ADENO-ASSOCIATED VIRUS VARIANT CAPSIDS AND USE FOR INHIBITING ANGIOGENESIS

CROSS-REFERENCE TO RELATED APPLICATIONS

[001] This application claims the benefit of United States Provisional Patent Application Serial Nos. 62/590,976, filed November 27, 2017 and 62/664,726, filed April 30, 2018, the full disclosures of each of which are incorporated herein by reference.

INCORPORATION BY REFERENCE OF A SEQUENCE LISTING PROVIDED AS A TEXT FILE

[002] A Sequence Listing is provided herewith as a text file, "090400-5010-WO-seq-listing.txt" created on November 26, 2018 and having a size of 238 KB. The contents of the text file are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

[003] The invention disclosed herein relates generally to the field of adeno-associated virus (AAV) virions comprising variant capsid proteins and the generation of such variant capsids using directed evolution techniques.

BACKGROUND OF THE DISCLOSURE

[004] Inherited retinal diseases encompass a large group of heterogenous genetic diseases that affect approximately 1 in 3000 people (greater than 2 million people worldwide) and are a major source of severe vision loss or blindness. Complex, multifactoral retinal diseases such as wet age related macular degeneration (wAMD) and diabetic retinopathy (DR) impact even more individuals, with 1.7 million Americans currently living with severe central vision loss associated with wAMD and almost one-third of adults over age 40 years with diabetes being visually impaired. These diseases are typically associated with the dysfunction or death of one or more types of cell of the retina, in some instances due to the absence of expression or function of a key protein, e.g. RPE65 in LCA2, in other instances due to gene mutations that create toxic gene products, e.g. dominant mutations that affect rhodopsin protein folding, or in yet other instances due to changes in retinal physiology induced by the ectopic expression of a protein, e.g. VEGF in wAMD.

[005] One approach to addressing this great unmet medical need is gene-based adeno-associated virus (AAV)-mediated therapy, in which a recombinant adeno associated virus (rAAV) is used to deliver a gene to one or more types of cells in the retina, for example to replace a missing gene, to correct a dominant defective gene, or to provide a template for continuous protein therapy. While AAV-based clinical gene therapy has been increasingly successful, it is still fraught with shortcomings with regard to viral vector properties, including, for example, targeting the desired cells of the retina with high efficiency. For example, multiple homologous primate AAV serotypes and numerous nonhuman primate serotypes have been identified and characterized, with AAV2 being the best characterized among the AAV serotypes and the first to be adapted as a gene delivery vehicle in the eye. However, these AAVs (including AAV2) have not been reported to be effective at transducing the deeper cell types of the retina when delivered via intravitreal administration. Accordingly, there is a need in the art for new AAV variants with superior transduction capabilities that will provide for more effective gene-based delivery to the cells of the retina for the treatment of ocular disease. There is a need in the art for such AAV variants which exhibit an enhanced retinal transduction profile -- in some instances broadly, in other instances preferentially to certain retinal cell types -- as compared to wild-type AAVs and AAV variants as known in the art.

[006] Naturally occurring AAV is a single stranded DNA virus that contains three open reading frames, *rep*, *cap,* and *aap*. The first gene, *rep*, encodes four proteins necessary for genome replication (Rep78, Rep68, Rep52, and Rep40), the second, *cap*, expresses three structural proteins (VP1-3) that assemble to form the viral capsid, and the third expresses the assembly activating protein (AAP) that is essential for capsid assembly. AAV is dependent upon the presence of a helper virus, such as an adenovirus or herpesvirus, for active replication. In the absence of a helper virus, AAV establishes a latent state in which its genome is maintained episomally or integrated into the host chromosome in the AAVS1 locus.

[007] *In vitro* and *in vivo*-directed evolution techniques may be used to select for AAV variants that offer an improvement over current AAV-based gene delivery vectors. Such directed evolution techniques are known in the art and described, *e.g.*, in PCT publication WO 2014/194132 and Kotterman & Schaffer (Nature Review Genetics, AOP, published online 20 May 2014; doi: 10.1038/nrg3742), both of which are incorporated herein in their entirety by reference. Directed evolution is a capsid

engineering approach that emulates natural evolution through iterative rounds of genetic diversification and selection processes, thereby enabling the accumulation of beneficial mutations that progressively improve the function of a biomolecule such as an AAV-based virion. In this approach, wild-type AAV *cap* genes are diversified to create large genetic libraries that are packaged to generate libraries of viral particles, and selective pressure is applied to isolate unique variants with superior phenotypes that can overcome gene delivery barriers.

[008] AAV variants have been disclosed in, for example, in United States Patent Numbers 9,193,956; 9;186;419; 8,632,764; 8,663,624; 8,927,514; 8,628,966; 8,263,396; 8,734,809; 8,889,641; 8,632,764; 8,691,948; 8,299,295; 8,802,440; 8,445,267; 8,906,307; 8,574,583; 8,067,015; 7,588,772; 7,867,484; 8,163,543; 8,283,151; 8,999,678; 7,892,809; 7,906,111; 7,259,151; 7,629,322; 7,220,577; 8,802,080; 7,198,951; 8,318,480; 8,962,332; 7,790,449; 7,282,199; 8,906,675; 8,524,446; 7,712,893; 6,491,907; 8,637,255; 7,186,522; 7,105,345; 6,759,237; 6,984,517; 6,962,815; 7,749,492; 7,259,151; and 6,156,303; United States Publication Numbers 2013/0295614; 2015/0065562; 2014/0364338; 2013/0323226; 2014/0359799; 2013/0059732; 2014/0037585; 2014/0056854; 2013/0296409; 2014/0335054 2013/0195801; 2012/0070899; 2011/0275529; 2011/0171262; 2009/0215879; 2010/0297177; 2010/0203083; 2009/0317417; 2009/0202490; 2012/0220492; 2006/0292117; and 2004/0002159; European Publication Numbers 2692731 A1; 2383346 B1; 2359865 B1; 2359866 B1; 2359867 B1; and 2357010 B1; 1791858 B1; 1668143 B1; 1660678 B1; 1664314 B1; 1496944 B1; 1456383 B1; 2341068 B1; 2338900 B1; 1456419 B1; 1310571 B1; 1456383 B1; 1633772 B1; and 1135468 B1; and International (PCT) Publication Numbers WO 2014/124282; WO 2013/170078; WO 2014/160092; WO 2014/103957; WO 2014/052789; WO 2013/174760; WO 2013/123503; WO 2011/038187; and WO 2008/124015; WO 2003/054197; however, none of these references disclose the embodiments and/or features and/or composition of matter structures of the AAV variants disclosed herein.

[009] All documents and references cited herein and in the referenced patent documents, are hereby incorporated herein by reference.

SUMMARY OF THE INVENTION

[0010] Provided herein are variant adeno-associated virus (AAV) capsid proteins having one or more modifications in amino acid sequence relative to a

parental AAV capsid protein, which, when present in an AAV virion, confer increased infectivity of one or more types of retinal cells as compared to the infectivity of the retinal cells by an AAV virion comprising an unmodified parental AAV capsid protein. Also provided are recombinant AAV virions and pharmaceutical compositions thereof comprising a variant AAV capsid protein as described herein, methods of making variant rAAV capsid proteins and virions, and methods for using these rAAV capsid proteins and virions in research and in clinical practice, for example in the delivery of nucleic acid sequences to one or more cells of the retina for the treatment of retinal disorders and diseases.

[0011] In some aspects of the disclosure, variant adeno-associated virus (AAV) capsid proteins are provided, these variant AAV capsid proteins having one or more modifications in amino acid sequence relative to a parental AAV capsid, which, when present in an AAV virion, confer increased infectivity of one or more types of retinal cells (e.g. a photoreceptor cell (e.g. rods; cones), a retinal ganglion cell (RGC), a glial cell (e.g. a Müller glial cell, a microglial cell), a bipolar cell, an amacrine cell, a horizontal cell, and/or a retinal pigmented epithelium (RPE) cell) as compared to the infectivity of the retinal cells by an AAV virion comprising a parental AAV capsid protein that does not comprise the amino acid sequence modification.

[0012] In some aspects of the disclosure, recombinant AAV (rAAV) virions are provided, these rAAV virions comprising a variant capsid protein as described herein, wherein the rAAV virions exhibit increased infectivity of one or more types of retinal cells (e.g. a photoreceptor cell (e.g. rods; cones), a retinal ganglion cell (RGC), a glial cell (e.g. a Müller glial cell, a microglial cell), a bipolar cell, an amacrine cell, a horizontal cell, and/or a retinal pigmented epithelium (RPE) cell) relative to the infectivity of the retinal cell by an AAV virion comprising a corresponding unmodified parental AAV capsid protein. In some embodiments, the rAAV virion exhibits increased infectivity of all retinal cells relative to the AAV virion comprising the parental AAV capsid protein. In other embodiments, the rAAV virion exhibits increased infectivity of certain cell types of the retina but not others relative of the AAV virion comprising the parental AAV capsid protein. Put another way, the rAAV virion exhibits increased infectivity that is preferential for certain cell types of the retina but not others, e.g. the rAAV demonstrates a preferentially increased infectivity of one or more cell types selected from photoreceptor cells, retinal ganglion cells, glial cells, bipolar cells, amacrine cells, horizontal cells, and/or

retinal pigmented epithelium (RPE) cells, but does not demonstrate increased infectivity of all cell types.

[0013] In some embodiments, the rAAV virion comprises a heterologous nucleic acid. In some such embodiments, the heterologous nucleic acid encodes an RNA that encodes a polypeptide. In other such embodiments, the heterologous nucleic acid sequence encodes an RNA that does not encode a polypeptide, e.g. the heterologous nucleic acid sequence encodes an RNA interference agent, a guide RNA for a nuclease, etc.

[0014] Also provided herein are pharmaceutical compositions comprising the subject infectious rAAV virions and a pharmaceutically acceptable carrier.

[0015] Also provided is the use of an rAAV virion comprising a variant capsid protein as herein described in a method of delivering a heterologous nucleic acid to a target cell (such as a retinal cell) by contacting the target cell with the rAAV virion. In some embodiments, the target cell is *in vivo*, such as in the eye of an individual in need of treatment for an ocular disease. In other embodiments, the target cell is *in vitro*.

[0016] Also provided are methods of treating an ocular disease by administering to a subject in need of such treatment an effective amount of rAAV virions comprising a variant capsid protein as herein described or a pharmaceutical composition comprising an effective amount of the rAAV virions.

[0017] Also provided is an isolated nucleic acid comprising a sequence encoding a variant AAV capsid protein as described herein and a host cell comprising the isolated nucleic acid. In yet other embodiments, the isolated nucleic acid and/or isolated host cell comprises the rAAV.

[0018] In some aspects, the variant AAV capsid protein comprises an insertion of from about 5 amino acids to about 20 amino acids (a "heterologous peptide", or "peptide insertion") in the GH-loop of the capsid protein, relative to a corresponding parental AAV capsid protein, wherein the variant capsid protein, when present in an AAV virion, confers increased infectivity of a retinal cell compared to the infectivity of a retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein. In some embodiments, the peptide comprises the sequence selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN

(SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), QANANEN (SEQ ID NO:22), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LANQDYTKTA (SEQ ID NO:31), LAHDITKNIA (SEQ ID NO:32), LAHPDTTKNA (SEQ ID NO:33), LAHQDTTKNA (SEQ ID NO:34), LANKTTNKDA (SEQ ID NO:35), LPISNENEHA (SEQ ID NO:36), LPQANANENA (SEQ ID NO:37), LAGKSKVIDA (SEQ ID NO:38), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40) and LAKDRAPSTA (SEQ ID NO:41). In some embodiments, the peptide consists essentially of the sequence selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), QANANEN (SEQ ID NO:22), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LANQDYTKTA (SEQ ID NO:31), LAHDITKNIA (SEQ ID NO:32), LAHPDTTKNA (SEQ ID NO:33), LAHQDTTKNA (SEQ ID NO:34), LANKTTNKDA (SEQ ID NO:35), LPISNENEHA (SEQ ID NO:36), LPQANANENA (SEQ ID NO:37), LAGKSKVIDA (SEQ ID NO:38), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40) and LAKDRAPSTA (SEQ ID NO:41). In some aspects, the variant AAV capsid protein comprises one or more amino acid substitutions relative to a corresponding parental AAV capsid protein, wherein the variant capsid protein, when present in an AAV virion, confers increased infectivity of a retinal cell compared to the infectivity of a retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein.

[0019] In related aspects, the variant AAV capsid protein comprises a peptide insertion and one or more amino acid substitutions relative to a corresponding parental AAV capsid protein, wherein the variant capsid protein, when present in an AAV virion, confers increased infectivity of a retinal cell compared to the infectivity

of a retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein.

[0020] Also disclosed herein is a variant AAV capsid protein comprising the heterologous peptide LAISDQTKHA (SEQ ID NO:28) and a P34A substitution relative to AAV2. In related embodiments, disclosed herein is an infectious recombinant AAV comprising a variant AAV capsid protein at least 90% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising a sequence encoding a VEGF inhibitor, preferably a VEGFa inhibitor, and a pharmaceutical composition comprising the same. In some embodiments, the heterologous nucleic acid sequence encoding a VEGF inhibitor is selected from a sequence encoding Aflibercept, Ranibizumab, a single-chain version of Ranibizumab (sc-Ranibizumab LH or HL), Brolucizumab, sc-Ranibizumab fused to the IgG Fc domain (sc-Ranibizumab-Fc), or Brolucizumab fused to the IgG Fc domain (Brolucizumab-Fc). In related embodiments, the recombinant AAV comprises a heterologous nucleic acid comprising two or more sequences, each of which encodes a VEGFa inhibitor (e.g. a first sequence encoding Aflibercept and a second sequence encoding Brolucizumab). In preferred embodiments, the heterologous nucleic acid sequence has a sequence of any one of SEQ ID NOs:65, 67, 69, 70, 72, 74, 76 or a sequence at least 90% identical thereto. In other related embodiments, a method for treating a patient with an eye disease associated with elevated intraocular VEGFa levels is provided, comprising administering to the patient, preferably via intravitreal injection, an effective amount of an infectious recombinant AAV comprising a variant AAV capsid protein at least 90% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising a sequence encoding a VEGF inhibitor.

[0021] Also disclosed herein is a variant AAV capsid protein comprising the heterologous peptide LAISDQTKHA (SEQ ID NO:28) and amino acid substitutions N312K, N449D, N551S, I698V, and L735Q relative to AAV2.

[0022] Also disclosed herein are methods for manufacture and/or delivery of an rAAV comprising a variant AAV capsid as disclosed herein. In addition, provided herein are kits comprising an rAAV comprising a variant AAV capsid as disclosed herein and for use in methods described herein.

[0023] In other embodiments, the AAV virion comprising the variant capsid protein in the preceding paragraphs may incorporate any of the preceding or subsequently disclosed embodiments. Indeed, it is appreciated that certain features of

the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[0024] The Summary of the Invention is not intended to define the claims nor is it intended to limit the scope of the invention in any manner.

[0025] Other features and advantages of the invention disclosed herein will be apparent from the following Figures, Detailed Description, and the Claims.

[0026] Before the present methods and compositions are described, it is to be understood that this invention is not limited to a particular method or composition described and as such may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0027] The invention disclosed herein is illustrated in the figures and description. However, while particular embodiments are illustrated in the figures, there is no intention to limit the invention to the specific embodiment or embodiments illustrated and/or disclosed. Rather, the invention disclosed herein is intended to cover all modifications, alternative constructions, and equivalents falling within the spirit and scope of the invention. As such, the figures are intended to be illustrative and not restrictive.

[0028] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limits of that range is also specifically disclosed. Each smaller range between any stated value or intervening value in a stated range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included or excluded in the range, and each range where

either, neither or both limits are included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

[0029] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, some potential and preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited. It is understood that the present disclosure supersedes any disclosure of an incorporated publication to the extent there is a contradiction.

[0030] As will be apparent to those of skill in the art upon reading this disclosure, each of the individual embodiments described and illustrated herein has discrete components and features which may be readily separated from or combined with the features of any of the other several embodiments without departing from the scope or spirit of the present invention. Any recited method can be carried out in the order of events recited or in any other order which is logically possible.

[0031] It is noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a recombinant AAV virion” includes a plurality of such virions and reference to “the photoreceptor cell” includes reference to one or more photoreceptor cells and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as “solely,” “only” and the like in connection with the recitation of claim elements, or use of a “negative” limitation.

[0032] The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed

BRIEF DESCRIPTION OF THE FIGURES

[0033] The invention is best understood from the following detailed description when read in conjunction with the accompanying drawings. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee. It is emphasized that, according to common practice, the various features of the drawings are not to-scale. On the contrary, the dimensions of the various features are arbitrarily expanded or reduced for clarity. Included in the drawings are the following figures.

[0034] **Figure 1** depicts embodiments of a directed evolution methodology. Step (a) depicts the generation of a viral capsid library comprising combinations of DNA mutation techniques and *cap* genes. Step (b) depicts the packaging of the viruses such that each viral particle is composed of a mutant capsid surrounding the *cap* gene encoding that capsid and purified. The capsid library is then placed under selective pressure *in vitro* or *in vivo*. In this aspect of the directed evolution technology, tissues or cellular material of interest are harvested for isolation of AAV variants that have successfully infected that target, and the successful viruses are recovered. Step (c) depicts the Stage 1 enrichment of successful clones through repeated selection. Step (d) depicts the Stage 2 enrichment of selected *cap* genes which undergo re-diversification and further selection steps to iteratively increase viral fitness. Step (e) depicts the variants, identified as hits during Vector Selection Stages 1 and 2, which will be manufactured as recombinant AAV vectors and characterized for the level of transduction of various cell types and tissue targets. By the nature of the AAV directed evolution process, variants that are disclosed herein have already demonstrated the ability to transduce retinal cells and deliver a genome (the genome encoding the variant *cap* gene) during the selection process.

[0035] **Figure 2** provides a retinal flat mount schematic showing where samples from which viral genomes are amplified, are collected across a broad area of the retina.

[0036] **Figure 3** shows a PCR amplification of viral genomes from the ganglion cell layer (GCL), inner nuclear layer (INL), photoreceptor/outer nuclear layer (ONL), and retinal pigment epithelia (RPE) layer retinal tissue from a representative round of selection. Both the right eye (top image) and left eye (bottom

image) were injected with library. Inner retina (in), middle retina (mid), and outer/peripheral retina (out) were sampled. Bands within red boxes represent successful amplification of viral genomes.

[0037] **Figure 4A-4D** shows frequency of motifs within sequencing analysis. Figure 4A provides Round 3 sequencing analysis. Figure 4B provides Round 4 sequencing analysis. Figure 4C provides Round 5 sequencing analysis. Figure 4D provides Round 6 sequencing analysis.

[0038] **Figure 5** provides a representative three-dimensional model of AAV2 containing a random heptamer following amino acid 587.

[0039] **Figure 6A-6W** provides an alignment of wild-type AAV SEQ ID NOS:1-11 showing amino acid locations between and across the wild-type (naturally occurring) serotypes AAV1, AAV2, AAV3A, AAV3B, and AAV4-10.

[0040] **Figure 7** provides fundus fluorescence images taken with a Heidelberg Spectralis™ of the retina of an African Green monkey following intravitreal administration of $2x10^{11}$ vector genomes (vg) of AAV2 delivering a GFP transgene under the control of the CMV promoter (AAV2.CMV.GFP). Images were taken at baseline (A) and at 14 days (B), 28 days (C), and 42 days (D) after injection.

[0041] **Figure 8** provides fundus fluorescence images taken with a Heidelberg Spectralis™ the retina of an African Green monkey following intravitreal administration of $2x10^{11}$ vector genomes (vg) of the novel AAV variant LAISDQTKHA+P34A delivering a GFP transgene under the control of the CMV promoter (LAISDQTKHA+P34A.CMV.GFP). Images taken at baseline (A) and at 14 days (B), 28 days (C), and 42 days (D) after injection.

[0042] **Figure 9** provides fundus fluorescence images taken with a Heidelberg Spectralis™ of the retinas of Cynomolgus monkeys following intravitreal administration of the novel AAV variant LAISDQTKHA+P34A delivering a GFP transgene under the control of the CAG promoter (LAISDQTKHA+P34A.CAG.EGFP). (A) The retina of a monkey injected intravitreally with $2x10^{11}$ vg of vector, imaged 14 days (A1), 21 days (A2), and 28 days (A3) after injection. (B) The retina of a monkey injected intravitreally with $1x10^{12}$ vg of vector, imaged 14 days (B1) and 21 days (B2) after injection.

[0043] **Figures 10A-10E** provide the results of immunohistochemical analysis of the retina of a monkey injected intravitreally with $1x10^{12}$ vg of the novel AAV variant LAISDQTKHA+P34A delivering a GFP transgene under the control of

the CAG promoter, analyzed three weeks after injection. All immunohistochemistry is provided alongside the corresponding fundus fluorescence image, with a red box to denote approximately where in the retina the analysis was performed. Figure 10A: Robust retinal pigment epithelium (RPE) and photoreceptor transduction was observed using a GFP-specific antibody (red). Cone photoreceptor immunostaining using an M/L opsin antibody is shown in white. Figures 10B and 10C: Robust rod and cone photoreceptor (Figure 10B) and RPE (Figure 10C) transduction was observed by direct EGFP fluorescence (green) and by immunohistochemistry using a GFP-specific antibody (red). Melanosomes in RPE appear black in the image. Figure 10D: Transduction of cone photoreceptors (identified by M/L opsin, white) and retinal ganglion cells (RGC) in and around the fovea was observed by direct EGFP fluorescence (green) and by immunohistochemistry using a GFP-specific antibody (red). Images in the middle panels are a higher magnification (63X) of the area denoted by a white box in the left panel. Figure 10E: Transduction of retinal ganglion cells (RGC) and the retinal ganglion cell layer was observed by direct EGFP fluorescence (right panels, green; lower right panel is a 63X magnification of the upper right panel); top left panel shows the region under brightfield illumination.

[0044] Figures 11A-11F provides data on the transduction of human retinal pigment epithelial (RPE) cells in vitro by recombinant AAV virus comprising the novel AAV variant LAISDQTKHA+P34A capsid and a GFP transgene under the control of the CAG promoter. Cells that were differentiated into RPE cells from a human embryonic stem cell line (Figures 11A and 11C) or from human fibroblast-derived induced pluripotent stem cells (FB-iPSC) (Figures 11B and 11D) were infected with novel AAV variant LAISDQTKHA+P34A.CAG.GFP or wild type control AAV2.CAG.GFP. Figures 11A and 11B: Immunofluorescence imaging of the cell cultures 7 days after infection at an MOI of 500 demonstrates that the novel AAV variant capsid (left panels) transduces RPE cells better than wild type AAV2 capsid (right panels). Figures 11C and 11D: Quantification of the percent of GFP-positive RPE cells in each culture by flow cytometry reveals that the novel AAV variant capsid provides for a significant, dose-dependent improvement in the number of cells transduced over wild type AAV2 capsid regardless of cell source. Figures 11E and 11F: Quantification of the amount of GFP in each culture by Western blot reveals that the novel AAV variant provides for significant improvement in expression of the transgene over wild type capsid regardless of cell source.

[0045] **Figures 12A-12F** depict embodiments of anti-VEGF proteins. Fig. 12A depicts the Aflibercept design, which consists of the human Flt1 signal peptide, VEGFR1 domain 2, and VEGFR2 domain 3 fused to the Fc region of human IgG1. Figs. 12B-C depict the Ranibizumab designs, which include a flexible protein linker to convert the two-chain antigen-binding fragment (Fab) into a single-chain Fab (scFab). Fig. 12B depicts the Light-Heavy (LH) form, which consists of the human Ig kappa light chain signal peptide, the variable light, constant light, variable heavy, and constant heavy 1 domains of Ranibizumab linked by the flexible peptide. Fig. 12C depicts the Heavy-Light (HL) form, which is similar except the signal peptide is derived from the human IgG heavy chain and the heavy and light domains are on opposite sides of the linker as compared to the LH form. Fig. 12D depicts the Brolucizumab design, which includes variable light and variable heavy domains linked by a flexible peptide. Fig. 12E depicts the sc-Ranibizumab LH-Fc design consists of the scFab LH form fused to the Fc region of human IgG1. Fig. 12F depicts the Brolucizumab-Fc design, which consists of the Brolucizumab fused to the Fc region of human IgG1. Red stripes represent complementarity-determining regions (CDRs). Genes were codon-optimized for improved expression from human cells and synthesized by GeneArt or GenScript and inserted into pAAV-CAG-SV40 pA vector between the CAG promoter and the SV40 polyA signal.

[0046] **Figures 13A-B** show the result of an ELISA to detect proteins that bind to VEGF. Fig. 13A shows VEGF-binding activity was detected in media from HEK293T cells transfected with Aflibercept (SEQ ID NO:65) or single-chain (sc) Ranibizumab (SEQ ID NOs:67, 69, and 70) expression plasmids but not from those mock-transfected or transfected with a GFP expression vector. Fig. 13B shows VEGF-binding activity was detected in media from HEK293T cells transfected with Aflibercept (SEQ ID NO:65), sc-Ranibizumab LH1 (SEQ ID NO:69), or Brolucizumab (SEQ ID NO:74) expression plasmids but not from those transfected with a GFP expression vector. The signal with Brolucizumab is very low, most likely due to poor recognition by the detection antibody. Error bars represent the standard deviation of quadruplicate transfection wells.

[0047] **Figures 14A-B** provide representative Western blots of media from HEK293T cells transfected with anti-VEGF constructs. Fig. 14A shows Aflibercept (SEQ ID NO:65) or sc-Ranibizumab (SEQ ID NOs:67, 69, and 70) expression plasmids. Both the clinical Eylea and the Aflibercept sample are reduced to separate

halves of the dimer, of apparent molecular mass of 58 kD (including glycosylation). The clinical Lucentis is reduced into separate light and heavy chains of 24 kD, whereas the sc-Ranibizumab proteins are not separated and migrate at approximately 48 kD. A higher quantity of the LH forms of the protein are present compared to the HL form of the protein, consistent with the protein quantification obtained through ELISA. Fig. 14B shows Aflibercept (SEQ ID NO:65), sc-Ranibizumab LH1 (SEQ ID NO:69), or Brolucizumab (SEQ ID NO:74) expression plasmids. The signal with Brolucizumab is low, most likely due to poor recognition by the detection antibody. The protein migrates at the correct molecular mass of 26 kD. There was no signal in any of the mock transfection or GFP negative control sample.

[0048] **Figures 15A-B** show the result of a competition ELISA to detect free VEGF after incubation with media from HEK293T cells transfected with anti-VEGF constructs. Fig. 15A shows Aflibercept (SEQ ID NO:65) or sc-Ranibizumab (SEQ ID NOs:67, 69, and 70) expression plasmids. The inhibition curves of the four anti-VEGF proteins from the transfected samples were very similar to the clinical comparator proteins Eylea and Lucentis. Aflibercept and Eylea competed for VEGF more strongly than the sc-Ranibizumab variants and Lucentis. All three forms of sc-Ranibizumab were nearly identical. Fig. 15B shows Aflibercept (SEQ ID NO:65), sc-Ranibizumab LH1 (SEQ ID NO:69), or Brolucizumab (SEQ ID NO:74) expression plasmids. There was no competition activity from the GFP negative control sample. Error bars represent the standard deviation of duplicate transfection wells.

[0049] **Figure 16** shows the result of a cellular VEGF neutralization assay. The assay uses HEK293 cells expressing VEGF receptor/beta-galactosidase fusion proteins that produce active beta-galactosidase upon VEGF binding. The cells are incubated with mixtures of VEGF and various dilutions of media from HEK293T cells transfected with Aflibercept (SEQ ID NO:65) or sc-Ranibizumab (SEQ ID NO:69) expression plasmids. The inhibition curves of the anti-VEGF proteins from the transfected samples demonstrate that the anti-VEGF proteins neutralize VEGF activity at levels equal to the clinical comparator proteins. Error bars represent the standard deviation of duplicate assay wells.

[0050] **Figures 17A-B** shows the result of a cellular VEGF neutralization assay performed with equal volumes of media from HEK293T cells transfected with anti-VEGF plasmids. Fig. 17A shows GFP, Aflibercept (SEQ ID NO:65), sc-Ranibizumab HL (SEQ ID NO:67), or sc-Ranibizumab LH1 (SEQ ID NO:69)

expression plasmids. All anti-VEGF constructs evaluated neutralized VEGF. Fig. 17B shows GFP, Aflibercept (SEQ ID NO:65), sc-Ranibizumab LH1 (SEQ ID NO:69), and Brolucizumab (SEQ ID NO:74) expression plasmids. All anti-VEGF constructs evaluated neutralized VEGF. There was a slight matrix effect from the GFP control sample at the dilutions assayed. Error bars represent the standard deviation of duplicate transfection wells.

[0051] **Figure 18** shows the result of an ELISA to detect VEGF in media from RPE cells transfected with Aflibercept (SEQ ID NO:65) or sc-Ranibizumab (SEQ ID NOs:67, 69, and 70) expression plasmids. A reduction in VEGF levels by both Aflibercept expression and sc-Ranibizumab expression was observed. The effect on VEGF levels by all three sc-Ranibizumab forms was similar. Error bars represent the standard deviation of quadruplicate transfection wells.

[0052] **Figure 19** shows the result of an ELISA to detect VEGF in media collected from RPE cells six or ten days after transduction with the R100 capsid (having the amino acid sequence set forth as SEQ ID NO:42) expressing Aflibercept (SEQ ID NO:65), sc-Ranibizumab (SEQ ID NOs:67 and 69), or Brolucizumab (SEQ ID NO:74) transgenes. The endogenous level of VEGF as indicated by the cells transduced with a GFP control vector was 4,500 to 8,300 pg/ml. Transduction with all of the anti-VEGF vectors resulted in undetectable levels of VEGF in the media. Error bars represent the standard deviation of quadruplicate transduction wells.

[0053] **Figure 20** shows the result of an ELISA to detect proteins that bind to VEGF in media collected from RPE cells six or ten days after transduction with the R100 capsid (having the amino acid sequence set forth as SEQ ID NO:42) expressing anti-VEGF transgenes. VEGF-binding activity was detected in media from cells transduced with Aflibercept (SEQ ID NO:65), sc-Ranibizumab (SEQ ID NOs:67 and 69), or Brolucizumab (SEQ ID NO:74) expression vectors but not from those transduced with a GFP expression vector. The signal with Brolucizumab is very low, most likely due to poor recognition by the detection antibody. Error bars represent the standard deviation of quadruplicate transduction wells.

[0054] **Figure 21** provides a representative Western blot of media collected from RPE cells six or ten days after transduction with the R100 capsid (having the amino acid sequence set forth as SEQ ID NO:42) expressing anti-VEGF transgenes. Both the clinical Eylea and the Aflibercept (SEQ ID NO:65) sample are reduced to separate halves of the dimer, of apparent molecular mass of 60 kD

(including glycosylation), as indicated by the black arrow. There was no band of the correct mobility in the GFP negative control sample. The clinical Lucentis is reduced into separate light and heavy chains of 24 kD, whereas sc-Ranibizumab HL and LH (SEQ ID NOs:67 and 69) are not separated and migrate at apparent molecular mass of 58 kD, as indicated by the gray arrow. The signal with Brolucizumab (SEQ ID NO:74) is low, most likely due to poor recognition by the detection antibody. The protein migrates at the correct molecular mass of 26 kD, as indicated by the stippled arrow.

