molecules are considered to be “homologous” to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical or similar. The term “homologous” necessarily refers to a comparison between at least two sequences (polynucleotide or polypeptide sequences). In accordance with the invention, two polynucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50%, 60%, 70%, 80%, 90%, 95%, or even 99% for at least one stretch of at least about 20 amino acids. In some embodiments, homologous polynucleotide sequences are characterized by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. For polynucleotide sequences less than 60 nucleotides in length, homology is typically determined by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. In accordance with the invention, two protein sequences are considered to be homologous if the proteins are at least about 50%, 60%, 70%, 80%, or 90% identical for at least one stretch of at least about 20 amino acids. In many embodiments, homologous protein may show a large overall degree of homology and a high degree of homology over at least one short stretch of at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50 or more amino acids. In many embodiments, homologous proteins share one or more characteristic sequence elements. As used herein, the term “characteristic sequence element” refers to a motif present in related proteins. In some embodiments, the presence of such motifs correlates with a particular activity (such as biological activity).

[000653] *Identity*: As used herein, the term “identity” refers to the overall relatedness between polymeric molecules, *e.g.*, between oligonucleotide and/or polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two polynucleotide sequences, for example, may be performed by aligning the two sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the

number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleotide sequences can be determined using methods such as those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; each of which is incorporated herein by reference in its entirety. For example, the percent identity between two nucleotide sequences can be determined, for example using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleotide sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix. Methods commonly employed to determine percent identity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., SIAM J Applied Math., 48:1073 (1988); incorporated herein by reference in its entirety. Techniques for determining identity are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., *et al.*, *Nucleic Acids Research*, 12(1), 387 (1984)), BLASTP, BLASTN, and FASTA Altschul, S. F. *et al.*, *J. Molec. Biol.*, 215, 403 (1990)).

[000654] *Inhibit expression of a gene*: As used herein, the phrase “inhibit expression of a gene” means to cause a reduction in the amount of an expression product of the gene. The expression product may be RNA transcribed from the gene (e.g. mRNA) or a polypeptide translated from mRNA transcribed from the gene. Typically a reduction in the level of mRNA results in a reduction in the level of a polypeptide translated therefrom. The level of expression may be determined using standard techniques for measuring mRNA or protein.

[000655] *In vitro*: As used herein, the term “*in vitro*” refers to events that occur in an artificial environment, e.g., in a test tube or reaction vessel, in cell culture, in a Petri dish, *etc.*, rather than within an organism (e.g., animal, plant, or microbe).

[000656] *In vivo*: As used herein, the term “*in vivo*” refers to events that occur within an organism (e.g., animal, plant, or microbe or cell or tissue thereof).

[000657] *Isolated*: As used herein, the term “isolated” is synonymous with “separated”, but carries with it the inference separation was carried out by the hand of man. In one embodiment, an isolated substance or entity is one that has been separated from at least some of the components with which it was previously associated (whether in nature or in an experimental setting). Isolated substances may have varying levels of purity in reference to the substances from which they have been associated. Isolated substances and/or entities may be separated from at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or more of the other components with which they were initially associated. In some embodiments, isolated agents are more than about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. As used herein, a substance is “pure” if it is substantially free of other components.

[000658] *Substantially isolated*: By “substantially isolated” is meant that the compound is substantially separated from the environment in which it was formed or detected. Partial separation can include, for example, a composition enriched in the compound of the present disclosure. Substantial separation can include compositions containing 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 97%, or at least about 99% by weight of the compound of the present disclosure, or salt thereof. Methods for isolating compounds and their salts are routine in the art. In some embodiments, isolation of a substance or entity includes disruption of chemical associations and/or bonds. In some embodiments, isolation includes only the separation from components with which the isolated substance or entity was previously combined and does not include such disruption.

[000659] *Modified*: As used herein, the term “modified” refers to a changed state or structure of a molecule or entity of the invention as compared with a parent or reference molecule or entity. Molecules may be modified in many ways including chemically, structurally, and functionally. In some embodiments, compounds and/or compositions of the present disclosure are modified by the introduction of non-natural amino acids, or non-natural nucleotides.

[000660] *Mutation*: As used herein, the term “mutation” refers to a change and/or alteration. In some embodiments, mutations may be changes and/or alterations to proteins (including peptides and polypeptides) and/or nucleic acids (including polynucleic acids). In some embodiments, mutations

comprise changes and/or alterations to a protein and/or nucleic acid sequence. Such changes and/or alterations may comprise the addition, substitution and or deletion of one or more amino acids (in the case of proteins and/or peptides) and/or nucleotides (in the case of nucleic acids and or polynucleic acids). In embodiments wherein mutations comprise the addition and/or substitution of amino acids and/or nucleotides, such additions and/or substitutions may comprise 1 or more amino acid and/or nucleotide residues and may include modified amino acids and/or nucleotides.

[000661] *Naturally occurring*: As used herein, “naturally occurring” means existing in nature without artificial aid or involvement of the hand of man

[000662] *Non-human vertebrate*: As used herein, a “non-human vertebrate” includes all vertebrates except *Homo sapiens*, including wild and domesticated species. Examples of non-human vertebrates include, but are not limited to, mammals, such as alpaca, banteng, bison, camel, cat, cattle, deer, dog, donkey, gayal, goat, guinea pig, horse, llama, mule, pig, rabbit, reindeer, sheep water buffalo, and yak.

[000663] *Nucleic acid*: As used herein, the term “nucleic acid”, “polynucleotide” and “oligonucleotide” refer to any nucleic acid polymers composed of either polydeoxyribonucleotides (containing 2-deoxy-D-ribose), or polyribonucleotides (containing D-ribose), or any other type of polynucleotide which is an N glycoside of a purine or pyrimidine base, or modified purine or pyrimidine bases. There is no intended distinction in length between the term “nucleic acid”, “polynucleotide” and “oligonucleotide”, and these terms will be used interchangeably. These terms refer only to the primary structure of the molecule. Thus, these terms include double- and single-stranded DNA, as well as double- and single stranded RNA.

[000664] *Off-target*: As used herein, “off target” refers to any unintended effect on any one or more target, gene and/or cellular transcript.

[000665] *Open reading frame*: As used herein, “open reading frame” or “ORF” refers to a sequence which does not contain a stop codon in a given reading frame.

[000666] *Operably linked*: As used herein, the phrase “operably linked” refers to a functional connection between two or more molecules, constructs, transcripts, entities, moieties or the like.