[0055] **Figure 22** shows the result of a competition ELISA to detect free VEGF after incubation with media collected from RPE cells six or ten days after transduction with the R100 capsid (having the amino acid sequence set forth as SEQ ID NO:42) expressing anti-VEGF transgenes. All anti-VEGF constructs competed for VEGF. There was no competition activity from the GFP negative control sample. Free VEGF levels are higher in the lowest dilutions due to the endogenous VEGF produced by the RPE cells. Error bars represent the standard deviation of duplicate assay wells.

[0056] **Figure 23** shows the result of a cellular VEGF neutralization assay performed with media collected from RPE cells six days after transduction with the R100 capsid (having the amino acid sequence set forth as SEQ ID NO:42) expressing anti-VEGF transgenes. All anti-VEGF constructs evaluated neutralized VEGF. There was no VEGF neutralization observed with media from the GFP control transduction. Error bars represent the standard deviation of duplicate assay wells.

DEFINITIONS

[0057] Unless otherwise defined, all scientific and technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this technology belongs.

[0058] Adeno-associated virus is a nonpathogenic parvovirus composed of a 4.7 kb single-stranded DNA genome within a non-enveloped, icosahedral capsid. The genome contains three open reading frames (ORF) flanked by inverted terminal repeats (ITR) that function as the viral origin of replication and packaging signal. The *rep* ORF encodes four nonstructural proteins that play roles in viral replication, transcriptional regulation, site-specific integration, and virion assembly. The *cap* ORF encodes three structural proteins (VP 1-3) that assemble to form a 60-mer viral capsid. Finally, an ORF present as an alternate reading frame within the *cap* gene produces

the assembly- activating protein (AAP), a viral protein that localizes AAV capsid proteins to the nucleolus and functions in the capsid assembly process.

[0059] There are several naturally occurring ("wild-type") serotypes and over 100 known variants of AAV, each of which differs in amino acid sequence, particularly within the hypervariable regions of the capsid proteins, and thus in their gene delivery properties. No AAV has been associated with any human disease, making recombinant AAV attractive for clinical applications.

[0060] For the purposes of the disclosure herein, the terminology "AAV" is an abbreviation for adeno-associated virus, including, without limitation, the virus itself and derivatives thereof. Except where otherwise indicated, the terminology refers to all subtypes or serotypes and both replication-competent and recombinant forms. The term "AAV" includes, without limitation, AAV type 1 (AAV-1 or AAV1), AAV type 2 (AAV-2 or AAV2), AAV type 3A (AAV-3A or AAV3A), AAV type 3B (AAV-3B or AAV3B), AAV type 4 (AAV-4 or AAV4), AAV type 5 (AAV-5 or AAV5), AAV type 6 (AAV-6 or AAV6), AAV type 7 (AAV-7 or AAV7), AAV type 8 (AAV-8 or AAV8), AAV type 9 (AAV-9 or AAV9), AAV type 10 (AAV-10 or AAV10 or AAVrh10), avian AAV, bovine AAV, canine AAV, caprine AAV, equine AAV, primate AAV, non-primate AAV, and ovine AAV. "Primate AAV" refers to AAV that infect primates, "non-primate AAV" refers to AAV that infect non-primate mammals, "bovine AAV" refers to AAV that infect bovine mammals, *etc.*

[0061] The genomic sequences of various serotypes of AAV, as well as the sequences of the native terminal repeats (TRs), Rep proteins, and capsid subunits are known in the art. Such sequences may be found in the literature or in public databases such as GenBank. See, e.g., GenBank Accession Numbers NC_002077.1 (AAV1), AF063497.1 (AAV1), NC_001401.2 (AAV2), AF043303.1 (AAV2), J01901.1 (AAV2), U48704.1 (AAV3A), NC_001729.1 (AAV3A), AF028705.1 (AAV3B), NC_001829.1 (AAV4), U89790.1 (AAV4), NC_006152.1 (AA5), AF085716.1 (AAV-5), AF028704.1 (AAV6), NC_006260.1 (AAV7), AF513851.1 (AAV7), AF513852.1 (AAV8) NC_006261.1 (AAV-8), AY530579.1 (AAV9), AAT46337 (AAV10) and AAO88208 (AAVrh10); the disclosures of which are incorporated by reference herein for teaching AAV nucleic acid and amino acid sequences. See also, e.g., Srivistava et al. (1983) J. Virology 45:555; Chiorini et al. (1998) J. Virology 71:6823; Chiorini et al. (1999) J. Virology 73: 1309; Bantel-Schaal

et al. (1999) J. Virology 73:939; Xiao et al. (1999) J. Virology 73:3994; Muramatsu et al. (1996) Virology 221:208; Shade et. al. (1986) J. Virol. 58:921; Gao et al. (2002) Proc. Nat. Acad. Sci. USA 99: 11854; Moris et al. (2004) Virology 33:375-383; international patent publications WO 00/28061, WO 99/61601, WO 98/11244; and U.S. Pat. No. 6,156,303.

[0062] The sequences of naturally existing cap (capsid) proteins associated with AAV serotypes are known in the art and include those disclosed herein as AAV1 (SEQ ID NO:1), AAV2 (SEQ ID NO:2), AAV3A (SEQ ID NO:3), AAV3B (SEQ ID NO:4), AAV4 (SEQ ID NO:5), AAV5 (SEQ ID NO:6), AAV6 (SEQ ID NO:7), AAV7 (SEQ ID NO:8), AAV8 (SEQ ID NO:9), AAV9 (SEQ ID NO:10), AAV10 (SEQ ID NO:11), and AAVrh10 (SEQ ID NO:12). The terms "variant AAV capsid protein" or “AAV variant’ refer to an AAV capsid protein comprising an amino acid sequence that includes at least one modification or substitution (including deletion, insertion, point mutation, etc.) relative to a naturally existing or “wild-type” AAV capsid protein sequence, e.g. as set forth in SEQ ID NO:l-12 herein. A variant AAV capsid protein may have about 80% identity or more to the amino acid sequence of a wild type capsid protein, for example, 85% identity or more, 90% identity or more, or 95% identity or more to the amino acid sequence of the wild type capsid protein, for example, 98% or 99% identity to the wild type capsid protein. A variant AAV capsid protein may not be a wild type capsid protein.

[0063] For the purposes of the disclosure herein, "AAV virion" or "AAV viral particle" refers to a viral particle composed of at least one AAV capsid protein and an encapsidated AAV polynucleotide.

[0064] For the purposes of the disclosure herein, the terminology “rAAV” is an abbreviation that refers to recombinant adeno-associated virus. "Recombinant," as applied to a polynucleotide means that the polynucleotide is the product of various combinations of cloning, restriction or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature. A recombinant virus is a viral particle comprising a recombinant polynucleotide. The terms respectively include replicates of the original polynucleotide construct and progeny of the original virus construct.

[0065] The term "rAAV vector" encompasses rAAV virions (i.e., rAAV viral particles) (e.g., an infectious rAAV virion), which by definition include an rAAV polynucleotide; and also encompasses polynucleotides encoding rAAV (e.g., a

single stranded polynucleotide encoding rAAV (ss-rAAV); a double stranded polynucleotide encoding rAAV (ds- rAAV), e.g., plasmids encoding rAAV; and the like).

[0066] If an AAV virion comprises a heterologous polynucleotide (i.e. a polynucleotide other than a wild-type AAV genome, e.g., a transgene to be delivered to a target cell, an RNAi agent or CRISPR agent to be delivered to a target cell, etc.), it is typically referred to as a "recombinant AAV (rAAV) virion" or an "rAAV viral particle." In general, the heterologous polynucleotide is flanked by at least one, and generally by two, AAV inverted terminal repeat sequences (ITRs).

[0067] The term "packaging" refers to a series of intracellular events that result in the assembly and encapsidation of an AAV particle. AAV "*rep*" and "*cap*" genes refer to polynucleotide sequences encoding replication and encapsidation proteins of adeno-associated virus. AAV *rep* and *cap* are referred to herein as AAV "packaging genes."

[0068] The terminology "helper virus" for AAV refers to a virus that allows AAV (e.g. wild-type AAV) to be replicated and packaged by a mammalian cell. A variety of such helper viruses for AAV are known in the art, including adenoviruses, herpesviruses and poxviruses such as vaccinia. The adenoviruses encompass a number of different subgroups, although Adenovirus type 5 of subgroup C is most commonly used. Numerous adenoviruses of human, non-human mammalian and avian origin are known and available from depositories such as the ATCC. Viruses of the herpes family include, for example, herpes simplex viruses (HSV) and Epstein-Barr viruses (EBV), as well as cytomegaloviruses (CMV) and pseudorabies viruses (PRV); which are also available from depositories such as ATCC.

[0069] The terminology "helper virus function(s)" refers to function(s) encoded in a helper virus genome which allow AAV replication and packaging (in conjunction with other requirements for replication and packaging described herein). As described herein, "helper virus function" may be provided in a number of ways, including by providing helper virus or providing, for example, polynucleotide sequences encoding the requisite function(s) to a producer cell in trans. For example, a plasmid or other expression vector comprising nucleotide sequences encoding one or more adenoviral proteins is transfected into a producer cell along with an rAAV vector.

[0070] The terminology "infectious" virus or viral particle is one that comprises a competently assembled viral capsid and is capable of delivering a polynucleotide component into a cell for which the viral species is tropic. The term does not necessarily imply any replication capacity of the virus. Assays for counting infectious viral particles are described elsewhere in this disclosure and in the art. Viral infectivity can be expressed as the ratio of infectious viral particles to total viral particles. Methods of determining the ratio of infectious viral particle to total viral particle are known in the art. See, e.g., Grainger et al. (2005) Mol. Ther. 11: S337 (describing a TCID50 infectious titer assay); and Zolotukhin et al. (1999) Gene Ther. 6:973. See also the Examples.

[0071] The term "tropism" as used herein refers to the preferential targeting by a virus (e.g., an AAV) of cells of a particular host species or of particular cell types within a host species. For example, a virus that can infect cells of the heart, lung, liver, and muscle has a broader (i.e., increased) tropism relative to a virus that can infect only lung and muscle cells. Tropism can also include the dependence of a virus on particular types of cell surface molecules of the host. For example, some viruses can infect only cells with surface glycosaminoglycans, while other viruses can infect only cells with sialic acid (such dependencies can be tested using various cells lines deficient in particular classes of molecules as potential host cells for viral infection). In some cases, the tropism of a virus describes the virus's relative preferences. For example, a first virus may be able to infect all cell types but is much more successful in infecting those cells with surface glycosaminoglycans. A second virus can be considered to have a similar (or identical) tropism as the first virus if the second virus also prefers the same characteristics (e.g., the second virus is also more successful in infecting those cells with surface glycosaminoglycans), even if the absolute transduction efficiencies are not similar. For example, the second virus might be more efficient than the first virus at infecting every given cell type tested, but if the relative preferences are similar (or identical), the second virus can still be considered to have a similar (or identical) tropism as the first virus. In some embodiments, the tropism of a virion comprising a subject variant AAV capsid protein is not altered relative to a naturally occurring virion. In some embodiments, the tropism of a virion comprising a subject variant AAV capsid protein is expanded (i.e., broadened) relative to a naturally occurring virion. In some embodiments, the tropism of a virion

comprising a subject variant AAV capsid protein is reduced relative to a naturally occurring virion.

[0072] The terminology "replication-competent" virus (e.g. a replication-competent AAV) refers to a phenotypically wild-type virus that is infectious, and is also capable of being replicated in an infected cell (i.e. in the presence of a helper virus or helper virus functions). In the case of AAV, replication competence generally requires the presence of functional AAV packaging genes. In general, rAAV vectors as described herein are replication-incompetent in mammalian cells (especially in human cells) by virtue of the lack of one or more AAV packaging genes. Typically, such rAAV vectors lack any AAV packaging gene sequences in order to minimize the possibility that replication competent AAV are generated by recombination between AAV packaging genes and an incoming rAAV vector. In many embodiments, rAAV vector preparations as described herein are those which contain few if any replication competent AAV (rcAAV, also referred to as RCA) (e.g., less than about 1 rcAAV per 10^2 rAAV particles, less than about 1 rcAAV per 10^4 rAAV particles, less than about 1 rcAAV per 10 rAAV particles, less than about 1 rcAAV per 10^{12} rAAV particles, or no rcAAV).

[0073] The term "polynucleotide" refers to a polymeric form of nucleotides of any length, including deoxyribonucleotides or ribonucleotides, or analogs thereof. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, and may be interrupted by non-nucleotide components. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The term polynucleotide, as used herein, refers interchangeably to double- and single-stranded molecules. Unless otherwise specified or required, any embodiment herein that comprises a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

[0074] A polynucleotide or polypeptide has a certain percent "sequence identity" to another polynucleotide or polypeptide, meaning that, when aligned, that percentage of bases or amino acids are the same when comparing the two sequences. Sequence similarity can be determined in a number of different manners. To determine sequence identity, sequences can be aligned using the methods and computer programs, including BLAST, available over the world wide web at

ncbi.nlm.nih.gov/BLAST/. Another alignment algorithm is FASTA, available in the Genetics Computing Group (GCG) package, from Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Of particular interest are alignment programs that permit gaps in the sequence. The Smith- Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. See J. Mol. Biol. 48: 443- 453 (1970).

[0075] The term "gene" refers to a polynucleotide that performs a function of some kind in the cell. For example, a gene can contain an open reading frame that is capable of encoding a gene product. One example of a gene product is a protein, which is transcribed and translated from the gene. Another example of a gene product is an RNA, e.g. a functional RNA product, e.g., an aptamer, an interfering RNA, a ribosomal RNA (rRNA), a transfer RNA (tRNA), a non-coding RNA (ncRNA), a guide RNA for nucleases, etc., which is transcribed but not translated.

[0076] The terminology "gene expression product" or "gene product" is a molecule resulting from expression of a particular gene, as defined above. Gene expression products include, e.g., a polypeptide, an aptamer, an interfering RNA, a messenger RNA (mRNA), an rRNA, a tRNA, a non-coding RNA (ncRNA), and the like.

[0077] The term “siRNA agent” ("small interfering" or "short interfering RNA" (or siRNA)) is an RNA duplex of nucleotides that is targeted to a gene interest (a "target gene"). An "RNA duplex" refers to the structure formed by the complementary pairing between two regions of a RNA molecule, forming a region of double stranded RNA (dsRNA). siRNA is "targeted" to a gene in that the nucleotide sequence of the duplex portion of the siRNA is complementary to a nucleotide sequence of the targeted gene. In some embodiments, the length of the duplex of siRNAs is less than 30 nucleotides. In some embodiments, the duplex can be 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10 nucleotides in length. In some embodiments, the length of the duplex is 19-25 nucleotides in length. In some embodiments, siRNA-mediated gene targeting is accomplished through the

use of DNA-directed RNA interference (ddRNAi) which is a gene silencing technique that utilizes DNA constructs to activate an animal cell's endogenous RNA interference (RNAi) pathways. Such DNA constructs are designed to express self-complementary double-stranded RNAs, typically short-hairpin RNAs (shRNA), that once processed bring about silencing of a target gene or genes. Any RNA, including endogenous mRNAs or viral RNAs, can be silenced by designing constructs to express double-stranded RNA complementary to the desired mRNA target. As such, the RNA duplex portion of an siRNA agent can be part of a short hairpin structure referred to as shRNA. In addition to the duplex portion, the hairpin structure may contain a loop portion positioned between the two sequences that form the duplex. The loop can vary in length. In some embodiments the loop is 5, 6, 7, 8, 9, 10, 11, 12 or 13 nucleotides in length. The hairpin structure can also contain 3' or 5' overhang portions. In some embodiments, the overhang is a 3' or a 5' overhang 0, 1, 2, 3, 4 or 5 nucleotides in length. In general, the level of expression product (e.g., mRNA, polypeptide, etc.) of a target gene is reduced by an siRNA agent (e.g., an siRNA, an shRNA, etc.) that contains specific double stranded nucleotide sequences that are complementary to at least a 19-25 nucleotide long segment (e.g., a 20-21 nucleotide sequence) of the target gene transcript, including the 5' untranslated (UT) region, the ORF, or the 3' UT region. In some embodiments, short interfering RNAs are about 19-25nt in length. See, e.g., PCT applications WO 00/44895, WO 99/32619, WO 01/75164, WO 01/92513, WO 01/29058, WO 01/89304, WO 02/16620, and WO 02/29858; and U.S. Patent Publication No. 2004/0023390 for descriptions of siRNA technology. The siRNA and/or shRNA can be encoded by a nucleic acid sequence, and the nucleic acid sequence can also include a promoter. The nucleic acid sequence can also include a polyadenylation signal. In some embodiments, the polyadenylation signal is a synthetic minimal polyadenylation signal.

[0078] The terminology "antisense RNA" encompasses RNA that is complementary to a gene expression product. For example, an antisense RNA targeted to a specific mRNA is an RNA-based agent (or can be a modified RNA) that is complementary to the mRNA, where hybridization of the antisense RNA to the mRNA alters the expression of the mRNA (e.g., via altering the stability of the RNA, altering the translation of the RNA, etc.). Also included in "antisense RNA" are nucleic acids encoding an antisense RNA.

[0079] With regards to "CRISPR/Cas9 agents", the term "CRISPR" encompasses Clustered regularly interspaced short palindromic repeats/CRISPR-associated (Cas) systems that evolved to provide bacteria and archaea with adaptive immunity against viruses and plasmids by using CRISPR RNAs (crRNAs) to guide the silencing of invading nucleic acids. The Cas9 protein (or functional equivalent and/or variant thereof, i.e., Cas9-like protein) naturally contains DNA endonuclease activity that depends on association of the protein with two naturally occurring or synthetic RNA molecules called crRNA and tracrRNA (also called guide RNAs). In some cases, the two molecules are covalently linked to form a single molecule (also called a single guide RNA ("sgRNA")). Thus, the Cas9 or Cas9-like protein associates with a DNA-targeting RNA (which term encompasses both the two-molecule guide RNA configuration and the single-molecule guide RNA configuration), which activates the Cas9 or Cas9-like protein and guides the protein to a target nucleic acid sequence.

[0080] If the Cas9 or Cas9-like protein retains its natural enzymatic function, it will cleave target DNA to create a double-strand break, which can lead to genome alteration (i.e., editing: deletion, insertion (when a donor polynucleotide is present), replacement, etc.), thereby altering gene expression. Some variants of Cas9 (which variants are encompassed by the term Cas9-like) have been altered such that they have a decreased DNA cleaving activity (in some cases, they cleave a single strand instead of both strands of the target DNA, while in other cases, they have severely reduced to no DNA cleavage activity). Cas9-like proteins with decreased DNA-cleavage activity (even no DNA-cleaving activity) can still be guided to a target DNA to block RNA polymerase activity. Alternatively, the Cas9 or Cas9-like protein may be modified by fusing a VP64 transcription activation domain to the Cas9 protein and codelivering the fusion protein with a MS2-P65-HSF1 helper protein and a single guide RNA comprising MS2 RNA aptamers at the tetraloop and stem-loop to form a Synergistic Activation Mediator (Cas9-SAM) complex in the cell that activates transcription. Thus enzymatically inactive Cas9-like proteins can be targeted to a specific location in a target DNA by a DNA-targeting RNA in order to block or activate transcription of the target DNA. The term "CRISPR/Cas9 agents" as used herein encompasses all forms of CRISPR/Cas9 as described above or as known in the art.

[0081] Detailed information regarding CRISPR agents can be found, for example in (a) Jinek et. al., Science. 2012 Aug 17;337(6096):816-21: "A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity"; (b) Qi et al., Cell. 2013 Feb 28; 152(5): 1173-83: "Repurposing CRISPR as an RNA-guided platform for sequence- specific control of gene expression", and (c) US patent application number 13/842,859 and PCT application number PCT/US13/32589; all of which are hereby incorporated by reference in their entirety. Thus, the term "CRISPR agent" as used herein encompasses any agent (or nucleic acid encoding such an agent), comprising naturally occurring and/or synthetic sequences, that can be used in the Cas9-based system (e.g., a Cas9 or Cas9-like protein; any component of a DNA-targeting RNA, e.g., a crRNA-like RNA, a tracrRNA-like RNA, a single guide RNA, etc.; a donor polynucleotide; and the like).

[0082] By "Zinc-finger nucleases" (ZFNs) it is meant artificial DNA endonucleases generated by fusing a zinc finger DNA binding domain to a DNA cleavage domain. ZFNs can be engineered to target desired DNA sequences and this enables zinc-finger nucleases to cleave unique target sequences. When introduced into a cell, ZFNs can be used to edit target DNA in the cell (e.g., the cell's genome) by inducing double strand breaks. For more information on the use of ZFNs, see, for example: Asuri et al., Mol Ther. 2012 Feb; 20(2):329-38; Bibikova et al. Science. 2003 May 2;300(5620):764; Wood et al. Science. 2011 Jul 15;333(6040):307; Ochiai et al. Genes Cells. 2010 Aug; 15(8):875-85; Takasu et. al., Insect Biochem Mol Biol. 2010 Oct; 40(10):759-65; Ekker et al, Zebrafish 2008 Summer; 5(2): 121-3; Young et al, Proc Natl Acad Sci U S A. 2011 Apr 26;108(17):7052-7; Goldberg et al, Cell. 2010 Mar 5;140(5):678-91; Geurts et al, Science. 2009 Jul 24;325(5939):433; Flisikowska et al, PLoS One. 2011;6(6):e21045. doi: 10.1371/journal.pone.0021045. Epub 2011 Jun 13; Hauschild et al, Proc Natl Acad Sci U S A. 2011 Jul 19;108(29): 12013-7; and Yu et al, Cell Res. 2011 Nov; 21(l 1): 1638-40; all of which are herein incorporated by reference for their teachings related to ZFNs. The term "ZFN agent" encompasses a zinc finger nuclease and/or a polynucleotide comprising a nucleotide sequence encoding a zinc finger nuclease.

[0083] The terminology "Transcription activator-like effector nuclease" or "TALEN" agents refers to Transcription activator-like effector nucleases (TALENs) are artificial DNA endonucleases generated by fusing a TAL (Transcription activator-like) effector DNA binding domain to a DNA cleavage domain. TALENS can be

quickly engineered to bind practically any desired DNA sequence and when introduced into a cell, TALENs can be used to edit target DNA in the cell (e.g., the cell's genome) by inducing double strand breaks. For more information on the use of TALENs, see, for example: Hockemeyer et al. Nat Biotechnol. 2011 Jul 7;29(8):731-4; Wood et al. Science. 2011 Jul 15;333(6040):307; Tesson et al. Nat Biotechnol. 2011 Aug 5;29(8):695-6; and Huang et. al., Nat Biotechnol. 2011 Aug 5;29(8):699-700; all of which are herein incorporated by reference for their teachings related to TALENs. The term "TALEN agent" encompasses a TALEN and/or a polynucleotide comprising a nucleotide sequence encoding a TALEN.

[0084] The terminology "control element" or "control sequence" refers to a nucleotide sequence involved in an interaction of molecules that contributes to the functional regulation of a polynucleotide, including replication, duplication, transcription, splicing, translation, or degradation of the polynucleotide. The regulation may affect the frequency, speed, or specificity of the process, and may be enhancing or inhibitory in nature. Control elements known in the art include, for example, transcriptional regulatory sequences such as promoters and enhancers. A promoter is a DNA region capable under certain conditions of binding RNA polymerase and initiating transcription of a coding region usually located downstream (in the 3' direction) from the promoter. Promoters may be ubiquitously acting, i.e. active in many cell types, e.g. CAG or CMV promoters; or tissue or cell specific, e.g. the rho promoter, which is active in rods, or the opsin promoter, which is active in cones.

[0085] The terminology "operatively linked" or "operably linked" refers to a juxtaposition of genetic elements, wherein the elements are in a relationship permitting them to operate in the expected manner. For instance, a promoter is operatively linked to a coding region if the promoter helps initiate transcription of the coding sequence. There may be intervening residues between the promoter and coding region so long as this functional relationship is maintained.

[0086] The terminology "expression vector" encompasses a vector comprising a polynucleotide region which encodes a polypeptide of interest, and is used for effecting the expression of the protein in an intended target cell. An expression vector may also comprise control elements operatively linked to the encoding region to facilitate expression of the protein in the target. The combination of control elements and a gene or genes to which they are operably linked for

expression is sometimes referred to as an "expression cassette," a large number of which are known and available in the art or can be readily constructed from components that are available in the art.

[0087] The term “heterologous" means derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared. For example, a polynucleotide introduced by genetic engineering techniques into a plasmid or vector derived from a different species is a heterologous polynucleotide. A promoter removed from its native coding sequence and operatively linked to a coding sequence with which it is not naturally found linked is a heterologous promoter. Thus, for example, an rAAV that includes a heterologous nucleic acid sequence encoding a heterologous gene product is an rAAV that includes a polynucleotide not normally included in a naturally-occurring, wild-type AAV, and the encoded heterologous gene product is a gene product not normally encoded by a naturally-occurring, wild type AAV.

[0088] The terminology "genetic alteration" and "genetic modification" (and grammatical variants thereof), are used interchangeably herein to refer to a process wherein a genetic element (e.g., a polynucleotide) is introduced into a cell other than by mitosis or meiosis. The element may be heterologous to the cell, or it may be an additional copy or improved version of an element already present in the cell. Genetic alteration may be effected, for example, by transfecting a cell with a recombinant plasmid or other polynucleotide through any process known in the art, such as electroporation, calcium phosphate precipitation, or contacting with a polynucleotide-liposome complex. Genetic alteration may also be effected, for example, by transduction or infection with a DNA or RNA virus or viral vector. Generally, the genetic element is introduced into a chromosome or mini-chromosome in the cell; but any alteration that changes the phenotype and/or genotype of the cell and its progeny is included in this term.

[0089] With regards to cell modification, the terminology "genetically modified" or "transformed" or "transfected" or “transduced” by exogenous DNA (e.g. via a recombinant virus) refers to when such DNA has been introduced inside the cell. The presence of the exogenous DNA results in permanent or transient genetic change. The transforming DNA may or may not be integrated (covalently linked) into the genome of the cell. A "clone" is a population of cells derived from a single cell or

common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth in vitro for many generations.

[0090] As used herein, a cell is said to be "stably" altered, transduced, genetically modified, or transformed with a genetic sequence if the sequence is available to perform its function during extended culture of the cell *in vitro* and/or for an extended period of time *in vivo*. Generally, such a cell is "heritably" altered (genetically modified) in that a genetic alteration is introduced which is also inheritable by progeny of the altered cell.

[0091] The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, lipidation, phosphorylation, or conjugation with a labeling component. Polypeptides such as anti-angiogenic polypeptides, neuroprotective polypeptides, and the like, when discussed in the context of delivering a gene product to a mammalian subject, and compositions therefor, refer to the respective intact polypeptide, or any fragment or genetically engineered derivative thereof, which retains the desired biochemical function of the intact protein. Similarly, references to nucleic acids encoding anti-angiogenic polypeptides, nucleic acids encoding neuroprotective polypeptides, and other such nucleic acids for use in delivery of a gene product to a mammalian subject (which may be referred to as "transgenes" to be delivered to a recipient cell), include polynucleotides encoding the intact polypeptide or any fragment or genetically engineered derivative possessing the desired biochemical function.

[0092] As used herein, an "isolated" plasmid, nucleic acid, vector, virus, virion, host cell, protein, or other substance refers to a preparation of the substance devoid of at least some of the other components that may also be present where the substance or a similar substance naturally occurs or is initially prepared from. Thus, for example, an isolated substance may be prepared by using a purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this disclosure are increasingly more isolated. An isolated plasmid, nucleic acid, vector, virus, host cell, or other substance is in some embodiments purified, e.g., from about 80% to about 90% pure, at least about 90%

pure, at least about 95% pure, at least about 98% pure, or at least about 99%, or more, pure.

[0093] As used herein, the terms "treatment," "treating," and the like, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment," as used herein, covers any treatment of a disease in a mammal, particularly in a human, and includes: (a) preventing the disease (and/or symptoms caused by the disease) from occurring in a subject which may be predisposed to the disease or at risk of acquiring the disease but has not yet been diagnosed as having it; (b) inhibiting the disease (and/or symptoms caused by the disease), i.e., arresting its development; and (c) relieving the disease (and/or symptoms caused by the disease), i.e., causing regression of the disease (and/or symptoms caused by the disease), i.e., ameliorating the disease and/or one or more symptoms of the disease. For example, the subject compositions and methods may be directed towards the treatment of retinal disease. Nonlimiting methods for assessing retinal diseases and the treatment thereof include measuring retinal function and changes thereof, e.g. changes in visual acuity (e.g. best-corrected visual acuity [BCVA], ambulation, navigation, object detection and discrimination), changes in visual field (e.g. static and kinetic visual field perimetry), clinical examination (e.g. slit lamp examination of the anterior and posterior segments of the eye), electrophysiological responsiveness to all wavelengths of light and dark (e.g. all forms of electroretinography (ERG) [full-field, multifocal and pattern], all forms of visual evoked potential (VEP), electrooculography (EOG), color vision, dark adaptation and/or contrast sensitivity; measuring changes in anatomy or health using anatomical and/or photographic measures, e.g. Optical Conherence Tomography (OCT), fundus photography, adaptive optics scanning laser ophthalmoscopy, fluorescence and/or autofluorescence; measuring ocular motility and eye movements (e.g. nystagmus, fixation preference, and stability), measuring reported outcomes (patient-reported changes in visual and non-visually-guided behaviors and activities, patient-reported outcomes [PRO], questionnaire-based assessments of quality-of-life, daily activities and measures of neurological function (e.g. functional Magnetic Resonance Imaging (MRI)).

[0094] The terms "individual," "host," "subject," and "patient" are used interchangeably herein, and refer to a mammal, including, but not limited to, humans; non-human primates, including simians; mammalian sport animals (e.g., horses); mammalian farm animals (e.g., sheep, goats, etc.); mammalian pets (dogs, cats, etc.); and rodents (e.g., mice, rats, etc.).

[0095] In some embodiments, the individual is a human who has previously been naturally exposed to AAV and as a result harbors anti-AAV antibodies (i.e., AAV neutralizing antibodies). In some embodiments, the individual is a human who has previously been administered an AAV vector (and as a result may harbor anti-AAV antibodies) and needs re-administration of vector for treatment of a different condition or for further treatment of the same condition. Based on positive results in clinical trials involving AAV gene delivery to, for example, liver, muscle, and retina - all tissues affected by neutralizing antibodies against this vehicle - there are many such therapeutic applications/disease targets.

[0096] The term "effective amount" as used herein is an amount sufficient to effect beneficial or desired clinical results. An effective amount can be administered in one or more administrations. For purposes of this disclosure, an effective amount of a compound (e.g., an infectious rAAV virion) is an amount that is sufficient to palliate, ameliorate, stabilize, reverse, prevent, slow or delay the progression of (and/or symptoms associated with) a particular disease state (e.g., a retinal disease). Accordingly, an effective amount of an infectious rAAV virion is an amount of the infectious rAAV virion that is able to effectively deliver a heterologous nucleic acid to a target cell (or target cells) of the individual. Effective amounts may be determined preclinically by, e.g., detecting in the cell or tissue the gene product (RNA, protein) that is encoded by the heterologous nucleic acid sequence using techniques that are well understood in the art, e.g. RT-PCR, western blotting, ELISA, fluorescence or other reporter readouts, and the like. Effective amounts may be determined clinically by, e.g. detecting a change in the onset or progression of disease using methods known in the art, e.g. fundus autofluorescence, fluorescein angiography, OCT, microperimetry, adaptive optics, etc. and the like, as described herein and as known in the art.

[0097] The terminology “retinal cell” refers herein to any of the cell types that comprise the retina, such as, without limitation, retinal ganglion (RG) cells, amacrine cells, horizontal cells, bipolar cells, photoreceptor cells, Müller glial cells,

microglial cells, and retinal pigmented epithelium (RPE). The terminology "photoreceptor cells" refers herein to, without limitation, rod cells or "rods" and cone cells or "cones". The terminology "Müller cells" or "Müller glia" refers to glial cells that support neurons in the vertebrate retina.

[0098] The terminology "directed evolution" refers to a capsid engineering methodology, *in vitro* and/or *in vivo*, which emulates natural evolution through iterative rounds of genetic diversification and selection processes, thereby accumulating beneficial mutations that progressively improve the function of a biomolecule. Directed evolution often involves an *in vivo* method referred to as "biopanning" for selection of AAV variants from a library which variants possess a more efficient level of infectivity of a cell or tissue type of interest.

DETAILED DESCRIPTION

[0099] Adeno-associated viruses (AAVs) are a family of parvoviruses with a 4.7 kb single-stranded DNA genome contained inside a non-enveloped capsid. The viral genome of a naturally occurring AAV has 2 inverted terminal repeats (ITR) – which function as the viral origin of replication and packaging signal – flanking 2 primary open reading frames (ORF): *rep* (encoding proteins that function in viral replication, transcriptional regulation, site-specific integration, and virion assembly) and *cap*. The *cap* ORF codes for 3 structural proteins that assemble to form a 60-mer viral capsid. Many naturally occurring AAV variants and serotypes have been isolated, and none have been associated with human disease.

[00100] Recombinant versions of AAV can be used as gene delivery vectors, where a marker or therapeutic gene of interest is inserted between the ITRs in place of *rep* and *cap*. These vectors have been shown to transduce both dividing and non-dividing cells *in vitro* and *in vivo* and can result in stable transgene expression for years in post-mitotic tissue. See *e.g.*, Knipe DM, Howley PM. *Fields' Virology*. Lippincott Williams & Wilkins, Philadelphia, PA, USA, 2007; Gao G-P, Alvira MR, Wang L, Calcedo R, Johnston J, Wilson JM. Novel adeno-associated viruses from rhesus monkeys as vectors for human gene therapy. *Proc Natl Acad Sci U S A* 2002; 99: 11854–9;Atchison RW, Casto BC, Hammon WM. Adenovirus-Associated Defective Virus Particles. *Science* 1965; 149: 754–6; Hoggan MD, Blacklow NR, Rowe WP. Studies of small DNA viruses found in various adenovirus preparations: physical, biological, and immunological characteristics. *Proc Natl Acad Sci U S A*

1966; 55: 1467–74; Blacklow NR, Hoggan MD, Rowe WP. Isolation of adenovirus-associated viruses from man. *Proc Natl Acad Sci U S A* 1967; 58: 1410–5; Bantel-Schaal U, zur Hausen H. Characterization of the DNA of a defective human parvovirus isolated from a genital site. *Virology* 1984; 134: 52–63; Mayor HD, Melnick JL. Small deoxyribonucleic acid-containing viruses (picodnavirus group). *Nature* 1966; 210: 331–2; Mori S, Wang L, Takeuchi T, Kanda T. Two novel adeno-associated viruses from cynomolgus monkey: pseudotyping characterization of capsid protein. *Virology* 2004; 330: 375–83; Flotte TR. Gene therapy progress and prospects: recombinant adeno-associated virus (rAAV) vectors. *Gene Ther* 2004; 11: 805–10.

[00101] Recombinant AAV (referred to herein simply as "AAV") has yielded promising results in an increasing number of clinical trials. However, there are impediments to gene delivery that may limit AAV's utility, such as anti-capsid immune responses, low transduction of certain tissues, an inability for targeted delivery to specific cell types and a relatively low carrying capacity. In many situations, there is insufficient mechanistic knowledge to effectively empower rational design with the capacity to improve AAV. As an alternative, directed evolution has emerged as a strategy to create novel AAV variants that meet specific biomedical needs. Directed evolution strategies harness genetic diversification and selection processes to enable the accumulation of beneficial mutations that progressively improve the function of a biomolecule. In this process, wild-type AAV *cap* genes are diversified by several approaches to create large genetic libraries that are packaged to generate libraries of viral particles, and selective pressure is then applied to isolate novel variants that can overcome gene delivery barriers. Importantly, the mechanistic basis underlying a gene delivery problem does not need to be known for directed evolution of function, which can thus accelerate the development of enhanced vectors.

[00102] Typically, the variants disclosed herein were generated through use of an AAV library and/or libraries. Such an AAV library or libraries is/are generated by mutating the *cap* gene, the gene which encodes the structural proteins of the AAV capsid, by a range of directed evolution techniques known by and readily available to the skilled artisan in the field of viral genome engineering. See e.g., Bartel et al. Am. Soc. Gene Cell Ther. 15th Annu. Meet. 20, S140 (2012); Bowles, D. et al. J. Virol. 77, 423-432 (2003); Gray et al. Mol. Ther. 18, 570-578 (2010); Grimm, D. et al. J. Virol. 82, 5887-5911; Koerber, J. T. et al. Mol. Ther. 16, 1703-1709 (2008); Li W. et al. Mol. Ther. 16, 1252-1260 (2008); Koerber, J. T. et al. Methods Mol. Biol. 434, 161-

170 (2008); Koerber, J. T. et al. Hum. Gene Ther. 18, 367-378 (2007); and Koerber, J. T. et al. Mol. Ther. 17, 2088-2095 (2009). Such techniques, without limitation, are as follows: i) Error-prone PCR to introduce random point mutations into the AAV *cap* open reading frame (ORF) at a predetermined, modifiable rate; ii) *In vitro* or *in vivo* viral recombination or "DNA shuffling" to generate random chimeras of AAV *cap* genes to yield a gene library with multiple AAV serotypes; iii) Random peptide insertions at defined sites of the capsid by ligation of degenerate oligonucleotides in the *cap* ORF; iv) Defined insertions of peptide-encoding sequences into random locations of the AAV *cap* ORF using transposon mutagenesis; v) Replacing surface loops of AAV capsids with libraries of peptide sequences bioinformationally designed based on the level of conservation of each amino acid position among natural AAV serotypes and variants to generate "loop-swap" libraries; vi) Random amino acid substitution at positions of degeneracy between AAV serotypes to generate libraries of ancestral variants (Santiago-Ortiz et al., 2015); and a combination of such techniques thereof.

[00103] DNA shuffling generates chimeras which combine their parental properties in unique and, often beneficial, ways; however, some may be incapable of packaging which, in effect, reduces the diversity of the library. Diversity concentration of the library is achieved through peptide insertion techniques such as, without limitation, iii-iv) above. Diversity of the library is also concentrated in techniques such as v) above, and such concentration is directed onto multiple hypervariable regions, which lie on surface exposed loops, of the AAV capsid. While many of the techniques generate variant capsids with only a small area of the capsid mutated, these techniques can be paired with additional mutagenesis strategies to modify the full capsid.

[00104] Once the AAV library or libraries is/are generated, viruses are then packaged, such that each AAV particle is comprised of a mutant capsid surrounding a *cap* gene encoding that capsid, and purified. Variants of the library are then subjected to *in vitro* and/or *in vivo* selective pressure techniques known by and readily available to the skilled artisan in the field of AAV. See e.g., Maheshri, N. et al. Nature Biotech. 24, 198-204 (2006); Dalkara, D. et al. Sci. Transl. Med. 5, 189ra76 (2013); Lisowski, L. et al. Nature. 506, 382-286 (2013); Yang, L. et al. PNAS. 106, 3946-3951 (2009); Gao, G. et al. Mol. Ther. 13, 77-87 (2006); and Bell, P. et al. Hum. Gene. Ther. 22, 985-997 (2011). For example, without limitation, AAV variants can be selected using

i) affinity columns in which elution of different fractions yields variants with altered binding properties; ii) primary cells – isolated from tissue samples or immortal cell lines that mimic the behavior of cells in the human body – which yield AAV variants with increased efficiency and/or tissue specificity; iii) animal models - which mimic a clinical gene therapy environment - which yield AAV variants that have successfully infected target tissue; iv) human xenograft models which yield AAV variants that have infected grafted human cells; and/or a combination of selection techniques thereof.

[00105] Once viruses are selected, they may be recovered by known techniques such as, without limitation, adenovirus-mediated replication, PCR amplification, Next Generation sequencing and cloning, and the like. Virus clones are then enriched through repeated rounds of the selection techniques and AAV DNA is isolated to recover selected variant *cap* genes of interest. Such selected variants can be subjected to further modification or mutation and as such serve as a new starting point for further selection steps to iteratively increase AAV viral fitness. However, in certain instances, successful capsids have been generated without additional mutation.

[00106] The AAV variants disclosed herein were generated at least in part through the use of *in vivo* directed evolution methodology, such as the techniques described above, involving the use of primate retinal screens following intravitreal administration. As such, the AAV variant capsids disclosed herein comprise one or more modifications in amino acid sequence that confer more efficient transduction of primate retinal cells than a corresponding parental AAV capsid protein. As used herein, a "corresponding parental AAV capsid protein" refers to an AAV capsid protein of the same wild-type or variant AAV serotype as the subject variant AAV capsid protein but that does not comprise the one or more amino acid sequence modifications of the subject variant AAV capsid protein.

[00107] In some embodiments, the subject variant AAV capsid protein comprises a heterologous peptide of from about 5 amino acids to about 20 amino acids inserted by covalent linkage into an AAV capsid protein GH loop, or loop IV, relative to a corresponding parental AAV capsid protein. By the "GH loop," or loop IV, of the AAV capsid protein it is meant the solvent-accessible portion referred to in the art as the GH loop, or loop IV, of AAV capsid protein. For the GH loop/loop IV of AAV capsid, see, e.g., van Vliet et al. (2006) *Mol. Ther.* 14:809; Padron et al. (2005) *J. Virol.* 79:5047; and Shen et al. (2007) *Mol. Ther.* 15:1955. Thus, for

example, the insertion site can be within about amino acids 411-650 of an AAV VP1 capsid protein. For example, the insertion site can be within amino acids 571-612 of AAV1 VP1, amino acids 570-611 of AAV2 VP1, within amino acids 571-612 of AAV3A VP1, within amino acids 571-612 of AAV3B VP1, within amino acids 569-610 of AAV4 VP1, within amino acids 560-601 of AAV5 VP1, within amino acids 571 to 612 of AAV6 VP1, within amino acids 572 to 613 of AAV7 VP1, within amino acids 573 to 614 of AAV8 VP1, within amino acids 571 to 612 of AAV9 VP1, or within amino acids 573 to 614 of AAV10 VP1, or the corresponding amino acids of any variant thereof. Those skilled in the art would know, based on a comparison of the amino acid sequences of capsid proteins of various AAV serotypes, where an insertion site "corresponding to amino acids of AAV2" would be in a capsid protein of any given AAV serotype. See also Figure 6 for an alignment of wild-type AAV SEQ ID NOS:1-11 which provides amino acid locations between and across the wild-type (naturally occurring) serotypes AAV1, AAV2, AAV3A, AAV3B, and AAV4-10.

[00108] In certain embodiments, the insertion site is a single insertion site between two adjacent amino acids located between amino acids 570-614 of VP1 of any wild-type AAV serotype or AAV variant, e.g., the insertion site is between two adjacent amino acids located in amino acids 570-610, amino acids 580-600, amino acids 570-575, amino acids 575-580, amino acids 580-585, amino acids 585-590, amino acids 590-600, or amino acids 600-614, of VP1 of any AAV serotype or variant. For example, the insertion site can be between amino acids 580 and 581, amino acids 581 and 582, amino acids 583 and 584, amino acids 584 and 585, amino acids 585 and 586, amino acids 586 and 587, amino acids 587 and 588, amino acids 588 and 589, or amino acids 589 and 590. The insertion site can be between amino acids 575 and 576, amino acids 576 and 577, amino acids 577 and 578, amino acids 578 and 579, or amino acids 579 and 580. The insertion site can be between amino acids 590 and 591, amino acids 591 and 592, amino acids 592 and 593, amino acids 593 and 594, amino acids 594 and 595, amino acids 595 and 596, amino acids 596 and 597, amino acids 597 and 598, amino acids 598 and 599, or amino acids 599 and 600. For example, the insertion site can be between amino acids 587 and 588 of AAV2, between amino acids 590 and 591 of AAV1, between amino acids 588 and 589 of AAV3A, between amino acids 588 and 589 of AAV3B, between amino acids 584 and 585 of AAV4, between amino acids 575 and 576 of AAV5, between amino acids 590 and 591 of AAV6, between amino acids 589 and 590 of AAV7, between

amino acids 590 and 591 of AAV8, between amino acids 588 and 589 of AAV9, or between amino acids 588 and 589 of AAV10.

[00109] In some embodiments, a peptide insertion disclosed herein has a length of 5 amino acids, 6 amino acids, 7 amino acids, 8 amino acids, 9 amino acids, 10 amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids. In another embodiment, a peptide insertion disclosed herein comprises from 1 to 4 spacer amino acids at the amino terminus (N-terminus) and/or at the carboxyl terminus (C-terminus) of any one of the peptide insertions disclosed herein. Exemplary spacer amino acids include, without limitation, leucine (L), alanine (A), glycine (G), serine (S), threonine (T), and proline (P). In certain embodiments, a peptide insertion comprises 2 spacer amino acids at the N-terminus and 2 spacer amino acids at the C-terminus. In other embodiments, a peptide insertion comprises 2 spacer amino acids at the N-terminus and 1 spacer amino acids at the C-terminus.

[00110] The peptide insertions disclosed herein have not been previously described and/or inserted into an AAV capsid. Without wishing to be bound by theory, the presence of any of the disclosed peptide insertions may act to lower the variant capsid's affinity for heparin sulfate which likely reduces binding to the extracellular matrix in the front of the primate retina. In addition, the peptide insertion motifs disclosed herein may confer enhanced transduction of primate retinal cells through the addition of a cell surface receptor binding domain.

[00111] In some preferred embodiments, the insertion peptide comprises an amino acid sequence of any one of the formulas below.

[00112] In some aspects, an insertion peptide can be a peptide of 7 to 10 amino acids in length, of Formula 1a:

$Y_1Y_2X_1X_2X_3X_4X_5X_6X_7Y_3$

Where each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Gln, Asn, His, Ile, and Ala

X_2 is selected from Ala, Gln, Asp, Ser, Lys, and Pro

X_3 is selected from Asp, Ile, Thr and Asn

X_4 is selected from Thr, Ser, Tyr, Gln, Glu, and Ala

X_5 is selected from Thr, Lys, and Asn

X_6 is selected from Lys, Asn, and Glu

X_7 is selected from Asn, Thr, Ile, His, Asp, and Ala.

[00113] In certain embodiments, the insertion peptide of Formula 1a comprises an amino acid sequence selected from QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), and QANANEN (SEQ ID NO:22).

[00114] In other aspects, an insertion peptide can be a peptide of 7 to 10 amino a acids in length, of Formula 1b:

$Y_1Y_2X_1X_2X_3X_4X_5X_6X_7Y_3$

Where each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Gln, Asn, His, and Ile

X_2 is selected from Ala, Gln, Asp, and Ser

X_3 is selected from Asp and Ile

X_4 is selected from Thr, Tyr, and Gln

X_5 is selected from Thr and Lys

X_6 is selected from Lys and Asn

X_7 is selected from Asn, Thr, Ile, and His

[00115] In certain embodiments, the insertion peptide of Formula 1b comprises an amino acid sequence selected from QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), NQDYTKT (SEQ NO:16), HDITKNI (SEQ ID NO:17), and HQDTTKN (SEQ ID NO:19).

[00116] In other aspects, an insertion peptide can be a peptide of 7 to 10 amino acids in length, of Formula 1c

$Y_1Y_2X_1X_2AspX_3ThrLysX_4Y_3$

Where each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Gln, Asn, His, and Ile

X_2 is selected from Ala, Gln, and Ser

X_3 is selected from Thr, Tyr, and Gln

X_4 is selected from Asn, Thr, and His

[00117] In certain embodiments, the insertion peptide of Formula 1c comprises an amino acid sequence selected from QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), NQDYTKT (SEQ NO:16), and HQDTTKN (SEQ ID NO:19).

[00118] In other aspects, an insertion peptide can be a peptide of 7 to 10 amino acids in length, of Formula 1d:

$Y_1Y_2X_1X_2AspX_3ThrThrX_4Y_3$

Where each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Gln and Ile

X_2 is selected from Ala and Ser

X_3 is selected from Thr and Gln

X_4 is selected from Asn and His

[00119] In certain embodiments, the insertion peptide of Formula 1d comprises an amino acid sequence selected from QADTTKN (SEQ ID NO:13) and ISDQTKH (SEQ ID NO:14).

[00120] In other aspects, an insertion peptide can be a peptide of 7 to 11 amino acids in length, of Formula Ie

$Y_1Y_2X_1X_2AsnX_3AsnGluX_4Y_3$

Where each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Gln and Ile

X_2 is selected from Ala and Ser

X_3 is selected from Glu and Ala

X_4 is selected from Asn and His

[00121] In other embodiments, an insertion peptide of Formula 1e comprises an amino acid sequence selected from ISNENEH (SEQ ID NO:21), and QANANEN (SEQ ID NO:22).

[00122] In yet another embodiment, an insertion peptide can be a peptide of 7 to 11 amino acids in length, of Formula IIa:

$Y_1Y_2X_1X_2DX_3TKX_4Y_3$.

Wherein each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from Q, N, A, H, and I;

X_2 is selected from Q, A, P, and S;

X_3 is selected from T, Y, S, and Q; and

X_4 is selected from T, N, A, and H.

[00123] In a further embodiment of a peptide insertion of an amino acid sequence of the formula $X_1X_2DX_3TKX_4$, the peptide insertion is selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA, NQDYTKT (SEQ NO:16), HQDTTKN (SEQ ID NO:19), and HPDTTKN (SEQ ID NO:18).

[00124] In some such embodiments, an insertion peptide can be a peptide of 7 to 11 amino acids in length, of Formula IIb:

$Y_1Y_2X_1X_2DX_3TKX_4Y_3$

[00125] Wherein each of Y_1-Y_3, if present, is independently selected from Ala, Leu, Gly, Ser, Thr, Pro

X_1 is selected from N, A, and H;

X_2 is selected from Q, P, and S;

X_3 is selected from T, Y, and S; and

X_4 is selected from T, N, and A.

[00126] In a further embodiment of a peptide insertion of an amino acid sequence of the formula $X_1X_2DX_3TKX_4$, the peptide insertion is selected from the group consisting of ASDSTKA, NQDYTKT (SEQ NO:16), HQDTTKN (SEQ ID NO:19), and HPDTTKN (SEQ ID NO:18).

[00127] In other embodiments, the insertion peptide comprises an amino acid sequence selected from KDRAPST (SEQ ID NO:26), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25) and GKSKVID (SEQ ID NO:23).

[00128] In some embodiments, the insertion peptide comprises an amino acid sequence selected from ASDSTKA (SEQ ID NO:15), QANANEN (SEQ ID NO:22), QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25) and KDRAPST (SEQ ID NO:26).

[00129] In other preferred embodiments, the insertion peptide has from 1 to 3 spacer amino acids (Y_1-Y_3) at the amino and/or carboxyl terminus of an amino acid sequence selected from QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14),

ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), QANANEN (SEQ ID NO:22), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25) and KDRAPST (SEQ ID NO:26). In certain such embodiments, the insertion peptide is selected from the group consisting of: LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LANQDYTKTA (SEQ ID NO:31), LAHDITKNIA (SEQ ID NO:32), LAHPDTTKNA (SEQ ID NO:33), LAHQDTTKNA (SEQ ID NO:34), LANKTTNKDA (SEQ ID NO:35), LPISNENEHA (SEQ ID NO:36), LPQANANENA (SEQ ID NO:37), LAGKSKVIDA (SEQ ID NO:38), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40) and LAKDRAPSTA (SEQ ID NO:41).

[00130] In some embodiments, the subject variant AAV capsid protein does not include any other amino acid sequence modifications other than a peptide insertion of from about 5 amino acids to about 20 amino acids in the GH loop, or loop IV. For example, in some embodiments, the subject variant AAV capsid protein comprises a peptide insertion comprising an amino acid sequence selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), QANANEN (SEQ ID NO:22), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LANQDYTKTA (SEQ ID NO:31), LAHDITKNIA (SEQ ID NO:32), LAHPDTTKNA (SEQ ID NO:33), LAHQDTTKNA (SEQ ID NO:34), LANKTTNKDA (SEQ ID NO:35), LPISNENEHA (SEQ ID NO:36), LPQANANENA (SEQ ID NO:37), LAGKSKVIDA (SEQ ID NO:38), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40) and LAKDRAPSTA (SEQ ID NO:41), and the variant AAV capsid does not include any other amino acid substitutions, insertions, or deletions (i.e., the variant AAV capsid protein comprises said insertion and is otherwise identical to the corresponding AAV capsid protein). Put another way, the

variant AAV capsid protein comprising said insertion is otherwise identical to the parental AAV capsid protein into which the peptide has been inserted. As another example, the subject variant AAV capsid protein comprises a peptide insertion having an amino acid sequence selected from QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), HPDTTKN (SEQ ID NO:18), HQDTTKN (SEQ ID NO:19), NKTTNKD (SEQ ID NO:20), ISNENEH (SEQ ID NO:21), QANANEN (SEQ ID NO:22), GKSKVID (SEQ ID NO:23), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LANQDYTKTA (SEQ ID NO:31), LAHDITKNIA (SEQ ID NO:32), LAHPDTTKNA (SEQ ID NO:33), LAHQDTTKNA (SEQ ID NO:34), LANKTTNKDA (SEQ ID NO:35), LPISNENEHA (SEQ ID NO:36), LPQANANENA (SEQ ID NO:37), LAGKSKVIDA (SEQ ID NO:38), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40) and LAKDRAPSTA (SEQ ID NO:41), wherein the peptide insertion is located between amino acids 587 and 588 of the VP1 of the AAV2 capsid or the corresponding amino acids of a VP1 of another parental AAV, e.g. between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, between amino acids 586 and 587 of VP1 of AAV4, between amino acids 577 and 578 of VP1 of AAV5, between amino acids 589 and 590 of VP1 of AAV7, between amino acids 590 to 591 of VP1 of AAV8 or AAV10, etc. wherein the variant AAV capsid protein sequence is otherwise identical to the corresponding parental AAV capsid protein sequence, e.g. any one of SEQ ID NOs:1-12.

[00131] In other embodiments, the subject variant AAV capsid protein, in addition to comprising a peptide insertion, e.g. as disclosed herein or as known in the art, in the GH loop, comprises from about 1 to about 100 amino acid substitutions or deletions, e.g. 1 to about 5, from about 2 to about 4, from about 2 to about 5, from about 5 to about 10, from about 10 to about 15, from about 15 to about 20, from about 20 to about 25, from about 25-50, from about 50-100 amino acid substitutions or deletions compared to the parental AAV capsid protein. Thus, in some embodiments, a subject variant capsid protein comprises an amino acid sequence having a sequence identity of 85% or more, 90% or more, 95% or more, or 98% or more, e.g. or 99%

identity to the corresponding parental AAV capsid, e.g. a wild type capsid protein as set forth in SEQ ID NOs:1-12.

[00132] In a further embodiment, the one or more amino acid substitutions are at amino acid residue(s) 1, 15, 34, 57, 66, 81, 101, 109, 144, 164, 176, 188, 196, 226, 236, 240, 250, 312, 363, 368, 449, 456, 463, 472, 484, 524, 535, 551, 593, 698, 708, 719, 721, and/or 735 of AAV2 VP1 capsid protein as numbered prior to insertion of the peptide, or the corresponding amino acid residue(s) of another AAV capsid protein. In some such embodiments, the one or more amino acid substitutions are selected from the group consisting of M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, and L735Q of AAV2 VP1 capsid protein as numbered prior to the insertion of the peptide, or the corresponding amino acid residue(s) of another AAV capsid protein .

[00133] In a preferred embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from ISDQTKH (SEQ ID NO:14), LGISDQTKHA (SEQ ID NO:29) and LAISDQTKHA (SEQ ID NO:28), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. In some embodiments, the one or more amino acid substitutions are selected from the group consisting of: M1L+L15P+P535S, P34A, P34A+S721L, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, Q164K+V708I, T176P, L188I, S196Y, G226E, G236V, I240T, N312K, N312K+N449D+D472N+N551S+I698V+L735Q, P363L, R484C+V708I, T456K and V708I. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype.

[00134] In a particularly preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29) between amino acids 587 and 588 of VP1 of AAV2 or the corresponding amino acids of another AAV capsid, and further comprises a P34A amino acid substitution at residue 34 relative to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding residue of another AAV capsid. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2 or the corresponding parental AAV capsid. In a particularly preferred embodiment, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPK**A**AERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAISDQTKHA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:42)

[00135] In another particularly preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29)

between amino acids 587 and 588 of AAV2 capsid protein or the corresponding position in the capsid protein of another AAV serotype and comprises an N312K amino acid substitution compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype and optionally further comprises N449D, D472N, N551S, I698V and/or L735Q amino acid substitutions compared to the amino acid sequence of AAV2 capsid or the corresponding substitutions in another AAV parental serotype. In another particularly preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29) between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype and comprises N312K, N449D, D472N, N551S, I698V and L735Q amino acid substitutions compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or substitutions at the corresponding residues in another AAV parental serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In a particularly preferred embodiment, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRL**K**FKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRT**D**TPSGTTTQSRLQFSQA
GASDIR**N**QSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKT**S**VDIEKVMITDEEEIRTTNP
VATEQYGSVSTNLQRGN**LAISDQTKHA**RQAATADVNTQGVLPGMVWQDRD
VYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAA

KFASFITQYSTGQVSVEIEWELQKENSKRWNPE**V**QYTSNYNKSVNVDFTVDT NGVYSEPRPIGTRYLTRN**Q** (SEQ ID NO:43)

[00136] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion located between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, amino acids 586 and 587 of AAV4, amino acids 577 and 578 of AAV5, amino acids 589 and 590 of AAV7, or amino acids 590 to 591 of AAV8 or AAV10, the peptide insertion comprising an amino acid sequence selected from ISDQTKH (SEQ ID NO:14), LGISDQTKHA (SEQ ID NO:29) and LAISDQTKHA (SEQ ID NO:28), and b) a valine to isoleucine substitution at amino acid 709 of AAV3A or AAV3B, an alanine to isoleucine substitution at position 709 of AAV1 or AAV6, an asparagine to isoleucine substitution at amino acid 707 of AAV4 or amino acid 709 of AAV9 or a threonine to isoleucine substitution at amino acid 710 of AAV7 or amino acid 711 of AAV8 or AAV10 or a glutamine to isoleucine substitution at amino acid 697 of AAV5 and is optionally otherwise identical to any one of SEQ ID NOs: 1 and 3-12. In preferred embodiments, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29) between amino acids 587 and 588 of AAV2 capsid and b) a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2, wherein the variant capsid protein comprises from 2 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions.

[00137] In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29) between amino acids 587 and 588 of AAV2 capsid and b) a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2 and is otherwise identical to the amino acid sequence of SEQ ID NO:2.

[00138] In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence ISDQTKH (SEQ ID NO:14) or comprising, consisting essentially of, or consisting of the amino acid sequence LAISDQTKHA (SEQ ID NO:28) or LGISDQTKHA (SEQ ID NO:29) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid

sequence of SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LGISDQTKHA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:44)

[00139] In a preferred embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from QADTTKN (SEQ ID NO:13) and LAQADTTKNA (SEQ ID NO:27), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V719M, S721L, L735Q and a combination thereof, preferably selected from S109T, P250S, A524T, A593E, I698V, V708I, and/or V719M. The peptide insertion site is preferably located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In a particularly preferred embodiment, the variant AAV

capsid comprises a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype and comprises an I698V amino acid substitution compared to the amino acid sequence of AAV2 or the corresponding substitution in another AAV parental serotype, wherein the substituted amino acid(s) do not naturally occur at the corresponding position. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the corresponding amino acid substitution is an I699V amino acid substitution compared to the amino acid sequence of AAV3A, AAV3B or AAV9 capsid, an I687V substitution compared to the amino acid sequence of AAV5 capsid, an I700V substitution compared to the amino acid sequence of AAV7, an I701V substitution compared to the amino acid sequence of AAV8 or AAV10. In a particularly preferred embodiment, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAQADTTKNA**RQAATADVNTQGVLPGMVWQD
RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFS
AAKFASFITQYSTGQVSVEIEWELQKENSKRWNPE**V**QYTSNYNKSVNVDFTV
DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:45)

[00140] In other preferred embodiments, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype and comprises a V719M amino acid substitution and optionally a V708I substitution compared to the amino acid sequence of AAV2 or the corresponding substitution in another AAV parental serotype, wherein the substituted amino acid(s) do not naturally occur at the corresponding position.

[00141] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion located between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, amino acids 586 and 587 of AAV4, amino acids 577 and 578 of AAV5, amino acids 589 and 590 of AAV7, or amino acids 590 to 591 of AAV8 or AAV10, the peptide insertion comprising an amino acid sequence selected from QADTTKN (SEQ ID NO:13) and LAQADTTKNA (SEQ ID NO:27), and b) a valine to isoleucine substitution at amino acid 709 of AAV3A or AAV3B, an alanine to isoleucine substitution at position 709 of AAV1 or AAV6, an asparagine to isoleucine substitution at amino acid 707 of AAV4 or amino acid 709 of AAV9 or a threonine to isoleucine substitution at amino acid 710 of AAV7 or amino acid 711 of AAV8 or AAV10 or a glutamine to isoleucine substitution at amino acid 697 of AAV5. In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion located between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, amino acids 586 and 587 of AAV4, amino acids 577 and 578 of AAV5, amino acids 589 and 590 of AAV7, or amino acids 590 to 591 of AAV8 or AAV10, the peptide insertion comprising an amino acid sequence selected from QADTTKN (SEQ ID NO:13) and LAQADTTKNA (SEQ ID NO:27), and b) a serine to threonine amino acid substitution at position 109 compared to the amino acid sequence of AAV1, AAV3A, AAV3B, AAV4, AAV7, AAV8, AAV9, or AAV10 or at position 108 compared to the amino acid sequence of AAV5 or AAV6. In preferred embodiments, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid and comprises a serine to threonine substitution at amino acid 109 (S109T) or a valine

to isoleucine amino acid substitution at amino acid 708 (V708I) compared to the amino acid sequence of AAV2, wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions and is preferably at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In other preferred embodiments, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype and comprises a serine to threonine substitution at amino acid 109 and a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2.