[000667] *Particle*: As used herein, a “particle” is a virus comprised of at least two components, a protein capsid and a polynucleotide sequence enclosed within the capsid.

[000668] *Patient*: As used herein, “patient” refers to a subject who may seek or be in need of treatment, requires treatment, is receiving treatment, will receive treatment, or a subject who is

under care by a trained professional for a particular disease or condition, such as for example Parkinson's Disease.

[000669] *Payload*: As used herein, "payload" refers to one or more polynucleotides or polynucleotide regions encoded by or within a viral genome or an expression product of such polynucleotide or polynucleotide region, e.g., a transgene, a polynucleotide encoding a polypeptide or multi-polypeptide or a modulatory nucleic acid or regulatory nucleic acid.

[000670] *Payload construct*: As used herein, "payload construct" is one or more polynucleotide regions encoding or comprising a payload that is flanked on one or both sides by an inverted terminal repeat (ITR) sequence. The payload construct is a template that is replicated in a viral production cell to produce a viral genome.

[000671] *Payload construct vector*: As used herein, "payload construct vector" is a vector encoding or comprising a payload construct, and regulatory regions for replication and expression in bacterial cells.

[000672] *Payload construct expression vector*: As used herein, a "payload construct expression vector" is a vector encoding or comprising a payload construct and which further comprises one or more polynucleotide regions encoding or comprising components for viral expression in a viral replication cell.

[000673] *Peptide*: As used herein, "peptide" is less than or equal to 50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

[000674] *Pharmaceutically acceptable*: The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[000675] *Pharmaceutically acceptable excipients*: The phrase "pharmaceutically acceptable excipient," as used herein, refers to any ingredient other than the compounds and/or active agents (e.g. as described herein) present in pharmaceutical compositions and having the properties of being substantially nontoxic and non-inflammatory in a subject such as a patient. In some embodiments, pharmaceutically acceptable excipients are vehicles capable of suspending and/or dissolving active agents. Excipients may include, for example: antiadherents, antioxidants, binders, coatings, compression aids, disintegrants, dyes (colors), emollients, emulsifiers, fillers (diluent), film formers

or coatings, flavors, fragrances, glidants (flow enhancers), lubricants, preservatives, printing inks, sorbents, suspension or dispersing agents, sweeteners, and waters of hydration. Exemplary excipients include, but are not limited to: butylated hydroxytoluene (BHT), calcium carbonate, calcium phosphate (dibasic), calcium stearate, croscarmellose, crosslinked polyvinyl pyrrolidone, citric acid, crospovidone, cysteine, ethylcellulose, gelatin, hydroxypropyl cellulose, hydroxypropyl methylcellulose, lactose, magnesium stearate, maltitol, mannitol, methionine, methylcellulose, methyl paraben, microcrystalline cellulose, polyethylene glycol, polyvinyl pyrrolidone, povidone, pregelatinized starch, propyl paraben, retinyl palmitate, shellac, silicon dioxide, sodium carboxymethyl cellulose, sodium citrate, sodium starch glycolate, sorbitol, starch (corn), stearic acid, sucrose, talc, titanium dioxide, vitamin A, vitamin E, vitamin C, and xylitol.

[000676] *Pharmaceutically acceptable salts*: Pharmaceutically acceptable salts of the compounds described herein. As used herein, “pharmaceutically acceptable salts” refers to derivatives or forms of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., as generated by reacting the free base group with a suitable organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycerophosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. In some embodiments a pharmaceutically

acceptable salt of the present disclosure can be synthesized salt prepared from the parent compound which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, Pa., 1985, p. 1418, Pharmaceutical Salts: Properties, Selection, and Use, P.H. Stahl and C.G. Wermuth (eds.), Wiley-VCH, 2008, and Berge et al., Journal of Pharmaceutical Science, 66, 1-19 (1977), each of which is incorporated herein by reference in its entirety.

[000677] *Pharmaceutically acceptable solvate*: The term "pharmaceutically acceptable solvate," as used herein, refers to a crystalline form of a compound of the invention wherein molecules of a suitable solvent are incorporated in the crystal lattice. A suitable solvent is physiologically tolerable at the dosage administered. For example, solvates may be prepared by crystallization, recrystallization, or precipitation from a solution that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), N-methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), N,N'-dimethylformamide (DMF), N,N'-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate." In some embodiments, the solvent incorporated into a solvate is of a type or at a level that is physiologically tolerable to an organism to which the solvate is administered (e.g., in a unit dosage form of a pharmaceutical composition).

[000678] *Pharmacokinetic*: As used herein, "pharmacokinetic" refers to any one or more properties of a molecule or compound as it relates to the determination of the fate of substances administered to a living organism. Pharmacokinetics is divided into several areas including the extent and rate of absorption, distribution, metabolism and excretion. This is commonly referred to as ADME where: (A) Absorption is the process of a substance entering the blood circulation; (D) Distribution is the dispersion or dissemination of substances throughout the fluids and tissues of the body; (M) Metabolism (or Biotransformation) is the irreversible transformation of parent

compounds into daughter metabolites; and (E) Excretion (or Elimination) refers to the elimination of the substances from the body. In rare cases, some drugs irreversibly accumulate in body tissue.

[000679] *Physicochemical*: As used herein, “physicochemical” means of or relating to a physical and/or chemical property.

[000680] *Preventing*: As used herein, the term “preventing” refers to partially or completely delaying onset of an infection, disease, disorder and/or condition; partially or completely delaying onset of one or more symptoms, features, or clinical manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying onset of one or more symptoms, features, or manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying progression from an infection, a particular disease, disorder and/or condition; and/or decreasing the risk of developing pathology associated with the infection, the disease, disorder, and/or condition, such as for example Parkinson’s Disease.

[000681] *Prodrug*: The present disclosure also includes prodrugs of the compounds described herein. As used herein, “prodrugs” refer to any substance, molecule or entity which is in a form predicate for that substance, molecule or entity to act as a therapeutic upon chemical or physical alteration. Prodrugs may be covalently bonded or sequestered in some way and which release or are converted into the active drug moiety prior to, upon or after administered to a mammalian subject. Preparation and use of prodrugs is discussed in T. Higuchi and V. Stella, “Pro-drugs as Novel Delivery Systems,” Vol. 14 of the A.C.S. Symposium Series, and in *Bioreversible Carriers in Drug Design*, ed. Edward B. Roche, American Pharmaceutical Association and Pergamon Press, 1987, both of which are hereby incorporated by reference in their entirety.