[00142] In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid and b) at least one amino acid substitution, wherein the amino acid sequence of the variant capsid does not comprise a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2 and does not comprise a serine to threonine substitution at amino acid 109 compared to the amino acid sequence of AAV2.

[00143] In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence QADTTKN (SEQ ID NO:13) or comprising, consisting essentially of, or consisting of the amino acid sequence LAQADTTKNA (SEQ ID NO:27) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence of SEQ ID NO:2.

[00144] In another preferred embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from HDITKNI (SEQ ID NO:17), IAHDITKNIA (SEQ ID NO:60) and LAHDITKNIA (SEQ ID NO:32), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the

substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, R389S, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. In some embodiments, the AAV capsid protein comprises one or more amino acid substitutions selected from S109T, R389S, A593E and/or V708I. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In one preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence HDITKNI (SEQ ID NO:17) or comprising, consisting essentially of, or consisting of the amino acid sequence IAHDITKNIA (SEQ ID NO:60) or LAHDITKNIA (SEQ ID NO:32) between amino acids 587 and 588 of AAV2 capsid and comprises an S109T amino acid substitution compared to the amino acid sequence of AAV2 capsid or the corresponding substitution in another AAV parental serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2.

[00145] In yet another embodiment, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence HDITKNI (SEQ ID NO:17) or comprising, consisting essentially of, or consisting of the amino acid sequence IAHDITKNIA (SEQ ID NO:60) or LAHDITKNIA (SEQ ID NO:32) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG

CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAHDITKNIA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:46)

[00146] In other embodiments, the variant capsid comprises a) a peptide insertion comprising, consisting essentially of, or consisting of the amino acid sequence LAHDITKNIA between amino acids 587 and 588 of AAV2 capsid and b) at least one amino acid substitution, wherein the amino acid sequence of the variant capsid does not comprise a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2. In yet other embodiments, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence DITKNIA (SEQ ID NO:61) or comprising, consisting essentially of or consisting of the amino acid sequence sequence IAHDITKNIA (SEQ ID NO:60) or LAHDITKNIA (SEQ ID NO:32) between amino acids 587 and 588 of AAV2 capsid and b) a V708I substitution compared to the amino acid sequence of AAV2. In other embodiments, the variant capsid comprises a) a peptide insertion comprising, consisting essentially of, or consisting of the amino acid sequence LAHDITKNIA (SEQ ID NO:32) between amino acids 587 and 588 of AAV2 capsid and b) two or more amino acid substitutions, wherein the amino acid sequence of the variant capsid comprises a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2.

[00147] In another preferred embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from NQDYTKT (SEQ ID NO:16) and LANQDYTKTA (SEQ ID NO:31), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E,

G236V, I240T, P250S, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. In some embodiments, the AAV capsid protein comprises one or more amino acid substitutions selected from S109T, S109T+S463Y, D368H and V708I. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In one preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence NQDYTKT (SEQ ID NO:16) or comprising, consisting essentially of, or consisting of the amino acid sequence LANQDYTKTA (SEQ ID NO:31) between amino acids 587 and 588 of AAV2 capsid and comprises a V708I amino acid substitution compared to the amino acid sequence of AAV2 capsid or the corresponding substitution in another AAV parental serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence NQDYTKT (SEQ ID NO:16) or comprising, consisting essentially of, or consisting of the amino acid sequence LANQDYTKTA (SEQ ID NO:31) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN

PVATEQYGSVSTNLQRGN**LANQDYTKTA**RQAATADVNTQGVLPGMVWQD
RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFS
AAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV
DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:47)

[00148] In other embodiments, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence NQDYTKT (SEQ ID NO:16) or comprising, consisting essentially of, or consisting of the amino acid sequence LANQDYTKTA (SEQ ID NO:31) between amino acids 587 and 588 of AAV2 capsid and b) an S109T amino acid substitution compared to the sequence of SEQ ID NO:2 and optionally an S463Y amino acid substitution, wherein the variant capsid is at least about 85%, at least about 90%, at least about 95%, at least about 98% identical to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In related embodiments, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence NQDYTKT (SEQ ID NO:16) or comprising, consisting essentially of, or consisting of the amino acid sequence LANQDYTKTA (SEQ ID NO:31) between amino acids 587 and 588 of AAV2 capsid and b) an S109T amino acid substitution compared to the amino acid sequence of SEQ ID NO:2 and is otherwise identical to the amino acid sequence of SEQ ID NO:2.

[00149] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion located between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, amino acids 586 and 587 of AAV4, amino acids 577 and 578 of AAV5, amino acids 589 and 590 of AAV7, or amino acids 590 to 591 of AAV8 or AAV10, the peptide insertion comprising an amino acid sequence selected from NQDYTKT (SEQ ID NO:16) and LANQDYTKTA (SEQ ID NO:31), and b) an asparagine to lysine amino acid substitution at position 313 compared to the amino acid sequence of AAV1 or AAV6, or at position 314 compared to the amino acid sequence of AAV9, or a serine to lysine substitution at position 312 of AAV3A or AAV3B or at position 315 of AAV8 or AAV10, or an arginine to lysine substitution at position 303 of AAV4 or AAV5, or at position 314 of AAV7. In another embodiment, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence NQDYTKT (SEQ ID NO:16) or comprising, consisting essentially of, or consisting of the amino acid sequence LANQDYTKTA (SEQ ID NO:31) between amino acids 587 and 588 of AAV2 capsid and b) an N312K amino

acid substitution, wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions.

[00150] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from PNSTHGS (SEQ ID NO:25) and LAPNSTHGSA (SEQ ID NO:40), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In one preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence PNSTHGS (SEQ ID NO:25) or comprising, consisting essentially of, or consisting of the amino acid sequence LAPNSTHGSA (SEQ ID NO:40) between amino acids 587 and 588 of AAV2 capsid and comprises a V708I amino acid substitution compared to the amino acid sequence of AAV2 capsid or the corresponding substitution in another AAV parental serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence PNSTHGS (SEQ ID NO:25) or comprising, consisting essentially of, or consisting of the amino acid sequence LAPNSTHGSA (SEQ ID NO:40) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some_embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ

ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAPNSTHGSA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ IDNO:48)

[00151] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from NKTTNKDA (SEQ ID NO:62) and LANKTTNKDA (SEQ ID NO:35), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In one preferred embodiment, the variant AAV capsid comprises a peptide insertion comprising the amino acid sequence NKTTNKDA (SEQ ID NO:62) or comprising, consisting essentially of, or consisting of the amino acid sequence LANKTTNKDA (SEQ ID NO:35) between amino acids 587 and 588 of AAV2 capsid and comprises an N449D amino acid substitution compared to the amino acid sequence of AAV2 capsid or the corresponding substitution in another AAV parental serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the

entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a) a peptide insertion comprising the amino acid sequence NKTTNKDA (SEQ ID NO:62) or comprising, consisting essentially of, or consisting of the amino acid sequence LANKTTNKDA (SEQ ID NO:35) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LANKTTNKDA**RQAATADVNTQGVLPGMVWQD
RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFS
AAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV
DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:49)

[00152] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from TNRTSPD (SEQ ID NO:24) and LATNRTSPDA (SEQ ID NO:39), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S,

N551S, A593E, I698V, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. In a related embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion located between amino acids 588 and 589 of VP1 of AAV1, AAV3A, AAV3B, AAV6 or AAV9, amino acids 586 and 587 of AAV4, amino acids 577 and 578 of AAV5, amino acids 589 and 590 of AAV7, or amino acids 590 to 591 of AAV8 or AAV10, the peptide insertion comprising an amino acid sequence selected from TNRTSPD (SEQ ID NO:24) and LATNRTSPDA (SEQ ID NO:39), and b) a valine to isoleucine substitution at amino acid 709 of AAV3A or AAV3B, an alanine to isoleucine substitution at position 709 of AAV1 or AAV6, an asparagine to isoleucine substitution at amino acid 707 of AAV4 or amino acid 709 of AAV9 or a threonine to isoleucine substitution at amino acid 710 of AAV7 or amino acid 711 of AAV8 or AAV10 or a glutamine to isoleucine substitution at amino acid 697 of AAV5. In other embodiments, the variant capsid protein comprises a) a peptide insertion comprising, consisting essentially of, or consisting of the amino acid sequence LATNRTSPDA (SEQ ID NO:39) between amino acids 587 and 588 of AAV2 capsid and b) a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2, wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions. In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence TNRTSPD (SEQ ID NO:24) between amino acids 587 and 588 of AAV2 capsid and b) a valine to isoleucine amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2.

[00153] In yet another embodiment, the variant capsid protein comprises a) a peptide insertion comprising the amino acid sequence TNRTSPD (SEQ ID NO:24) or comprising, consisting essentially of, or consisting of the amino acid sequence LATNRTSPDA (SEQ ID NO:39) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence of SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least

about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:
MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LATNRTSPDA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:50)

[00154] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from GKSKVID (SEQ ID NO:23) and LAGKSKVIDA (SEQ ID NO:38), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid comprises a peptide insertion located between

amino acids 587 and 588 of AAV2 capsid comprising the amino acid sequence GKSKVID (SEQ ID NO:23) or comprising, consisting essentially of, or consisting of the amino acid sequence LAGKSKVIDA (SEQ ID NO:38) and is otherwise identical to the amino acid sequence of SEQ ID NO:2. In other embodiments, the variant AAV capsid comprises a) a peptide insertion comprising, consisting essentially of, or consisting of the amino acid sequence LAGKSKVIDA (SEQ ID NO:38) between amino acids 587 and 588 of AAV2 capsid and comprises at least one amino acid substitution.

[00155] In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAGKSKVIDA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:51)

[00156] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from ASDSTKA (SEQ ID NO:15) and LAASDSTKAA (SEQ ID NO:30), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at

the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence ASDSTKA (SEQ ID NO:15) or comprising, consisting essentially of, or consisting of the amino acid sequence LAASDSTKAA (SEQ ID NO:30) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAASDSTKAA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:52)

[00157] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the

peptide insertion comprises an amino acid sequence selected from KDRAPST (SEQ ID NO:26) and LAKDRAPTSA (SEQ ID NO:41), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence KDRAPST (SEQ ID NO:26) or comprising, consisting essentially of, or consisting of the amino acid sequence LAKDRAPTSA (SEQ ID NO:41) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAKDRAPSTA**RQAATADVNTQGVLPGMVWQDR

DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:53)

[00158] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from HQDTTKN (SEQ ID NO:19) and LAHQDTTKNA (SEQ ID NO:34), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at one or more of the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence HQDTTKN (SEQ ID NO:19) or comprising, consisting essentially of, or consisting of the amino acid sequence LAHQDTTKNA (SEQ ID NO:34) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG

CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LAHQDTTKNA**RQAATADVNTQGVLPGMVWQD
RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFS
AAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV
DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:54)

[00159] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from ISNENEH (SEQ ID NO:21) and LPISNENEHA (SEQ ID NO:36), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at one or more of the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence ISNENEH (SEQ ID NO:21) or comprising, consisting essentially of, or consisting of the amino acid sequence LPISNENEHA (SEQ ID NO:36) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ

ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LPISNENEHA**RQAATADVNTQGVLPGMVWQDR
DVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSA
AKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT
NGVYSEPRPIGTRYLTRNL (SEQ ID NO:55)

[00160] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from QANANEN (SEQ ID NO:22) and LPQANANENA (SEQ ID NO:37), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence QANANEN (SEQ ID NO:22) or comprising, consisting essentially of, or consisting of the amino acid sequence LPQANANENA (SEQ ID NO:37) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid

has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYK
YLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQ
ERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEP
DSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAPSGLGTNTMAT
GSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNH
LYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFR
PKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG
CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFS
YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTQSRLQFSQA
GASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSL
VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTN
PVATEQYGSVSTNLQRGN**LPQANANENA**RQAATADVNTQGVLPGMVWQD
RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFS
AAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV
DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:56)

[00161] In another embodiment, a variant AAV capsid protein is provided comprising a) a peptide insertion in the GH-loop of the capsid protein, wherein the peptide insertion comprises an amino acid sequence selected from HPDTTKN (SEQ ID NO:18) and LAHPDTTKNA (SEQ ID NO:33), and b) one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid(s) do not naturally occur at the corresponding positions: M1L, L15P, P34A, N57D, N66K, R81Q, Q101R, S109T, R144K, R144M, Q164K, T176P, L188I, S196Y, G226E, G236V, I240T, P250S, N312K, P363L, D368H, N449D, T456K, S463Y, D472N, R484C, A524T, P535S, N551S, A593E, I698V, V708I, V719M, S721L, L735Q and a combination thereof. Preferably, the peptide insertion site is located between amino acids 587 and 588 of AAV2 capsid or the corresponding position in the capsid protein of another AAV serotype. The variant AAV capsid may have at least about 85%, at least about 90%, at least about 95%, at least about 98%, or greater amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2. In yet another

embodiment, the variant capsid comprises a peptide insertion comprising the amino acid sequence HPDTTKN (SEQ ID NO:18) or comprising, consisting essentially of, or consisting of the amino acid sequence LAHPDTTKNA (SEQ ID NO:33) between amino acids 587 and 588 of AAV2 capsid and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the variant AAV capsid has an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98% sequence identity to or is 100% identical to the following amino acid sequence:

[00162] MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKD DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYL KYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTAPGK KRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAA PSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTST RTWALPTYNNHLYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRD WQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSE YQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFP SQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPS GTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTG ATKYHLNGRDSLVNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEK VMITDEEEIRTTNPVATEQYGSVSTNLQRGN**<u>LAHPDTTKNA</u>**RQAATADVNT QGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIK NTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSN YNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:57).

[00163] In several aspects, a variant AAV capsid protein is provided comprising one or more amino acid substitutions relative to a corresponding parental AAV capsid protein, wherein the variant capsid protein, when present in an AAV virion, confers increased infectivity of a retinal cell compared to the infectivity of a retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein.

[00164] In some embodiments, a variant AAV capsid protein comprises a P34A amino acid substitution compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or a P33A amino acid substitution compared to the amino acid sequence of AAV5 capsid (SEQ ID NO:6). In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at

least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2 or SEQ ID NO:6 and comprises a P34A or P33A amino acid substitution compared to the amino acid sequence of AAV2 or AAV5 capsid respectively. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence comprising a P34A amino acid substitution compared to the amino acid sequence set forth in SEQ ID NO 2 and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In related embodiments, the variant capsid protein comprises a P34A amino acid substitution compared to the amino acid sequence of SEQ ID NO:2, wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2.

[00165] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 164 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid does not naturally occur at the corresponding position. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 164 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the rAAV virion comprises a glutamine to lysine amino acid substitution at amino acid 164 compared to amino acid sequence of AAV1, AAV2 or AAV6 or at amino acid 165 compared to the amino acid sequence of AAV7, AAV8, or AAV10; or comprises a serine to lysine substitution at amino acid 160 of AAV5 or comprises an alanine to lysine substitution at amino acid 164 of AAV9. In related embodiments, the variant capsid protein comprises an amino acid substitution at amino acid 164 (e.g. Q164K) compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2), wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence comprising a Q164K amino acid substitution compared to the amino acid sequence set forth in SEQ ID

NO:2 and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In other embodiments the variant capsid protein comprises Q164K and V708I amino acid substitutions compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding substitutions in another AAV parental serotype (i.e. other than AAV2) and is at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:2.

[00166] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 698 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid does not naturally occur at the corresponding position. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 698 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the rAAV virion comprises an isoleucine to valine amino acid substitution at amino acid 698 compared to amino acid sequence of AAV2, or at amino acid 699 compared to the amino acid sequence of AAV3A, AAV3B, or AAV9, or at amino acid 687 of AAV5, or at amino acid 700 of AAV7, or at amino acid 701 of AAV8 or AAV10. In related embodiments, the variant capsid protein comprises an amino acid substitution at amino acid 699 (e.g. I698V) compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2), wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence comprising an I698V amino acid substitution compared to the amino acid sequence set forth in SEQ ID NO:2 and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2.

[00167] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 109 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2). In some preferred embodiments, the variant capsid

protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 109 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the variant capsid protein comprises a serine to threonine amino acid substitution at position 109 compared to the amino acid sequence of AAV1, AAV3A, AAV3B, AAV4, AAV7, AAV8, AAV9 , or AAV10 or at position 108 compared to the amino acid sequence of AAV5 or AAV6. In related embodiments, the variant capsid protein comprises an S109T amino acid substitution compared to the amino acid sequence AAV2, wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions. In other related embodiments, the variant capsid protein comprises an S109T amino acid substitution and an A593E amino acid substitution compared to the amino acid sequence of AAV2. In some embodiments the variant capsid protein comprises S109T and A493V and optionally A593E and/or V708I amino acid substitutions compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding substitutions in another AAV parental serotype (i.e. other than AAV2) and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2. In some preferred embodiments the variant capsid protein comprises S109T, A493V, A593E and V708I amino acid substitutions compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding substitutions in another AAV parental serotype (i.e. other than AAV2) and is at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2. In other preferred embodiments, the variant capsid protein comprises S109T and V708I amino acid substitutions compared to the amino acid sequence of AAV2 capsid and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 or is otherwise identical to the amino acid sequence of SEQ ID NO:2.

[00168] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 593 compared to the amino acid sequence of

AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2). In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 593 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the variant capsid protein comprises a glycine to glutamate amino acid substitution at amino acid 594 compared to the amino acid sequence of AAV1, AAV3A, AAV6, or AAV9, or at amino acid 583 of AAV5, or at amino acid 596 of AAV8 or AAV10, or an arginine to glutamate amino acid substitution at amino acid 594 of AAV3B, or an aspartate to glutamate amino acid substitution at amino acid 592 of AAV4 or a glutamine to glutamate amino acid substitution at position 595 of AAV7. In other embodiments, the variant capsid protein comprises an A593E amino acid substitution compared to the amino acid sequence of AAV2 and does not comprise one or more of the following amino acid substitutions compared to the amino acid sequence of AAV2: I19V, V369A, K26R, N215D, G355S, V46A and S196P. In related embodiments, the variant capsid protein comprises A593E and N596D amino acid substitutions compared to the amino acid sequence of AAV2 and has at least about 85%, at least about 90%, at least about 95%, at least about 98% or at least about 99% identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2. In other embodiments, the variant capsid comprises A593E and N596D amino acid substitutions compared to the amino acid sequence of AAV2 and is otherwise identical to the amino acid sequence of AAV2. In other embodiments, the variant capsid comprises A593E and V708I amino acid substitutions compared to the amino acid sequence of AAV2 and has at least about 85%, at least about 90%, at least about 95%, at least about 98% or at least about 99% identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2. In other embodiments, the variant capsid comprises A593E and V708I amino acid substitutions compared to the amino acid sequence of AAV2 and is otherwise identical to the amino acid sequence of AAV2.

[00169] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental

serotype (i.e. other than AAV2) wherein the substituted amino acid does not naturally occur at the corresponding position. Preferably, the rAAV virion does not comprise a proline to serine substitution at amino acid 250 compared to AAV2 or a corresponding amino acid in another AAV parental serotype. In some embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 708 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In preferred embodiments, the variant capsid protein comprises a valine to isoleucine (V708I) substitution at amino acid 708 compared to the amino acid sequence of AAV2 capsid and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 or is otherwise identical to the amino acid sequence of SEQ ID NO:2, wherein the variant capsid protein does not comprise a P250S amino acid substitution. In some embodiments, the variant capsid protein comprises a valine to isoleucine substitution at amino acid 709 of AAV3A or AAV3B, an alanine to isoleucine substitution at position 709 of AAV1 or AAV6, an asparagine to isoleucine substitution at amino acid 707 of AAV4 or amino acid 709 of AAV9 or a threonine to isoleucine substitution at amino acid 710 of AAV7 or amino acid 711 of AAV8 or AAV10 or a glutamine to isoleucine substitution at amino acid 697 of AAV5. In related embodiments, the variant capsid protein comprises a V708I amino acid substitution compared to the amino acid sequence of AAV2, wherein the variant capsid protein comprises from 2 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions and wherein the variant capsid protein does not comprise a P250S amino acid substitution. In other embodiments, the variant capsid protein comprises a V708I amino acid substitution and also comprises an A593E and/or an S109T amino acid substitution compared to the amino acid sequence of AAV2. In other related embodiments, the variant capsid comprises V708I and A593E amino acid substitutions compared to the amino acid sequence of AAV2, wherein the variant capsid protein is otherwise identical to the amino acid sequence of AAV2. In other related embodiments, the variant capsid comprises V708I and S109T amino acid substitutions compared to the amino acid sequence of AAV2, wherein the variant capsid protein is otherwise

identical to the amino acid sequence of AAV2. In other embodiments, the variant capsid protein comprises V708I and V719M amino acid substitutions compared to the amino acid sequence of AAV2 and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 or is otherwise identical to the amino acid sequence of SEQ ID NO:2. In other embodiments, the variant capsid protein comprises V708I and R733C amino acid substitutions compared to the amino acid sequence of AAV2 and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 or is otherwise identical to the amino acid sequence of SEQ ID NO:2. In other embodiments, the variant capsid protein comprises V708I and G727D amino acid substitutions compared to the amino acid sequence of AAV2 and has at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 or is otherwise identical to the amino acid sequence of SEQ ID NO:2.

[00170] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 196 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid does not naturally occur at the corresponding position and is optionally other than proline. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 196 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) and is optionally other than an S196P substitution. In preferred embodiments, the variant capsid protein comprises a serine to tyrosine amino acid substitution at amino acid 196 of AAV2 or AAV9 or at amino acid 197 of AAV7, AAV8 or AAV10 or at amino acid 186 of AAV5; or an alanine to tyrosine substitution at amino acid 196 of AAV1 or AAV6; or a methionine to tyrosine substitution at amino acid 191 of AAV4; or a threonine to tyrosine substitution at amino acid 196 of AAV3A or AAV3B. In a related embodiment, the variant capsid

protein comprises an amino acid sequence comprising an S196Y amino acid substitution compared to the amino acid sequence set forth in SEQ ID NO:2 and is otherwise identical to the amino acid sequence set forth in SEQ ID NO:2. In related embodiments, the variant capsid protein comprises an amino acid substitution at amino acid 196 other than an S196P substitution (e.g. comprises an S196Y substitution) compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2), wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2.

[00171] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 175 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid does not naturally occur at the corresponding position. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 175 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the variant capsid comprises a Q175H amino acid substitution compared to the amino acid sequence of AAV2 as set forth in SEQ ID NO:2 or a glutamine to histidine substitution at the corresponding position in another AAV parental serotype. In related embodiments, the variant capsid protein comprises an amino acid substitution at amino acid 175 (e.g. Q175H) compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2), wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2.

[00172] In other embodiments a variant AAV capsid protein comprises an amino acid substitution at amino acid 64 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2) or the corresponding position in another AAV parental serotype (i.e. other than AAV2), wherein the substituted amino acid does not naturally occur at the corresponding position. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least

about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO 2 and comprises an amino acid substitution at amino acid 64 compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2). In some embodiments, the rAAV virion comprises a P64S amino acid substitution compared to the amino acid sequence of AAV2 as set forth in SEQ ID NO:2 or a proline to serine substitution at the corresponding position in another AAV parental serotype. In related embodiments, the variant capsid protein comprises an amino acid substitution at amino acid 64 (e.g. P64S) compared to the amino acid sequence of AAV2 capsid (SEQ ID NO:2), wherein the variant capsid protein comprises from 1 to 5, from 5 to 10, or from 10 to 15 amino acid substitutions compared to the amino acid sequence of an AAV2 capsid protein set forth in SEQ ID NO:2.

[00173] In other embodiments, a variant AAV capsid protein comprises an amino acid sequence at least 85%, at least 90%, at least 95% or at least 98% identical to a wild-type AAV capsid sequence selected from the group consisting of SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 8, 10,11 and 12 and also comprises i) one or more amino acid substitutions selected from the group consisting of P34A, S109T+V708I, A593E+N596D, V708I+V719M, V708I+G727D, S109T+A493V+A593E+V708I, V708I+R733C, Q164K, and I698V and/or (ii) a peptide insertion selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), PQANANEN (SEQ ID NO:63), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), HQDTTKN (SEQ ID NO:19), HPDTTKN (SEQ ID NO:18), NKTTNKD (SEQ ID NO:20), GKSKVID (SEQ ID NO:23), PISNENEH (SEQ ID NO:64), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LAHDITKNIA (SEQ ID NO:32), LPQANANENA (SEQ ID NO:37), LANQDYTKTA (SEQ ID NO:31), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40), LAKDRAPSTA (SEQ ID NO:41), LAHQDTTKNA (SEQ ID NO:34), LAHPDTTKNA (SEQ ID NO:33), LANKTTNKDA (SEQ ID NO:35), LAGKSKVIDA (SEQ ID NO:38), and LPISNENEHA (SEQ ID NO:36). In some embodiments, the variant AAV capsid comprises the specified one or more amino

acid substitutions and/or peptide insertions and is otherwise identical to a sequence selected from the group consisting of SEQ ID NOS: 1-12.

[00174] In some embodiments, a variant AAV capsid protein is an ancestral capsid protein. By an ancestral capsid protein it is meant an evolutionary ancestor of a capsid protein that is found in nature today, e.g. AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAVrh10, AAV11, AAV12, AAV13, which is generated in silico by random amino acid substitution at positions of degeneracy between AAV capsid proteins that are found in nature today. One nonlimiting example of an ancestral capsid is provided below, wherein the positions of degeneracy (residues 264, 266, 268, 448, 459, 460, 467, 470, 471, 474, 495, 516, 533, 547, 551, 555, 557, 561, 563, 577, 583, 593, 596, 661, 662, 664, 665, 710, 717, 718, 719, 723) are marked as an "X" :

[00175] MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQ
DDGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNP
YLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAP
GKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPLGEPP
AGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITT
STRTWALPTYNNHLYKQISSXSXGXTNDNHYFGYSTPWGYFDFNRFHCHFSP
RDWQRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSD
SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYF
PSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLXRTQST
GGTAGXXELLFSQXGPXXMSXQAKNWLPGPCYRQQRVSKTLXQNNNSNFA
WTGATKYHLNGRXSLVNPGVAMATHKDDEXRFFPSSGVLIFGKXGAGXNNT
XLXNVMXTXEEEIKTTNPVATEXYGVVAXNLQSSNTAPXTGXVNSQGALPG
MVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPA
NPPXXFXXAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYAKSX
NVDFAVXXXGVYXEPRPIGTRYLTRNL (SEQ ID NO:58)

[00176] In some embodiments, the ancestral capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence set forth in SEQ ID NO:58. In some embodiments, the ancestral capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of

the amino acid sequence of AAV2, e.g. as set forth in SEQ ID NO 2. In some embodiments, the ancestral capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, or greater, amino acid sequence identity to the entire length of the amino acid sequence of the ancestral sequence disclosed in SEQ ID NO:58 or in SEQ ID NO:2 and comprises one or more amino acid residues selected from the group consisting of: Alanine (A) at 264, Alanine (A) at 266, Serine (S) at 268, Alanine (A) at 448, Threonine (T) at 459, Arginine (R) at 460, Alanine (A) at 467, Serine (S) at 470, Asparagine (N) at 471, Alanine (A) at 474, Serine (S) at 495, Asparagine (D) at 516, Asparagine (D) at 533, Glutamine (Q) at 547, Alanine (A) at 551, Alaninet (A) at 555, Glutamic acid (E) at 557, Methionine (M) at 561, Serine (S) at 563, Glutamine (Q) at 577, Serine (S) at 583, Valine (V) at 593, Threonine (T) at 596, Alanine (A) at 661, Valine (V) at 662, Threonine (T) at 664, Proline (P) at 665, Threonine (T) at 710, Aspartic Acid (D) at 717, Asparagine (N) at 718, Glutamic acid (E) at 719, and Serine (S) at 723. In some preferred embodiments, the variant capsid protein comprises an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, in some instances 100% amino acid sequence identity to the entire length of the following amino acid sequence and comprises one or more amino acid residues selected from the group consisting of: Alanine (A) at 264, Alanine (A) at 266, Serine (S) at 268, Alanine (A) at 448, Threonine (T) at 459, Arginine (R) at 460, Alanine (A) at 467, Serine (S) at 470, Asparagine (N) at 471, Alanine (A) at 474, Serine (S) at 495, Asparagine (D) at 516, Asparagine (D) at 533, Glutamine (Q) at 547, Alanine (A) at 551, Alanine (A) at 555, Glutamic acid (E) at 557, Methionine (M) at 561, Serine (S) at 563, Glutamine (Q) at 577, Serine (S) at 583, Valine (V) at 593, Threonine (T) at 596, Alanine (A) at 661, Valine (V) at 662, Threonine (T) at 664, Proline (P) at 665, Threonine (T) at 710, Aspartic Acid (D) at 717, Asparagine (N) at 718, Glutamic acid (E) at 719, and Serine (S) at 723:

[00177] MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQ
DDGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNP
YLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAP
GKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPLGEPP
AGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITT
STRTWALPTYNNHLYKQISSASAGSTNDNHYFGYSTPWGYFDFNRFHCHFSP

RDWQRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSD
SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYF
PSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST
GGTAGTRELLFSQAGPSNMSAQAKNWLPGPCYRQQRVSKTLSQNNNSNFAW
TGATKYHLNGRDSLVNPGVAMATHKDDEDRFFPSSGVLIFGKQGAGANNTA
LENVMMTSEEEIKTTNPVATEQYGVVASNLQSSNTAPVTGTVNSQGALPGM
VWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPANP
PAVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYAKSTNV
DFAVDNEGVYSEPRPIGTRYLTRNL (SEQ ID NO:59).