[000682] *Proliferate*: As used herein, the term “proliferate” means to grow, expand, replicate or increase or cause to grow, expand, replicate or increase. “Proliferative” means having the ability to proliferate. “Anti-proliferative” means having properties counter to or in opposition to proliferative properties.

[000683] *Prophylactic*: As used herein, “prophylactic” refers to a therapeutic or course of action used to prevent the spread of disease.

[000684] *Prophylaxis*: As used herein, a “prophylaxis” refers to a measure taken to maintain health and prevent the spread of disease.

[000685] *Protein of interest*: As used herein, the terms “proteins of interest” or “desired proteins” include those provided herein and fragments, mutants, variants, and alterations thereof.

[000686] *Purified*: As used herein, “purify,” “purified,” “purification” means to make substantially pure or clear from unwanted components, material defilement, admixture or imperfection.

“Purified” refers to the state of being pure. “Purification” refers to the process of making pure.

[000687] *Region*: As used herein, the term “region” refers to a zone or general area. In some embodiments, when referring to a protein or protein module, a region may comprise a linear sequence of amino acids along the protein or protein module or may comprise a three dimensional area, an epitope and/or a cluster of epitopes. In some embodiments, regions comprise terminal regions. As used herein, the term “terminal region” refers to regions located at the ends or termini of a given agent. When referring to proteins, terminal regions may comprise N- and/or C-termini. N-termini refer to the end of a protein comprising an amino acid with a free amino group. C-termini refer to the end of a protein comprising an amino acid with a free carboxyl group. N- and/or C-terminal regions may therefore comprise the N- and/or C-termini as well as surrounding amino acids. In some embodiments, N- and/or C-terminal regions comprise from about 3 amino acid to about 30 amino acids, from about 5 amino acids to about 40 amino acids, from about 10 amino acids to about 50 amino acids, from about 20 amino acids to about 100 amino acids and/or at least 100 amino acids. In some embodiments, N-terminal regions may comprise any length of amino acids that includes the N-terminus, but does not include the C-terminus. In some embodiments, C-terminal regions may comprise any length of amino acids, which include the C-terminus, but do not comprise the N-terminus.

[000688] In some embodiments, when referring to a polynucleotide, a region may comprise a linear sequence of nucleic acids along the polynucleotide or may comprise a three dimensional area, secondary structure, or tertiary structure. In some embodiments, regions comprise terminal regions. As used herein, the term “terminal region” refers to regions located at the ends or termini of a given agent. When referring to polynucleotides, terminal regions may comprise 5’ and 3’ termini. 5’ termini refer to the end of a polynucleotide comprising a nucleic acid with a free phosphate group. 3’ termini refer to the end of a polynucleotide comprising a nucleic acid with a free hydroxyl group. 5’ and 3’ regions may therefore comprise the 5’ and 3’ termini as well as surrounding nucleic acids. In some embodiments, 5’ and 3’ terminal regions comprise from about 9 nucleic acids to about 90 nucleic acids, from about 15 nucleic acids to about 120 nucleic acids, from about 30 nucleic acids to about 150 nucleic acids, from about 60 nucleic acids to about 300 nucleic acids and/or at least 300 nucleic acids. In some embodiments, 5’ regions may comprise any length of nucleic acids that

includes the 5' terminus, but does not include the 3' terminus. In some embodiments, 3' regions may comprise any length of nucleic acids, which include the 3' terminus, but does not comprise the 5' terminus.

[000689] *RNA or RNA molecule*: As used herein, the term “RNA” or “RNA molecule” or “ribonucleic acid molecule” refers to a polymer of ribonucleotides; the term “DNA” or “DNA molecule” or “deoxyribonucleic acid molecule” refers to a polymer of deoxyribonucleotides. DNA and RNA can be synthesized naturally, e.g., by DNA replication and transcription of DNA, respectively; or be chemically synthesized. DNA and RNA can be single-stranded (i.e., ssRNA or ssDNA, respectively) or multi-stranded (e.g., double stranded, i.e., dsRNA and dsDNA, respectively). The term “mRNA” or “messenger RNA”, as used herein, refers to a single stranded RNA that encodes the amino acid sequence of one or more polypeptide chains.

[000690] *RNA interference*: As used herein, the term “RNA interference” or “RNAi” refers to a sequence specific regulatory mechanism mediated by RNA molecules which results in the inhibition or interference or “silencing” of the expression of a corresponding protein-coding gene.

[000691] *Sample*: As used herein, the term “sample” refers to an aliquot, subset or portion taken from a source and/or provided for analysis or processing. In some embodiments, a sample is from a biological source such as a tissue, cell or component part (e.g. a body fluid, including but not limited to blood, mucus, lymphatic fluid, synovial fluid, cerebrospinal fluid, saliva, amniotic fluid, amniotic cord blood, urine, vaginal fluid and semen). In some embodiments, a sample may be or comprise a homogenate, lysate or extract prepared from a whole organism or a subset of its tissues, cells or component parts, or a fraction or portion thereof, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, or organs. In some embodiments, a sample is or comprises a medium, such as a nutrient broth or gel, which may contain cellular components, such as proteins or nucleic acid molecule. In some embodiments, a “primary” sample is an aliquot of the source. In some embodiments, a primary sample is subjected to one or more processing (e.g., separation, purification, etc.) steps to prepare a sample for analysis or other use.

[000692] *Self-complementary viral particle*: As used herein, a “self-complementary viral particle” is a particle comprised of at least two components, a protein capsid and a polynucleotide sequence encoding a self-complementary genome enclosed within the capsid.

[000693] *Sense strand*: As used herein, the term “the sense strand” or “the second strand” or “the passenger strand” of a siRNA molecule refers to a strand that is complementary to the antisense strand or first strand. The antisense and sense strands of a siRNA molecule are hybridized to form a duplex structure. As used herein, a “siRNA duplex” includes a siRNA strand having sufficient complementarity to a section of about 10-50 nucleotides of the mRNA of the gene targeted for silencing and a siRNA strand having sufficient complementarity to form a duplex with the siRNA strand.

[000694] *Signal Sequences*: As used herein, the phrase “signal sequences” refers to a sequence which can direct the transport or localization.

[000695] *Single unit dose*: As used herein, a “single unit dose” is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event. In some embodiments, a single unit dose is provided as a discrete dosage form (e.g., a tablet, capsule, patch, loaded syringe, vial, etc.).

[000696] *Similarity*: As used herein, the term “similarity” refers to the overall relatedness between polymeric molecules, e.g. between polynucleotide molecules (e.g. DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of percent similarity of polymeric molecules to one another can be performed in the same manner as a calculation of percent identity, except that calculation of percent similarity takes into account conservative substitutions as is understood in the art.

[000697] *Small/short interfering RNA*: As used herein, the term “small/short interfering RNA” or “siRNA” refers to an RNA molecule (or RNA analog) comprising between about 5-60 nucleotides (or nucleotide analogs) which is capable of directing or mediating RNAi. Preferably, a siRNA molecule comprises between about 15-30 nucleotides or nucleotide analogs, more preferably between about 16-25 nucleotides (or nucleotide analogs), even more preferably between about 18-23 nucleotides (or nucleotide analogs), and even more preferably between about 19-22 nucleotides (or nucleotide analogs) (e.g., 19, 20, 21 or 22 nucleotides or nucleotide analogs). The term “short” siRNA refers to a siRNA comprising 5-23 nucleotides, preferably 21 nucleotides (or nucleotide analogs), for example, 19, 20, 21 or 22 nucleotides. The term “long” siRNA refers to a siRNA comprising 24-60 nucleotides, preferably about 24-25 nucleotides, for example, 23, 24, 25 or 26 nucleotides. Short siRNAs may, in some instances, include fewer than 19 nucleotides, e.g., 16, 17 or 18 nucleotides, or as few as 5 nucleotides, provided that the shorter siRNA retains the ability to

mediate RNAi. Likewise, long siRNAs may, in some instances, include more than 26 nucleotides, e.g., 27, 28, 29, 30, 35, 40, 45, 50, 55, or even 60 nucleotides, provided that the longer siRNA retains the ability to mediate RNAi or translational repression absent further processing, e.g., enzymatic processing, to a short siRNA. siRNAs can be single stranded RNA molecules (ss-siRNAs) or double stranded RNA molecules (ds-siRNAs) comprising a sense strand and an antisense strand which hybridized to form a duplex structure called siRNA duplex.

[000698] *Split dose*: As used herein, a “split dose” is the division of single unit dose or total daily dose into two or more doses.

[000699] *Stable*: As used herein “stable” refers to a compound or entity that is sufficiently robust to survive isolation to a useful degree of purity from a reaction mixture, and preferably capable of formulation into an efficacious therapeutic agent.

[000700] *Stabilized*: As used herein, the term “stabilize”, “stabilized,” “stabilized region” means to make or become stable. In some embodiments, stability is measured relative to an absolute value. In some embodiments, stability is measured relative to a reference compound or entity.

[000701] *Subject*: As used herein, the term “subject” or “patient” refers to any organism to which a composition in accordance with the invention may be administered, e.g., for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include animals (e.g., mammals such as mice, rats, rabbits, non-human primates, and humans) and/or plants. In some embodiments, the subject may be an infant, neonate, or a child under the age of 12 years old. In some embodiments, the subject may be in utero.

[000702] *Substantially*: As used herein, the term “substantially” refers to the qualitative condition of exhibiting total or near-total extent or degree of a characteristic or property of interest. One of ordinary skill in the biological arts will understand that biological and chemical phenomena rarely, if ever, go to completion and/or proceed to completeness or achieve or avoid an absolute result. The term “substantially” is therefore used herein to capture the potential lack of completeness inherent in many biological and chemical phenomena.

[000703] *Substantially equal*: As used herein as it relates to time differences between doses, the term means plus/minus 2%.

[000704] *Substantially simultaneously*: As used herein and as it relates to plurality of doses, the term typically means within about 2 seconds.

[000705] *Suffering from*: An individual who is “suffering from” a disease, disorder, and/or condition has been diagnosed with or displays one or more symptoms of a disease, disorder, and/or condition such as for example Parkinson’s Disease.

[000706] *Susceptible to*: An individual who is “susceptible to” a disease, disorder, and/or condition has not been diagnosed with and/or may not exhibit symptoms of the disease, disorder, and/or condition but harbors a propensity to develop a disease or its symptoms. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition (for example, cancer) may be characterized by one or more of the following: (1) a genetic mutation associated with development of the disease, disorder, and/or condition; (2) a genetic polymorphism associated with development of the disease, disorder, and/or condition; (3) increased and/or decreased expression and/or activity of a protein and/or nucleic acid associated with the disease, disorder, and/or condition; (4) habits and/or lifestyles associated with development of the disease, disorder, and/or condition; (5) a family history of the disease, disorder, and/or condition; and (6) exposure to and/or infection with a microbe associated with development of the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will develop the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will not develop the disease, disorder, and/or condition.

[000707] *Sustained release*: As used herein, the term “sustained release” refers to a pharmaceutical composition or compound release profile that conforms to a release rate over a specific period of time.

[000708] *Synthetic*: The term “synthetic” means produced, prepared, and/or manufactured by the hand of man. Synthesis of polynucleotides or polypeptides or other molecules of the present invention may be chemical or enzymatic.

[000709] *Targeting*: As used herein, “targeting” means the process of design and selection of nucleic acid sequence that will hybridize to a target nucleic acid and induce a desired effect.

[000710] *Targeted Cells*: As used herein, “targeted cells” refers to any one or more cells of interest. The cells may be found *in vitro*, *in vivo*, *in situ* or in the tissue or organ of an organism. The organism may be an animal, preferably a mammal, more preferably a human and most preferably a patient.

[000711] *Therapeutic Agent*: The term “therapeutic agent” refers to any agent that, when administered to a subject, has a therapeutic, diagnostic, and/or prophylactic effect and/or elicits a desired biological and/or pharmacological effect.

[000712] *Therapeutically effective amount*: As used herein, the term “therapeutically effective amount” means an amount of an agent to be delivered (*e.g.*, nucleic acid, drug, therapeutic agent, diagnostic agent, prophylactic agent, *etc.*) that is sufficient, when administered to a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition such as for example Parkinson’s Disease. In some embodiments, a therapeutically effective amount is provided in a single dose. In some embodiments, a therapeutically effective amount is administered in a dosage regimen comprising a plurality of doses. Those skilled in the art will appreciate that in some embodiments, a unit dosage form may be considered to comprise a therapeutically effective amount of a particular agent or entity if it comprises an amount that is effective when administered as part of such a dosage regimen.

[000713] *Therapeutically effective outcome*: As used herein, the term “therapeutically effective outcome” means an outcome that is sufficient in a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition.