[00178] In other embodiments, a variant AAV capsid protein comprises an amino acid sequence at least 85%, at least 90%, at least 95% or at least 98% identical to a wild-type AAV capsid sequence selected from the group consisting of the ancestral variant disclosed herein as SEQ ID NO:58, comprises one or more amino acid residues selected from the group consisting of: Alanine (A) at 264, Alanine (A) at 266, Serine (S) at 268, Alanine (A) at 448, Threonine (T) at 459, Arginine (R) at 460, Alanine (A) at 467, Serine (S) at 470, Asparagine (N) at 471, Alanine (A) at 474, Serine (S) at 495, Asparagine (D) at 516, Asparagine (D) at 533, Glutamine (Q) at 547, Alanine (A) at 551, Alanine (A) at 555, Glutamic acid (E) at 557, Methionine (M) at 561, Serine (S) at 563, Glutamine (Q) at 577, Serine (S) at 583, Valine (V) at 593, Threonine (T) at 596, Alanine (A) at 661, Valine (V) at 662, Threonine (T) at 664, Proline (P) at 665, Threonine (T) at 710, Aspartic Acid (D) at 717, Asparagine (N) at 718, Glutamic acid (E) at 719, and Serine (S) at 723; and also comprises i) one or more amino acid substitutions selected from the group consisting of P34A, S109T+V708I, A593E+N596D, V708I+V719M, V708I+G727D, S109T+A493V+A593E+V708I, V708I+R733C, Q164K, and I698V and/or (ii) a peptide insertion selected from the group consisting of QADTTKN (SEQ ID NO:13), ISDQTKH (SEQ ID NO:14), ASDSTKA (SEQ ID NO:15), NQDYTKT (SEQ ID NO:16), HDITKNI (SEQ ID NO:17), PQANANEN (SEQ ID NO:63), TNRTSPD (SEQ ID NO:24), PNSTHGS (SEQ ID NO:25), KDRAPST (SEQ ID NO:26), HQDTTKN (SEQ ID NO:19), HPDTTKN (SEQ ID NO:18), NKTTNKD (SEQ ID NO:20), GKSKVID (SEQ ID NO:23), PISNENEH (SEQ ID NO:64), LAQADTTKNA (SEQ ID NO:27), LAISDQTKHA (SEQ ID NO:28), LGISDQTKHA (SEQ ID NO:29), LAASDSTKAA (SEQ ID NO:30), LAHDITKNIA (SEQ ID NO:32), LPQANANENA (SEQ ID NO:37), LANQDYTKTA (SEQ ID

NO:31), LATNRTSPDA (SEQ ID NO:39), LAPNSTHGSA (SEQ ID NO:40), LAKDRAPSTA (SEQ ID NO:41), LAHQDTTKNA (SEQ ID NO:34), LAHPDTTKNA (SEQ ID NO:33), LANKTTNKDA (SEQ ID NO:35), LAGKSKVIDA (SEQ ID NO:38), and LPISNENEHA (SEQ ID NO:36). In some embodiments, the variant AAV capsid comprises the specified one or more amino acid substitutions and/or peptide insertions and is otherwise identical to SEQ ID NO:59.

[00179] The AAV variants disclosed herein were generated through the use of *in vivo* directed evolution involving the use of primate retinal screens following intravitreal administration. In some embodiments, the variant capsid proteins disclosed herein, when present in an AAV virion, confer increased transduction of a retinal cell compared to the transduction of the retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein or wild-type AAV. For example, in some embodiments, the variant capsid proteins disclosed herein, when present in an AAV virion, confer more efficient transduction of primate retinal cells than AAV virions comprising the corresponding parental AAV capsid protein or wild-type AAV capsid protein, e.g. the retinal cells take up more AAV virions comprising the subject variant AAV capsid protein than AAV virions comprising the parental AAV capsid protein or wild-type AAV. In some such embodiments, the AAV variant virion or variant rAAV exhibits at least 2-fold, at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased transduction of a retinal cell, compared to the transduction of the retinal cell by a wild-type AAV virion or rAAV comprising the corresponding parental AAV capsid protein. In certain such embodiments, the variant capsid proteins disclosed herein, when present in an AAV virion, confer broader transduction of the primate retinal cells than AAV virions comprising the corresponding parental AAV capsid protein or wild type AAV capsid protein. In other words, the variant AAV virion transduces cell types not transduced by virions comprising the corresponding parental AAV capsid protein, and hence more types of cells in the retina than the corresponding parental AAV virion. In some embodiments, the AAV variant virion preferentially transduces a retinal cell, e.g., a subject rAAV virion infects a retinal cell with 2-fold, 5- fold, 10-fold, 15-fold, 20-fold, 25-fold, 50-fold, or more than 50-fold, specificity than another retinal cell or a non-retinal cell, e.g., a cell outside the eye. In some embodiments, the transduced retinal cell is a photoreceptor cell (e.g., rods;

cones). In some embodiments, the retinal cell is a retinal ganglion cell (RGC). In some embodiments, the retinal cell is a retinal epithelial cell (RPE cell). In some embodiments, the retinal cell is a Müller glial cell. In some embodiments, the retinal cell is a microglial cell. In some embodiments, the retinal cell is an amacrine cell. In some embodiments, the retinal cell is a bipolar cell. In some embodiments, the retinal cell is a horizontal cell. An increase in transduction of a retinal cell, e.g. increased efficiency of transduction, broader transduction, more preferential transduction, etc. may be readily assessed in vitro or in vivo by any number of methods in the art for measuring gene expression. For example, the AAV may be packaged with a genome comprising an expression cassette comprising a reporter gene, e.g. a fluorescent protein, under the control of a ubiquitous or tissue specific promoter, and the extent of transduction assessed by detecting the fluorescent protein by, e.g., fluorescence microscopy. As another example, the AAV may be packaged with a genome comprising a bar coded nucleic acid sequence, and the extent of transduction assessed by detecting the nucleic acid sequence by, e.g., PCR. As another example, the AAV may be packaged with a genome comprising an expression cassette comprising a therapeutic gene for the treatment of a retinal disease, and the extent of transduction assessed by detecting the treatment of the retinal disease in an afflicted patient that was administered the AAV.

[00180] Ocular diseases that can be treated using a variant rAAV vector or virion and/or method disclosed herein include, but are not limited to, monogenic diseases, complex genetic diseases, acquired diseases, and traumatic injuries. Examples of monogenic diseases include, but are not limited to, Bardet-Biedl syndrome; Batten's Disease; Bietti's Crystalline Dystrophy; choroideremia; chorioretinal atrophy; chorioretinal degeneration; cone or cone-rod dystrophies (autosomal dominant, autosomal recessive, and X-linked); congenital stationary night blindness (autosomal dominant, autosomal recessive, and X-linked); disorders of color vision, including achromatopsia (including ACHM2, ACHM3, ACHM4, and ACHM5), protanopia, deuteranopia, and tritanopia; Friedreich's ataxia; Leber's congenital amaurosis (autosomal dominant and autosomal recessive), including, but not limited to, LCA1, LCA2, LCA3, LCA4, LCA6, LCA7, LCA8, LCA12, and LCA15; Leber's Hereditary Optic Neuropathy; macular dystrophy (autosomal dominant and autosomal recessive), including, but not limited to, acute macular degeneration, Best vitelliform macular dystrophy, pattern dystrophy, North Carolina

Macular Dystrophy, inherited drusen, Sorsby's fundus dystrophy, malattia levantanese, and genetically-determined retinopathy of prematurity; ocular-retinal developmental disease; ocular albinism; optic atrophies (autosomal dominant, autosomal recessive, and X-linked); retinitis pigmentosa (autosomal dominant, autosomal recessive, X-linked, and mitochondrially-inherited traits), examples of which include RP1, RP2, RP3, RP10, RP20, RP38, RP40, and RP43; X-linked retinoschisis; Stargardt disease; and Usher syndrome, including, but not limited to, USH1B, USH1C, USH1D, USH1F, USH1G, USH2A, USH2C, USH2D, AND USH3. Examples of complex genetic diseases include, but are not limited to, glaucoma (open angle, angle-closure, low-tension, normal-tension, congenital, neovascular, pigmentary, pseudoexfoliation); age-related and other forms of macular degeneration, both exudative and non-exudative forms (autosomal dominant and autosomal recessive), such as acute macular degeneration, vitelliform macular degeneration; retinopathy of prematurity; and Vogt Koyanagi-Harada (VKH) syndrome. Examples of acquired diseases include, but are not limited to, acute macular neuroretinopathy; anterior ischemic optic neuropathy and posterior ischemic optic neuropathy; Behcet's disease; branch retinal vein occlusion; choroidal neovascularization; diabetic retinopathy, including proliferative diabetic retinopathy and associated complications; diabetic uveitis; edema, such as macular edema, cystoid macular edema and diabetic macular edema; epiretinal membrane disorders; macular telangiectasia; multifocal choroiditis; non-retinopathy diabetic retinal dysfunction; ocular tumors; optic atrophies; retinal detachment; retinal disorders, such as central retinal vein occlusion, proliferative vitreoretinopathy (PVR), retinal arterial and venous occlusive disease, vascular occlusion, uveitic retinal disease; uveal effusion; retinal infective and infiltrative disease; optic nerve diseases such as acquired optic atrophy. Examples of traumatic injuries include, but are not limited to, histoplasmosis; optic nerve trauma; ocular trauma which affects a posterior ocular site or location; retinal trauma; viral infection of the eye; viral infection of the optic nerve; a posterior ocular condition caused by or influenced by an ocular laser treatment; posterior ocular conditions caused by or influenced by a photodynamic therapy; photocoagulation, radiation retinopathy; and sympathetic ophthalmia.

[00181] In another embodiment, a variant capsid disclosed herein comprises a heterologous nucleic acid comprising a nucleotide sequence encoding a gene product such as, without limitation, an interfering RNA, a long non-coding RNA, a

short non-coding RNA, an antisense RNA, an aptamer, a polypeptide, a secreted antibody, a single chain antibody, a V_{HH} domain, a soluble receptor, an affibody, a knottin, a DARPin, a centurin, a chaperone, a site-specific nuclease that provides for site-specific knock-down of gene function or a modified site-specific nuclease that provides for gene-specific activation of transcription.

[00182] A rAAV variant virion disclosed herein comprises a heterologous nucleic acid comprising a nucleotide sequence encoding a gene product. In some embodiments, the gene product is an interfering RNA. In some embodiments, the gene product is a long non-coding RNA. In some embodiments, the gene product is a short non-coding RNA. In some embodiments, the gene product is an antisense RNA. In some embodiments, the gene product is an aptamer. In some embodiments, the gene product is a polypeptide. In some embodiments, the gene product is a secreted antibody. In some embodiments, the gene product is a single chain antibody. In some embodiments, the gene product is a V_{HH} domain. In some embodiments, the gene product is a soluble receptor. In some embodiments, the gene product is an affibody. In some embodiments, the gene product is a knottin. In some embodiments, the gene product is a DARPin. In some embodiments, the gene product is a centurin. In some embodiments, the gene product is a chaperone. In some embodiments, the gene product is a site-specific nuclease that provide for site-specific knock-down of gene function.

[00183] The uses of the gene product include, but are not limited to, enhancing the level of a factor in a cell, enhancing the level of a factor in a neighboring cell through secretion of a factor, decreasing the level of a factor in a cell, or decreasing the level of a factor in a neighboring cell through secretion of a factor. The gene product can be designed to supplement the level of a defective of missing gene product, decrease the level of a defective of missing gene product, introduce a new supporting gene product, supplement the level of a supporting gene product, decrease the level of a hindering gene product, or both decrease the level of a hindering gene product and introduce or supplement the level of a supporting gene product.

[00184] Gene products delivered by the subject AAV variants can be used to alter the level of gene products or gene product activity directly or indirectly linked to retinal diseases and trauma. Genes whose gene products are directly or indirectly linked to genetic diseases include, e.g., ADP-ribosylation factor-like 6

(ARL6); BBSome interacting protein 1 (BBIP1); BBSome protein 1 (BBS1); BBSome protein 2 (BBS2); BBSome protein 4 (BBS4); BBSome protein 5 (BBS5); BBSome protein 7 (BBS7); BBSome protein 9 (BBS9); BBSome protein 10 (BBS10); BBSome protein 12 (BBS12); centrosomal protein 290 kDa (CEP290); intraflagellar transport protein 172 (IFT172); intraflagellar transport protein 27 (IFT27); inositol polyphosphate-5-phosphatase E (INPP5E); inwardly-rectifying potassium channel subfamily J member 13 (KCNJ13); leucine zipper transcription factor like-1 (LZTFL1); McKusick-Kaufman syndrome protein (MKKS); Meckel syndrome type 1 protein (MKS1); nephronophthisis 3 protein (NPHP1); serologically-defined colon cancer antigen 8 (SDCCAG8); tripartite motif-containing protein 32 (TRIM32); tetratricopeptide repeat domain 8 (TTC8); Batten disease protein (CLN3); Rab escort protein 1 (CHM); (PRDM13); (RGR; (TEAD1); arylhydrocarbon-interacting receptor protein-like 1 (AIPL1); cone-rod otx-like photoreceptor homeobox transcription factor (CRX); guanylate cyclase activating protein 1A (GUCA1A); retinal-specific guanylate cyclase (GUCY2D); phosphatidylinositol transfer membrane-associated family member 3 (PITPNM3); prominin 1 (PROM1); peripherin (PRPH); peripherin 2 (PRPH2); regulating synaptic membrane exocytosis protein 1 (RIMS1); semaphorin 4A (SEMA4A); human homolog of C. elegans unc119 protein (UNC119); ATP-binding cassette transporter - retinal (ABCA4); ADAM metallopeptidase domain 9 (ADAM9); activating transcription factor 6 (ATF6); chromosome 21 open reading frame 2 (C21orf2); chromosome 8 open reading frame 37 (C8orf37); calcium channel; voltage-dependent; alpha 2/delta subunit 4 (CACNA2D4); cadherin-related family member 1 (protocadherin 21) (CDHR1); ceramide kinase-like protein (CERKL); cone photoreceptor cGMP-gated cation channel alpha subunit (CNGA3); cone cyclic nucleotide-gated cation channel beta 3 subunit (CNGB3); cyclin M4 (CNNM4); guanine nucleotide binding protein (G protein); alpha transducing activity polypeptide 2 (GNAT2); potassium channel subfamily V member 2 (KCNV2); Phosphodiesterase 6C (PDE6C); Phosphodiesterase 6H (PDE6H); proteome of centriole 1 centriolar protein B (POC1B); RAB28 member of RAS oncogene family (RAB28); retina and anterior neural fold homeobox 2 transcription factor (RAX2); 11-cis retinol dehydrogenase 5 (RDH5); RP GTPase regulator-interacting protein 1 (RPGRIP1); tubulin tyrosine ligase-like family member 5 (TTLL5); L-type voltage-gated calcium channel alpha-1 subunit (CACNA1F); retinitis pigmentosa GTPase regulator (RPGR); (GNAT1);

(PDE6B); (RHO); CABP4); GPR179); (GRK1); GRM6); LRIT3); SLC24A1); TRPM1); NYX); OPN1LW); OPN1MW); blue cone opsin (OPN1SW); frataxin (FXN); (IMPDH1); (OTX2); CRB1); DTHD1GDF6); IFT140); IQCB1); LCA5); LRAT); NMNAT1); RD3); RDH12); RPE65); SPATA7); TULP1); mitochondiral genes (KSS, LHON, MT-ATP6, MT-TH, MT-TL1, MT-TP, MT-TS2, mitochondrially encoded NADH dehydrogenases [MT-ND]); (BEST1);C1QTNF5EFEMP1); ELOVL4); FSCN2); GUCA1B); HMCN1); IMPG1); RP1L1); TIMP3); DRAM2); MFN2); NR2F1); optic atrophy 1 (OPA1); TMEM126A); TIMM8A); CA4); HK1); KLHL7); NR2E3); NRL); OR2W3); PRPF3); PRPF4); PRPF6); PRPF8); PRPF31); ROM1); retinitis pigmentosa protein 1 (RP1); RP9); SNRNP200); SPP2); TOPORS); ARL2BP); C2orf71); CLRN1); CNGA1); CNGB1); CYP4V2); DHDDS); DHX38); EMC1); EYS); FAM161A); GPR125); HGSNAT); IDH3B); IMPG2); KIAA1549); KIZ); MAK); MERTK); MVK); NEK2); NEUROD1); PDE6A); PDE6G); PRCD); RBP3); RLBP1); SLC7A14); USH2A); ZNF408); ZNF513); OFD1); RP2); retinoschisin (RS1); ABHD12); CDH23); CEP250); CIB2); DFNB31); GPR98); HARS); MYO7A); PCDH15); USH1C); USH1G); NDP); PGK1); CAPN5); FZD4); ITM2B); LRP5); MIR204); RB1); TSPAN12); C12orf65); CDH3); MFRP); OAT); PLA2G5); RBP4); RGS9); RGS9BP); ARMS2; ERCC6); FBLN5); HTRA1); TLR3); and TLR4).

[00185] Genes whose gene products induce or promote apoptosis are referred to herein as "pro-apoptotic genes" and the products of those genes (mRNA; protein) are referred to as "pro-apoptotic gene products." Pro-apoptotic targets include, e.g., Bax gene products; Bid gene products; Bak gene products; Bad gene products; Bcl-2; Bcl-X1. Anti-apoptotic gene products include X-linked inhibitor of apoptosis.

[00186] Genes whose gene products induce or promote angiogenesis are referred to herein as "pro-angiogenic genes" and the products of those genes (mRNA; protein) are referred to as "pro-angiogenic gene products." Pro-angiogenic targets include, e.g., vascular endothelial growth factor (VEGFa, VEGFb, VEGFc, VEGFd); vascular endothelial growth factor receptor 1 (VEGFR1); vascular endothelial growth factor receptor 2 (VEGFR2); Fms-Related Tyrosine Kinase 1 (Flt1); placenta growth factor (PGF); Platelet-derived growth factor (PDGF); angiopoietins; sonic hedgehog. Genes whose gene products inhibit angiogenesis are referred to herein as "anti-angiogenic genes" and the products of those genes (mRNA; protein) are referred to as

"anti-angiogenic gene products." Anti-angiogenic gene products include endostatin; tumstatin; angiostatin; pigment epithelium-derived factor (PEDF), and fusion proteins or antibodies that are specific for pro-angiogenic targets and/or their receptors, e.g. the anti-VEGF fusion proteins sFLT1 or Eylea, the VEGF-specific antibodies Lucentis™ and Avastin™, etc.

[00187] In some embodiments, the gene product(s) delivered by the subject AAV variants act to inhibit angiogenesis. In certain preferred embodiments, the gene product(s) delivered by the subject AAV variants act to inhibit the activity of one or more mammalian VEGF proteins selected from the group consisting of VEGFa, VEGFb, VEGFc, VEGFd and PGF. In particularly preferred embodiments, the gene product(s) delivered by the subject AAV variants inhibit the activity of VEGFa. VEGFa has 9 isoforms generated by alternative splicing, the most physiologically relevant of which is VEGF165. VEGFa levels have been found to be elevated in the vitreous of patients with wet age-related macular degeneration, diabetic macular edema and retinal vein occlusion. Gene product(s) which inhibit the activity of VEGFa in the eye and which are therefore effective to treat patients with elevated vitreous VEGFa include, but are not limited to, Aflibercept, Ranibizumab, Brolucizumab, Bevacizumab, and soluble fms-like tyrosine kinase 1 (sFLT1) (GenBank Acc. No. U01134). In some embodiments, an infectious recombinant AAV (rAAV) virion is provided comprising (i) a variant AAV capsid protein as herein described and (ii) a heterologous nucleic acid comprising multiple sequences, each of which encodes a distinct VEGFa inhibitor.

[00188] In one preferred embodiment, the gene product is Aflibercept. Aflibercept (EYLEA®) is a recombinant fusion protein comprising extracellular domains of human VEGF receptors 1 and 2 fused to the Fc portion of human IgG1. Aflibercept acts as a soluble decoy receptor that binds VEGFa and PGF with greater affinity than the native receptors. The approved dose of intravitreal Aflibercept injection is 2.0 mg, the dosing of which varies according to indication. Aflibercept is indicated for the treatment of neovascular (wet) age-related macular degeneration, macular edema following retinal vein occlusion, diabetic macular edema and diabetic retinopathy. In a particularly preferred embodiment, a novel codon-optimized nucleic acid sequence encoding Aflibercept (corresponding to Figure 12A) is provided comprising or consisting of:

[00189] ATGGTTTCTTACTGGGACACCGGCGTGCTGCTGTGTGCCC
TGCTTTCTTGTCTGCTGCTGACCGGCTCTAGCAGCGGCTCTGATACCGGCA
GACCCTTCGTGGAAATGTACAGCGAGATCCCCGAGATCATCCACATGACC
GAGGGCAGAGAGCTGGTCATCCCTTGCAGAGTGACAAGCCCCAACATCAC
CGTGACTCTGAAGAAGTTCCCTCTGGACACACTGATCCCCGACGGCAAGA
GAATCATCTGGGACAGCCGGAAGGGCTTCATCATCAGCAACGCCACCTAC
AAAGAGATCGGCCTGCTGACCTGTGAAGCCACCGTGAATGGCCACCTGTA
CAAGACCAACTACCTGACACACAGACAGACCAACACCATCATCGACGTGG
TGCTGAGCCCTAGCCACGGCATTGAACTGTCTGTGGGCGAGAAGCTGGTG
CTGAACTGTACCGCCAGAACCGAGCTGAACGTGGGCATCGACTTCAACTG
GGAGTACCCCAGCAGCAAGCACCAGCACAAGAAACTGGTCAACCGGGAC
CTGAAAACCCAGAGCGGCAGCGAGATGAAGAAATTCCTGAGCACCCTGA
CCATCGACGGCGTGACCAGAAGTGACCAGGGCCTGTACACATGTGCCGCC
AGCTCTGGCCTGATGACCAAGAAAAACAGCACCTTCGTGCGGGTGCACGA
GAAGGACAAGACCCACACCTGTCCTCCATGTCCTGCTCCAGAACTGCTCG
GCGGACCTTCCGTGTTCCTGTTTCCTCCAAAGCCTAAGGACACCCTGATGA
TCAGCAGAACCCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAG
GATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAA
CGCCAAGACCAAGCCTAGAGAGGAACAGTACAATAGCACCTACAGAGTG
GTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTGAACGGCAAAGAGTA
CAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCA
TCTCCAAGGCCAAGGGCCAGCCTAGGGAACCCCAGGTTTACACACTGCCT
CCAAGCAGGGACGAGCTGACAAAGAACCAGGTGTCCCTGACCTGCCTGGT
CAAGGGCTTCTACCCTTCCGATATCGCCGTGGAATGGGAGAGCAATGGCC
AGCCTGAGAACAACTACAAGACAACCCCTCCTGTGCTGGACAGCGACGGC
TCATTCTTCCTGTACAGCAAGCTGACAGTGGACAAGAGCAGATGGCAGCA
GGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACT
ACACCCAGAAGTCCCTGAGCCTGTCTCCTGGCAAATGA (SEQ ID NO:65).

[00190] In some embodiments, a nucleic acid sequence encoding Aflibercept is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:65 or to nucleotides 79-1377 of SEQ ID NO:65 (without the underlined nucleotides encoding the Flt1 signal sequence). In related

embodiments, the gene product(s) delivered by the subject AAV variant(s) is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:65 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variants comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence:

[00191] MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPE IIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYK EIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTA RTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS DQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:66)

[00192] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to amino acids 27-458 of SEQ ID NO:66 (corresponding to the amino acid sequence of Aflibercept without the underlined signal peptide sequence).

[00193] In another preferred embodiment, the gene product is a single-chain version of Ranibizumab (sc-Ranibizumab). Ranibizumab (LUCENTIS®) is a monoclonal IgG1 antibody fragment (Fab) that binds to and blocks all isoforms of VEGFa. LUCENTIS® is expressed in bacteria as two separate chains (light and heavy) which are joined by a disulfide bond between the constant light (CL) and constant heavy 1 (CH1) domains. The approved dose of intravitreal Ranibizumab is either 0.3 or 0.5 mg in 0.05 mL depending on the indication. Ranibizumab is approved for the treatment of wet age-related macular degeneration, macular edema following retinal vein occlusion, diabetic macular edema and diabetic retinopathy. In a particularly preferred embodiment, a novel codon-optimized nucleic acid sequence

encoding a single chain Heavy-Light (HL) form of Ranibizumab (sc-Ranibizumab HL) corresponding to Figure 12C is provided, the nucleic acid sequence comprising or consisting of:

[00194] ATGGACTGGACCTGGTCCATCCTGTTTCTGGTGGCTGCCG
CCACAGGCACATACTCTGAAGTGCAGCTGGTGGAATCTGGCGGCGGACTT
GTTCAACCTGGCGGCTCTCTGAGACTGAGCTGTGCCGCCTCTGGCTACGAC
TTTACCCACTACGGCATGAACTGGGTCCGACAGGCCCCTGGCAAAGGCCT
TGAATGGGTCGGATGGATCAACACCTACACCGGCGAGCCAACATACGCCG
CCGACTTCAAGCGGAGATTCACCTTCAGCCTGGACACCAGCAAGAGCACC
GCCTACCTCCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTA
CTGCGCCAAGTATCCCTACTACTACGGCACCAGCCACTGGTACTTCGACGT
GTGGGGACAGGGCACACTGGTCACAGTGTCTAGCGCCTCTACAAAGGGCC
CCAGCGTTTTCCCACTGGCTCCTAGCAGCAAGTCTACCTCCGGTGGAACAG
CCGCTCTGGGCTGTCTGGTCAAGGACTACTTTCCCGAGCCTGTGACCGTGT
CCTGGAATAGCGGAGCACTGACAAGCGGCGTGCACACCTTTCCAGCCGTG
CTGCAAAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCAAG
CAGCTCTCTGGGCACCCAGACCTACATCTGCAATGTGAACCACAAGCCTA
GCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGAC
ACACCTCGGCGGAAGCTCTGGAAGCGGCTCTGGATCTACCGGCACAAGCT
CTAGCGGAACAGGCACAAGCGCTGGCACAACCGGAACAAGCGCTTCTAC
ATCTGGCTCTGGTTCTGGCGGAGGCGGAGGATCAGGTGGTGGTGGATCTG
CTGGCGGAACAGCTACAGCTGGCGCCTCTTCTGGCAGCGACATTCAGCTG
ACACAGAGCCCTTCTAGCCTGAGCGCCTCTGTGGGCGACAGAGTGACCAT
CACATGTAGCGCCAGCCAGGACATCTCCAACTACCTGAACTGGTATCAGC
AGAAGCCCGGCAAGGCCCCTAAGGTGCTGATCTACTTTACCAGCAGCCTG
CACTCCGGCGTGCCCAGCAGATTTTCTGGATCTGGCTCCGGCACCGACTTC
ACCCTGACAATATCTAGCCTCCAGCCTGAGGACTTCGCCACCTACTACTGC
CAGCAGTACAGCACCGTGCCTTGGACATTTGGCCAGGGCACAAAGGTGGA
AATCAAGCGGACAGTGGCCGCTCCTAGCGTGTTCATCTTTCCACCTAGCGA
CGAGCAGCTGAAGTCTGGCACAGCCTCTGTCGTGTGCCTGCTGAACAACT
TCTACCCCAGAGAAGCCAAGGTGCAGTGGAAAGTGGACAACGCCCTCCAG
TCCGGCAACAGCCAAGAGTCTGTGACCGAGCAGGACAGCAAGGACTCCA
CCTACAGCCTGTCCAGCACACTGACACTGAGCAAGGCCGACTACGAGAAG

CACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTTTCTAGCCCTGT
GACCAAGAGCTTCAACCGGGGCGAGTGTTGA (SEQ ID NO:67)

[00195] In some embodiments, a nucleic acid sequence encoding sc-Ranibizumab HL is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:67 or to nucleotides 58-1575 of SEQ ID NO:67 (without the underlined nucleotides encoding the Human IGHV7-8 signal sequence). In related embodiments, the gene product(s) delivered by the subject AAV variant(s) is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:67 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variant(s) comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence:

[00196] MDWTWSILFLVAAATGTYSEVQLVESGGGLVQPGGSLRLSC
AASGYDFTHYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSL
DTSKSTAYLQMNSLRAEDTAVYYCAKYPYYYGTSHWYFDVWGQGTLVTVS
SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THLGGSSGSGSGSTGTSSSGTGTSAGTTGTSASTSGSGSGGGGGSGGGGSAGG
TATAGASSGSDIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKA
PKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTF
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC (SEQ ID NO:68).

[00197] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to amino acids 20-524 of SEQ ID NO:68 (corresponding to the amino acid sequence of sc-Ranibizumab HL without the underlined signal peptide sequence).