[000714] *Total daily dose*: As used herein, a “total daily dose” is an amount given or prescribed in 24 hour period. It may be administered as a single unit dose.

[000715] *Transfection*: As used herein, the term “transfection” refers to methods to introduce exogenous nucleic acids into a cell. Methods of transfection include, but are not limited to, chemical methods, physical treatments and cationic lipids or mixtures.

[000716] *Treating*: As used herein, the term “treating” refers to partially or completely alleviating, ameliorating, improving, relieving, delaying onset of, inhibiting progression of, reducing severity of, and/or reducing incidence of one or more symptoms or features of a particular infection, disease, disorder, and/or condition. For example, “treating” cancer may refer to inhibiting survival, growth, and/or spread of a tumor. Treatment may be administered to a subject who does not exhibit signs of a disease, disorder, and/or condition and/or to a subject who exhibits only early signs of a disease, disorder, and/or condition for the purpose of decreasing the risk of developing pathology associated with the disease, disorder, and/or condition such as for example Parkinson’s Disease.

[000717] *Unmodified*: As used herein, “unmodified” refers to any substance, compound or molecule prior to being changed in any way. Unmodified may, but does not always, refer to the wild type or native form of a biomolecule or entity. Molecules or entities may undergo a series of modifications whereby each modified substance, compound, molecule or entity may serve as the “unmodified” starting molecule for a subsequent modification.

[000718] *Vector*: As used herein, a “vector” is any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule. Vectors of the present disclosure may be produced recombinantly and may be based on and/or may comprise adeno-associated virus (AAV) parent or reference sequence. Such parent or reference AAV sequences may serve as an original, second, third or subsequent sequence for engineering vectors. In non-limiting examples, such parent or reference AAV sequences may comprise any one or more of the following sequences: a polynucleotide sequence encoding a polypeptide or multi-polypeptide, which sequence may be wild-type or modified from wild-type and which sequence may encode full-length or partial sequence of a protein, protein domain, or one or more subunits of a protein; a polynucleotide comprising a modulatory or regulatory nucleic acid which sequence may be wild-type or modified from wild-type; and a transgene that may or may not be modified from wild-type sequence. These AAV sequences may serve as either the “donor” sequence of one or more codons (at the nucleic acid level) or amino acids (at the polypeptide level) or “acceptor” sequences of one or more codons (at the nucleic acid level) or amino acids (at the polypeptide level).

[000719] *Viral construct vector*: As used herein, a “viral construct vector” is a vector which comprises one or more polynucleotide regions encoding or comprising Rep and or Cap protein.

[000720] *Viral construct expression vector*: As used herein, a “viral construct expression vector” is a vector which comprises one or more polynucleotide regions encoding or comprising Rep and or Cap that further comprises one or more polynucleotide regions encoding or comprising components for viral expression in a viral replication cell.

[000721] *Viral genome*: As used herein, a “viral genome” is a polynucleotide encoding at least one inverted terminal repeat (ITR), at least one regulatory sequence, and at least one payload. The viral genome is derived by replication of a payload construct from the payload construct expression vector. A viral genome encodes at least one copy of the payload construct.

EQUIVALENTS AND SCOPE

[000722] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the appended claims.

[000723] In the claims, articles such as “a,” “an,” and “the” may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include “or” between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention includes embodiments in which more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process.

[000724] It is also noted that the term “comprising” is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term “comprising” is used herein, the term “consisting of” is thus also encompassed and disclosed.

[000725] Unless otherwise defined, 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 invention belongs. Methods and materials are described herein for use in the present disclosure; other, suitable methods and materials known in the art can also be used.

[000726] Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or subrange within the stated ranges in different embodiments of the invention, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

[000727] In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from any one or more of the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the invention (*e.g.*, any nucleic acid or protein encoded thereby; any method of

production; any method of use; *etc.*) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

[000728] All cited sources, for example, references, publications, databases, database entries, and art cited herein, are incorporated into this application by reference, even if not expressly stated in the citation. In case of conflicting statements of a cited source and the instant application, the statement in the instant application shall control.

[000729] Section and table headings are not intended to be limiting.

EXAMPLES

Example 1. Design of Payloads: AADC polynucleotides

[000730] AADC polynucleotides are designed to comprise at a minimum a nucleic acid sequence encoding an AADC protein.

[000731] Once designed, the sequence is engineered or synthesized or inserted in a plasmid or vector and administered to a cell or organism. Suitable plasmids or vectors are any which transduce or transfect the target cell.

[000732] Adeno-associated viral (AAV) particles may be used.

[000733] Administration results in the processing of the AADC polynucleotide to generate the AADC protein which alters the etiology of the disease, in this case Parkinson's Disease.

[000734] In one non-limiting example, plasmids containing an AADC polynucleotide of the invention have a CMV promoter and encode AADC. In some embodiments the open reading frame of the AADC protein mRNA is codon optimized.

[000735] AADC polynucleotides, listed ITR to ITR, suitable for use in AAV particles include those in Table 2.

Table 2. ITR to ITR AADC polynucleotides

Construct	SEQ ID NO
AADC Polynucleotide	979

[000736] The start and stop positions of various regions of the AADC polynucleotides are given are relative to the ITR to ITR AADC polynucleotides described in Table 2. In Table 3, ITR is inverted terminal repeat, MCS is multiple cloning site, CMV is cytomegalovirus, Ie1 is immediate-

early 1, hBglobin is human beta-globin, AADC is region encoding the AADC polypeptide, and poly(A) is the polyadenylation signal.

Table 3. Component regions of AADC polynucleotides

	AADC Polynucleotide (SEQ ID NO: 979)			
Region	Start	Stop	Length of Region	SEQ ID NO of region
5' ITR	1	141	141	980
MCS	189	206	18	981
CMV enhancer	213	515	303	982
CMV promoter	516	719	204	983
Ie1 exon 1	734	867	134	984
Ie1 intron partial	868	899	32	985
hBglobin intron 2	900	1246	347	986
hBglobin exon 3	1247	1299	53	987
AADC	1338	2777	1440	988
MCS	2820	2837	18	989
Poly(A)	2838	3314	477	990
3' ITR	3386	3526	141	991

Example 2. Design of AADC polynucleotides to treat Parkinson's Disease

[000737] AADC polynucleotides are designed to comprise at a minimum a nucleic acid sequence encoding an AADC protein.

[000738] Once designed, the sequence is engineered or synthesized or inserted in a plasmid or vector and administered to a cell or organism. Suitable plasmids or vectors are any which transduce or transfect the target cell.

[000739] Adeno-associated viral (AAV) particles may be used.

[000740] Administration results in the processing of the AADC polynucleotide to generate the AADC protein which alters the etiology of the disease, in this case Parkinson's Disease.

Example 3. Administration of AAV Particles

[000741] AAV particles are infused into the substantia nigra, and in particular, the substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA) of patients having Parkinson's Disease and identified as qualified for treatment according to methods known in the art.

[000742] One method of administration contemplated for use in the methods described herein is real-time convection-enhanced delivery (RCD) of AAV particle compositions by co-infusion of

gadoteridol (a magnetic resonance (MR) contrast agent) and T1 or T2 magnetic resonance imaging (MRI), which can predict areas of subsequent AADC gene expression. As described in Richardson, *et al.*, 2011, the accuracy of cannula placement and initial infusate distribution may be safely determined by saline infusion without significantly altering the subsequent distribution of the tracer agent (Richardson, *et al.*, 2011, *Neurosurgery*, 69(1):154-163). T2 RCD provides detection of intraparenchymal convection-enhanced delivery in the uninjured brain and may predict subsequent distribution of a transgene after AAV particle infusion. Subjects undergo saline infusion/T2 acquisition, immediately followed by gadoteridol infusion/T1 acquisition in the putamen and brainstem. Distribution volumes and spatial patterns are analyzed. Gadoteridol and AAV-encoded AADC are co-infused under alternating T2/T1 acquisition in the thalamus, and hyperintense areas are compared with areas of subsequent transgene expression. Ratios of distribution volume to infusion volume are expected to be similar between saline and gadoteridol RCD. Spatial overlap should correlate well between T2 and T1 images. The second infusate will follow a spatiotemporal pattern similar to that of the first, filling the target area before developing extra-target distribution. Areas of AADC expression should correlate well with areas of both T1 and T2 hyperintensity observed during RCD (Richardson, *et al.*, 2011, *Neurosurgery*, 69(1):154-163).

[000743] Convection-enhanced delivery (CED) of macromolecules directly into the brain parenchyma has been known for over two decades. CED is a term that denotes the use of a pressure gradient to generate bulk flow within the brain parenchyma, *i.e.* convection of macromolecules within the interstitial fluid driven by infusing a solution through a cannula placed directly in the targeted structure. This method allows therapeutic agents to be homogeneously distributed through large volumes of brain tissue by bypassing the blood brain barrier and surpassing simple diffusion (Richardson, *et al.*, 2011, *Stereotact. Funct. Neurosurg.* 89:141–151).

[000744] Salegio, *et al.* recently demonstrated the distribution of nanoparticles of different sizes, including micelles (~15 nm in size), AAV (~20–25 nm) and liposomes (~65 nm), within the CNS of rodents and NHPs (Salegio *et al.*, 2014, *Frontiers in Neuroanatomy*, vol. 8, article 9: pp. 1-8). Simple injections cannot engage the perivascular system, and specialized infusion cannulae are required, enabling constant pressures to be exerted at the tip of the cannula such that the interstitial hydrostatic pressure is exceeded and infusate can flow out into the tissue. Simple needles generate significant reflux; thus, reflux-resistant cannulas have been developed to counter this tendency. The advent of platforms for MRI-guided convection-enhanced infusions further refined understanding of

the mechanics of perivascular flow, and it was demonstrated that perivascular distribution of liposomes was linear with respect to time, the slope of the curve was increased in myelinated regions, and cessation of infusion prevented further expansion in the volume of distribution. (Richardson, *et al.*, 2011, *Stereotact. Funct. Neurosurg.* 89:141–151; Salegio *et al.*, 2014, *Frontiers in Neuroanatomy*, vol. 8, article 9: pp. 1-8).

[000745] Intraparenchymal rAAV injections are known to result in robust but relatively local transduction. Such local delivery methods are advantageous when attempting gene therapy for neurological disorders that result from neuropathology that is localized to a specific anatomical region or anatomical circuitry such as in the case of Parkinson's disease. However, in treatments requiring more widespread CNS transduction, intraparenchymal injections are impractical. Treatment of neurological disorders attributable to inborn errors of metabolism and/or single-gene defects, or those that affect motor neurons of the spinal cord can require transduction of large proportions of the brain or spinal cord, respectively. Development of less invasive trans-BBB delivery methods for vectors is an extremely important endeavor. Numerous attempts to use molecules that are known to interact with various active transport mechanisms (probably receptor-mediated) to convey proteins across the BBB have been reported with varying results. Given the large number of AAV serotypes available, one or more serotypes may bind a cell-entry receptor capable of transporting the AAV capsid across the BBB (Manfredsson, *et al.*, 2009, "AAV9: a potential blood-brain barrier buster." *Molecular Therapy* 17(3):403-405).

Vector and stereotaxic infusion

[000746] A stereotactic approach may be used to surgically deliver the AADC polynucleotides. Although individuals with AADC deficiency lack epinephrine and norepinephrine, these patients should maintain stable blood pressure and heart rates during the surgery. There should be no notable intracerebral hemorrhages in the postoperative computed tomography (CT) or MRI scans. The needle tracts, as shown on the MRI scans, should show accurate injection into the substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA). The patients will be discharged from the hospital about one week after the surgery (Hwu, W.L., *et al.*, 2012. Gene therapy for aromatic L-amino acid decarboxylase deficiency. *Sci. Transl. Med.* Vol. 4, 134ra61).

[000747] Subjects of treatment receive the AAV-vector composition vector, safely delivered to substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA) via bilateral infusions, or alternatively, intrastrially (into the caudate nucleus and putamen), or into the subthalamic nucleus

(STN), for example optionally using the FDA-approved SMARTFLOW® neuroventricular cannula (SurgiVision, Inc.) specifically designed for clinical application, with or without the aid of the CLEARPOINT® system to help the treating neurosurgeon(s) target and observe the delivery of the therapeutic agent in the brain (*See, for example, San Sebastian, et al., 2014, Mol. Ther. Methods Clin. Dev.* 3: 14049; *See, for example, Feng and Maguire-Zeiss, 2010, CNS Drugs* 24(3):177-192).