[00198] In another particularly preferred embodiment, a novel codon-optimized nucleic acid sequence encoding a single chain Light-Heavy (LH) form of Ranibizumab (sc-Ranibizumab LH) corresponding to Figure 12B is provided, the nucleic acid sequence comprising or consisting of:

[00199] ATGGTCCTCCAGACACAGGTGTTCATCAGCCTGCTGCTGT
GGATCTCTGGCGCCTACGGCGATATCCAGCTGACACAGAGCCCTAGCAGC
CTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGTAGCGCCAGCCA
GGACATCAGCAACTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCC
CTAAGGTGCTGATCTACTTTACCAGCAGCCTGCACAGCGGCGTGCCCAGC
AGATTTTCTGGCTCTGGCAGCGGCACCGACTTCACCCTGACAATATCTAGC
CTCCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCACCGT
GCCTTGGACATTTGGCCAGGGCACCAAGGTGGAAATCAAGCGGACAGTGG
CCGCTCCTAGCGTGTTCATCTTTCCACCTAGCGACGAGCAGCTGAAGTCTG
GCACAGCCTCTGTCGTGTGCCTGCTGAACAACTTCTACCCCAGAGAAGCC
AAGGTGCAGTGGAAGGTGGACAACGCCCTCCAGAGCGGCAATAGCCAAG
AGAGCGTGACCGAGCAGGACAGCAAGGACTCTACCTACTCTCTGAGCAGC
ACACTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAAGTGTACGCCTG
CGAAGTGACCCACCAGGGCCTTTCTAGCCCTGTGACCAAGAGCTTCAACA
GAGGCGAGTGTGGCGGCAGCTCTGGAAGCGGATCTGGAAGCACAGGCAC
AAGCTCTAGCGGAACCGGAACAAGCGCTGGCACAACAGGCACATCTGCC
AGCACAAGCGGTTCTGGTTCTGGCGGAGGCGGAGGATCTGGTGGTGGCGG
ATCTGCTGGCGGAACAGCTACAGCTGGTGCCTCTTCTGGATCCGAGGTGC
AGCTGGTTGAATCTGGCGGTGGACTGGTTCAGCCAGGCGGATCTCTGAGA
CTGTCTTGTGCCGCCAGCGGCTACGATTTCACCCACTACGGCATGAACTGG
GTCCGACAGGCCCCTGGCAAAGGCCTTGAATGGGTCGGATGGATCAACAC
CTACACCGGCGAGCCAACATACGCCGCCGACTTCAAGCGGAGATTCACCT
TCAGCCTGGACACCTCCAAGAGCACCGCCTACCTCCAGATGAACAGCCTG
AGAGCCGAGGACACCGCCGTGTACTACTGCGCCAAGTATCCCTACTACTA
CGGCACCAGCCACTGGTACTTCGACGTGTGGGGACAGGGCACACTGGTCA
CAGTGTCTAGCGCCTCTACAAAGGGCCCCAGCGTTTTCCCACTGGCTCCTA
GCAGCAAGAGCACATCAGGCGGAACTGCTGCCCTGGGCTGTCTGGTCAAG
GACTACTTTCCTGAGCCTGTGACCGTGTCCTGGAACAGCGGAGCACTGAC
ATCTGGCGTGCACACCTTTCCAGCCGTGCTCCAAAGCAGCGGCCTGTATTC
TCTGTCCAGCGTCGTGACAGTGCCTAGCAGCTCTCTGGGCACCCAGACCTA

CATCTGCAATGTGAACCACAAGCCTAGCAACACCAAGGTCGACAAGAAG
GTGGAACCCAAGAGCTGCGACAAGACCCACCTCTGA (SEQ ID NO:69)

[00200] In another particularly preferred embodiment, a novel codon-optimized nucleic acid sequence encoding a single chain Light-Heavy (LH) form of Ranibizumab (sc-Ranibizumab LH) corresponding to Figure 12B is provided, the nucleic acid sequence comprising or consisting of:

[00201] ATGGTGCTCCAGACCCAGGTGTTTATTTCACTGCTGCTGT
GGATTAGCGGGGCTTACGGAGACATTCAGCTGACCCAGAGTCCTTCATCT
CTGAGCGCCTCCGTGGGCGACAGGGTGACCATCACATGCTCTGCCAGCCA
GGATATCTCCAACTATCTGAATTGGTACCAGCAGAAGCCCGGCAAGGCCC
CTAAGGTGCTGATCTATTTCACCAGCTCCCTGCACAGCGGAGTGCCATCCC
GCTTCTCCGGCTCTGGCAGCGGCACCGACTTTACCCTGACAATCTCTAGCC
TCCAGCCAGAGGATTTCGCCACATACTATTGCCAGCAGTACAGCACCGTG
CCCTGGACATTTGGCCAGGGCACCAAGGTGGAGATCAAGCGGACAGTGGC
CGCCCCAAGCGTGTTCATCTTTCCCCCTAGCGACGAGCAGCTGAAGTCTGG
CACCGCCAGCGTGGTGTGCCTGCTGAACAATTTCTATCCCAGAGAGGCCA
AGGTGCAGTGGAAGGTGGATAACGCCCTCCAGTCCGGCAATTCTCAGGAG
AGCGTGACCGAGCAGGACTCCAAGGATTCTACATACAGCCTGTCCTCTAC
CCTGACACTGTCCAAGGCCGACTATGAGAAGCACAAGGTGTACGCATGCG
AGGTGACCCACCAGGGCCTGAGCTCCCCAGTGACAAAGAGCTTTAACAGG
GGAGAGTGTGGAGGATCTAGCGGATCCGGATCTGGAAGCACCGGCACATC
CTCTAGCGGAACCGGCACAAGCGCCGGCACCACAGGCACCTCCGCCTCTA
CAAGCGGCAGCGGATCTGGCGGAGGAGGAGGATCCGGAGGAGGAGGATC
TGCCGGCGGCACCGCCACAGCCGGCGCCTCCTCTGGCTCCGAGGTGCAGC
TGGTGGAGTCTGGAGGAGGCCTGGTGCAGCCTGGAGGCTCCCTGAGGCTG
TCTTGCGCAGCAAGCGGCTATGATTTCACCCACTACGGAATGAACTGGGT
GCGCCAGGCACCTGGCAAGGGCCTGGAGTGGGTGGGCTGGATCAATACCT
ATACAGGCGAGCCAACCTACGCCGCCGACTTTAAGCGGAGATTCACATTT
TCCCTGGATACCAGCAAGTCCACAGCCTACCTCCAGATGAACAGCCTGAG
GGCAGAGGACACCGCCGTGTACTATTGCGCCAAGTATCCTTACTATTACG
GCACAAGCCACTGGTACTTCGACGTGTGGGGACAGGGCACCCTGGTGACA
GTGAGCTCCGCCAGCACCAAGGGCCCATCCGTGTTTCCTCTGGCCCCATCT
AGCAAGTCTACCAGCGGAGGAACAGCCGCCCTGGGATGTCTGGTGAAGG
ACTACTTCCCAGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCT

CCGGCGTGCACACATTTCCCGCCGTGCTCCAGTCCTCTGGCCTGTATAGCC
TGAGCTCCGTGGTGACCGTGCCTTCTAGCTCCCTGGGCACCCAGACATACA
TCTGTAACGTGAATCACAAGCCTTCAAATACCAAAGTCGATAAAAAAGTG
GAACCAAAATCCTGTGATAAAACCCATCTGTGA (SEQ ID NO:70).

[00202] In some embodiments, a nucleic acid sequence encoding sc-Ranibizumab LH is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:69 or SEQ ID NO:70 or to nucleotides 61-1578 of SEQ ID NO:69 or SEQ ID NO:70 (without the underlined nucleotides encoding the Ig kappa signal sequence). In related embodiments, the gene product(s) delivered by the subject AAV variant(s) is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:69 or SEQ ID NO:70 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variant(s) comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence:

[00203] MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTIT
CSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSSGSGSGSTGTSSSGTG
TSAGTTGTSASTSGSGSGGGGGSGGGGSAGGTATAGASSGSEVQLVESGGGL
VQPGGSLRLSCAASGYDFTHYGMNWVRQAPGKGLEWVGWINTYTGEPTYA
ADFKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPYYYGTSHWYFDV
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
DKKVEPKSCDKTHL (SEQ ID NO:71)

[00204] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to

amino acids 21-525 of SEQ ID NO:71 (corresponding to the amino acid sequence of sc-Ranibizumab LH without the underlined signal peptide sequence).

[00205] In another preferred embodiment, a novel nucleic acid sequence encoding a single chain Light-Heavy (LH) form of Ranibizumab fused to the Fc region of human IgG1 (sc-Ranibizumab-Fc) corresponding to Figure 12E is provided, the nucleic acid sequence comprising or consisting of:

[00206] ATGGTCCTCCAGACACAGGTGTTCATCAGCCTGCTGCTGT
GGATCTCTGGCGCCTACGGCGATATCCAGCTGACACAGAGCCCTAGCAGC
CTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGTAGCGCCAGCCA
GGACATCAGCAACTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCC
CTAAGGTGCTGATCTACTTTACCAGCAGCCTGCACAGCGGCGTGCCCAGC
AGATTTTCTGGCTCTGGCAGCGGCACCGACTTCACCCTGACAATATCTAGC
CTCCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCACCGT
GCCTTGGACATTTGGCCAGGGCACCAAGGTGGAAATCAAGCGGACAGTGG
CCGCTCCTAGCGTGTTCATCTTTCCACCTAGCGACGAGCAGCTGAAGTCTG
GCACAGCCTCTGTCGTGTGCCTGCTGAACAACTTCTACCCCAGAGAAGCC
AAGGTGCAGTGGAAGGTGGACAACGCCCTCCAGAGCGGCAATAGCCAAG
AGAGCGTGACCGAGCAGGACAGCAAGGACTCTACCTACTCTCTGAGCAGC
ACACTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAAGTGTACGCCTG
CGAAGTGACCCACCAGGGCCTTTCTAGCCCTGTGACCAAGAGCTTCAACA
GAGGCGAGTGTGGCGGCAGCTCTGGAAGCGGATCTGGAAGCACAGGCAC
AAGCTCTAGCGGAACCGGAACAAGCGCTGGCACAACAGGCACATCTGCC
AGCACAAGCGGTTCTGGTTCTGGCGGAGGCGGAGGATCTGGTGGTGGCGG
ATCTGCTGGCGGAACAGCTACAGCTGGTGCCTCTTCTGGATCCGAGGTGC
AGCTGGTTGAATCTGGCGGTGGACTGGTTCAGCCAGGCGGATCTCTGAGA
CTGTCTTGTGCCGCCAGCGGCTACGATTTCACCCACTACGGCATGAACTGG
GTCCGACAGGCCCCTGGCAAAGGCCTTGAATGGGTCGGATGGATCAACAC
CTACACCGGCGAGCCAACATACGCCGCCGACTTCAAGCGGAGATTCACCT
TCAGCCTGGACACCTCCAAGAGCACCGCCTACCTCCAGATGAACAGCCTG
AGAGCCGAGGACACCGCCGTGTACTACTGCGCCAAGTATCCCTACTACTA
CGGCACCAGCCACTGGTACTTCGACGTGTGGGGACAGGGCACACTGGTCA
CAGTGTCTAGCGCCTCTACAAAGGGCCCCAGCGTTTTCCCACTGGCTCCTA
GCAGCAAGAGCACATCAGGCGGAACTGCTGCCCTGGGCTGTCTGGTCAAG
GACTACTTTCCTGAGCCTGTGACCGTGTCCTGGAACAGCGGAGCACTGAC

ATCTGGCGTGCACACCTTTCCAGCCGTGCTCCAAAGCAGCGGCCTGTATTC
TCTGTCCAGCGTCGTGACAGTGCCTAGCAGCTCTCTGGGCACCCAGACCTA
CATCTGCAATGTGAACCACAAGCCTAGCAACACCAAGGTCGACAAGAAG
GTGGAACCCAAGAGCTGCGACAAGACCCACACCTGTCCTCCATGTCCTGC
TCCAGAACTGCTCGGCGGACCTTCCGTGTTCCTGTTTCCTCCAAAGCCTAA
GGACACCCTGATGATCAGCAGAACCCCTGAAGTGACCTGCGTGGTGGTGG
ATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGC
GTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAATA
GCACCTACAGAGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTG
AACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCC
TATCGAGAAAACCATCTCCAAGGCCAAGGGCCAGCCTAGGGAACCCCAG
GTTTACACACTGCCTCCAAGCAGGGACGAGCTGACAAAGAACCAGGTGTC
CCTGACCTGCCTGGTCAAGGGCTTCTACCCTTCCGATATCGCCGTGGAATG
GGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCCTGTGC
TGGACAGCGACGGCTCATTCTTCCTGTACAGCAAGCTGACAGTGGACAAG
AGCAGATGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGC
CCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGTCTCCTGGCAAAT
GAGCCACGCGTAACACGTGCATGCGAGAGATCTGA (SEQ ID NO:72).

[00207] In some embodiments, a nucleic acid sequence encoding sc-Ranibizumab-Fc is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:72 or to nucleotides 61-2277 of SEQ ID NO:72 (without the underlined nucleotides encoding the Ig kappa signal sequence). In related embodiments, the gene product(s) delivered by the subject AAV variants is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:72 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variant(s) comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence:

[00208] MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTIT
CSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS

SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSSGSGSGSTGTSSSGTG
TSAGTTGTSASTSGSGSGGGGGSGGGGSAGGTATAGASSGSEVQLVESGGGL
VQPGGSLRLSCAASGYDFTHYGMNWVRQAPGKGLEWVGWINTYTGEPTYA
ADFKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPYYYGTSHWYFDV
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
DKKVEPKSCDKTHLDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 73)

[00209] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to amino acids 21-752 of SEQ ID NO:73 (corresponding to the amino acid sequence of sc-Ranibizumab-Fc without the underlined signal peptide sequence)

[00210] In another preferred embodiment, the gene product is Brolucizumab. Brolucizumab (RTH258) is a single chain variable fragment (scFv) that binds to and blocks all isoforms of VEGFa. Brolucizumab is currently in Phase III clinical studies evaluating 3 mg and 6 mg doses for the treatment of wet age-related macular degeneration. In a particularly preferred embodiment, a novel codon-optimized nucleic acid sequence encoding Brolucizumab (corresponding to Figure 12D) is provided, the nucleic acid sequence comprising or consisting of:

[00211] ATGGTCCTCCAGACACAGGTGTTCATCAGCCTGCTGCTGT
GGATCTCTGGCGCCTATGGCGAGATCGTGATGACACAGAGCCCCAGCACA
CTGTCTGCCAGCGTGGGAGACAGAGTGATCATCACATGCCAGGCCAGCGA
GATCATCCACAGCTGGCTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCC
CTAAGCTGCTGATCTACCTGGCCTCTACACTGGCCAGCGGAGTGCCTAGC
AGATTTTCTGGCTCTGGATCTGGCGCCGAGTTCACCCTGACAATCTCTAGC
CTCCAGCCTGACGACTTCGCCACCTACTACTGCCAGAACGTGTACCTGGCC
AGCACCAACGGCGCCAATTTTGGCCAGGGCACCAAGCTGACAGTGCTTGG

CGGAGGCGGAGGTTCTGGTGGCGGAGGAAGTGGCGGCGGAGGATCAGGC
GGTGGTGGATCTGAAGTGCAGCTGGTGGAATCAGGCGGAGGACTGGTTCA
ACCTGGCGGCTCTCTGAGACTGAGCTGTACCGCCTCTGGCTTCTCCCTGAC
CGACTACTACTACATGACCTGGGTCCGACAGGCCCCTGGCAAAGGACTTG
AGTGGGTCGGATTCATCGACCCCGACGACGATCCTTACTACGCCACATGG
GCCAAGGGCAGATTCACCATCAGCCGGGACAACAGCAAGAACACCCTGT
ACCTCCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGT
GCCGGCGGAGATCACAATAGCGGCTGGGGACTCGATATCTGGGGCCAGG
GAACACTGGTCACCGTGTCTAGTTGA (SEQ ID NO:74).

[00212] In some embodiments, a nucleic acid sequence encoding Brolucizumab is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:74 or to nucleotides 61-816 of SEQ ID NO:74 (without the underlined nucleotides encoding the Ig kappa signal sequence). In related embodiments, the gene product(s) delivered by the subject AAV variants is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:74 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variants comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence:

[00213] MVLQTQVFISLLLWISGAYGEIVMTQSPSTLSASVGDRVIITC
QASEIIHSWLAWYQQKPGKAPKLLIYLASTLASGVPSRFSGSGSGAEFTLTISS
LQPDDFATYYCQNVYLASTNGANFGQGTKLTVLGGGGGSGGGGSGGGGSG
GGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLTDYYYMTWVRQAPGKGLE
WVGFIDPDDDPYYATWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAG
GDHNSGWGLDIWGQGTLVTVSS (SEQ ID NO:75)

[00214] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to

amino acids 21-271 of SEQ ID NO:75 (corresponding to the amino acid sequence of Brolucizumab without the underlined signal peptide sequence).

[00215] In another preferred embodiment, a novel nucleic acid sequence encoding Brolucizumab fused to the Fc region of human IgG1 (Brolucizumab-Fc) corresponding to Figure 12F is provided, the nucleic acid sequence comprising or consisting of:

[00216] ATGGTCCTCCAGACACAGGTGTTCATCAGCCTGCTGCTGT
GGATCTCTGGCGCCTATGGCGAGATCGTGATGACACAGAGCCCCAGCACA
CTGTCTGCCAGCGTGGGAGACAGAGTGATCATCACATGCCAGGCCAGCGA
GATCATCCACAGCTGGCTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCC
CTAAGCTGCTGATCTACCTGGCCTCTACACTGGCCAGCGGAGTGCCTAGC
AGATTTTCTGGCTCTGGATCTGGCGCCGAGTTCACCCTGACAATCTCTAGC
CTCCAGCCTGACGACTTCGCCACCTACTACTGCCAGAACGTGTACCTGGCC
AGCACCAACGGCGCCAATTTTGGCCAGGGCACCAAGCTGACAGTGCTTGG
CGGAGGCGGAGGTTCTGGTGGCGGAGGAAGTGGCGGCGGAGGATCAGGC
GGTGGTGGATCTGAAGTGCAGCTGGTGGAATCAGGCGGAGGACTGGTTCA
ACCTGGCGGCTCTCTGAGACTGAGCTGTACCGCCTCTGGCTTCTCCCTGAC
CGACTACTACTACATGACCTGGGTCCGACAGGCCCCTGGCAAAGGACTTG
AGTGGGTCGGATTCATCGACCCCGACGACGATCCTTACTACGCCACATGG
GCCAAGGGCAGATTCACCATCAGCCGGGACAACAGCAAGAACACCCTGT
ACCTCCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGT
GCCGGCGGAGATCACAATAGCGGCTGGGGACTCGATATCTGGGGCCAGG
GAACACTGGTCACCGTGTCTAGTGACAAGACCCACACCTGTCCTCCATGTC
CTGCTCCAGAACTGCTCGGCGGACCTTCCGTGTTCCTGTTTCCTCCAAAGC
CTAAGGACACCCTGATGATCAGCAGAACCCCTGAAGTGACCTGCGTGGTG
GTGGATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGA
CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTAC
AATAGCACCTACAGAGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTG
GCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTG
CTCCTATCGAGAAAACCATCTCCAAGGCCAAGGGCCAGCCTAGGGAACCC
CAGGTTTACACACTGCCTCCAAGCAGGGACGAGCTGACAAAGAACCAGGT
GTCCCTGACCTGCCTGGTCAAGGGCTTCTACCCTTCCGATATCGCCGTGGA
ATGGGAGAGCAATGGCCAGCCTGAGAACAACTACAAGACAACCCCTCCTG
TGCTGGACAGCGACGGCTCATTCTTCCTGTACAGCAAGCTGACAGTGGAC

AAGAGCAGATGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGTCTCCTGGCA
AATGAGCCACGCGTAACACGTGCATGCGAGAGATCTGA (SEQ ID NO:76).

[00217] In some embodiments, a nucleic acid sequence encoding Brolucizumab-Fc is provided comprising a nucleic acid sequence having at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, or greater, nucleic acid identity to the entire length of the nucleic acid sequence set forth in SEQ ID NO:76 or to nucleotides 61-1530 of SEQ ID NO:76 (without the underlined nucleotides encoding the Ig kappa signal sequence). In related embodiments, the gene product(s) delivered by the subject AAV variants is encoded by a nucleic acid sequence consisting of or comprising the nucleic acid sequence of SEQ ID NO:76 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In other related embodiments, the gene product(s) delivered by the subject AAV variant(s) comprises an amino acid sequence at least about at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to the following amino acid sequence.

[00218] MVLQTQVFISLLLWISGAYGEIVMTQSPSTLSASVGDRVIITC
QASEIIHSWLAWYQQKPGKAPKLLIYLASTLASGVPSRFSGSGSGAEFTLTISS
LQPDDFATYYCQNVYLASTNGANFGQGTKLTVLGGGGGSGGGGSGGGGSG
GGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLTDYYYMTWVRQAPGKGLE
WVGFIDPDDDPYYATWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAG
GDHNSGWGLDIWGQGTLVTVSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 77).

[00219] In other related embodiments, the AAV variant(s) comprises a heterologous nucleic acid comprising a nucleotide sequence that encodes an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical or 100% identical to amino acids 21-498 of SEQ ID NO:77 (corresponding to the amino acid sequence of Brolucizumab-Fc without the underlined signal peptide sequence).

[00220] In particularly preferred embodiments, an infectious recombinant AAV (rAAV) virion is provided comprising a variant AAV capsid protein comprising a peptide insertion in the GH-loop of the capsid protein relative to a corresponding parental AAV capsid protein, wherein the peptide insertion comprises the amino acid sequence ISDQTKH (SEQ ID NO:14) or LAISDQTKHA (SEQ ID NO:28) and a heterologous nucleic acid encoding a polypeptide that inhibits the activity of VEGF, preferably VEGFa, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell. In some embodiments, the insertion site is between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2) or the corresponding position in the capsid protein of another AAV serotype. Preferably, the variant AAV capsid protein also comprises a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype.

[00221] In some embodiments, an rAAV virion is provided comprising a variant AAV capsid protein comprising (i) a peptide insertion between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2), or the corresponding position in the capsid protein of another AAV serotype of the capsid protein relative to a corresponding parental AAV capsid protein, and (ii) a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype, and a heterologous nucleic acid comprising a sequence encoding Aflibercept. In preferred embodiments, the nucleic acid sequence encoding Aflibercept consists of or comprises the nucleic acid sequence of SEQ ID NO:65 or a nucleic acid at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In a particularly preferred embodiment, an rAAV virion is provided comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising the nucleic acid sequence of SEQ ID NO:65, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell. In other related embodiments, the heterologous nucleic acid further comprises one or more sequences each encoding an additional VEGFa inhibitor preferably selected from Ranibizumab, sc-Ranibizumab HL, sc-

Ranibizumab LH, sc-Ranibizumab-Fc, Brolucizumab, and Brolucizumab-Fc. In related embodiments, a pharmaceutical composition comprising such an rAAV is provided. In other related embodiments, a method for treating VEGFa-associated ocular disease is provided comprising administering to a subject in need thereof an effective amount of an rAAV virion comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising the nucleic acid sequence of SEQ ID NO:65 and optionally one or more additional nucleic acid sequences, each encoding a distinct VEGFa inhibitor. The rAAV may be administered by subretinal, suprachoroidal, topical, intracameral or intravitreal injection, but is preferably administered via intravitreal injection. In some embodiments, the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; macular edema following retinal vein occlusion; retinal neovascularization resulting from retinal vein occlusion; diabetic macular edema, diabetic retinopathy (including all stages of non-proliferative diabetic retinopathy and proliferative diabetic retinopathy), myopic macular degeneration, branch retinal vein occlusion, hemi-retinal vein occlusion, and central retinal vein occlusion; retinopathy of prematurity; idiopathic choroidal neovascularization; myopia macular degeneration and secondary retinal and choridal neovascularization; retinal telangiectasia; neovascular glaucoma; vitreous hemorrhage; retinal and choroidal neovascularization secondary to retinal diseases, including but not limited to uvetis, trauma, retinal degenerative disorders, genetic retinal and/or choroidal disease, tumors of the eye, corneal and iris neovascularization. In some preferred embodiments, the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; diabetic macular edema; macular edema following retinal vein occlusion; diabetic retinopathy; and myopic choroidal neovascularization.

[00222] In some embodiments, an rAAV virion is provided comprising a variant AAV capsid protein comprising (i) a peptide insertion between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2), or the corresponding position in the capsid protein of another AAV serotype of the capsid protein relative to a corresponding parental AAV capsid protein, and (ii) a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype, and a heterologous nucleic acid comprising a nucleotide sequence encoding Ranibizumab, sc-Ranibizumab HL, sc-

Ranibizumab LH, or sc-Ranibizumab-Fc. In preferred embodiments, the nucleic acid sequence encoding a sc-Ranibizumab consists of or comprises the nucleic acid sequence set forth in any one of SEQ ID NOs:67, 69, 70 and 72, or is at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In a particularly preferred embodiment, an rAAV virion is provided comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising the nucleic acid sequence of any one of SEQ ID NOs: 67, 69, 70 and 72, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell. In other related embodiments, the heterologous nucleic acid further comprises one or more additional nucleic acid sequences each encoding a distinct VEGFa inhibitor preferably selected from Aflibercept, Brolucizumab, and Brolucizumab-Fc. In related embodiments, a pharmaceutical composition comprising such an rAAV is provided. In other related embodiments, a method for treating an eye disease associated with elevated intraocular VEGFa is provided comprising administering to a subject in need thereof an effective amount of an rAAV virion comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid sequence comprising the nucleic acid sequence of any one of SEQ ID NOs: 67, 69, 70 and 72. Preferably, the rAAV is administered via intravitreal injection. In some embodiments, the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; macular edema following retinal vein occlusion; retinal neovascularization resulting from retinal vein occlusion; diabetic macular edema, diabetic retinopathy (including all stages of non-proliferative diabetic retinopathy and proliferative diabetic retinopathy), myopic macular degeneration, branch retinal vein occlusion, hemi-retinal vein occlusion, and central retinal vein occlusion; retinopathy of prematurity; idiopathic choroidal neovascularization; myopia macular degeneration and secondary retinal and choridal neovascularization; retinal telangiectasia; neovascular glaucoma; vitreous hemorrhage; retinal and choroidal neovascularization secondary to retinal diseases, including but not limited to uvetis, trauma, retinal degenerative disorders, genetic retinal and/or choroidal disease, tumors of the eye, corneal and iris neovascularization. In some preferred embodiments, the VEGFa-

associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; diabetic macular edema; macular edema following retinal vein occlusion; diabetic retinopathy; and myopic choroidal neovascularization.

[00223] In some embodiments, an rAAV virion is provided comprising a variant AAV capsid protein comprising (i) a peptide insertion between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2), or the corresponding position in the capsid protein of another AAV serotype of the capsid protein relative to a corresponding parental AAV capsid protein, and (ii) a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype, and a heterologous nucleic acid comprising a nucleotide sequence encoding Brolucizumab or Brolucizumab-Fc. In preferred embodiments, the nucleotide sequence encoding Brolucizumab or Brolucizumab-Fc consists of or comprises the nucleic acid sequence set forth in SEQ ID NO:74 or SEQ ID NO:76 or is at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical thereto. In a particularly preferred embodiment, an rAAV virion is provided comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising the nucleic acid sequence of SEQ ID NO:74 or SEQ ID NO:76, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell. In other related embodiments, the heterologous nucleic acid further comprises one or more nucleotide sequences each encoding a distinct VEGFa inhibitor preferably selected from Aflibercept, Ranibizumab, sc-Ranibizumab HL, sc-Ranibizumab LH, and sc-Ranibizumab-Fc. In related embodiments, a pharmaceutical composition comprising such an rAAV is provided. In other related embodiments, a method for treating an eye disease associated with elevated intraocular VEGFa is provided comprising administering to a subject in need thereof an effective amount of an rAAV virion comprising a variant AAV capsid protein having an amino acid sequence at least 90% identical to the sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid sequence comprising the nucleic acid sequence of SEQ ID NO:74 or SEQ ID NO:76. Preferably, the rAAV is administered via intravitreal injection. In some embodiments, the VEGFa-associated ocular disease is selected from wet

(neovascular, exudative) age-related macular degeneration; macular edema following retinal vein occlusion; retinal neovascularization resulting from retinal vein occlusion; diabetic macular edema, diabetic retinopathy (including all stages of non-proliferative diabetic retinopathy and proliferative diabetic retinopathy), myopic macular degeneration, branch retinal vein occlusion, hemi-retinal vein occlusion, and central retinal vein occlusion; retinopathy of prematurity; idiopathic choroidal neovascularization; myopia macular degeneration and secondary retinal and choridal neovascularization; retinal telangiectasia; neovascular glaucoma; vitreous hemorrhage; retinal and choroidal neovascularization secondary to retinal diseases, including but not limited to uvetis, trauma, retinal degenerative disorders, genetic retinal and/or choroidal disease, tumors of the eye, corneal and iris neovascularization. In some preferred embodiments, the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; diabetic macular edema; macular edema following retinal vein occlusion; diabetic retinopathy; and myopic choroidal neovascularization.

[00224] Genes whose gene products function as immune modulators, e.g., complement factors, toll-like receptors, are called "immunomodulatory genes". Exemplary immunomodulatory genes include cytokines, chemokines, and the fusion proteins or antibodies that are specific for them and/or their receptors, e.g. the anti-IL-6 fusion protein Rilonacept™, the Complement Factor H-specific antibody lampamizumab, etc. Genes whose gene products function as neuroprotective factors, e.g., platelet derived growth factor receptor (PDGFR); glial derived neurotrophic factor (GDNF); rod-derived con viability factor (RdCVF); fibroblast growth factor (FGF); neurturin (NTN); ciliary neurotrophic factor (CNTF); nerve growth factor (NGF); neurotrophin-4 (NT4); brain derived neurotrophic factor (BDNF); epidermal growth factor. Genes whose gene products function as light responsive opsins, e.g., opsin; rhodopsin; channel rhodopsin; halo rhodopsin.

[00225] In some cases, a gene product of interest is a site-specific endonuclease that provide for site-specific knock-down of gene function, e.g., where the endonuclease knocks out an allele associated with a retinal disease. For example, where a dominant allele encodes a defective copy of a gene that, when wild-type, is a retinal structural protein and/or provides for normal retinal function, a site-specific endonuclease can be targeted to the defective allele and knock out the defective allele.

[00226] In addition to knocking out a defective allele, a site-specific nuclease can also be used to stimulate homologous recombination with a donor DNA that encodes a functional copy of the protein encoded by the defective allele. Thus, e.g., a subject rAAV virion can be used to deliver both a site-specific endonuclease that knocks out a defective allele, and can be used to deliver a functional copy of the defective allele, resulting in repair of the defective allele, thereby providing for production of a functional retinal protein (e.g., functional retinoschisin, functional RPE65, functional peripherin, etc.). See, e.g., Li et al. (2011) *Nature* 475:217. In some embodiments, a rAAV virion disclosed herein comprises a heterologous nucleotide sequence that encodes a site-specific endonuclease; and a heterologous nucleotide sequence that encodes a functional copy of a defective allele, where the functional copy encodes a functional retinal protein. Functional retinal proteins include, e.g., retinoschisin, RPE65, retinitis pigmentosa GTPase regulator (RGPR)-interacting protein-1, peripherin, peripherin-2, and the like.

[00227] Site-specific endonucleases that are suitable for use include, e.g., meganucleases; zinc finger nucleases (ZFNs); transcription activator-like effector nucleases (TALENs); and Clustered regularly interspaced short palindromic repeats/CRISPR-associated (Cas), where such site-specific endonucleases are non-naturally occurring and are modified to target a specific gene. Such site-specific nucleases can be engineered to cut specific locations within a genome, and non-homologous end joining can then repair the break while inserting or deleting several nucleotides. Such site-specific endonucleases (also referred to as "INDELs") then throw the protein out of frame and effectively knock out the gene. See, e.g., U.S. Patent Publication No. 2011/0301073.

[00228] In some embodiments of the variant rAAV vector disclosed herein, a nucleotide sequence encoding a gene product of interest is operably linked to a constitutive promoter. Suitable constitutive promoters include e.g. cytomegalovirus promoter (CMV) (Stinski et al. (1985) *Journal of Virology* 55(2): 431-441), CMV early enhancer/chicken β-actin (CBA) promoter/rabbit β-globin intron (CAG) (Miyazaki et al. (1989) *Gene* 79(2): 269-277, CB^{SB} (Jacobson et al. (2006) *Molecular Therapy* 13(6): 1074-1084), human elongation factor 1α promoter (EF1α) (Kim et al. (1990) *Gene* 91(2): 217-223), human phosphoglycerate kinase promoter (PGK) (Singer-Sam et al. (1984) *Gene* 32(3): 409-417, mitochondrial heavy-strand promoter (Loderio et al. (2012) *PNAS* 109(17): 6513-6518), ubiquitin promoter (Wulff et al.