[000748] For example, during the surgery, two target points are determined in the substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA) that are sufficiently separated from each other in dorsolateral directions and identified on a magnetic resonance image. One burr hole is trepanned in each side of the cranial bone, through which the vector is injected into the two target points via the two-track insertion route. The AAV-vector-containing solution is prepared to a concentration of 1.5×10^{12} vector genome/ml, and 50 μ l per point of the solution is injected at 1 μ l/min; each patient receives 3×10^{11} vector genome of the AAV-vector construct.

[000749] Neutralizing antibody titers against AAV2 are determined by measuring β -galactosidase activities in HEK293 cells transduced with 5×10^3 vector genome/cell of AAV2 vectors expressing β -galactosidase in various dilutions of sera.

PET

[000750] The AADC expression level in the substantia nigra are assessed on PET imaging with FMT six days before surgery and at one- and six-months after gene transfer. All patients cease taking dopaminergic medications 18 hours before PET and take 2.5mg/kg of carbidopa orally one hour before FMT injection. Subsequently, 0.12mCi/kg of FMT in saline is infused into an antecubital vein, and a 90-minute dynamic acquisition sequence is obtained. The PET and magnetic resonance imaging data are co-registered with a fusion processing program (Syntegra; Philips, Amsterdam, The Netherlands) to produce the fusion images. Radioactivities within volumes of interest drawn in the nigrostriatal pathway are calculated between 80 and 90 minutes after tracer injection. A change in nigrostriatal pathway FMT uptake from baseline to 24 weeks is assessed using the substantia nigra to striatal ratio of radioactivity.

Statistical analysis

[000751] Values at baseline and 6 months after gene transfer are compared using Student's t-test (paired analyses). A two-sided P value <0.05 is taken to indicate significant differences. Two-way analysis of variance with Bonferroni correction of P values is used for the short-duration response to

levodopa. (See, for example, Muramatsu, *et al.*, 2010, “A phase I study of aromatic L-amino acid decarboxylase gene therapy for Parkinson’s disease.” *Mol. Ther.* 18:1731–1735).

[000752] Safety and tolerability of bilateral administration of AAV-vector compositions using real-time image-guided infusion into the brains of Parkinson’s Disease subjects may be monitored for up to or after 9 months post-surgery. Broad coverage of targeted areas (substantia nigra pars compacta (SNpc) and ventral tegmental area (VTA)) and widespread AADC protein distribution in the striatum should be achieved without inducing any adverse effects.

[000753] *Changes in growth and motor skills:* The patients should gain weight and exhibit improvement in their motor scores after gene transfer, within a year, post-treatment. Weight will be measured at 3 to 6 months after gene transfer. All patients initially should have raw scores of zero on the Alberta Infant Motor Scale (AIMS) and very low raw scores for the Peabody Developmental Motor Scale, Second Edition (PDMS-II). After the gene transfer, all of the patients should show continuous increases in their raw scores on these two scales, which indicates that their motor functions have improved. The Comprehensive Developmental Inventory for Infants and Toddlers (CDIIT) covers both cognition and motor development. All of the patients should show low raw CDIIT scores before gene transfer, and the subsequent increase in scores demonstrate improvement in both motor and cognitive functions.

Subjective improvements after gene transfer

[000754] To document the symptoms that are more difficult to quantify, spouses, guardians or caretakers of the patients are asked to fill out a questionnaire at the end of the study. The symptoms of the oculogyric crises should lessen, and eye deviations and sleep disruptions, for example, are some mild symptoms of the oculogyric crises that may remain after gene therapy. Subjects may experience increased emotional stability, and/or some improvements in sweating and hyperthermia (a common manifestation of body temperature instability in hot weather). There should be no detectable abnormality in heart rate variability as assessed by 24-hour Holter monitoring either before or after gene transfer. Before gene therapy, patients that were bedridden and showed little spontaneous movement may exhibit less severe ptosis (drooping of the upper eyelid) one to two weeks after the gene transfer. According to previous studies, dyskinesia may occur one month after gene transfer, but upon observation of a decrease in dyskinesia, motor development should start (Hwu, W.L., *et al.*, 2012. Gene therapy for aromatic L-amino acid decarboxylase deficiency. *Sci. Transl. Med.* Vol. 4, 134ra61). Subjects may exhibit increased head control after three months,

sitting with support after six to nine months, sitting up from the prone position after thirteen months, and holding toys and standing with support sixteen months after the gene transfer, for example. Anti-AAV2 antibodies should be negative in the patients before gene therapy, and the titers may increase slightly after gene transfer.

PET scans and CSF analyses

[000755] PET scans and CSF analyses are completed for the treated patients. Six months after gene transfer, PET scans should reveal that uptake of 6-[18F] fluorodopa (FDOPA) increase from baseline in the combined (right and left) treatment sites. The CSF analysis should reveal increases in the levels of homovanillic acid (HVA, a metabolite of dopamine) and 5-hydroxyindoleacetic acid (HIAA, a metabolite of serotonin). However, the levels of L-DOPA and 3-O-methyldopa may remain elevated (Hwu, W.L., *et al.*, 2012. Gene therapy for aromatic L-amino acid decarboxylase deficiency. *Sci. Transl. Med.* Vol. 4, 134ra61).

Example 4. Administration of AADC Polynucleotides

[000756] AAV particle compositions are infused into the putamen of patients having Parkinson's Disease using the administration methods described in Example 3. The dose, number of patients and volume are outlined in Table 4.

Table 4. Study Design

Study No.	Number of Patients	Dose	Volume
1	6	3×10^{11} vg	100 ul per putamen
2	6	9×10^{11} vg	300 ul per putamen
3	10	2.3×10^{11} vg	100 ul per putamen
4	10	7.5×10^{11} vg	100 ul per putamen
5	5	7.5×10^{11} vg	450 ul per putamen
6	Up to 20	1.4×10^{12} vg	Up to 900 ul per putamen
7	Up to 20	4.8×10^{12} vg	Up to 900 ul per putamen
8	Up to 20	8.8×10^{12} vg	Up to 900 ul per putamen

[000757] During the course of the study the safety and tolerability of the infusion of the AADC polynucleotide-containing recombinant adeno-associated virus (AAV) vector compositions in human patients diagnosed with Parkinson's Disease is evaluated. Patients are evaluated preoperatively and monthly postoperatively for six months, using multiple measures, including the Global Syntonia Scale (GDS) (*see Comella, et al.*, 2003, *Movement Disorders*, 18(3):303–312), L-DOPA challenge test, UPDRS scores, motor state diaries, and laboratory tests. Using diaries that separate the day into half-hour segments, the caregivers of the patients will record their mobility during the four days before admission and for another four days at six months after admission to the

study site. The patient caregivers are trained to rate subject's condition as sleeping, immobile, mobile without troublesome dyskinesias, or mobile with troublesome dyskinesias. The total number of hours spent in each of these categories is calculated, and the differences between the baseline and the six-month scores are compared between the groups. The short-duration response to levodopa is evaluated at baseline and 6 months after gene transfer; subjects take 100 mg of levodopa orally with 25mg benserazide after 20 hours without dopaminergic medication. Motor symptoms based on GDS and plasma levodopa concentrations are assessed at baseline and 30 minutes, 1, 2, 3, and 4 hours after levodopa intake (*See, for example, Muramatsu, et al., 2010, "A phase I study of aromatic L-amino acid decarboxylase gene therapy for Parkinson's disease." Mol. Ther. 18:1731-1735*).

[000758] While the present invention has been described at some length and with some particularity with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the invention.

[000759] All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, section headings, the materials, methods, and examples are illustrative only and not intended to be limiting.

CLAIMS

We claim:

1. An aromatic L-amino acid decarboxylase (AADC) polynucleotide comprising an AADC sequence region which has at least 95% identity to SEQ ID NO: 979.
2. The AADC polynucleotide of claim 1, wherein the AADC sequence region comprises a promoter region, an enhancer region, a multiple cloning site (MCS) region and a polyadenylation (poly(A)) signal region.
3. The AADC polynucleotide of claim 2, wherein the AADC sequence region comprises at least one 5' inverted terminal repeat (ITR) region and one 3' ITR region.
4. The AADC polynucleotide of claim 3, wherein one or more of the 5' ITRs are located 5' to the MCS region and one or more of the 3' ITRs are located 3' to the poly(A) signal.
5. The AADC polynucleotide of claim 3, wherein the AADC sequence region comprises a first exon region, a first intron region, a second intron region and a second exon region.
6. The AADC polynucleotide of claim 5, wherein the enhancer region and the promoter region are derived from CMV.
7. The AADC polynucleotide of claim 6, wherein the first exon region is immediate-early 1 (ie1) exon 1 or fragments thereof, the first intron region is ie1 intron 1 or fragments thereof, the second intron region is human beta-globin (hBglobin) intron 2 or fragments thereof and the second exon region is hBglobin exon 3 or fragments thereof.
8. The AADC polynucleotide of claim 2, wherein the poly(A) signal is derived from human growth hormone.
9. A plasmid or vector encoding the AADC polynucleotide of any of claims 1-8.
10. The plasmid or vector of claim 9 which is or is derived from an adeno-associated virus (AAV).
11. A recombinant AAV virus comprising the AAV plasmid or vector of claim 10.
12. The recombinant AAV virus of claim 11, comprising a capsid serotype selected from the group consisting of AAV2, PHP.B, PHP.A, AAV1, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3,

AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/rh.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38,

AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T, AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101, AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2, AAV Shuffle 100-1, AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8, AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12,

AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, AAVF9/HSC9, PHP.B (AAV-PHP.B), PHP.A (AAV.PHP.A), G2B-26, G2B-13, TH1.1-32, TH1.1-35, AAVPHP.B2, AAVPHP.B3, AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3, AAVG2B4, and/or AAVG2B5, and variants thereof.

13. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAV2.
14. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAVrh10.
15. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAV9 (hu14).
16. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAV-DJ.
17. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAV9.47.
18. The recombinant AAV virus of claim 12, wherein the capsid serotype is AAV-DJ8.
19. The AADC polynucleotide of claim 1, wherein the AADC sequence region has at least 99% identity SEQ ID NO: 979.

20. A pharmaceutical composition comprising an adeno-associated virus (AAV) particle, said AAV particle comprising an AAV capsid and a vector genome, said vector genome comprising at least one AADC sequence region with at least 95% identity to SEQ ID NO: 900.
21. The pharmaceutical composition of claim 20, wherein the AADC sequence region has at least 99% identity SEQ ID NO: 979.
22. The pharmaceutical composition of claim 20, wherein at least 70% of the AAV particles contain a vector genome.
23. A method of reducing periods of dyskinesia in a subject comprising administering to said subject the pharmaceutical composition of claims 20-22.
24. The method of claim 23, wherein the decrease in periods of dyskinesia is shown by improvement in off time and motor fluctuations by at least 30%.
25. The method of claim 24, wherein the improvement lasts for at least 6 hours.
26. The method of any of claims 23-26, wherein the subject has Parkinson's Disease.
27. A method of improving the sleep-wake cycle of a subject comprising administering to said subject the pharmaceutical composition of claims 20-22.
28. The method of claim 27, where the subject's amount of rapid eye movement (REM) sleep is decreased as compared to the subject's amount of REM sleep prior to administration of the pharmaceutical composition.
29. The method of claim 27, wherein the subject's amount of non-REM (NREM) sleep is increased as compared to the subject's amount of REM sleep prior to administration of the pharmaceutical composition.
30. The method of any of claims 27-29, wherein the subject has Parkinson's Disease.
31. A method of treating a sleep disorder of a subject comprising administering to said subject the pharmaceutical composition of claims 20-22.
32. The method of claim 31, wherein the sleep disorder is insomnia.
33. The method of any of claims 31 or 32, wherein the subject has Parkinson's Disease.
34. A method of increasing the level of AADC protein in a subject comprising administering the pharmaceutical composition of claims 20-22.

FIG. 1

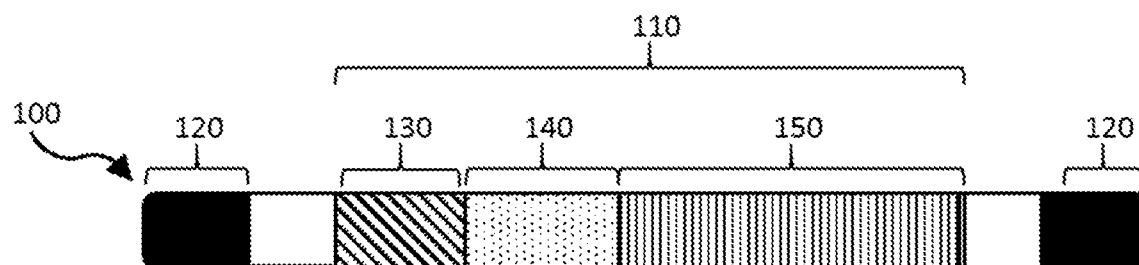


FIG. 1