(1990) *FEBS Letters* 261: 101-105). In other embodiments, a nucleotide sequence encoding a gene product of interest is operably linked to an inducible promoter. In some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a tissue-specific or cell type-specific regulatory element. For example, in some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a photoreceptor-specific regulatory element (e.g., a photoreceptor-specific promoter), e.g., a regulatory element that confers selective expression of the operably linked gene in a photoreceptor cell. Suitable photoreceptor-specific regulatory elements include, e.g., a rhodopsin promoter; a rhodopsin kinase promoter (Young et al. (2003) *Ophthalmol. Vis. Sci.* 44:4076); a beta phosphodiesterase gene promoter (Nicoud et al. (2007) *J. Gene Med.*9:1015); a retinitis pigmentosa gene promoter (Nicoud et al. (2007) supra); an interphotoreceptor retinoid-binding protein (IRBP) gene enhancer (Nicoud et al. (2007) supra); an IRBP gene promoter (Yokoyama et al. (1992) *Exp Eye Res.* 55:225), an opsin gene promoter (Tucker et al. (1994) *PNAS* 91:2611-2615), a retinoschisin gene promoter (Park et al. (2009) *Gene Therapy* 16(7): 916-926), a CRX homeodomain protein gene promoter (Furukawa et al. (2002) *The Journal of Neuroscience* 22(5): 1640-1647), a guanine nucleotide binding protein alpha transducing activity polypeptide 1 (GNAT1) gene promoter (Lee et al. (2010) *Gene Therapy* 17:1390-1399), a neural retina-specific leucine zipper protein (NRL) gene promoter (Akimoto et al. (2006) *PNAS* 103(10): 3890-3895), human cone arrestin (hCAR) promoter (Li et al. (2002) *Biochemistry and Molecular Biology* 43: 1375-1383), and the PR2.1, PR1.7, PR1.5, and PR1.1 promoters (Ye et al. (2016) *Human Gene Therapy* 27(1): 72-82)). In some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a retinal pigment epithelia (RPE) cell-specific regulatory element (e.g., a RPE-specific promoter), e.g., a regulatory element that confers selective expression of the operably linked gene in a RPE cell. Suitable RPE-specific regulatory elements include, e.g., an RPE65 gene promoter (Meur et al. (2007) *Gene Therapy* 14: 292-303), a cellular retinaldehyde-binding protein (CRALBP) gene promoter (Kennedy et al. (1998) *Journal of Biological Chemistry* 273: 5591-5598), a pigment epithelium-derived factor (PEDF aka serpin F1) gene promoter (Kojima et al. (2006) *Molecular and Cellular Biochemistry* 293(1-2): 63-69), and a vitelliform macular dystrophy (VMD2) promoter (Esumi et al. (2004) *The Journal of Biological Chemistry* 279(18): 19064-19073). In some instances, a nucleotide sequence encoding a gene product of interest

is operably linked to a Müller glia cell-specific regulatory element (e.g., a glial-specific promoter), e.g., a regulatory element that confers selective expression of the operably linked gene in a retinal glial cell. Suitable glial-specific regulatory elements include, e.g., a glial fibrillary acidic protein (GFAP) promoter (Besnard et al. (1991) *Journal of Biological Chemistry* 266(28): 18877-18883). In some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a bipolar cell-specific regulatory element (e.g., a bipolar-specific promoter), e.g., a regulatory element that confers selective expression of the operably linked gene in a bipolar cell. Suitable bipolar-specific regulatory elements include, e.g., a GRM6 promoter (Cronin et al. (2014) *EMBO Molecular Medicine* 6(9): 1175-1190).

[00229] For the purposes of the invention, the disclosure herein provides an isolated nucleic acid comprising a nucleotide sequence that encodes a variant AAV capsid protein as described above. An isolated nucleic acid can be an AAV vector, e.g., a recombinant AAV vector.

[00230] The disclosure herein also provides a method of treating a retinal disease, the method comprising administering to an individual in need thereof an effective amount of a rAAV variant virion comprising a transgene of interest as described above and disclosed herein. One of ordinary skill in the art would be readily able to determine an effective amount of the subject rAAV virion and that the disease had been treated by testing for a change in one or more functional or anatomical parameters, e.g. visual acuity, visual field, electrophysiological responsiveness to light and dark, color vision, contrast sensitivity, anatomy, retinal health and vasculature, ocular motility, fixation preference, and stability.

[00231] Nonlimiting methods for assessing retinal function and changes thereof include assessing visual acuity (e.g. best-corrected visual acuity [BCVA], ambulation, navigation, object detection and discrimination), assessing visual field (e.g. static and kinetic visual field perimetry), performing a clinical examination (e.g. slit lamp examination of the anterior and posterior segments of the eye), assessing electrophysiological responsiveness to all wavelengths of light and dark (e.g. all forms of electroretinography (ERG) [full-field, multifocal and pattern], all forms of visual evoked potential (VEP), electrooculography (EOG), color vision, dark adaptation and/or contrast sensitivity). Nonlimiting methods for assessing anatomy and retinal health and changes thereof include Optical Conherence Tomography (OCT), fundus photography, adaptive optics scanning laser ophthalmoscopy (AO-

SLO), fluorescence and/or autofluorescence; measuring ocular motility and eye movements (e.g. nystagmus, fixation preference, and stability), measuring reported outcomes (patient-reported changes in visual and non-visually-guided behaviors and activities, patient-reported outcomes [PRO], questionnaire-based assessments of quality-of-life, daily activities and measures of neurological function (e.g. functional Magnetic Resonance Imaging (MRI)).

[00232] In some embodiments, an effective amount of the subject rAAV virion results in a decrease in the rate of loss of retinal function, anatomical integrity, or retinal health, e.g. a 2-fold, 3-fold, 4-fold, or 5-fold or more decrease in the rate of loss and hence progression of disease, for example, a 10-fold decrease or more in the rate of loss and hence progression of disease. In some embodiments, the effective amount of the subject rAAV virion results in a gain in visual function, retinal function, an improvement in retinal anatomy or health, and/or an improvement in ocular motility and/or improvement in neurological function, e.g. a 2-fold, 3-fold, 4-fold or 5-fold improvement or more in retinal function, retinal anatomy or health, and/or improvement in ocular motility, e.g. a 10-fold improvement or more in retinal function, retinal anatomy or health, and/or improvement in ocular motility. As will be readily appreciated by the ordinarily skilled artisan, the dose required to achieve the desired treatment effect will typically be in the range of 1×10^8 to about 1×10^{15} recombinant virions, typically referred to by the ordinarily skilled artisan as 1×10^8 to about 1×10^{15} "vector genomes".

[00233] A subject rAAV virion can be administered via intraocular injection, for example by intravitreal injection, by subretinal injection, by suprachoroidal injection, or by any other convenient mode or route of administration that will result in the delivery of the rAAV virion to the eye. Other convenient mancestodes or routes of administration include, without limitation, intravenous, intra-arterial, periocular, intracameral, subconjunctival and sub-tenons injections and topical administration and intranasal. When administered via intravitreal injection, the subject rAAV virion is able to move through the vitreous and traverse the internal limiting membrane (also referred to herein as an inner limiting membrane, or "ILM"; a thin, transparent acellular membrane on the surface of the retina forming the boundary between the retina and the vitreous body, formed by astrocytes and the end feet of Müller cells), and/or moves through the layers of the retina more efficiently,

compared to the capability of an AAV virion comprising the corresponding parental AAV capsid protein.

[00234] A variant capsid protein disclosed herein is isolated, e.g., purified. In some embodiments, a variant capsid protein disclosed herein is included in an AAV vector or a recombinant AAV (rAAV) virion. In other embodiments, such AAV variant vectors and/or AAV variant virions are used in an *in vivo* or *ex vivo* method of treating ocular disease in the primate retina.

[00235] The disclosure herein further provides host cells such as, without limitation, isolated (genetically modified) host cells comprising a subject nucleic acid. A host cell according to the invention disclosed herein, can be an isolated cell, such as a cell from an *in vitro* cell culture. Such a host cell is useful for producing a subject rAAV variant virion, as described herein. In one embodiment, such a host cell is stably genetically modified with a nucleic acid. In other embodiments, a host cell is transiently genetically modified with a nucleic acid. Such a nucleic acid is introduced stably or transiently into a host cell, using established techniques, including, but not limited to, electroporation, calcium phosphate precipitation, liposome-mediated transfection, and the like. For stable transformation, a nucleic acid will generally further include a selectable marker, e.g., any of several well-known selectable markers such as neomycin resistance, and the like. Such a host cell is generated by introducing a nucleic acid into any of a variety of cells, e.g., mammalian cells, including, e.g., murine cells, and primate cells (e.g., human cells). Exemplary mammalian cells include, but are not limited to, primary cells and cell lines, where exemplary cell lines include, but are not limited to, 293 cells, COS cells, HeLa cells, Vero cells, 3T3 mouse fibroblasts, C3H10T1/2 fibroblasts, CHO cells, and the like. Exemplary host cells include, without limitation, HeLa cells (e.g., American Type Culture Collection (ATCC) No. CCL-2), CHO cells (e.g., ATCC Nos. CRL9618, CCL61, CRL9096), 293 cells (e.g., ATCC No. CRL-1573), Vero cells, NIH 3T3 cells (e.g., ATCC No. CRL-1658), Huh-7 cells, BHK cells (e.g., ATCC No. CCL10), PC12 cells (ATCC No. CRL1721), COS cells, COS-7 cells (ATCC No. CRL1651), RAT1 cells, mouse L cells (ATCC No. CCLI.3), human embryonic kidney (HEK) cells (ATCC No. CRL1573), HLHepG2 cells, and the like. A host cell can also be made using a baculovirus to infect insect cells such as Sf9 cells, which produce AAV (see, e.g., U.S. Pat. No. 7,271,002; U.S. patent application Ser. No. 12/297,958). In some embodiments, a genetically modified host cell includes, in addition to a nucleic acid

comprising a nucleotide sequence encoding a variant AAV capsid protein, as described above, a nucleic acid that comprises a nucleotide sequence encoding one or more AAV rep proteins. In other embodiments, a host cell further comprises an rAAV variant vector. An rAAV variant virion can be generated using such host cells. Methods of generating an rAAV virion are described in, e.g., U.S. Patent Publication No. 2005/0053922 and U.S. Patent Publication No. 2009/0202490.

[00236] The disclosure herein additionally provides a pharmaceutical composition comprising: a) the rAAV variant virion, as described above and disclosed herein; and b) a pharmaceutically acceptable carrier, diluent, excipient, or buffer. In some embodiments, the pharmaceutically acceptable carrier, diluent, excipient, or buffer is suitable for use in a human or non-human patient. Such excipients, carriers, diluents, and buffers include any pharmaceutical agent that can be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, glycerol and ethanol. Pharmaceutically acceptable salts can be included therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. Additionally, auxiliary substances, such as wetting or emulsifying agents, surfactants, pH buffering substances, and the like, may be present in such vehicles. A wide variety of pharmaceutically acceptable excipients are known in the art and need not be discussed in detail herein. Pharmaceutically acceptable excipients have been amply described in a variety of publications, including, for example, A. Gennaro (2000) "Remington: The Science and Practice of Pharmacy," 20th edition, Lippincott, Williams, & Wilkins; Pharmaceutical Dosage Forms and Drug Delivery Systems (1999) H. C. Ansel et al., eds., 7^{th} ed., Lippincott, Williams, & Wilkins; and Handbook of Pharmaceutical Excipients (2000) A. H. Kibbe et al., eds., 3^{rd} ed. Amer. Pharmaceutical Assoc. In some aspects of the present invention, the present invention provides a pharmaceutical composition comprising about 1×10^8 to about 1×10^{15} recombinant viruses or 1×10^8 to about 1×10^{15} vector genomes, wherein each said recombinant virus comprises a genome encoding one or more gene products.

[00237] Some embodiments of the invention are exemplified in the following items 1 to 36:

1. A variant adeno-associated virus (AAV) capsid protein comprising a peptide insertion in the GH-loop of the capsid protein relative to a corresponding

parental AAV capsid protein, wherein the peptide insertion comprises the amino acid sequence ISDQTKH (SEQ ID NO:14), and wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell.

2. The variant AAV capsid protein of item 1, wherein the peptide insertion comprises the amino acid sequence Y_1Y_2ISDQTKHY_3, wherein each of Y_1-Y_3 is independently selected from Ala, Leu, Gly, Ser, Thr, and Pro.

3. The variant AAV capsid protein of item 2, wherein the peptide insertion comprises the amino acid sequence LAISDQTKHA (SEQ ID NO:28).

4. The variant AAV capsid protein of any one of items 1-3, wherein the insertion site is between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2) or the corresponding position in the capsid protein of another AAV serotype.

5. The variant AAV capsid protein of any one of items 1-4, wherein the capsid protein comprises one or more amino acid substitutions relative to VP1 capsid of AAV2 (SEQ ID NO:2) or one or more corresponding substitutions in another AAV serotype.

6. The variant AAV capsid protein of any one of items 1-5, wherein the capsid protein comprises a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype.

7. The variant AAV capsid protein of any one of items 1-6, wherein the capsid protein comprises (i) the amino acid sequence ISDQTKH (SEQ ID NO:14) and (ii) a P34A amino acid substitution, and is at least 90% identical, at least 95% identical or at least 99% identical to the sequence set forth as SEQ ID NO:42.

8. The variant AAV capsid protein of item 7, wherein the capsid protein consists essentially of the amino acid sequence set forth as SEQ ID NO:42.

9. A recombinant AAV (rAAV) virion comprising a variant AAV capsid protein according to any one of items 1-8 and a heterologous nucleic acid comprising a nucleotide sequence encoding a gene product.

10. The rAAV of item 9, wherein the gene product is a polypeptide.

11. The rAAV of item 10, wherein the heterologous nucleic acid comprises a nucleotide sequence encoding a polypeptide that inhibits the activity of vascular endothelial growth factor (VEGF).

12. The rAAV of item 11, wherein the nucleotide sequence encodes a fusion protein.

13. The rAAV of item 12, wherein the nucleotide sequence encodes Aflibercept (Eylea).

14. The rAAV of item 13, wherein the nucleotide sequence is at least 90% identical, at least 95% identical or at least 99% identical to the nucleic acid sequence set forth as SEQ ID NO: 65 or to nucleotides 79-1377 of SEQ ID NO:65 and preferably encodes the amino acid sequence set forth as SEQ ID NO:66 or amino acids 27-458 of SEQ ID NO:66.

15. The rAAV of item 11, wherein the nucleotide sequence encodes a monoclonal antibody or antigen binding fragment thereof.

16. The rAAV of item 15, wherein the nucleotide sequence encodes Ranibizumab (Lucentis).

17. The rAAV of item 15, wherein the nucleotide sequence (i) comprises a sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence of SEQ ID NO:67 (sc-Ranibizumab HL) or to nucleotides 58-1575 of SEQ ID NO:67 and encodes the amino acid sequence set forth as SEQ ID NO:68 or (ii) encodes the amino acid sequence of amino acids 20-524 of SEQ ID NO:68.

18. The rAAV of item 15, wherein the nucleotide sequence (i) has a sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence of SEQ ID NO:69 (sc-Ranibizumab LH1) or SEQ ID NO:70 (sc-Ranibizumab LH2) or to nucleotides 61-1578 of SEQ ID NO:69 or SEQ ID NO:70 and encodes the amino acid sequence set forth as SEQ ID NO:71 or (ii) encodes the amino acid sequence of amino acids 21-525 of SEQ ID NO:71.

19. The rAAV of item 15, wherein the nucleotide sequence (i) has a sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence of SEQ ID NO:72 (sc-Ranibizumab-Fc) or to nucleotides 61-2277 of SEQ

ID NO:72 and encodes the amino acid sequence set forth as SEQ ID NO:73 or (ii) encodes the amino acid sequence of amino acids 21-752 of SEQ ID NO:73.

20. The rAAV of item 15, wherein the nucleotide sequence encodes Brolucizumab.

21. The rAAV of item 20, wherein the nucleotide sequence has a sequence at least 90% identical, at least 95% identical or at least 99% identical to the nucleic acid sequence set forth as SEQ ID NO:74 or to nucleotides 61-816 of SEQ ID NO:74 and preferably encodes the amino acid sequence set forth as SEQ ID NO:75 or the amino acid sequence of amino acids 21-271 of SEQ ID NO:75.

22. The rAAV of item 15, wherein the nucleotide sequence (i) has a sequence at least 90% identical, at least 95% identical or at least 99% identical to the sequence of SEQ ID NO:76 (Brolucizumab-Fc) or to nucleotides 61-1530 of SEQ ID NO:76 and encodes the amino acid sequence set forth as SEQ ID NO:77 or (ii) encodes the amino acid sequence of amino acids 21-498 of SEQ ID NO:77.

23. The rAAV of item 11, wherein the heterologous nucleic acid comprises (i) a sequence encoding Aflibercept, preferably wherein the sequence encoding aflibercept is at least 90% identical, at least 95% identical or at least 99% identical to the nucleic acid sequence set forth as SEQ ID NO: 65 and encodes the amino acid sequence set forth as SEQ ID NO:66 and (ii) a sequence encoding Brolucizumab, preferably wherein the sequence encoding Brolucizumab is at least 90% identical, at least 95% identical or at least 99% identical to the nucleic acid sequence set forth as SEQ ID NO: 74 or SEQ ID NO:76 and preferably encodes the amino acid sequence set forth as SEQ ID NO:75 or SEQ ID NO:77.

24. The rAAV of any one of items 9-23, wherein the nucleotide sequence encoding a gene product is operably linked to an expression control sequence.

25. A pharmaceutical composition comprising an rAAV according to any of items 11-24 and a pharmaceutically acceptable carrier.

26. A method for delivering a VEGF inhibitor to a retinal cell, choroidal cell, lenticular cell, ciliary cell, iris cell, optic nerve cell and/or corneal cell in a subject comprising administering to the subject an rAAV virion according to any one of items 11-24 or a pharmaceutical composition according to item 24.

27. The method of item 26, wherein the rAAV virion or pharmaceutical composition is administered intravitreally to the subject.

28. A method for treating a VEGFa-associated ocular disease selected from wet (neovascular, exudative) age-related macular degeneration; macular edema following retinal vein occlusion; retinal neovascularization resulting from retinal vein occlusion; diabetic macular edema, diabetic retinopathy (including all stages of non-proliferative diabetic retinopathy and proliferative diabetic retinopathy); myopic macular degeneration; branch retinal vein occlusion, hemi-retinal vein occlusion, and central retinal vein occlusion; retinopathy of prematurity; idiopathic choroidal neovascularization; myopia macular degeneration and secondary retinal and choridal neovascularization; retinal telangiectasia; neovascular glaucoma; vitreous hemorrhage; retinal and choroidal neovascularization secondary to retinal diseases, including but not limited to uvetis, trauma, retinal degenerative disorders, genetic retinal and/or choroidal disease, tumors of the eye, corneal and iris neovascularization in a subject in need of such treatment by administering to the subject an effective amount of an rAAV according to any one of items 11-24 or a pharmaceutical composition according to item 25.

29. The method of item 28, wherein the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; diabetic macular edema; macular edema following retinal vein occlusion; diabetic retinopathy; and myopic choroidal neovascularization.

30. The method of any one of items 26 to 29, wherein the rAAV comprises a capsid protein consisting essentially of the amino acid sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising a sequence encoding Aflibercept, preferably wherein the sequence encoding Aflibercept has the sequence set forth in SEQ ID NO:65.

31. The method of any one of items 26 to 29, wherein the rAAV comprises a capsid protein consisting essentially of the amino acid sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising a sequence encoding Ranibizumab, sc-Ranibizumab HL, sc-Ranibizumab LH, or sc-Ranibizumab-Fc, preferably wherein the sequence encoding sc-Ranibizumab HL, sc-Ranibizumab LH,

or sc-Ranibizumab-Fc has the sequence set forth in any one of SEQ ID NOs:67, 69, 70 and 72.

32. The method of any one of items 26 to 29, wherein the rAAV comprises a capsid protein consisting essentially of the amino acid sequence set forth as SEQ ID NO:42 and a heterologous nucleic acid comprising a sequence encoding brolicizumab or brolicizumab-Fc, preferably wherein the sequence encoding brolicizumab or brolicizumab-Fc has the sequence set forth in SEQ ID NO:74 or SEQ ID NO:76.

33. The method of any one of items 28-32, wherein the rAAV or pharmaceutical composition is administered intravitreally to the subject.

34. The method of any one of items 26-33, wherein the subject is a human.

35. An isolated nucleic acid comprising a nucleotide sequence that encodes a variant AAV capsid protein according to any one of items 1-8.

36. An isolated, genetically modified host cell comprising the nucleic acid of item 35.

EXAMPLES

[00238] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

[00239] General methods in molecular and cellular biochemistry can be found in such standard textbooks as Molecular Cloning: A Laboratory Manual, 3rd Ed. (Sambrook et al., Harbor Laboratory Press 2001); Short Protocols in Molecular Biology, 4th Ed. (Ausubel et al. eds., John Wiley & Sons 1999); Protein Methods (Bollag et al., John Wiley & Sons 1996); Nonviral Vectors for Gene Therapy (Wagner et al. eds., Academic Press 1999); Viral Vectors (Kaplift & Loewy eds., Academic Press 1995); Immunology Methods Manual (I. Lefkovits ed., Academic

Press 1997); and Cell and Tissue Culture: Laboratory Procedures in Biotechnology (Doyle & Griffiths, John Wiley & Sons 1998), the disclosures of which are incorporated herein by reference. Reagents, cloning vectors, and kits for genetic manipulation referred to in this disclosure are available from commercial vendors such as BioRad, Stratagene, Invitrogen, Sigma-Aldrich, and ClonTech.

[00240] **Example 1**

[00241] Intravitreal Injection and Tissue Harvesting. A single male cynomolgus macaque (*macaca fascicularis*) age 4-10 years old and weighing at least 4 kg was dosed via intravitreal injection through the sclera (approximately 3 mm behind the limbus using a procedure and delivery device suitable for human use). The animal was anesthetized and given topical anesthetic. 100 µL of the library was administered to each eye.

[00242] Euthanasia was performed by trained veterinary staff using 100 mg/kg pentobarbital sodium intravenous injection on day 14±3. Eyes were nucleated and stored at 4°C until dissection.

[00243] Tissue Dissection. Eyes were cut along the ora serrata with a scalpel, and the anterior segment was removed. Relief cuts were made into the retina around the fovea to enable flat mounting of the retina, and the vitreous was removed. Six samples of the retina from each quadrant (superior, inferior, nasal, and temporal) were collected, as shown in Figure 2, and cellular material corresponding to RPE cells, photoreceptors, biopolar cells, amacrine cells, horizontal cells, and/or ganglion cells was isolated.

[00244] Directed Evolution. The directed evolution process is shown in Figure 1A-1E. Briefly, a viral capsid library comprising 20+ proprietary combinations of DNA mutation technique and *cap* genes is created (Figure 1A). Viruses are then packaged (Figure 1B) — such that each particle is composed of a mutant capsid surrounding the *cap* gene encoding that capsid — and purified. The capsid library is placed under selective pressure *in vivo*. The tissue or cellular material of interest is harvested to isolate AAV variants that have successfully infected that target, and the successful viruses are recovered. Successful clones are enriched through repeated selection (Stage I – Figure 1D). Selected *cap* genes then undergo proprietary re-diversification and are enriched through further selection steps to iteratively increase viral fitness (Stage 2 – Figure 1D). Variants identified during Vector Selection Stages 1 and 2 demonstrate the ability to transduce primate retina cells (Figure 1E).

[00245] Successful Recovery of AAV Capsid Genomes: Rounds 1-6. The capsids recovered from each round of selection were used to package the library injected to initiate the subsequent round of selection. Recovery of capsid genes from tissue represents successful internalization of library vectors into the tissue of interest. Following Round 4, additional re-diversification of the library was incorporated prior to library packaging and injection for Round 5. Recovery of viral genomes from RPE, PR, inner nuclear layer (INL), and ganglion cell layer (GCL) retinal tissue from a representative round of selection are shown in Figure 3. Bands within boxes represent successful recovery of viral genomes.

[00246] Sequencing Analysis: Rounds 3-6. During rounds 3-6, sequencing was performed on individual clones within the library to determine the frequency of variants within the population. Variants were evaluated for the presence of motifs within the sequencing data. Variants were grouped into motifs based on the presence of a unifying variation (for example, a specific point mutation or specific peptide insertion sequence in a consistent location within the capsid) that occurred in multiple sequences. Motifs representing at least 5% of the sequenced population in two or more rounds of the selection or at least 10% of the sequenced population in one or more rounds of the selection are represented in Figure 4A (Round 3 sequencing analysis), 4B (Round 4 sequencing analysis), 4C (Round 5 sequencing analysis), and 4D (Round 6 sequencing analysis).

[00247] Several representative clones that were identified as conferring increased infectivity of retinal cells are listed in Table 1 below (each clone contains the identified substitution(s) and/or peptide insertion and is otherwise identical to SEQ ID NO:2; the selection round, number of sequences and frequency (in parentheses) are listed for each clone):

Table 1. Amino acid sequence modifications to the AAV VP1 capsid protein that confer increased infectivity of one or more cells of the retina. Substitutions listed in column 2 are based on the amino acid sequence for wild type AAV2, i.e. in the absence of inserted peptide.

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
588~LAISDQTKHA~ (SEQ ID NO:28)	None	Round 4, 5, 6	Round 3, 5, 6	Round 4, 5
588~LAISDQTKHA~ (SEQ ID NO:28)	+M1L+L15P +P535S	Round 6 1 (1.61%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+P34A	Round 5 1 (1.89%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+P34A+S731L			Round 5 1 (1.82%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+N57D	Round 4 1 (1.33%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+N66K			Round 5 1 (1.82%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+R81Q	Round 6 1 (1.61%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+Q101R			Round 4 1 (2.27%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+S109T	Round 3 1 (1.85%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+R144K			Round 5 1 (1.82%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+R144M			Round 5 1 (1.82%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+Q164K			Round 4 1 (2.27%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+Q164K+V708I	Rounds 3 and 4 2 (3.7%) 1 (1.33%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+T176P	Round 4 1 (1.33%)		
588~LAISDQTKHA~	+L188I		Round 5	

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
(SEQ ID NO:28)			1 (2.27%)	
588~LAISDQTKHA~ (SEQ ID NO:28)	+S196Y	Round 4 1 (1.33%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+G226E			Round 4 1 (2.27%)
588~LAISDQTKHA~ (SEQ ID NO:28)	+G236V	Round 4 1 (1.33%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+I240T	Round 3 1 (1.85%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+N312K	Round 4 1 (1.33%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+P363L	Round 6 1 (1.61%)		
588~LAISDQTKHA~ (SEQ ID NO:28)	+T456K	Round 6 1 (1.61%)		
588-LAISDQTKHA~ (SEQ ID NO:28)	+I698V	Round 5 1 (1.89%)		
588-LAISDQTKHA~ (SEQ ID NO:28)	+V708I	Round 4, 5, 6	Round 3, 4, 5	Round 4, 5
588~LAISDQTKHA~ (SEQ ID NO:28)	+V708I+R484C		Round 5 1 (2.27%)	
588~LAISDQTKHA~ (SEQ ID NO:28)	N312K+N449D+N551S+I698V+L735Q	Engineered		Engineered
588~LGISDQTKHA~ (SEQ ID NO:29)	None	Round 5 1 (1.89%)		
588~LAQADTTKNA~ (SEQ ID NO:27)	None	Round 3, 4, 5, 6	Round 3, 4, 5	Round 4, 5
588~LAQADTTKNA~ (SEQ ID NO:27)	+E36D		Round 5 1 (2.27%)	
588~LAQADTTKNA~	+P250S	Round 6		

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
(SEQ ID NO:27)		1 (1.61%)		
588~LAQADTTKNA~ (SEQ ID NO:27)	+A524T	Round 3 1 (1.85%)		
588~LAQADTTKNA~ (SEQ ID NO:27)	+A593E	Round 4 1 (1.33%)		
588~LAQADTTKNA~ (SEQ ID NO:27)	+I698V	Rounds 5 and 6 1 (1.61%) 1 (1.89%)		
588~LAQADTTKNA~ (SEQ ID NO:27)	+V708I	Round 3, 4, 5, 6	Round 3, 4, 5	
588~LAQADTTKNA~ (SEQ ID NO:27)	+V708I+V719M		Rounds 3 and 4 1 (2.08%) 2 (4.55%)	
588~LAQADTTKNA~ (SEQ ID NO:27)	+V719M		Round 4 1 (2.27%)	
588~LAHQDTTKNA~ (SEQ ID NO:34)	None	Round 5 2 (3.77%)		
588~LANQDYTKTA~ (SEQ ID NO:31)	None	Rounds 3, 4 and 5 5 (9.26%) 1 (1.33%) 3 (5.66%)	Rounds 3, 4 and 5 2 (4.17%) 2 (4.55%) 2 (2.27%)	Round 5 1 (1.82%)
588~LANQDYTKTA~ (SEQ ID NO:31)	+S109T+S463Y	Round 3 1 (1.85%)		
588~LANQDYTKTA~ (SEQ ID NO:31)	+D368H	Round 3 1 (1.85%)		
588~LANQDYTKTA~ (SEQ ID NO:31)	+V708I	Round 4 1 (1.33%)	Round 3 1 (2.08%)	

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
588~LAHDITKNIA~ (SEQ ID NO:32)	None	Rounds 3, 4 5 and 6 1 (1.85%) 1 (1.33%) 1 (1.89%) 2 (3.23%)		
588~LAHDITKNIA~ (SEQ ID NO:32)	+S109T	Round 4 1 (1.33%)		
588~LAHDITKNIA~ (SEQ ID NO:32)	+R389S	Round 5 1 (1.89%)		
588~LAHDITKNIA~ (SEQ ID NO:32)	+A593E	Round 3 1 (1.85%)		
588~LAHDITKNIA~ (SEQ ID NO:32)	+V708I	Round 4, 5		
588~IAHDITKNIA~ (SEQ ID NO: 60)	+V708I		Round 3 1 (2.08%)	
588~LAPNSTHGSA~ (SEQ ID NO:40)	+V708I	Round 3 1 (1.85%)		
588~LANKTTNKDA~ (SEQ ID NO:35)	None		Round 5 1 (2.27%)	
588~LANKTTNKDA~ (SEQ ID NO:35)	+N449D			Round 4 1 (2.17%)
588~LAHPDTTKNA~ (SEQ ID NO:33)		Round 6 1 (1.61%)		
588~LATNRTSPDA~ (SEQ ID NO:39)		Round 6 1 (1.61%)		
588~LPQANANENA~ (SEQ ID NO:37)		Round 5 1 (1.89%)		
588~LAASDSTKAA~ (SEQ ID NO:30)		Rounds 3 and 4 1 (1.85%) 1 (1.33%)		

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
588~LAKDRAPSTA~ (SEQ ID NO:41)		Round 3 1 (1.85%)		
588~LPISNENEHA~ (SEQ ID NO:36)				Round 4 1 (2.17%)
588~LAGKSKVIDA~ (SEQ ID NO:38)				Round 5 1 (1.82%)
NONE	P34A	Round 5 1 (1.89%)	Rounds 4, 5 3 (6.82%) 1 (2.27%)	Round 4 1 (2.17%)
NONE	P64S	Round 3 1 (1.85%)	Round 4 1 (2.27%)	
NONE	S109T	Round 4 2 (2.67%)	Rounds 3, 4, 5 4 (8.33%) 1 (2.27%) 1 (2.27%)	
NONE	S109T+P8L		Round 3 1 (2.08%)	
NONE	S109T+Q120R		Round 3 1 (2.08%)	
NONE	S109T+A493V +A593E+V708I	Round 3 1 (1.85%)		
NONE	Q164K	Rounds 4 and 5 2 (2.67%) 1 (1.89%)	Round 4 1 (2.27%)	
NONE	Q175H	Round 3 1 (1.85%)		Round 4 1 (2.17%)
NONE	S196Y	Round 3 1 (1.85%)	Round 4 1 (2.27%)	

Insertion	Substitution	Pan-Retinal	RPE	Photo-receptor
NONE	A593E	Rounds 3, 4, 5 3 (5.56%) 7 (9.33%) 1 (1.89%)	Rounds 3, 4, 5 12 (25%) 7 (15.9%) 14(31.8%)	Round 4 1 (2.17%)
NONE	A593E+Q464R		Round 3 1 (2.08%)	
NONE	A593E+N596D		Round 4 1 (2.27%)	
NONE	A593E+N596D +T491A		Round 3 2 (4.17%)	
NONE	A593E+V708I	Rounds 3, 4 2 (3.7%) 2 (2.67%)	Rounds 3, 4, 5 4 (8.33%) 1 (2.27%) 1 (2.27%)	
NONE	I698V	Round 5 1 (1.89%)	Round 5 1 (2.27%)	
NONE	V708I	Rounds 3, 4, 2 (3.7%) 5 (6.67%)	Rounds 3, 4, 5 1 (2.08%) 4 (9.09%) 4 (9.09%)	
NONE	V708I+V719M		Round 4 2 (4.55%)	
NONE	V708I+G727D		Round 5 1 (2.27%)	
NONE	V708I+R733C			Round 4 1 (2.17%)

[00248] Also identified as a capsid having increased infectivity of one or more cells of the retina was a clone having the following ancestral VP1 capsid sequence:

[00249] MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQ DDGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNP YLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAP GKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPLGEPP AGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITT STRTWALPTYNNHLYKQISSASAGSTNDNHYFGYSTPWGYFDFNRFHCHFSP RDWQRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSD SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYF PSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST GGTAGTRELLFSQAGPSNMSAQAKNWLPGPCYRQQRVSKTLSQNNNSNFAW TGATKYHLNGRDSLVNPGVAMATHKDDEDRFFPSSGVLIFGKQGAGANNTA LENVMMTSEEEIKTTNPVATEQYGVVASNLQSSNTAPVTGTVNSQGALPGM VWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPANP PAVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYAKSTNV DFAVDNEGVYSEPRPIGTRYLTRNL. (SEQ ID NO:59)

[00250] This ancestral capsid variant is evolved from the ancestral capsid SEQ ID NO:58, in which the positions of degeneracy (residues 264, 266, 268, 448, 459, 460, 467, 470, 471, 474, 495, 516, 533, 547, 551, 555, 557, 561, 563, 577, 583, 593, 596, 661, 662, 664, 665, 710, 717, 718, 719, 723) evolved to comprise Alanine (A) at 264, Alanine (A) at 266, Serine (S) at 268, Alanine (A) at 448, Threonine (T) at 459, Arginine (R) at 460, Alanine (A) at 467, Serine (S) at 470, Asparagine (N) at 471, Alanine (A) at 474, Serine (S) at 495, Asparagine (D) at 516, Asparagine (D) at 533, Glutamine (Q) at 547, Alanine (A) at 551, Alaninet (A) at 555, Glutamic acid (E) at 557, Methionine (M) at 561, Serine (S) at 563, Glutamine (Q) at 577, Serine (S) at 583, Valine (V) at 593, Threonine (T) at 596, Alanine (A) at 661, Valine (V) at 662, Threonine (T) at 664, Proline (P) at 665, Threonine (T) at 710, Aspartic Acid (D) at 717, Asparagine (N) at 718, Glutamic acid (E) at 719, and Serine (S) at 723.

[00251] The AAV variant virions disclosed herein may incorporate reasonable rational design parameters, features, modifications, advantages, and variations that are readily apparent to those skilled in the art in the field of engineering AAV viral vectors.

[00252] **Example 2**

[00253] Directed evolution was employed to discover novel adeno-associated virus (AAV) variants with superior gene delivery to retinal cells following intravitreal (IVT) administration, a route of administration with significant advantages over other methods of gene delivery to the human eye (Example 1). The cell tropism following intravitreal administration of the novel AAV variant comprising a P34A substitution and the peptide LAISDQTKHA (SEQ ID NO:28) inserted at amino acid 588 (LAISDQTKHA+P34A; SEQ ID NO:42) was assessed *in vivo* in non-human primates (NHP) as a representative example of the ability of ISDQTKH (SEQ ID NO:14)-containing AAV variants to transduce retinal cells.

[00254] Recombinant AAV virions comprising either an AAV2 capsid or the novel variant capsid LAISDQTKHA+P34A (SEQ ID NO:42) and a genome comprising a green fluorescent protein (GFP) transgene operably linked to a CMV promoter (AAV2.CMV.GFP and LAISDQTKHA+P34A.CMV.GFP, respectively) or a CAG promoter (AAV2.CAG.EGFP and LAISDQTKHA+P34A.CAG.EGFP, respectively) were manufactured using standard methods. African Green Monkeys (Figures 7, 8) or Cynomolgus macaques (Figure 9) were injected intravitreally with various doses of vector ranging from $4x10^{10}$ vg to $1x10^{12}$ vg per eye (see figure legends for details) and the transduction of retinal cells was assessed in life by fundus fluorescence imaging with a Heidelberg Spectralis™.

[00255] Intravitreal delivery of AAVs comprising the novel variant LAISDQTKHA+P34A (SEQ ID NO:42) resulted in broader and more robust transgene expression across the NHP retina than AAV2 (Figures 7-9). Images reveal that the novel AAV variant capsid provides for robust expression within the center of the fovea (an area rich in cones); in the parafoveal ring (an area rich in retinal ganglion cells), and in the periphery (an area rich in many types of cells including rods, Muller glia, amacrine cells, bipolar cells) as early as 2 weeks after injection. In contrast, and consistent with results reported by others, wild type AAV2 provides for weaker expression that is primarily in the parafoveal ring and can only be detected at later time points. Immunohistochemical analysis of various regions of the retina performed 3 weeks after injection confirmed that many types of retinal cells, including retinal pigment epithelial cells, rod and cone photoreceptors, and retinal

ganglion cells, had been successfully transduced throughout the retina (Figures 10A-10E).

[00256] This study illustrates superior gene delivery by the ISDQTKH-comprising variant following a clinically preferred route of administration as compared to the clinically relevant AAV2. Similar efficacy is achievable with other variants comprising this peptide insertion motif. Likewise, similar efficacy is achievable with other variants disclosed herein that were identified using the same directed evolution approach.

[00257] **Example 3**

[00258] The cell tropism of the novel AAV variant LAISDQTKHA+P34A (SEQ ID NO:42) for retinal pigment epithelial (RPE) cells and photoreceptor (PR) cells was assessed in vitro in use RPE cells and PR cells generated from fibroblast-derived human induced pluripotent stem cells (FB-iPSC) or human embryonic stem cells (ESC).

[00259] AAV virions comprising either an AAV2 capsid or the novel variant capsid LAISDQTKHA+P34A (SEQ ID NO:42) and a genome comprising a green fluorescent protein (EGFP) transgene operably linked to a CAG promoter (AAV2.CAG.EGFP and LAISDQTKHA+P34A.CAG.EGFP, respectively) were manufactured using standard methods. Human RPE cell cultures were generated from the human embryonic stem cell line ESI-017 or human fibroblast-derived induced pluripotent stem cells (FB-iPSC) using a 45-day differentiation protocol. Maturation into RPE cells was confirmed by detecting the expression of mature RPE markers including RPE65 and BEST1; the synthesis of VEGF and PEDF; and the ability to phagocytose rod outer segments. PR cultures were generated by a multi-step eye cup formation paradigm and confirmed to comprise PRs by detecting the expression of Recoverin and S Opsin after 179 days in culture.

[00260] Relative to AAV2, LAISDQTKHA+P34A (SEQ ID NO:42) provided for significantly higher transduction efficiency of and transgene expression in human RPE cultures seven days post-infection as determined by immunofluorescence (Figures 11A-B), flow cytometry (2.7-fold increase; Figures 11C-D) and Western blot analysis (Figures 11E-F). Robust transduction and expression was likewise achieved using LAISDQTKHA+P34A.CAG.EGFP in human

PR cultures by 32 days post-infection. This study illustrates the superior ability of ISDQTKH (SEQ ID NO:14)-comprising variants to deliver genes to retinal cells.

[00261] **Example 4**

[00262] Design and construction of anti-VEGF expression vectors. The amino acid sequence of Aflibercept consists of the human Flt1 signal peptide, VEGFR1 domain 2, and VEGFR2 domain 3 fused to the Fc region of human IgG1 (Figure 12A; SEQ ID NO:66). The amino acid sequences of the light and heavy chains of Ranibizumab were joined by a flexible protein linker to convert the two-chain antigen-binding fragment (Fab) into a single-chain Fab (scFab). The Light-Heavy (LH) form consists of the human Ig kappa light chain signal peptide, the variable light, constant light, variable heavy, and constant heavy 1 domains of Ranibizumab linked by the flexible peptide (Figure 12B; SEQ ID NO:71). The Heavy-Light (HL) form is similar except the signal peptide is derived from the human IgG heavy chain and the heavy and light domains are on opposite sides of the linker as compared to the LH form (Figure 12C; SEQ ID NO:68). The Brolucizumab design includes variable light and variable heavy domains linked by a flexible peptide, with the human Ig kappa light chain signal peptide for secretion from mammalian cells (Figure 12D; SEQ ID NO:75). The open reading frames were codon-optimized for improved expression from human cells and synthesized by GeneArt or GenScript and provided in a standard plasmid cloning vector. The DNA of interest was excised from this plasmid with the restriction enzymes PstI and BglII and inserted into pAAV-CAG-SV40 pA plasmid between the CAG promoter and the SV40 polyA signal. The sc-Ranibizumab-Fc design consists of the LH form of sc-Ranibizumab fused to the Fc region of human IgG1 from the Aflibercept design (Figure 12E; SEQ ID NO:73). The Brolucizumab-Fc design consists of Brolucizumab fused to the Fc region of human IgG1 from the Aflibercept design (Figure 12F; SEQ ID NO:77). The sc-Ranibizumab LH, Brolucizumab, and Fc regions were amplified by PCR from the initial cloning vectors with extensions containing a site for the TypeIIS restriction enzyme BsmBI at the 3' end (sc-Ranibizumab LH and Brolucizumab) or 5' end (Fc). The resulting PCR products were digested with the restriction enzymes PstI and BsmBI (sc-Ranibizumab LH and Brolucizumab) or BsmBI and BglII (Fc) and inserted into pAAV-CAG-SV40 pA plasmid between the CAG promoter and the SV40 polyA signal. The ligation reactions were used to transform E. coli and positive clones were identified by restriction digest. Clones were then grown at a larger scale and plasmid DNA purified

with the Qiagen Endo-Free Maxiprep kit. The identity of the plasmids was verified by restriction digest and sequencing. The pAAV-CAG-SV40 polyA plasmid contains AAV2 inverted terminal repeats (ITRs), which allow the anti-VEGF sequences to be packaged inside AAV capsids and delivered to cells of interest in the retina via intravitreal administration.

[00263] HEK293T cells were mock transfected or transfected with plasmid containing either GFP or an anti-VEGF transgene (sc-RNBZ HL (SEQ ID NO:67), sc-RNBZ LH1 (SEQ ID NO:69) and sc-RNBZ-LH2 (SEQ ID NO:70), AFLB (SEQ ID NO:65), BRO (SEQ ID NO:74)) under the control of the CAG promoter using FuGene6 transfection reagent in two separate experiments. Media was collected at 48 hr post-transfection and assayed with the Aflibercept ELISA kit (Eagle Biosciences, Immunoguide IG-AA115). Anti-VEGF proteins were detected by the HRP-anti-IgG Fc provided as a reagent in the kit (mock, GFP, and AFLB) or HRP-anti-IgG H+L (sc-RNBZ HL, sc-RNBZ LH1, and sc-RNBZ LH2). Concentrations were calculated relative to clinical Eylea (mock, GFP, and AFLB) or Lucentis (sc-RNBZ HL, sc-RNBZ LH1, sc-RNBZ LH2, and BRO). In the first of two experiments, Aflibercept expression was about 15 ug/ml and sc-Ranibizumab expression ranged from 1.6 to 2.8 ug/ml, with the LH forms expressing similar concentrations and the HL form expression approximately a two-fold lower concentration (Figure 13A). In the second experiment, Aflibercept expression was about 50 ug/ml and sc-Ranibizumab LH1 expression was about 4.0 ug/ml (Figure 13B). The signal with Brolucizumab was very low, most likely due to poor recognition by the detection antibody. No VEGF binding activity was detected in media from mock or GFP transfections.

[00264] **Example 5**

[00265] To visualize the anti-VEGF proteins directly and confirm the size of the proteins, Western blot analysis of media from cells transfected with GFP, Aflibercept (SEQ ID NO:65), sc-Ranibizumab (SEQ ID NOs:67, 69, and 70), or Brolucizumab (SEQ ID NO:74) expression plasmids was performed (Figure 14). Media from transfected HEK293T cells was run on a Bolt 4-12% Bis-Tris Plus gel (Invitrogen Cat# NW04122BOX) and the separated proteins were transferred to nitrocellulose with an iBlot2 device. The blot was probed with HRP-conjugated goat anti-human IgG Fc (Thermo Cat# 31413, left panel) or goat anti-human IgG Fab (Thermo Cat# 31482, right panel) using an iBind Flex device, and visualized with

SuperSignal West Dura Chemiluminescent Substrate (Thermo Cat# 34076). Images were captured with an iBright FL1000 imager.

[00266] The Aflibercept sample appears similar to the clinical comparator protein Eylea. There was no signal in the negative control samples. The clinical comparator protein Lucentis is reduced into separate light and heavy chains of 24 kD whereas the sc-Ranibizumab proteins run at about 48 kD due to the existence of a polypeptide linker binding the light and heavy chains into a single protein. A higher quantity of the LH forms of the protein are present compared to the HL form of the protein, consistent with the protein quantification obtained through ELISA (Figure 13A). The Brolucizumab signal is low, most likely due to poor recognition by the detection antibody. The protein migrates at the correct molecular mass of 24 kD.

[00267] **Example 6**

[00268] As an additional method to determine VEGF-binding activity, a VEGF competition ELISA was performed (Figure 15). Clinical comparator proteins Eylea or Lucentis and media from transfected HEK293T cells were incubated with 13 pM VEGF at room temperature overnight. Samples were assayed for free VEGF using the Quantikine VEGF ELISA kit (R&D Systems Cat# DVE00). In the first of two experiments, the inhibition curves of the four anti-VEGF proteins from the transfected samples were very similar to the clinical Eylea and Lucentis. Aflibercept and Eylea competed for VEGF more strongly than the sc-Ranibizumab variants and Lucentis (Figure 15A). All three forms of sc-Ranibizumab (SEQ ID NOs:67, 69, and 70) were nearly identical. In the second experiment, all anti-VEGF constructs competed for VEGF (Figure 15B). There was no competition activity from the GFP negative control sample.

[00269] **Example 7**

[00270] To confirm that the anti-VEGF proteins expressed from transfected cells block the binding of VEGF to its receptor and thus its function, equal concentrations of clinical comparator proteins and media from transfected HEK293T cells were mixed with 20 ng/ml VEGF and placed on PathHunter KDR cells (DiscoverX 93-0996Y1). These cells express VEGF receptor/beta-galactosidase fusion proteins that produce active beta-galactosidase upon VEGF binding. The cells were lysed 22 hr later and assayed for beta-galactosidase activity. The inhibition curves of the anti-VEGF proteins from the transfected samples are equal to the clinical comparator proteins, demonstrating that the expressed proteins block VEGF

function in a cell-based assay (Figure 16). In two subsequent experiments, the cellular VEGF neutralization assay was also performed with equal volumes of media from HEK293T cells transfected with anti-VEGF constructs. In the first of these experiments, GFP, Aflibercept (SEQ ID NO:65), sc-Ranibizumab HL (SEQ ID NO:67), or sc-Ranibizumab LH1 (SEQ ID NO:69) expression plasmids were evaluated. All anti-VEGF constructs evaluated neutralized VEGF (Figure 17A). The sc-Ranibizumab LH form neutralized VEGF more strongly than the sc-Ranibizumab HL form. In the second experiment, GFP, Aflibercept (SEQ ID NO:65), sc-Ranibizumab LH1 (SEQ ID NO:69), or Brolucizumab (SEQ ID NO:74) expression plasmids were mixed with 8 ng/ml VEGF and placed on PathHunter KDR cells (DiscoverX 93-0996Y1). The cells were lysed 18 hr later and assayed for beta-galactosidase activity. Again, all anti-VEGF constructs evaluated neutralized VEGF (Figure 17B). There was a slight matrix effect from the GFP control sample at the dilutions assayed.

[00271] **Example 8**

[00272] Retinal pigment epithelia (RPE) cells were mock transfected or transfected with plasmid containing either GFP or an anti-VEGF transgene under the control of the CAG promoter using FuGeneHD transfection reagent. Media was collected at 48 hr post-transfection. The transfection efficiency of the RPE cells was extremely low, as evidenced by the number of GFP-expressing cells (data not shown), and thus, VEGF-binding activity was undetectable in media from these transfections. The total concentration of VEGF in the media was assessed to determine if low concentrations of the anti-VEGF agents could reduce RPE secretion of VEGF. Media was collected 48 hr post-transfection and assayed with the Quantikine VEGF ELISA kit (R&D Systems Cat# DVE00). A large reduction in VEGF levels following Aflibercept (SEQ ID NO:65) expression and a slight reduction in VEGF levels following sc-Ranibizumab (SEQ ID NOs:67, 69, and 70) expression was observed (Figure 18). The effect on VEGF levels by all three sc-Ranibizumab forms were similar. Once delivered by more efficient AAV transduction, the anti-VEGF transgenes resulted in the production of higher concentrations of anti-VEGF proteins, which was quantitated by the Aflibercept ELISA kit.

[00273] **Example 9**

[00274] AAV expression plasmids carrying genes for Aflibercept (SEQ ID NO:65), sc-Ranibizumab (SEQ ID NOs:67 and 69), or Brolucizumab (SEQ ID

NO:74) were used to package viral DNA in the R100 variant capsid (having the amino acid sequence set forth as SEQ ID NO:42). Mature RPE cells were transduced 30 days after seeding in 12-well plates at MOI 5,000 with these vectors in a volume of 1.0 ml X-Vivo10 media. Media was changed three days after transduction, collected and replaced six days after transduction, and collected and replaced again ten days after transduction.

[00275] The total concentration of VEGF in the media was assayed with the Quantikine VEGF ELISA kit (R&D Systems Cat# DVE00) to determine the effect of transduction with the anti-VEGF vectors on the level of free detectable endogenous VEGF secreted by the RPE cells into the media (Figure 19). The endogenous level of VEGF as indicated by the cells transduced with a GFP control vector was 4,500 pg/ml in the day 6 sample and 8,300 pg/ml in the day 10 sample. Transduction with all of the anti-VEGF vectors resulted in little to no detectable VEGF in the media. It is likely that the amount of VEGF secreted by the RPE cells has not changed, but rather that the VEGF in the media was bound by the anti-VEGF proteins such that it was undetectable by the ELISA. Additional experiments including Western blot can be performed to determine the total amount of bound and unbound VEGF.

[00276] Media from the RPE transductions was also assayed with the Aflibercept ELISA kit (Eagle Biosciences, Immunoguide IG-AA115). Anti-VEGF proteins were detected with an HRP-anti-IgG H+L antibody (ThermoFisher Cat# 31410). Concentrations were calculated relative to clinical Eylea (AFLB and GFP) or Lucentis (sc-RNBZ HL, sc-RNBZ LH1, and BRO). Aflibercept (SEQ ID NO:65) expression was about 1,800 ng/ml in the day 6 sample and 2,800 ng/ml in the day 10 sample. sc-Ranibizumab expression ranged from 700 ng/ml for the HL (SEQ ID NO:67) day 6 sample to 1,700 ng/ml for the LH (SEQ ID NO:69) day 10 sample (Figure 20). The signal with Brolucizumab (SEQ ID NO:74) was very low, most likely due to poor recognition by the detection antibody. No VEGF binding activity was detected in media from the GFP transduction.

[00277] **Example 10**

[00278] To visualize the anti-VEGF proteins directly and confirm the size of the proteins, Western blot analysis of media from transduced RPE cells was performed (Figure 21). Equal volumes of day 6 and day 10 media were run on Bolt 4-12% Bis-Tris Plus gels (Invitrogen Cat# NW04122BOX) and the separated proteins were transferred to nitrocellulose with an iBlot2 device. The blot was probed with

HRP-conjugated goat anti-human IgG Fc (Thermo Cat# 31413, left panel) or goat anti-human IgG Fab (Thermo Cat# 31482, right panel) using an iBind Flex device, and visualized with SuperSignal West Dura Chemiluminescent Substrate (Thermo Cat# 34076). Images were captured with a ChemiDoc MP imager.

[00279] The Aflibercept (SEQ ID NO:65) samples appear similar to the clinical comparator protein Eylea (black arrow). There was no band of the correct mobility in the GFP negative control sample. The clinical Lucentis is reduced into separate light and heavy chains of 24 kD, whereas sc-Ranibizumab HL (SEQ ID NO:67) and LH (SEQ ID NO:69) are not separated and migrate at apparent molecular mass of 58 kD, as indicated by the gray arrow. The signal with Brolucizumab (SEQ ID NO:74) is low, most likely due to poor recognition by the detection antibody. The protein migrates at the correct molecular mass of 26 kD, as indicated by the stippled arrow. Protein levels are fairly similar in the day 6 and day 10 samples.

[00280] **Example 11**

[00281] As an additional method to determine VEGF-binding activity, a VEGF competition ELISA was performed (Figure 22). Equal volumes of media from transduced RPE cells were incubated with 13 pM VEGF at room temperature overnight. Samples were assayed for free VEGF using the Quantikine VEGF ELISA kit (R&D Systems Cat# DVE00). Media from the cells transduced with all anti-VEGF constructs competed for VEGF. Results were similar for the day 6 and day 10 samples. There was no competition activity from the GFP negative control sample. Free VEGF levels are higher in the lowest dilutions due to the endogenous VEGF produced by the RPE cells.

[00282] **Example 12**

[00283] To compare the VEGF neutralization activity of the anti-VEGF proteins expressed in RPE cells from the viral vectors, equal volumes of media from transduced RPE cells were mixed with 8 ng/ml VEGF and placed on PathHunter KDR cells (DiscoverX 93-0996Y1) (Figure 23). The cells were lysed 18 hr later and assayed for beta-galactosidase activity. Media from cells transduced with all anti-VEGF constructs neutralized VEGF. There was no VEGF neutralization observed with media from the GFP control transduction.

[00284] The preceding merely illustrates the principles of the invention. It will be appreciated that those skilled in the art will be able to devise various arrangements which, although not explicitly described or shown herein, embody the

principles of the invention and are included within its spirit and scope. Furthermore, all examples and conditional language recited herein are principally intended to aid the reader in understanding the principles of the invention and the concepts contributed by the inventors to furthering the art, and are to be construed as being without limitation to such specifically recited examples and conditions.

[00285] Moreover, all statements herein reciting principles, aspects, and embodiments of the invention as well as specific examples thereof, are intended to encompass both structural and functional equivalents thereof. Additionally, it is intended that such equivalents include both currently known equivalents and equivalents developed in the future, i.e., any elements developed that perform the same function, regardless of structure. The scope of the present invention, therefore, is not intended to be limited to the exemplary embodiments shown and described herein. Rather, the scope and spirit of the present invention is embodied by the appended claims.

WHAT IS CLAIMED IS:

1. A recombinant adeno-associated virus (rAAV) virion comprising (a) a variant adeno-associated virus (AAV) capsid protein comprising a peptide insertion in the GH-loop of the capsid protein relative to a corresponding parental AAV capsid protein, wherein the peptide insertion comprises the amino acid sequence ISDQTKH (SEQ ID NO:14), and (b) a heterologous nucleic acid comprising a nucleotide sequence encoding a polypeptide that inhibits the activity of vascular endothelial growth factor (VEGF), wherein the nucleotide sequence is selected from the group consisting of:

(i) the nucleotide sequence set forth as SEQ ID NO: 69 (sc-ranibizumab-LH1),

(ii) the nucleotide sequence set forth as SEQ ID NO:65 (aflibercept),

(iii) the nucleotide sequence set forth as SEQ ID NO:74 (brolucizumab),

(iv) the nucleotide sequence set forth as SEQ ID NO:67 (sc-ranibizumab-HL),

(v) the nucleotide sequence set forth as SEQ ID NO:70 (sc-ranibizumab-LH2),

(vi) the nucleotide sequence set forth as SEQ ID NO:72 (sc-ranibizumab-LH-Fc),

(vii) the nucleotide sequence set forth as SEQ ID NO:76 (brolucizumab-Fc), and

(viii) a nucleotide sequence at least 90%, at least 95%, at least 98% or at least 99% identical to any of (i)-(vii).

2. The rAAV according to claim 1, wherein the peptide insertion comprises the amino acid sequence Y_1Y_2ISDQTKHY_3, wherein each of Y_1-Y_3 is independently selected from Ala, Leu, Gly, Ser, Thr, and Pro.

3. The rAAV according to claim 2, wherein the peptide insertion comprises the amino acid sequence LAISDQTKHA (SEQ ID NO:28).

4. The rAAV according to any one of claims 1-3, wherein the insertion site is between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2 (SEQ ID NO:2) or the corresponding position in the capsid protein of another AAV serotype.

5. The rAAV according to any one of claims 1-4, wherein the capsid protein comprises one or more amino acid substitutions relative to VP1 capsid of AAV2 (SEQ ID NO:2) or one or more corresponding substitutions in another AAV serotype.

6. The rAAV according to any one of claims 1-5, wherein the capsid protein comprises a P34A amino acid substitution relative to VP1 capsid of AAV2 (SEQ ID NO:2) or the corresponding substitution in another AAV serotype.

7. The rAAV according to any one of claims 1-6, wherein the capsid protein comprises (i) the amino acid sequence ISDQTKH (SEQ ID NO:14) and (ii) a P34A amino acid substitution, and is at least 90% identical, at least 95% identical or at least 99% identical to the sequence set forth as SEQ ID NO:42.

8. The rAAV according to claim 7, wherein the capsid protein consists essentially of the amino acid sequence set forth as SEQ ID NO:42.

9. The rAAV according to claim 8, wherein the nucleotide sequence is at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or is 100% identical to the entire length of the sequence set forth as SEQ ID NO:69 (sc-Ranibizumab LH) or to nucleotides 61-1578 of SEQ ID NO:69 and encodes the amino acid sequence set forth as SEQ ID NO:71 or encodes the amino acid sequence of amino acids 21-525 of SEQ ID NO:71.

10. The rAAV according to claim 9, wherein the nucleotide sequence comprises nucleotides 61-1578 of SEQ ID NO:69 and preferably comprises nucleotides 1-1578 of SEQ ID NO:69.

11. The rAAV according to claim 8, wherein the nucleotide sequence is at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or is 100% identical to the entire length of the sequence set forth as SEQ ID NO:65 (aflibercept) or to nucleotides 79-1377 of SEQ ID NO:65 and encodes the amino acid sequence set forth as SEQ ID NO:66 or encodes the amino acid sequence of amino acids 27-458 of SEQ ID NO:66.

12. The rAAV according to claim 11, wherein the nucleotide sequence comprises nucleotides 79-1377 of SEQ ID NO:65 and preferably comprises nucleotides 1-1377 of SEQ ID NO:65.

13. The rAAV according to claim 8, wherein the nucleotide sequence is at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or 100% identical to the entire length of the sequence set forth as SEQ ID NO:74 (brolucizumab) or to nucleotides 61-816 of SEQ ID NO:74 and encodes the amino acid sequence set forth as SEQ ID NO:75 or encodes the amino acid sequence of amino acids 21-271 of SEQ ID NO:75.

14. The rAAV according to claim 13, wherein the nucleotide sequence comprises nucleotides 61-816 of SEQ ID NO:74 and preferably comprises nucleotides 1-816 of SEQ ID NO:74.

15. The rAAV according to claim 8, wherein the nucleotide sequence is least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or is 100% identical to the entire length of the sequence set forth as SEQ ID NO:67 (sc-ranibizumab-HL) or to nucleotides 58-1575 of SEQ ID NO:67 and encodes the amino acid sequence set forth as SEQ ID NO:68 or encodes the amino acid sequence of amino acids 20-524 of SEQ ID NO:68.

16. The rAAV according to claim 15, wherein the nucleotide sequence comprises nucleotides 58-1575 of SEQ ID NO:67 and preferably comprises nucleotides 1-1575 of SEQ ID NO:67.

17. The rAAV of claim 8, wherein the heterologous nucleic acid comprises (i) a nucleotide sequence at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or 100% identical to the nucleic acid sequence set forth as SEQ ID NO: 65 and which encodes the amino acid sequence set forth as SEQ ID NO:66 and (ii) a nucleotide sequence at least 90% identical, at least 95% identical, at least 98% identical, at least 99% identical or 100% identical to the nucleic acid sequence set forth as SEQ ID NO: 74 and which encodes the amino acid sequence set forth as SEQ ID NO:75.

18. The rAAV of any one of claims 1-17, wherein the nucleotide sequence encoding a polypeptide that inhibits the activity of vascular endothelial growth factor (VEGF) is operably linked to an expression control sequence.

19. The rAAV of any of claims 1-18, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the corresponding parental AAV capsid protein for the retinal cell.

20. A pharmaceutical composition comprising an rAAV according to any of claims 1-19 and a pharmaceutically acceptable carrier.

21. A method for delivering a VEGF inhibitor to a retinal cell, choroidal cell, lenticular cell, ciliary cell, iris cell, optic nerve cell and/or corneal cell in a subject comprising administering to the subject an rAAV virion according to any one of claims 1-19 or a pharmaceutical composition according to claim 20.

22. The method of claim 21, wherein the rAAV virion or pharmaceutical composition is administered intravitreally to the subject.

23. A method for treating a VEGFa-associated ocular disease selected from wet (neovascular, exudative) age-related macular degeneration; macular edema following retinal vein occlusion; retinal neovascularization resulting from retinal vein occlusion; diabetic macular edema, diabetic retinopathy (including all stages of non-proliferative diabetic retinopathy and proliferative diabetic retinopathy); myopic macular degeneration; branch retinal vein occlusion, hemi-retinal vein occlusion, and central retinal vein occlusion; retinopathy of prematurity; idiopathic choroidal neovascularization; myopia macular degeneration and secondary retinal and choridal neovascularization; retinal telangiectasia; neovascular glaucoma; vitreous hemorrhage; retinal and choroidal neovascularization secondary to retinal diseases, including but not limited to uvetis, trauma, retinal degenerative disorders, genetic retinal and/or choroidal disease, tumors of the eye, corneal and iris neovascularization in a subject in need of such treatment by administering to the subject an effective amount of an rAAV according to any one of claims 1-19 or a pharmaceutical composition according to claim 20.

24. The method of claim 23, wherein the VEGFa-associated ocular disease is selected from wet (neovascular, exudative) age-related macular degeneration; diabetic macular edema; macular edema following retinal vein occlusion; diabetic retinopathy; and myopic choroidal neovascularization.

25. The method of claim 23 or 24, wherein the rAAV or pharmaceutical composition is administered intravitreally to the subject.

26. The method of any one of claims 21 to 25, wherein the subject is a human.